भारतीय पादप रोगविज्ञान संस्था, नई दिल्ली, भारत
Indian Phytopathological Society, New Delhi, India

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2020- INTERNATIONAL YEAR OF PLANT HEALTH

सातवां अंतर्राष्ट्रीय सम्मेलन

संयुक्त राष्ट्र सतत् विकास लक्ष्य प्राप्ति में पादपरोग विज्ञान

जनवरी 16–20, 2020 नई दिल्ली, भारत

7th International Conference

Phytopathology in Achieving UN Sustainable Development Goals

January 16-20, 2020, New Delhi, India

सारांश
Abstracts

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FOREWORD

Indian Phytopathological Society, ICAR and IARI are organising, 11 crop protection societies of India and abroad are co-organising and International Society for Plant Pathology is collaborating 7th International Conference on "Phytopathology in Achieving UN Sustainable Developmental Goals" at ICAR-IARI, New Delhi from 16-20th January, 2020. This mega event is witnessed by the participation from 32 countries of the world.

India along with other countries signed the declaration on the 2030 Agenda for Sustainable Development, comprising of 17 Sustainable Development Goals (SDGs) at the Sustainable Development Summit of the United Nations in September 2015. Research and Information System for developing countries (RIS) through its work programme on SDGs in collaboration with UN in India pursued a research agenda to explore various facets of India's negotiations, adoption and implementation of SDGs. In this context, plant protection societies from India and abroad involved in agriculture sector could partially contribute in fulfilling the SDGs by addressing the issues of .plant health as it has been recognized by the UN to commemorate 2020 as **International Year of Plant Health.** With this background, Indian Phytopathological Society in collaboration with 12 crop protection societies of the world has planned to bring the world plant pathologists/microbiologists/ biotechnologists on a common platform to discuss the issues related to plant health inflicted by biotic and abiotic factors, the threat they pose to global agriculture and method, techniques and strategies to combat them.

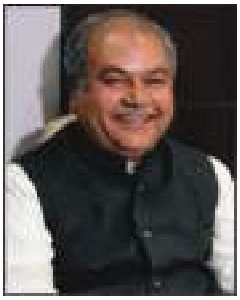
To achieve the goal, the 7th International Conference is divided into 20 themes and comprised of plenary lectures, keynote & invited lectures, contributory oral papers, contributory posters, invited corporate lectures and Farmers-Scientists-Industries interface. On this auspicious occasion, the society is publishing a book entitled "**Souvenir cum Abstract"** involving the messages and the abstracts of presentations. At this juncture, I like to complement and congratulate all my colleagues of the publication committee who spent their valuable time in compiling the book consisting the abstracts of presentations which may be extremely useful to the researchers, scholars, students, readers and extension personnel.

.

(M.P. Thakur)

नरेन्द्र सिंह तोमर
NARENDRA SINGH TOMAR

कृषि एवं किसान कल्याण,
ग्रामीण विकास तथा पंचायती राज मंत्री
भारत सरकार
कृषि भवन, नई दिल्ली
**MINISTER OF AGRICULTURE & FARMERS, WELFARE,
RURAL DEVELOPMENT AND PANCHAYATI RAJ
GOVERNMENT OF INDIA
KRISHI BHAWAN, NEW DELHI**



Message

I am glad to learn that the Indian Phytopathological Society (IPS) is organizing 7th International Conference on “Phytopathology in Achieving UN Sustainable Development Goals” during January 16-20, 2020 at ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi.

The crop losses that are being inflicted by different diseases are the major constraints in achieving the targeted productivity of crop plants globally. The situation is further aggravated by appearance of new pathotypes of various diseases under the influence of climate change. The conference on the aforementioned specific theme is thus timely and in right direction. I hope that the conference will provide a global platform to exchange ideas on the emerging issues pertaining to crop diseases and their management. The deliberations during the conference will certainly be of vast use to augment crop productivity by reducing the impact of crop diseases. I am convinced on the recommendations emanating from the conference will ultimately contribute towards accomplishing the focused theme.

I wish every success to the 7th International Conference on “Plant Pathology - 2020”.

7/1/20

Dated: **(Narendra Singh Tomar)**
New Delhi

Office: 'G' Wing, Ground Floor, Krishi Bhawan, New Delhi- 110001, Tel.: 011-23782373, 23782327 Fax: 011-23386876
Resi.: 3 Krishna Menon Marg, New Delhi-110001, Ph.: 011-23794697 / 98, Fax: 011-23794696

कैलाश चौधरी
KAILASH CHOUDHARY

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भारत सरकार
MINISTER OF STATE FOR AGRICULTURE
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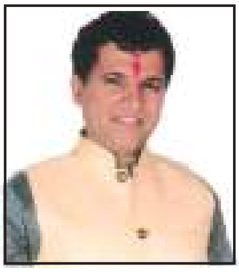

Message

It is a matter of great pleasure that the Indian Phytopathological Society (IPS) is organizing 7th International Conference on Plant Pathology during January 16-20, 2020 at ICAR-Indian Agricultural Research Institute, New Delhi. The theme for conference "Phytopathology in Achieving UN Sustainable Development Goals" is covering plant pathological technologies from agriculture sector which will help in fulfilling the SDGs by addressing the plant health as it has been recognized by the UN to commemorate 2020 as International Year of Plant Health. The Conference will be an outstanding approach for plant pathologists from around the world to come together, share information and to solve problems. I strongly believe that this conference would address the alarming issues in today's agriculture both under Indian as well as global perspectives.

I wish my best for the success of the 7th International Conference on Plant Pathology 2020.

(Kailash Choudhary)

Dated 04.01.2020
New Delhi

Office : 199Q, Krishi Bhawan, New Delhi-110 001. Tel. : +91-11-23782343, 23388165 Fax : 23074190

परशोत्तम रूपाला
PARSHOTTAM RUPALA

राज्य मंत्री
कृषि एवं किसान कल्याण
भारत सरकार
Minister of State For
Agriculture & Farmers Welfare
Government of India
D.O. No..................MOS(A&FW)/VIP/2019-20/

Message

Its gives me immense pleasure that the Indian Phytopathological Society (IPS) is organizing 7th International Conference on Plant Pathology during January 16-20, 2020 at ICAR-Indian Agricultural Research Institute, New Delhi in the theme "Phytopathology in Achieving UN Sustainable Development Goals". The conference is going to address plant pathological technologies of agriculture especially the field of plant protection. India being a farming based economy will be highly benefitted through this international meet particularly on crop losses caused by different biotic threats.

Hence the Conference will provide opportunities to the farmers and stakeholders of agriculture sector as a whole so as to discuss the ongoing management practices for diseases and pests. I am confident that this conference would help in formulating new strategies keeping in view the recent updates on eco-friendly and sustainable disease management.

I wish all success of the 7th International Conference on Plant Pathology 2020.

(Parshottam Rupala)

Dated:
New Delhi

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FNA, FNASc, FNAAS
SECRETARY & DIRECTOR GENERAL

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DEPARTMENT OF AGRICULTURAL RESEARCH & EDUCATION
AND
INDIAN COUNCIL OF AGRICULTURAL RESEARCH
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Message

I am delighted to know that the Indian Phytopathological Society (IPS) is organizing 7th International Conference on "Phytopathology in Achieving UN Sustainable Development Goals" from January 16-20, 2020 at Indian Agricultural Research Institute, New Delhi, India.

Global agriculture has been noticeably threatened by plant diseases which adversely affect agricultural productivity, profitability, and finally livelihood of the farmers. India along with other countries signed the declaration on the 2030 Agenda comprising of 17 Sustainable Development Goals (SDGs) at the Sustainable Development Summit of the United Nations in September 2015. Keeping these issues in mind, I appreciate the need of this conference on the theme "Phytopathology in Achieving UN Sustainable Development Goals". I have no doubts that the conference will provide opportunities to the world scientific communities to discuss, share and understand their views in the improvement of crop health in particular and in enhancing crop productivity in general.

I wish this event a great success in all aspects.

(T. MOHAPATRA)

Dated the 14th January, 2020
New Delhi

कृषि वैज्ञानिक चयन मंडल
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डॉ. पी. के. चक्रवर्ती
सदस्य (पौध विज्ञान)
Dr. P.K. Chakrabarty ARS, *FNAAS*
Member (Plant sciences)

January 12, 2020

Message

I am pleased to know that the Indian Phytopathological Society (IPS) has organized 7th International Conference on "Phytopathology in Achieving UN Sustainable Development Goals" during January 16-20, 2020 at ICAR-Indian Agricultural Research Institute, New Delhi, India. The conference will address all essential aspects of crop diseases and their management. I am sure there will be a threadbare discourse among the delegates from India and abroad as well on tackling those biotic stresses adopting multipronged strategies. The outcome of the conference will provide a useful document with respect to the basic and applied researches which will definitely contribute to the development of agricultural sciences and ultimately the farmers' security.

I extend my best wishes to the organizers and take this opportunity to wish the entire participants' endeavour for greater cause.

I further wish the International Conference a grand success.

P. K. Chakrabarty

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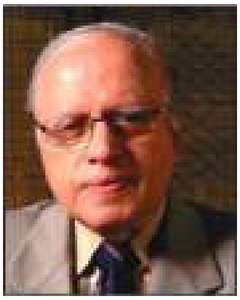

M S Swaminathan
Founder Chairman
M S Swaminathan Research Foundation
Third Cross Street, Taramani Institutional Area
Chennai - 600 113 (India)

Message

I am very happy that the 7thInternational Conference will be held from January 16-20, 2020 under the auspices of the Indian Phytopathological Society. The science of phytopathology is exceedingly important for crop security. In fact, the wheat revolution would not have been possible but for the advances made in phytopathology. I hope the conference will help to bring together the latest advances in the control and management of crop diseases. I wish the conference great success.

Dated: Sep. 27, 2019 **(M S Swaminathan)**

डॉ. आनन्द कुमार सिंह
उपमहानिदेशक (फसल विज्ञान)
Dr. Anand Kumar Singh
Deputy Director General
(Crop Science)

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INDIAN COUNCIL OF AGRICULTURAL RESEARCH
KRISHI BHAWAN, DR. RAJENDRA PRASAD ROAD, New Delhi-110001

Message

I am happy to learn that 7th International Conference on "Phytopathology in Achieving UN Sustainable Development Goals" is organized by the Indian Phytopathological Society (IPS) during January 16-20, 2020 at ICAR-Indian Agricultural Research Institute, New Delhi, India. I believe that the conference will attempt to cover important aspects of crop protection covering plant diseases and other such biotic stresses in a holistic manner. The galaxy of learned delegates will converse the issues concerning pertinent goals of total 17 Sustainable Development Goals (SDGs). The proceedings will serve as a guiding document for future Research & Development initiatives. I hope that it will further open up avenues for an ideal scientific interactions and collaborations among the participants and other stakeholders. The discourse will definitely add to the overall upliftment of Indian cum global agriculture sector and also contribute for nutritional and economic security of farming communities.

I congratulate the organizers and wish the participants for a fruitful event.

(Anand Kumar Singh)

Date: 2nd January' 2020
New Delhi

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Message

It gives me pleasure to know that the Indian Phytopathological Society (IPS) will organize its 7th International Conference on "Phytopathology in Achieving UN Sustainable Development Goals" during January 16-20, 2020 at the campus of Indian Agricultural Research Institute, New Delhi, India.

Diseases cause substantial losses to the productivity of agricultural food crops. The exhaustive agriculture with high fertilizer responsive crop varieties attracted newer problems, which were not serious in earlier days. At the same time emergence of new virulent races or biotypes are common features in places grown with disease resistant crop varieties. The impact of global climate change on disease scenario of agricultural crop plants is well evident.

I understand that these issues will be discussed in different sessions during the Conference among the world scientific communities and I hope resultant deliberations will be of immense use in formulating strategies for managing the plant diseases. Further, it will help in fulfilling the Sustainable Development Goals (SDGs) by addressing the plant health issues.

I welcome the entire delegates of the conference to this historic campus at New Delhi. I wish for the success of this event.

(A K Singh)

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Dr. M.P. Thakur
President

No. IPS/Pre./2019

Message

It is my pleasure to express my feelings and gratitude to all the esteemed members of Indian Phytopathological Society (IPS), New Delhi that with their kind support, guidance and consent only, it could have been possible to organise this mega event on the eve of 2020 as **International Year of Plant Health** being declared by United Nation General Assembly. IPS being the third world's largest and one of the oldest society of Plant Pathology happily agreed and came forward along with 12 most prominent societies/institute to act as **Co-organisers** in joining hands with IPS in organising this important unforgettable event during this great occasion on a topic "**Phytopathology in Achieving UN Sustainable Development Goals**". This topic is most relevant to the entire globe in avoiding yield losses, minimising the excessive use of pesticides, sustaining agricultural production, productivity, consumption, alleviating poverty, ending hunger and empowering women keeping pace with time in food, nutritional, income and employment security to the growing population. The losses in yield of different crops caused by newly emerging plant diseases *viz*., wheat blast, soybean rusts etc. are enormous and can be addressed by the scientific community via participating and discussing in this type of scientific event.

I hope, the organisation of this kind of mega event by IPS in collaboration with other academic societies/institute will open up a new avenues to jointly solve these problems within and outside the country. I congratulate one and all the members of the Organising Committee of 7th International Conference for their painstaking efforts in bringing the Souvenir and extend my best wishes for the grand success of the conference.

3/10/19

(M.P.Thakur)
President

Indian Phytopathological Society

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website: www.ipsdis.org

Dr. Dinesh Singh
Secretary

No. IPS/Sec/2019/00374
Dated: January 10, 2020

MESSAGE

The Indian Phytopathological society (IPS is a third largest professional society in the world in the area of plant pathology and established in February 28, 1947 at the Division of Mycology & Plant Pathology, Indian Agricultural Research Institute, New Delhi by Dr. B. B. Mundkur and other eminent scientists of Plant Pathology. The IPS is an international scientific organization and is fully devoted in advancement of plant health science through publishing journal, newsletter and books. The society provides platform to scientific community, planners and end users to participate in the exchange of latest research & development knowledge and information in the field of plant pathology and related science and also provide s scientific communication, collaboration and professional development.

In present context, plant pathological technology from agriculture sector could be added to this work programme as a part and partial contributor which will help in fulfilling the 17 sustainable development goals of United Nations by addressing the plant health as it has been recognized by the UN to commemorate 2020 as International Year of Plant Health. The society always looks toward the recent development in research in the field of plant pathology to fulfill future societal requirements and scientific opportunities.

Keeping this in view, society has taken an initiative to organize 7th International conference on Phytopathology in Achieving UN Sustainable Development Goals to be held January 16- 20, 2020 in order to emphasize the need for protecting crops from various plant pathogens to achieving global food and livelihood security. The conference will serve as a common platform where advanced techniques for diagnosis and detection of pathogens, characterization, and identification of source of resistance for breeding strategies, Bioprospecting in disease management, progress in chemical control, genomic & bioinformatics, and transgenic resistance, as well as host pathogen interaction & immunity, workshops on cereal rust and wilt of solanaceous crops will be discussed. A special session on farmers- scientists- industry interface will also be held during conference. I am very much sure; the conference will provide a platform to a large scientific community to share their knowledge and experiences to younger generation which they can properly utilize in their future research programme.

(Dinesh Singh)

INTERNATIONAL SOCIETY FOR PLANT PATHOLOGY
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Date: September 19, 2019

The International Society for Plant Pathology extends warm congratulates to the **Indian Phytopathological Society** for the successful organization of the:

7th International Conference on Phytopathology in Achieving UN Sustainable Development Goals

to be held January 16-20, 2020 in New Delhi, India.

We look forward to learning from the critical discussions held during the meeting on how managing crop diseases can contribute globally to higher crop productivity and environmental sustainability!

Best regards,

Jan E Leach

Jan E. Leach
ISPP President

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Date: 25.12.2019

Message

It gives me great pleasure to note that Indian Phytopathological Society, New Delhi is organizing *International Conference on Phytopathology in Achieving UN Sustainable Development Goals* at New Delhi from Jan. 16-20, 2020where diverse stakeholders of plant protection are going to participate. This is a very timely and well thought of topic for deliberations.

The role of plant protection is of paramount importance specially in Asia-Pacific region where huge losses are occurred annually due to endemic and introduced pests. The challenges in the region are many as climate change risks are looming large, pests and diseases are going transboundary, access to technology is often an issue for smallholder farmers and capacity building is too specific and not focused towards agriculturalvalue chain.The Economic and Social Commission for Asia and the Pacific (ESCAP) reported in July 2019 that Asia is far behind towards achieving SDGs and not even at half way mark of what was expected till 2018. This is a dismal situation and lot of efforts are needed wherein the discipline of plant protection can play a significant role by avoiding or managing diseases and pests and by boosting trade through SPS compliances.Besides, adopting and implementing the Agricultural Innovation System initiated by Tropical Agricultural Platform of FAO can also enhance the contribution of plant protection towards achieving SDGs.

I am sure the Conference will focus on relevant areas and come out with implementable recommendations.I wish the Conference and the Organizers a grand success.

Dr. Ravi Khetarpal
Executive Secretary
APAARI, Bangkok

Sri Lanka Association for Mycology and Plant Pathology (SLAMPP)

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SLAMPP President's Message

It gives me immense pleasure to write this message on behalf of the Sri Lanka Association for Mycology and Plant Pathology (SLAMPP), the Co-organizer of the IPS 7th International Conference on 'Phytopathology in Achieving UN Sustainable Development Goals (SDGs)', to be held in New Delhi, India from 16-20, January, 2019.

SLAMPP is greatly honored to be a co-organizer of this historic meeting, held in the year 2020 which is proclaimed as the "International Year of Plant Health (IYPH)" by the United Nations, aiming at increasing the awareness among the general public and policymakers on plant health and food security. Year 2020 also coincides with the 73th year of long journey of the Indian Phytopathological Society (IPS), taking Plant Pathology forward and tackling the threat of disease that continues to challenge the agriculture and horticulture in India

The theme of the conference 'Phytopathology in Achieving UN Sustainable Development Goals' is timely. Sustainable intensification of agriculture and minimizing crop loss by ensuring plant health are vital for feeding the growing global population and ensuring zero hunger. The wide variety of Technical Sessions, including some most timely and current issues that are likely to be challenging the mankind and global agriculture, reflects the great diversity that the Plant Pathology community can offer to the world.

The conference will no doubt be a platform for the researchers and experts in Plant Health from leading scientific and academic institutions from across the region will meet in New Delhi to share the latest scientific findings, advances and innovations. It will also be an opportunity to initiate new collaborations and regional networks to protect plants and secure supply of food, feed and fibre and achieve global livelihood and biosecurity.

New Delhi, the conference venue and the capital of India, has rich history and vibrant culture. SLAMPP joins the Indian Phytopathological Society in very warmly welcoming all participants to New Delhi. I wish the Conference a grand success.

Dr Ganga Devi Sinniah
President, Sri Lanka Association for Plant Pathology and Mycology

(Secretariat: Department of Botany, University of Peradeniya, Peradeniya, Sri Lanka, www.slampp.org.lk)
Affiliation: Plant Pathology Division, Tea Research Institute of Sri Lanka, Talawakelle, Sri Lanka

Prof. A. N. Mukhopadhyay
Ph.D.D. Sc.(h.c), FNAAS, HFIPS
Former Vice Chancellor, Assam Agric. University
Director General, Tea Research Association
Dean, College of Agriculture GBPUAT.

Message

I am extremely happy and delighted to know that 7th International conference on "Phytopathology in achieving UN sustainable development goals" is being organized by Indian Phytopathological Society one of the most premier plant pathology societies of the world. As per United Nations goal plant protection scientists can play a major role in increasing productivity and production of agricultural crops. As per recent estimates India is losingnearly two lakhs eighty five thousand crores rupees worth food materials due to pests and diseases. Even a meager 25 – 30% savings of loses can feed millions of people and overcome the food and nutritional hunger faced in our country.

Indiscriminate use of chemical pesticides has posed a serious problem affecting human and animal health. In this context research on Bio-intensive pest and disease management strategy can play very significant role not only by reducing the use of pesticides but also increase the farmer's profit through low cost technologyof Bioagent use for management of plant diseases. The planner and policy maker need to promote such technology for large scale use in the farmer's fields.

I am sure the International Conference in the presence of eminent scientists from India and abroad will pave the way for very successful in planning and formulating strategies for future plant protection programme under sustainable agriculture.

I congratulate Dr. M. P. Thakur, President IPS, Dr. P. Chakrabarty, President Elect and Dr. Dinesh Singh, Secretary IPS and other executive members for their dedicated and untiring efforts in making this programme a grand success.

My very best wishes for the Crowning Success of this important National Event.

(A. N. Mukhopadhyay)

Prof. M. S. Reddy
Founder & Chairman, Asian PGPR
Society for Sustainable Agriculture
Auburn University, AL, USA
Tel: +1334-559-1971
Email: prof.m.s.reddy@gmail.com

Message

Greetings!

On behalf of the Asian PGPR Society for Sustainable Agriculture and its allied Chapters of India, Indonesia, Sri Lanka, Malaysia, Uzbekistan & Pakistan,I take a great pride in welcoming all of you to participate in the **7th International Conference on "Phytopathology in Achieving UN Sustainable Development Goals"**to be held at ICAR-IARI, New Delhi from 16th to 20thJanuary 2020 organized by the Indian Phytopathological Society (IPS). The IPS is a professional Society for promoting the cause of science of Phytopathology which focuses in the field of Mycology, Plant Pathology, Bacteriology, Virology, Phytoplasmology and Nematology. The IPS organizing this prestigious conference in association with more than 12 prominent national and international plant protection societies and/or institutions. The main aim of this conference is to celebrate the year 2020 as the International Year of Plant Health among the world renowed invited Plant Pathologists, Microbiologists, Mycologists, Nematologists, Virologists, Bitechnologistsetc to discuss various devastated objectives related to plant pathogens, the threats they pose to global sustainable agriculture and identify the integrated disease management strategies for their threats.

Agriculture is the world's largest industry. It employs more than one billion people and generates over $1.4 trillion dollars' worth of food annually. The need for sustainable agriculture is increasingly urgent. Demand for agricultural commodities is rising rapidly as the world's population grows. Agriculture's deep connections to the world economy, human societies and biodiversity make it one of the most important frontiers for conservation around the globe.

How to address the escalating demands of a 10 billion population by 2050 with dwindling soil fertility and increasing chemical inputs intoxicating the agriculture industry? A higher global standard of living is driving up demand for food, resulting in record high global grain prices during recent years. Experts are projecting that by 2050, food production must increase by approximately 80-100% to meet demand. Doubling the world's food supply is the grand challenge for the next generation of agricultural scientists. Land constraints dictate that much of the increased production must come from existing agricultural lands. According to the FAO, past efforts to increase productivity has led to global degradation of farmland at an alarming rate. Future technology must lead to increased production in a sustainable manner. Thus, achieving Global food security would require every sustainable and economically viable practice to chip-in and balance the productivity vs.demand equation. A dynamic approach to predict growth requirements of crop plants and deployment of able technologies that would sustain the quality of land while meeting the productivity demands would be the need-of-the-hour.

In Asia, though PGPR research has picked up, there is a need to widen the scope and perspectives of its application to several agricultural crops. Especially, PGPR applications need to be projected as viable alternatives or supplements to chemical fertilizers. At this juncture, the functioning of a society like “**Asian PGPR Society of Sustainable Agriculture**” is critical. Though Asian countries are competing and syndicating in PGPR research, a consolidated plan to bring forth sustainable, scalable and economic solutions to control plant diseases, improve soil health and enhance Agro-ecosystem using PGPR is essential. Asian PGPR Society is instrumental in bringing researchers, academicians and entrepreneurs on to a common platform for exchange of ideas, promoting public-private partnerships and promoting research integration among public and private agencies involved in PGPR research. Presently, local, regional, and multi-national agricultural product companies are investing in basic research aimed at improving drought tolerance and nutrient uptake. Hence, the research must be focused on the new concept of rhizo-engineering based on favorably partitioning of the exotic biomolecules, which create a unique setting for the interaction between plant and microbes. Future research in rhizosphere biology will rely on the development of molecular and biotechnological approaches to increase our knowledge of rhizosphere biology and to achieve an integrated management of soil microbial populations. Fresh alternatives should be explored for the use of bioinoculants for other high value crops such as vegetables, fruits, and flowers. Plant-associated microbesare being tested for sources of new genes, sources of metabolites that affect plant gene transcription, and as potential inoculants for crops. Studies on PGPR fit very well with these goals, and for this reason, our research area is receiving renewed interest.

I strongly believe that these scientific innovations can reach farmers only with purposeful and effective partnerships. As agricultural scientists,the world is looking to us to provide solutions to food challenges that the world is facing. Never have so many people been dependent upon few farmers for food. We’re the ones who will have to make the decisions in the future, and we have to start now.So, to all the participants in this conference, let me encourage you to share, learn, reach out and build personal relationships throughout this conference that can lead to a productive partnership.Although there clearly are challenges facing plant pathology and many other agriculturally related disciplines, it seems important to keep these issues in some perspective.

Let me take this opportunity to express my sincere appreciation to all of the organizers, co-organizers, sponsors and as well as to all of you for coming here to share and keep abreast of what is new in Plant Pathology and allied subjects.Additional thanks goes to the local organizing team for service above and beyond the call of duty regarding local management, hospitality, and other intricate organizing activities that permitted relaxed deadlines for conference participants.

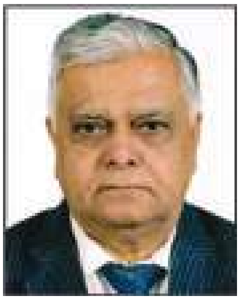
Finally, *on behalf of the local organizers, I* welcome you all to this multicultural city of New Delhi. I hope that you will take advantage of the many sights to see in the city,as well as the many natural and man-made wonders nearby, during your stay.

I *sincerely hope, that this conference will deliberate and discuss all the different facets of this exciting conference* on **“Phytopathology in Achieving UN Sustainable Development Goals”** *and* continue to arouse a high level of international interest *and come up with recommendations that will lead to a better, healthier and merrier world.* The IPS and its related societies need to continuously work to keep the importance of agricultural research in front of federal and state decision makers, and to monitor trends and provide departments and government agencies with the best possible data regarding nationwide educational trends and the skills being sought by employers.

I wish the conference a great success.

MSReddy

Prof. M. S. Reddy
Auburn, Alabama, USA
November 25, 2019



Dr C. D. Mayee

Former Chairman, ASRB, former President IPS
President South Asia Biotechnology Centre

Message

It is a matter of great happiness that the new year 2020 comes with the '7th International Conference on Phytopathology in Achieving the UN Sustainable Development Goals '(SDG) from Jan 16-20, 2020. I congratulate the Indian Phytopathological Society, New Delhi for having organized the most appropriate theme for this conference and that too with a bang to celebrate the International Year of Plant Health-2020.

Cut across the UN SDG's, I find that this conference can contribute towards meeting the Goals 2, 12 and 13 meant for zero hunger, responsible production and climate action, respectively. Understanding and management of crop diseases which takes a heavy toll of crop production will ease the flow of healthy food to the poor and remove hunger. The crop protection practices that are needed for the next decades will have to include bio-safety as a component so that the climate change mitigation can be achieved. I am sure the conference shall through light on the new areas of crop protection.

I wish the conference a grand success and look forward for the proceedings of the meet.

Dated: Dec. 31, 2019
Nagpur

(C.D. MAYEE)

Bushan L. Jalali,
F.N.A.Sc., F.N.A.A.S.
Ex. Director of Research
Cchav,Hisar (Haryana)

Message

I am immensely delighted that the Indian Phtopathological Society is organizing 7th. International Conference on ***“Phytopathology in Achieving UN Sustainable Development Goals”*** during 16.-20th.January, 2020 at New Delhi. Plant pathogens are responsible for huge crop losses and pose a potential threat to the sustainability of agriculture. Some minor and new plant diseases have started gaining momentum due to climate change. These are imminent challenges before plant pathologists, and I nurture a hope that this conference will pragmatically deliberate upon.

For the sustainable plant health management, strategies have to be prioritized and innovated, keeping in view the shifting disease situation which is greatly influenced by changing food production systems, climate variability, extreme weather events and exim policies of different countries. innovative ways and approaches for mitigation of adverse impact of plant diseases are of vital concern to plant pathologists. For the sustainable crop production through holistic plant health under varying agro-ecological and socio-economic conditions, we need reprioritization of R&D programmes in an interdisciplinary mode. In view of this global scenario, holding this International Conference is quite fitting and timely, to meet UN Development Goals.

I hope the innovative ideas and thoughts emanating during this conference will be of immense value in tailoring the need-based management strategies for different cropping systems and help in facilitating future research programmes.

I extend my best wishes for the grand success of this conference.

Dated: January 1, 2020

(B. L. Jalali)

Prof. C. MANOHARACHARY
M.Sc., Ph.D., FNASc., FNAAS, FBS, FPSI, FAPS, FMSc, FIMS
Hon. NASI Senior Scientist
Coordinator (UGC SAP), Dean, Development & UGC Affairs
Co-ordinator, AICOPTAX (MOEF)
Vice-Chancellor, Oriental University (Indore, MP)
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Message

Plant pathology is composed of many disciplines. India has had a rich agricultural heritage. Some farmers still follow ancient practices while modern agricultural graduates have been utilizing the recent technologies. There is a great need to renew our Plant Pathology in view of climate change. Disease management is crucial for the growing population as the Indian population will be reaching the highest in the world by 2050. Therefore, we need to develop strategies for disease managements. Disease management is another branch where plant pathologist is directly related as plant doctor. To practice disease management in the field is a challenging job. There is a need for accurate identification of plant pathogen, early diagnosis of disease, characterization of disease symptoms, conservation of plant pathogens and disease management through IPM, IDM, Judiciously employing fungicides, breeding for disease resistant varieties, phytosanitation etc.,

Plant Pathology offers a great scope for research, product development, teaching extension and plant health management. The rapid growth of Indian agriculture has to meet food security and has been creating serious problems. Ensuring an integrated bio-security in the agricultural environment contributes a lot for bio-security and conservation of biodiversity. In recent times, there has been application of nanotechnology in the management of plant diseases. Organic agriculture is globally accepted movement in respect of sustainable agricultural production and ecofriendly approach. India with different bio geographical regions and environmental variables along with crop diversity needs immediate attention for the fastidious development of suitable solutions to control crop losses. Fungicides may play important role in improving food quality, but fungicidal resistance that has been developed by Plant Pathogens has been creating problems.

Contd page 2

Fungal contamination in the storage godowns leads to loss of product and mycotoxin contamination resulting in severe health issues. Newly developed techniques such as bioinformatic tools will help a lot in understanding complications of plant pathology however it is essential that a sound metholodology has to be established for interaction of plant pathologists with farmers based on field experiences. I appreciate the efforts and valuable contributions provided from various plant pathologists from India and abroad and also by the IPS in making Plant Pathology a great science and happening science. I am sure that the Indian agriculture will become stronger and stronger in the years to come by producing the necessary food by ensuring food security besides controlling number of diseases. I congratulate the concerted efforts of the Indian Phytopathological Society for bringing together plant pathologists, microbiologists, biotechnologists, and agricultural scientists of India and abroad on to a common platform to discuss the issues related to plant pathogens, disease management and development of future strategies to combat the diseases and ensure food security and sustainable global agriculture. I wish the distinguished plant pathologists and participants a happy time and fruitful deliberations.

Date:

Signature

Y.S. Ahlawat, Ph.D

Professor of Virology (Retd)
Advanced Centre for Plant Virology
Division of Plant Pathology
Indian Agricultural Research Institute, New Delhi

Message

It gives me pleasure to know that Indian Phytopathological Society is organizing 7th International conference on "Phytopathology in Achieving UN Sustainable Development Goals" to be held from January 16-20, 2020 at ICAR-IARI, New Delhi.I would like to thank and express my sincere gratitude to the organizers including Dr. Dinesh Singh, Secretary, IPS for providing me an opportunityto convey a message about the conference. The **Sustainable Development Goals (SDGs)** place greater demands on the scientific community addressing climate change, renewable energy, food, health and water provision requires coordinated global monitoring and modelling of many factors — social, economic and environmental. Some synergies and trade-offs depend on scale — for instance, greater fertilizer use might increase food production and incomes locally, but would exacerbate pollution. Climate-change mitigation tends to happen at a local scale, but the consequences are global. The organizers of this conference have planned 20 scientific sessions on important aspects of phytopathology such as Disease Diagnostics, climate change influencing plant diseases, Epidemiology and forecasting systems and Transgenics in management of plant diseases. There will be plenary speakers and key note speakers of national and international repute. The conference will provide opportunity to delegates to present both contributory oral and poster papers. It is interesting that the conference will be supported by inviting corporate lectures on prospects and constraints. The organizers have also a provision of Farmers-Scientists-Industries interface which will help the end users in farm sector and industries. Scientists need to support the SDGs. We must help to integrate monitoring and evaluation mechanisms into policy-making at all levels and ensure that information of the conference is easily available to all. I strongly feel that the outcome of the conference will help the farming community in particular and others in general. I wish a great success to the conference.

(Y.S. Ahlawat)

PANJAB UNIVERSITY
CHANDIGARH-160014

Dr. S. S. Chahal
Honorary Emeritus Professor
(Former Vice Chancellor, MPUAT (Raj),
DBU and Khalsa University (Pb.)

Message

Establishment of the Indian Phytopathological Society (IPS) seventy years ago, has played a pivotal role in development of plant pathology as a knowledge intense, integral component of agricultural education in India. Becoming synonymous with the subject, it has provided forum for mutual interaction, dissemination of knowledge and inspiring young minds to kindle their interest in the subject which has now become an advance science, once known as a “cut and burn” technology only. Evolution of plant pathology is largely associated with evolution of agricultural education in India. Devastating pathogenic potential of microorganisms in intensive agriculture made plant pathology an indispensable subject in Agricultural Universities and All India Coordinated Research Projects of the Indian Council of Agricultural Research. There is now great understanding and advancement of knowledge of both the living systems of host and pathogen and lately the third system also of bio control agent under varied environments. Emphasis on use of chemicals which were considered handy, curative and effective is reduced because of their non desirable effects on environment and human health. Host plant resistance has attracted talent for investigation of genetic improvement against pathogens with in depth molecular studies with technological advancements. Omics (genomics, proteomics, ionomics, metabolomics, transcriptomics) approach has broader implications in developing disease resistance through genetic improvement in crops. The field of omics has tremendous potential to assess diseases with high precision in diagnosis and understanding of pathogenic mechanisms. Next Generation Sequencing (NGS) technology has helped to generate huge amount of genotypic data with which it is now expected to go beyond omics approachfor better disease control in crop plants.

It is heartening that IPS, in its continuing commitments, is organising 7th International Conference (16-20 January, 2020) under the theme:”Phytopathology in Achieving UN Sustainable Development Goals” and also celebrating the International Year of Plant Health. The deliberations are meticulously planned under 20 technical sessions to cover almost all the aspects related to plant pathology. It is expected that the conference will provide an excellent forum for sharing latest information and catalyse opening of new vistas in plant pathology.

All my good wishes for the success of this mega event of IPS.

S.S. Chahal

(S. S. Chahal)
Honorary Fellow, IPS

Correspondence: # 98, Sector 21-A, Chandigarh- . (M) 9855978629Email. chahalsspau@yahoo.com

Dr. A.K. Misra, ARS, FPSI, FISMPP, FINSOPP, FSDSH, FCHAI, FUPAAS
Ex. Project Coordinator AICRP (STF) &
Ex. Head, Division of Crop Protection, CISH, Lucknowand Past President, IPS

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Message

I am happy that Indian Phytopathological Society, a premier society of the world, has planned to bring the world plant pathologistson a common platformby organising 7th International Conferencefrom January 16-20, 2020, at New Delhi.The conference theme is rightly titled as “Phytopathology in Achieving UN Sustainable Development Goals”. World plant pathologists’ have great responsibility and role to playin achievingthis goal and fight against malnutrition and hunger. It is the duty of plant pathologists to boost production by protecting our crops from various diseases caused by various pathogens and minimize post harvest spoilage of fruits, vegetables, spices, flowers, plantations, forest, food crops, etc. Human population is growing in world and food production needs to be increased with the same land and resources. Growing healthy crop without field diseases and post harvest spoilage loss, is the priority of plant pathologists tokeep pace with growing human population and provide them enough calories for their healthy life.

During the period of 72 years, since its inception of the Indian Phytopathological Society, it has successfully organised six international conferences and it a seventh in the series. The society is having nearly 2,000 members located in more than 50 countries. They include research scientists, teachers, extension professionals, students, technicians, agricultural field representatives and pestmanagement personnel. Definitely it will be a great opportunity for the members and others also to share their experience in the frontier areas of research on plant pathology. The conference is designed with twenty technical sessions with plenary lectures, invited lectures, contributory papers, contributory posters, invited corporate lectures and farmers-scientists-industries interface,which will be very informative, useful and interesting for the participants/delegates of the conference.

I wish the international conference a grand success.

Dated : 28.10.2016

(A.K. Misra)

Dr. P. Chowdappa
Former Director
ICAR-Central Plantation Crops Research Institute
Kasaragod
and
Former President
Indian Phytopathological Society
New Delhi

Message

I would like to congratulate the executive committee of the Indian Phytopathological Society fortimely organizing 7th International Conference on **"Phytopathology in Achieving UN Sustainable Development Goals**" during January 16-20, 2020 at ICAR-Indian Agricultural Research Institute, New Delhi.

Of the 7 billion global population, about 800 million do not have enough food to eat and majority of the them live in developing countries. By 2050, the world population is estimated to reach 9 billion. Plant pests and diseases are responsible for losses of 20 to 40% of global food production. Due to increasing global trade and a changing climate, plant diseases pose a major threat to food security today than ever before. Emergence of new races of pathogen potentially threaten the production of food. To cite an example, migration of 13 -A2 clonal lineage of *Phytophthorainfestans* from Europe, during 2013, devastating tomato and potato in India. Plant pathogens also impact on environment sustainability, forest health, recreational horticulture, human and animal health.

The technological developments, such as introduction of biotechnological toolsand nanotechnology would help in rapid detection and management of new and emerging clonal lineages of plant pathogens.

I sincerely hope that this conference will deliberate and discuss all the different facets of Plant Pathologyand come up with recommendations that will lead to formulate strategies for effective plant disease management to ensure higher productivity and sustainability.

I wish the conference great success

(P.Chowdappa)

Punjab Agricultural University
Department of Plant Pathology
Ludhiana-141004, India

Dr. T.S. Thind
Ph.D., PDF (France), FPSI, Fulbright Fellow
Honorary Adjunct Professor

Message

It is a matter of great pleasure that the Indian Phytopathological Society (IPS) is organizing 7th International Conference on "Phytopathology in achieving UN Sustainable Development Goals" during 16-20 January, 2019 at New Delhi. The theme of the conference is in consonance with the Sustainable Development Goals, particularly SDG-2 on Zero Hunger, set out by the United Nations in 2015. The IPS in the past years has been regularly providing such platforms to address plant health issues facing agriculture and to find out sustainable solutions.

The science of plant pathology can play much needed role in alleviating hunger and malnutrition through development of affordable solutions for devastating plant diseases leading to increase in food production. It holds promise to ensure quality produce by containing microbial invasions and toxin contamination in food crops. Plant pathologists have an important role to play in meeting food security needs of the nation by developing technologies for ensuring proper crop health. There is an urgent need to produce more food per unit area for feeding rapidly increasing human population. The present day agriculture is faced with many challenges and one among the most serious challenges is the changing climate. Agriculture will have to cope with weather fluctuations that can affect the survival, distribution and multiplication of plant pathogens apart from shift in pathogenic microbial flora. We need to act ahead of the pathogens in our efforts to ensure normal crop yields. Cutting edge biotechnologies such as CRISPR gene editing systems and RNA interference are being exploited to rapidly develop crop varieties having resistance to specific pathogen races.

Crop protection has come a long way from the predominantly chemical-based approaches to more environment friendly technologies including green chemistry. There is a need to develop bio-intensive modules for managing pests and pathogens. Decision support systems need to be developed for important diseases for their timely, more efficient management. There is a need to adopt information technology at a larger scale to facilitate quick dissemination of new crop protection solutions among the farmers and other stake holders.

Much progress has been made in different spheres of plant pathology over the past some years. This international conference will provide an ideal opportunity to the plant pathologists from India and other countries to have useful interactions on the emerging issues related to crop health in the present day agriculture. I do hope that the conference deliberations will come up with novel ideas of research on plant diseases that would help us to reach the targets set out in SDGs.

I wish the organizers a grand success and fruitful deliberations to the participants.

TSThind

Dated: 27/09/2019

(TS Thind)

Indian Phytopathological Society
(Regn. No. S399 of 1949-50 under Societies Registraion Act XXI of 1860)
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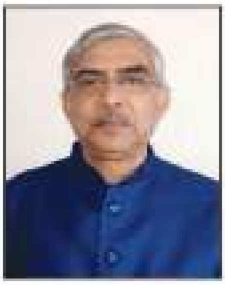
Prof. B.N. Chakraborty
FNAAS, FNABS, FRSC, FAScT, FIPS, FISMPP,FNRS, FISPC, FMSI, FIMS
Former President, IPS



Message

I am happy to be associated with the forthcoming 7th International Conference on "***Phytopathology in Achieving UN Sustainable Development Goals***" organized by the Indian Phytopathological Society, New Delhi during January 16-20, 2020. I am glad to know that IPS in collaboration with International Society of Plant Pathology (ISPP) along with 12 most prominent plant protection societies within and outside the country, who are the Co-organizers of the conference are celebrating 2020 as the International Year of Plant Health. I congratulate the organizers for having chosen appropriate theme for the conference.

When we look at the United Nations Sustainable Development Goals, we see 17 objectives against which we must measure our progress. We know that inclusive and sustainable growth are imperative for the health of our planet and for the continued success of our enterprises. We need to take the creative sparks behind our most innovative products and solutions and put then to work for the greater good.

I also congratulate the efforts of the organizers for shouldering the responsibilities in order to sustain the activities of the Indian Phytopathological Society in upholding the objectives of the society and encouraging the scientists, students and teachers to share their knowledge through such events. I hope the deliberation bring out fruitful solutions and recommendations based on the research contributions made by the participating scientists.

I wish the conference all the success.

(B.N. Chakraborty)

Prof. (Dr.) R.N. Pandey
Immediate Past President, IPS

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Message

It is a matter of great pleasure that *Indian Phytopathological Society*, New Delhi is organizing its 7th International Conference on **"Phytopathology in Achieving UN Sustainable Development Goals"** in collaboration with other institutes of reputeto celebrate the 'Year 2020 as International Year of Plant Health'at Division of Plant Pathology, ICAR- IARI, New Delhi, with the aim to bring the world plant pathologists/microbiologists/biotechnologists, etc. on a common platform to discuss the issues of plant health i.e. biotic and abiotic stresses related to plant pathogens, poor soil health and extremeweatherfactors which pose the threats to global agriculture and to draw a road map for future course of actionto combat the stresses for achieving global food and livelihood security. The Conference is planned to hold the sessions on twenty theme areas encompassing Taxonomy of plant pathogens, Disease diagnostics, Host pathogen interaction & plant immunity, Epidemiology and forecasting of plant diseases, Post-harvest diseases and mycotoxins, Bio-prospecting, Breeding strategies, Transgenics and related approaches in Disease management, Genomics and bioinformatics, Human resource development, International trade and biosecurity, Extension plant pathology: challenges in implementation, Plant pathologists entrepreneurship and policy perspectives for food security and Farmers-Scientists-Industries interface, etc.

Plant Pathology in our country has advanced very well. Eco-friendly, remunerativetechnologies, efficient in sustainable management of the plant diseases have been generated by the scientists all over the globe for the use of farmers. Molecular detections of plant pathogens, host plant resistance to pathogens, bio-intensive approaches useful under organic farming and climate change, etc. help in management of the diseases and reduction of crop yield losses.

Indian Phytopathological Society, the third largest society in the world has contributed immensely in updating the information in different field of plant pathology through publication of journal: Indian Phytopathology, Newsletter, books and organizing National and Zonal conferences, brain storming sessions on immerging issues of plant diseases and to draw road map for future course of action to combat them.I express greetings and congratulations to the members, office bearers, etc. of the society for their dedication to achieve the mandate of the society.

The planning of the conference is quite timely and hope that this will provide a common platform to academia, students, KVK personnel, farmers and other stakeholders to share their rich experiences and knowledge about the latest development in aspects of Plant Pathology and to draw a road map for policy makers for implementations to tackle the stresses responsible for yield reduction of plants.

I take this opportunity to express my gratitude with thanks to Dr. Trilochan Mohapatra, Secretary, DARE and Director General, ICAR; Dr. A. K. Singh, Director, ICAR - IARI, Dr. Anand Kumar Singh, DDG, Crops & Hort. Science, ICAR, for their encouragement and support to organize the Conference.

I take this opportunity to thank and congratulate Dr. M.P. Thakur, President, IPS& Director (Instructions), IGKV, Raipur, Dr. P.K. Chakrabarty, President Elect, IPS and Member (ASRB), DARE, New Delhi, Dr. Dinesh Singh, Secretary, IPS and the members of Organizing Committeesand all those who have put their efforts to make the Conference a success and wish the conference a grand success.

RNPandey

December 7, 2019

(R. N. Pandey)

NBPGR

Dr Kuldeep Singh
Director
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi

03 October 2019

Message

One of the major constraints in sustainable productivity of field crops is the loss caused by plant pathogens. Although pathogens are known to infect a large number of crops and crop produce, the situation attains alarming proportions when recommended management practices sometimes fail to manage the disease. Further, the indiscriminate use of pesticides has led to resistance development, accumulation of residues in food and contamination of the environment. There is an urgent need to develop innovative ways to help reduce our dependence on the chemical pesticides and thereby safeguard the food chain and the environment. ICAR-NBPGR is playing a key role in developing environment friendly and sensitive diagnostics for pathogens in the plant genetic resources exchanged globally.

It is a pleasure to know that the Indian Phytopathological Society is organizing the 7th International Conference on "Phytopathology in Achieving UN Sustainable Development Goals" during January 16-20, 2020 at ICAR-IARI Campus, New Delhi with an aim to provide an ideal opportunity for the interaction of scientists/ policy makers/corporate sectors towards developing holistically integrated future strategies envisaging plant disease management to ensure higher productivity and sustainability. I hope the Conference would result in useful recommendations and formulation of sound strategies required for effective disease management.

I wish the conference a great success

7.10.15

Kuldeep Singh

Former Assoc. Dean and Professor Plant Pathology
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Dr. Naresh Mehta
President- INSOPP

Message

It gives me an immense pleasure to note that Indian Phytopathological Society (IPS), New Delhi is organizing an International Symposium on “Phytopathology in Achieving UN Sustainable Development Goals”during January 16-20, 2020 at IARI, New Delhi, India where scientists, academicians, researchers, students, extension workers and farmers are going to participate. The theme of the symposium is very well planned andtopic selected for the deliberations are befitting to the need of the hour keeping in view the efforts being made for sustainable agricultural development for doubling the farmer’s income.

It is well known that proposed “International Year of Plant Health” by UN General Assembly 2020 which is in commemorate with SustainableDevelopment Summit of the United Nations held in September 2015.India has signed the declaration on the Agenda for SustainableDevelopment, comprising of 17 Sustainable Development Goals (SDGs) at the Research and Information System(RIS) for developing countries through its programme on SDGs. Indiapursued a research agenda to explore various facets of India’s negotiations, adoption andimplementation of SDGs which is utmost required since plant pathological techniques from agriculturesector would play a pivotal role in this programme. I am confident that various plenary lectures, technical sessions, keynote addresses, invited lectures, contributing oral presentations and invited corporate lectures will provide adequate tools forsustainable disease management which will help in fulfilling the SDGs as well as doubling the farmer’s income by 2022 as vision of Govt. of India.

On my behalf as president of Indian Society of Plant pathologist, Ludhiana (INSOPP) and on behalf of INSOPP colleagues extend a heartiest and sincerely wishesto Indian Phytopathological Society (IPS), New Delhifor organizing this International symposium. I am sure that conference deliberationswill result in meaningful recommendations which would be helpful in achieving the goals. I congratulate my colleagues of IPS in organizing the symposium and wish the conference to be a great success.

Dated: Oct. 1, 2019

(Dr. Naresh Mehta)

डा० रश्मि अग्रवाल, (एफ.एन.ए.ए.एस.)
अध्यक्ष

Dr. Rashmi Aggarwal (FNAAS)
Head

पादप रोग विज्ञान संभाग
भा.कृ.अनु.प.–भारतीय कृषि अनुसंधान संस्थान
नई दिल्ली–110012 (भारत)
Division of Plant Pathology
ICAR - Indian Agricultural Research Institute
New Delhi-110012 (INDIA)

Message

I am extremely happy to know that Indian Phytopathological Society (IPS) is organizing 7th International Conference on "*Phytopathology in Achieving UN Sustainable Development Goals*" From 16th January, 2020 to 20th January, 2020 in ICAR- Indian Agricultural Research Institute, New Delhi. It is my pleasure and proud privilege to welcome all the delegates attending this International Conference. With advancement in Science and Technology especially the genomics revolution has contributed enormously to research and disease management applications in plant pathology. This development has rapidly increased our understanding of the molecular mechanisms underpinning pathogenesis and resistance, contributed novel markers for rapid pathogen detection and diagnosis, and offered further insights into the genetics of pathogen populations on a larger scale. The availability of whole genome resources coupled with next-generation sequencing (NGS) technologies has helped in developing genomics-based approaches to improve disease resistance in crops.

We thank all the delegates who have contributed towards Plenary Lectures, Invited Oral presentations and poster presentations covering all aspects of Plant Pathology. This conference would not have been possible without the hard work and dedication of the members of the Core Committee and organizing Committees. I profusely thank Dr. A.K. Singh, Director, IARI for his continuous support in making this meeting possible. Many thanks to the members of Advisory Committee for their professional advice.

Our Co-organizers are integral to the success of the Conference and deserve appreciation of all the delegates.

The conference will also provide an opportunity to the participants to visit the capital city of the Republic of India which represents a unique amalgam of ancient history and modernity.

Once again, I extend heartiest welcome to all the delegates along with my good wishes for a happy and fruitful conference

(Rashmi Aggarwal)
Head (Plant Pathology)

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INDIAN PHYTOPATHOLOGICAL SOCIETY

IPS 7th International Conference

"Phytopathology in Achieving UN Sustainable Development Goals"

January 16-20, 2020

IARI Pusa Campus, New Delhi, India

TECHNICAL SESSIONS

Session 1 : Taxonomy of plant pathogens

Chairman: Dr. U.N. Saikia **Co-Chairman:** Dr. N. Mathivanan

Rapporteurs: Dr. RakeshMehra, Dr. P. Kishore Varma

Convener: Dr. P. Chowdappa **Co-Conveners:** Dr. S.K. Singh, Dr. R.N. Kharwar

Session 2: Plant disease diagnostics

Chairman: Dr. S.M. Paul Khurana **Co-Chairman:** Dr. S.C. Chatterjee

Rapporteurs: Dr. T. Makeshkumar, Dr. R. Thangavelu

Convener: Dr. B.N. Chakrabarty **Co-Conveners:** Dr. V.K. Baranwal, Dr. S. Umesha

Session 3 : Population genetics and pathogen diversity

Chairman: Dr. Laszlo Kredics

Co-Chairman: Dr. V. Devappa **Rapporteurs:** Dr. M.B. Patil, Dr. Pankaj Baiswar

Convener: Dr. Rashmi Aggarwal **Co-Conveners:** Dr. D.K. Ghosh, Dr. K.K. Pandey

Session 4 : Host pathogen interaction and plant immunity

Chairman: Dr. B.N. Chakraborty **Co-Chairman:** Dr. A.P. Suryawanshi

Rapporteurs: Dr. R. Ramesh, Dr. S.D. Somwanshi

Convener: Dr. Jagdish Kumar **Co-Convener:** Dr. M.S. Patil; Dr. A.S. Krishnamoorthy

Session 5 : Climate change influencing plant diseases

Chairman: Dr. C. Chattopadhyay **Co-Chairman:** Dr. S. Desai

Rapporteurs: Dr. T.S.S.K. Patro, Dr.Tasvina R. Borah

Convener: Dr. InduSawant **Co-Conveners:** Dr. Om Gupta, Dr. S. Desai

Session 6 : Epidemiology and forecasting of plant diseases

Chairman: Dr. V.S. Thakur **Co-Chairman:** Dr. S.K. Gupta

Rapporteurs: Dr. P.K. Bhattacharya, Dr. R.K. Mishra

Convener: Dr. S.S. Sharma **Co-Conveners:** Dr. M. Srinivas Prasad, Dr. R. Vishwanathan

Session 7: Plant health management vis-à-vis human health

Chairman: Dr.Srikanta Das **Co-Chairman:** Dr. R.R. Pandey

Rapporteurs: Dr. S.S. Vaish, Dr. Anjanayya Reddy

Convener: Dr. Shrikant Das **Co-Conveners:** Dr. M. Srinivas Prasad, Dr. R. Vishwanathan

Session 8: Post-harvest diseases and mycotoxins

Chairman: Dr. Ashok Bhattacharyya **Co-Chairman:** Dr.Naresh Mehta

Rapporteurs: Dr.Ayon Roy, Dr.Yogendra Singh

Convener: Dr. A. P. Suryawanshi **Co-Conveners:**Dr. B.K. Pandey, Dr. V. Devappa

Session 9: Disease management in organic and protected cultivation

Chairman: Prof. R.N. Pandey **Co-Chairman:** Dr. Amitabh Basu

Rapporteurs: Dr. K.K. Mishra (MP), Dr. ChandaKushwaha

Convener: Dr. S.K. Sharma **Co-Conveners:** Dr. K. D. Thakur, Dr. R.P. Singh

Session 10: Breeding strategies for plant disease resistance

Chairman: Dr. D.K. Yadav **Co-Chairman:** Dr. Mohan Totawar, Dr. R.D. Prasad

Rapporteurs: Dr. Subrata Dutta, Dr.Gireesh Chand

Convener: Dr. Ramesh Chand **Co-Conveners:** Dr. S. Jahgirdar, Dr. M. S. Saharan

Session 11: Bio-prospecting in disease management

Chairman: Dr. H.B. Singh **Co-Chairman:** Dr. Anil S. Kotasthane

Rapporteurs: Dr. S.K. Tripathi, Dr. H.K. Chourasia

Convener: Dr.Pratibha Sharma **Co-Conveners:** Dr. R. N. Pandey, Dr. V. Shanmugam

Session 12 : Progress in chemical control of plant diseases

Chairman: Dr.Gerd Stammler **Co-Chairman:** Dr. R.M. Gade

Rapporteurs: Dr. K.S. Hooda, Dr.Sanjeev Kumar

Convener: Dr. T.S. Thind **Co-Conveners:**Dr. K.P. Singh, Dr. Robin Gogoi

Session 13: Workshop on Wilt disease of solanaceous crops

Chairman: Dr. D.S. Singh **Co-Chairman:** Dr. Anwar Ali

Rapporteurs: Dr. Ram Dutta, Dr. ShahidAhamad

Convener: Dr. Dinesh Singh **Co-Conveners:** Dr. L.C. Borah, Dr. R. Ramesh

Session 14 : Genomics and bioinformatics

Chairman: Dr. N.K. Singh **Co-Chairman:** Dr. V.K. Baranwal

Rapporteurs: Dr. C.G. Sangeetha, Dr. Meenu Gupta

Convener: Dr. S.J. Eapen **Co-Conveners:** Dr. A. Kumar, Dr. K.K. Mondal

Session 15 : Transgenics and related approaches for disease management

Chairman: Dr. R.S. Chauhan **Co-Chairman:** Dr. Bikash Mandal

Rapporteurs: Dr. Prashant Jambhulkar, Dr. S.S. Sharma

Convener: Dr. M. Krishna Reddy **Co-Conveners:** Dr. R. Selvarajan

Session 16 : Human resource development in plant pathology

Chairman: Dr. R.C. Aggarwal (DDG-Edn) **Co-Chairman:** Dr. M.K. Naik

Rapporteurs: Dr. Jasvir Kaur, Dr. Kamal Khilari

Convener: Dr. R. K. Mittal **Co-Conveners:** Dr. A. K. Misra, Dr. H.B. Singh

Session 17: International trade and biosecurity

Chairman: Dr. T.S. Thind **Co-Chairman:** Dr. Rajan

Rapporteurs: Dr.RituMawar, Dr. S. Chandra Nayak

Convener: Dr. S. C. Dubey **Co-Conveners:** Dr. Celia Chalam, Dr. Kavita Gupta

Session 18 : Extension plant pathology: challenges in implementation

Chairman: Dr. J.P. Sharma **Co-Chairman:** Dr. Om Gupta

Rapporteurs: Dr. V.K. Singh, Dr. P.K. Shukla

Convener: Dr. M. P. Thakur **Co-Conveners:** Dr. M. B. Patil, Dr. Ved Ratan

Session 19: Plant pathologists entrepreneurship and policy perspectives for food security

Chairman: Dr. R.K. Mittal **Co-Chairman:** Dr. R.N. Kharwar

Rapporteurs: Dr. Nidhi Didwania, Dr.Susheel Kr. Singh

Convener: Dr. V.I. Benagi **Co-Conveners:** Dr. Krishna Kumar, Dr. Pankaj Baiswar

Session 20: Farmers-Scientists-Industries interface

Chairman: Dr. M.P. Thakur **Co-Chairman:** Dr. Randhir Singh,Poswal,
Dr. Bhagirath Choudhary,Dr. RajendraBarwale

Rapporteurs: Dr. Rakesh K. Gangwar, Dr. Vindewari Prasad

Convener: Dr. R.N. Padaria **Co-Conveners:** Asitava Sen, Dr. Ajit Kumar

Session 21: Workshop on Rust diseases of cereals

Chairman: Dr. D.V. Singh **Co-Chairman:** Dr. Sai Sree Uppala

Rapporteurs: Dr. K.K. Mishra, Dr. Pramod Prasad

Convener: Dr. S.C. Bhardwa **Co-Conveners:** Dr. A.N. Mishra, Dr. P.P.S. Pannu

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Plenary Lectures

PL (01): Role of plant protection and innovation in achieving sustainable development goals in Asia-Pacific

Ravi Khetarpal

Executive Secretary, Asia Pacific Association of Agricultural Research Institutions, Bangkok-10100, Thailand;
E-mail: ravi.khetarpal@apaari.org

The seventeen Sustainable Goals (SDGs) of United Nations aims to rid the world of poverty and hunger by 2030, and to make it safe from the worst effects of climate change. It's an ambitious plan and it was hoped that we can succeed. However, the recent report from UNESCAP hints that Asia Pacific countries could not even reach half the mark for what was to be achieved by 2019. This calls for accelerated efforts towards achieving the targets. FAO of UN has developed 5 key principles involving 20 action points for working towards the SDGs. The role of plant protection in that direction becomes very important though never worked out independently. The science and development aspects of plant protection can contribute significantly towards achieving certain SDGs by increasing agricultural production, by reducing losses caused by pests and diseases and also by mitigating the negative impacts of the climate change scenarios. Also the increase in use of eco-friendly approaches in manging plant diseases contribute towards environmental sustainability and conservation of biodiversity. Besides, now the role of Agricultural Innovation System as recently initiated and implemented by FAO through its Tropical Agricultural Platform has been considered as an important step towards achieving SDGs. The importance of innovation in plant protection needs to be exploited and the blending of technical skills with functional skills would build capacity to accelerate the efforts for achieving the targets. There are challenges but there are opportunities too. The countries in Asia Pacific region need to understand not only the SDGs much better but also the role plant protection science can play to achieve certain targets and indicators to track the progress and to contribute effectively towards achieving the goals.

PL (02): Chitooligosaccharides as pathogen-associated molecular patters to induce immunity in plants

Appa Rao Podile

JC Bose Fellow, Vice Chancellor, University of Hyderabad, Hyderabad – 500 046, Telangana

Plants and microbes have coevolved over millions of years assessing each other chemical constituents. The chemicals from plants are recognized by microbes and vice versa, and the outcome of interaction of the chemical signaling would decide the nature of interaction between the interacting partners. We have been working on a variety of chemical signals from the living partners in plant-pathogen interactions. Less has been studied about the recalcitrant fungal cell wall polymer, the chitin. This talk is intended to address a few following questions. Do plants recognize the insoluble chitin to decide its response? What would be the plant's response, if chitin is recognized? How does the plant's response influence the outcome of interaction? The speaker would bring in the experience of working with chitiooligosaccharides for over a decade and discuss he developments in this area of host-pathogen interactions.

PL (03): Science and technology for a sustainable future: adventures in plant disease resistance genetics

Robert F. Park

Plant Breeding Institute, The University of Sydney, Australia; E-mail: robert.park@sydney.edu.au

The 2030 Agenda for Sustainable Development, adopted by all United Nations Member States in 2015, provides a shared blueprint for peace and prosperity. It is based on 17 Sustainable Development Goals (SDGs), which recognize that ending poverty and other deprivations must go hand-in-hand with strategies to improve health and education, reduce inequality, and spur economic growth. Achieving SDG 2, Zero Hunger, presents significant challenges especially when viewed against the backdrop of an increasing global population, climate change, and the need to minimise the environmental impacts of human activities. The World Health Organisation has estimated that already, about one third of the world's population is well fed, one third underfed, and one third is starving. Plant diseases are a significant contributor to this imbalance, with conservative estimates of global losses to plant diseases in the order of 10%, both from direct loss of yield and also from contamination causing reduced quality and in some cases, toxins in food and fodder products. Wheat is the most commonly consumed cereal in the world, with global production of about 600 million tonnes in 2007, and demand predicted to increase by more than 1.5% annually up to 2020. A recent publication estimated that diseases reduce global wheat production by 21.5%. Some 31 wheat pests and pathogens were identified as problematic: 17 were fungi, 9 invertebrates, 4 viruses and 1 a phytoplasma. Significantly, the study found that just four of these 31 pests and pathogens accounted for half of all losses, with the most damaging being leaf rust, followed by Fusarium head-blight/scab, then *Septoria tritici* blotch and stripe (yellow) rust. To put these losses into perspective, it was estimated in 2015 that global annual losses to the fourth ranked stripe rust were 5.47 million tonnes (US$ 979 million). Maintaining current yield and quality, and reducing the current impact of diseases to meet future demand and achieve SDG 2 will require sustained commitment, sound science, and good policy. This presentation will provide an overview of the impact of rust diseases in food production, and provide examples of how new genomic approaches are being used to accelerate the development of new cereals with resistance to these damaging pathogens and the diseases they cause.

PL (04): Assessing the global burden of pathogens and pests on major food crops

S. Savary[1], L. Willocquet[1], S.J. Pethybridge[2], P.D. Esker[3], N. McRoberts[4] and A. Nelson[5]

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Crop losses to pathogens and pests (P&Ps) reduce agricultural production and food security; they also impact societies and the environment, since they affect economic fabrics and drain environmental resources. But what is the magnitude of these effects? The landscape of plant pathology is made up of "stars": potato late blight, rice blast, wheat stripe rust. And therefore, it consists also of neglected diseases – one might think of rice brown spot, wheat spot blotch, the virus diseases of cassava, and many others. Quantitative measures of these impacts would determine the value of better plant health, enable defining intervention points, and provide the necessary baseline for research policies – which are the most important diseases, and why? Despite these needs, there is no global data base on disease crop losses, for a number of reasons. One is the sheer diversity of plant pathogens; another is the difficulty for measurement, combined with metric issues; a third is the cost of field experiments and surveys; and a fourth is the inherent variability of crop health over time, seasons, and space, within field and from plots to continents. This presentation will report a recent effort (Savary et al. 2019, Nature Ecology & Evolution 3, 430–439) to quantify losses in wheat, rice, potato, soybean, and maize globally, through an international expert survey. Our results document losses associated with 137 P&Ps on these five crops. Our analysis further allows identifying P&Ps causing chronic or emerging losses, at regional to global scales. This work enables better positioning plant pathology with major challenges of our times: global and climate change, food (in) security, and the state of the biosphere.

PL (05): Scenarios for sustainable management of plant parasitic nematodes

Becky B. Westerdahl[1]

Department of Entomology and Nematology, University of California, Davis, CA 95616, USA

Plant parasitic nematodes are plant stressors that cause significant yield reductions worldwide. Prior to the development of soil fumigation, cultural practices were developed for management of plant parasitic nematodes; but were utilized with limited success. The restricted availability of fumigants and other nematicides, has stimulated a return to research into more sustainable management scenarios. Recent developments offer new tools to fine tune the use of cultural and biological practices for local cropping systems. The commercial availability of biological nematicides, of products with newer and safer modes of action, of the increasing availability of nematode resistant cultivars, of the development or selection of cover crop varieties for use against particular nematode species, and the use of green manures, biofumigation, and trap cropping are promising techniques. Combining these with a strong nematode control and certification program for nursery crops, the development of molecular techniques for identification of plant parasitic nematodes, online databases to rapidly search out nematode resistant crops, computerized soil temperature monitoring equipment plus computer models for calculating nematode degree days, and modeling population cycling, plus a greater understanding of nematode biology and population dynamics have made it possible to develop promising scenarios to reduce damaging nematode populations and increase yields.

PL (06): *Trichoderma* the most powerful arsenal for plant disease management

A.N. Mukhopadhyay

Former Vice-Chancellor, Assam Agric. University, Jorhat, Director General Tea Research Association and Dean, G.B. Pant University of Agriculture and Technology, Pantnagar, 'Sangini' 151 Akanksha, Udyan II, Raibareilly Road, Lucknow-226025, U.P. INDIA; E-mail: amar.mukhopadhyay@gmail.com

During last decade, species of *Trichoderma* have emerged as most powerful bioprotectants for management of wide variety of plant diseases. This is more true in the context of the fact that there is considerable public pressure and pressure from environmental scientists to reduce emphasis on chemical protectants and use bioprotectants. The genus *Trichoderma* by virtue of its broad spectrum action against a number of plant diseases caused by fungi, bacteria, viruses and even nematodes has occupied the top position among the bioprotectants developed for plant disease management. *Trichoderma* based biopesticides have been proved successful in a large number of field, vegetable, fruit and flowering crops for the management of diseases. Because of its eco-friendly nature and low cost when compared with chemical protectants, the technology has been very widely adapted all over the world. The literature accumulated on the subject during last decade is quite vast. *Trichoderma* strains exert biocontrol against phytoppathogens either indirectly by competing for nutrients and space, modifying the environmental conditions, or promoting plant growth and plant defensive mechanisms and antibiosis or directly by mechanisms such as mycoparasitism. These indirect and direct mechanisms may act coordinately and their importance in the biocontrol process depends on the *Trichoderma* strain, the antagonized fungus, the crop plant, and the environmental conditions, including nutrient availability, pH, temperature, moisture and iron concentrations. *Trichoderma* species are plant symbiont opportunistic virulent organisms, able to colonize plant root by mechanisms similar to those of mycorrhizal fungi. Root colonization by *Trichoderma* species frequently enhances root growth and development, crop productivity, resistance to abiotic stress and the uptake and use of nutrients. Root-fungus association also stimulate plant defensive mechanisms. *Trichoderma* added directly to rhizosphere or as seed treatment protects plant against numerous classes of pathogens, e.g. those that produce aerial infections, including fungal, bacterial, nematodes and viral pathogens. This reveals induction of resistance mechanisms similar to the hypersensitive response (HR), systemic acquired resistance (SAR) and induced systemic resistance (ISR) in plants. The low cost technology has opened up a new vista for plant disease management and is likely to be a boon for seed industries who would like to provide protection to seeds as well as plants against a large number of seed, soil- borne and foliar diseases.

PL (07): Asian PGPR and IPS: Win-win global relationship for sustainable crop productivity, education and collaboration

M. S. Reddy and S. Lalitha

Asian PGPR Society, Department of Entomology & Plant Pathology, Auburn University, AL, USA & Periyar University, Salem, Tamilnadu, India

Asian PGPR Society salutes Indian Phytopathological Society for organizing the 7th International Conference on “Phytopathology in Achieving UN Sustainable Development Goals” at ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India, during January 16-20, 2020. Research collaborators among these two societies have conducted PGPR research on various crops which include: row crops, legumes, vegetables, rice, ornamentals and spices. The rationale of mytalk is that there is a great need for environmentally-friendly microbial technologies in Asia particularly, India. Agriculture in this continent is plagued by two main constraints. The first is the depletion of nutrient supply in the agricultural soils, and consequently, the sizable gap between achievable and actual yields in various crops. The second main constraint is crop protection. Devastating pathogens lead to 15-30% average crop losses annually. Despite the constraints, the Asian continent has made great strides in agricultural production. Sustainable approaches are those that are not aimed solely at maximizing short-term production but rather those that consider long-term production gains, the ecology of agricultural systems, and profitability of farmers. Further, sustainable solutions result in empowerment of women, farm laborers, and rural communities. My talk deals with restructuring the crop rhizospheres for improving and sustaining the nutrient supply in the soils and enhancing the health and yield of crops through sustainable practices based on microbial technologies. By microbial technologies, we mean the principles of microbial ecology, which encompass inoculation of crops with beneficial microorganisms and the use of cultural practices that enrich indigenous beneficial microorganisms in individual agricultural fields. There are two main outcomes or effects from beneficial microorganisms: enhanced plant-growth and crop protection, both of which represent the two main constraints to agriculture. My network partnership around the globe has correctly identified the use of microbial inoculants to provide holistic health and sustainable crop yields. Each partner in our network has made substantial contributions to agriculture in research with plant-associated rhizobacteria. These research leaders bring their expertise together in building a Partnership in higher education. Several large development projects in agriculture failed after initiation because of new pest and soil health problems. There is an urgent need to promote integrated pest/disease management at a faster rate and it is driven by emphasizing organically-produced food, conservation of biodiversity, unpolluted environment, and sustainable agriculture. However, the adoption of biopesticides by farmers in Asia is still in its infancy. While already threatened by the unforeseen drought spells, crops suffer the frequent outbreaks of pests that lead to total crop failure. Because of such crop failures, the resource poor farmers cannot afford expensive crop protection technologies, and remain poor. Strengthening relationships among our societies through development, training, educationfor propagation of low-cost technologies would certainly help in the improvement of our farmers' economic situations and thereby eliminate the cycle of poverty.

PL (08): Genome Editing for Stress Tolerance of Rice

Viswanathan Chinnusamy

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PL (09): Tospovirus-host interactions in the omics era

R. Pappu

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Tospoviruses continue to be one of the major production constraints to a wide range of legumes, ornamentals and vegetable crops in many parts of the world. Transmitted by several species of thrips in a persistent and propagative manner, the viruses have a wide host range that include numerous weeds making disease management difficult. Among more than 32 tospoviruses, Tomato spotted wilt virus (TSWV) is the first recognized tospovirus and is one of the most prolific and economically important viruses. An integrated disease management approach is needed that includes vector management, cultural practices and growing virus resistant cultivars. As in case of many other viruses, growing virus resistant cultivars offers the most effective and ecofriendly tactic for tospovirus management. Much progress has been made in developing resistant cultivars of tomato and pepper against Tomato spotted wilt virus, the most prolific member of the tospovirus group. The resistance is governed by *Sw5* and *Tsw* in tomato and pepper, respectively. However, over the years, resistant breaking TSWV strains have emerged in several parts of the world. The search for new and effective sources of resistance should continue to ensure the sustainability of crop product. One potentially useful approach is to use genomics and transcriptomics to understand the interaction between tospoviruses and their hosts and use this information to identify potential markers and then subsequently genes that could confer resistance. Identification of susceptibility genes could be useful in genome editing approaches such as CRISPR-cas. With this long term goal, we have been using next generation sequencing to determine the small RNA profiles of TSWV in TSWV infected resistant and susceptible tomato cultivars. This approach provided insights into the processing of the TSWV genome different tomato genotypes. The virus-specific small RNAs were used to mine the tomato transcriptome to identify the potential targets among the host genes and pathways. Next generations sequencing combined with genomic and transcriptomic profiling is being increasingly used to gain insights into host-virus interactions and has started to yield practical information that could be useful in identifying new resistant genes leading to their incorporation into existing cultivars or development of new cultivars.

Award Lectures

Presidential Address

AL (01): Advances in mushroom production: Key to food, nutritional and employment security

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Mushroom is an excellent source of nutrition, tonic, medicine and dietary food items being produced and consumed by the peoples from Asian and European countries. Mushrooms are source of multiple nutrients and phytochemicals. These are rich in crude fibre, protein, vitamins B, C and D (including niacin, riboflavin, thiamine, and folate), minerals (potassium, phosphorus, calcium, magnesium, iron and copper), contain low fat, low calories and no starch. They provide carbohydrates of high quality and enrich the diet which can be of direct benefit to the human health and fitness. They are often considered to provide a fair substitute for meat, with at least a comparable nutritional value to many vegetables. It is now well recognized as an eco-friendly alternative for agro-waste recycling in Punjab, Haryana, Bihar, Chhattisgarh etc. with tremendous capabilities not only to provide better nutrition but also medicinal attributes for the vast vegetarian population. Mushroom farming is a potential biotechnological process wherein the waste plant materials (200 billion tons) can be converted into best valuable food. Protein conversion efficiency and productivity of mushrooms per unit area and time is also far superior than plant and animal sources.The world production of mushroom is about 40 million tones. China, USA, Netherlands, Poland, Spain, France, Italy, Ireland, Canada and UK are the leading mushroom producers in the world. India hardly produce 0.13 million tons of mushroom and not being recognised as a major mushroom producing country in the world. There have been lot of technological advancements in mushroom industry these days. There are changes in mushroom spawn production from use of non absorbent cotton plugs to poly-fill to filter bags, from milk bottles to glucose bottles to polypropylene bags to liquid spawn. Composting methods for button mushroom production have changed from long method to short method having Phase I and II to phase III. Production technologies of oyster and shiitake have been changed from log cultivation to bag cultivation to total automation for bottle cultivation and reduction in time of shiitake crops from 3 months to 1.5 months. Large number of new species has been introduced. Biofortification or value addition of mushroom with many other established recepies is becoming very common to enhance quality and address the demand for ready made or ready-to-make food products. Changes in production technology and diversification have led to exponential growth of mushroom production world over. It has the capacity to double or triple the farmers income within a year compared to any other agriculture/horticulture and allied activities. Thus, mushroom cultivation has witnessed a tremendous growth. It has proved as potential source of employment generation and supporting the local economy by contributing to subsistence food security, nutrition, and medicine; generating additional employment and income through local, regional and national trade and offering opportunities for processing enterprises in tribal dominating rural India.

Mundkur Memorial Award

AL (02): Exploring potentials of PGPMs in sustainable crop disease management

M.K. Naik

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Free living; root colonizing bacteria and fungi have been studied for the past century as possible inoculants for increasing plant productivity. Plant growth promoting microbes (PGPMs) are characterized by a number of functions which include improvement of plant establishment, increased availability of plant nutrients, enhancement of nutrient uptake, improvement of soil structure and protection against diseases. More specifically, fluorescent Pseudomonads under plant growth promoting rhizobacteria (PGPR) have received attention owing to their catabolic versatability, root colonizing ability and their capacity to produce a wide range of secondary metabolites. There are a varieties of biocontrol mechanism is to suppress fungal and bacterial pathogens by fluorescent *Pseudomonas* sp. by producing antibiotics, siderophores, hydrocyanic acid (HCN), enzymes and phytohormones. Antibiotics produced by species of Pseudomonas are deleterious to the growth or metabolic activities of other microorganisms. Antifungal compounds such as 2, 4-diacetyl phloroglucinol (Phl), pyoleuteorin (Plt), pyrrolnitrin (Prn), HCN and phenazines (Phz) contribute to disease suppression in various host pathogen systems. The use of fluorescent Pseudomonads for inducing systemic resistance against phytopathogens has been well documented. Various isolates of fluorescent Pseudomonas promoting the growth and vigour of chilli and rice seedlings have been identified. An increased activity of PAL, total phenol and â-1,3glucanase due to application of *P. fluorescens* isolates in chilli plants challenge inoculated with *F. solani* the cause of wilt of chilli .The treatments of rice seeds with an endophytic isolates (EP-5) recorded maximum PAL activity in rice against sheath blight fungus. However, when the rice seedlings were root-dipped, the PAL activity was maximum on the 7 day after challenge inoculation. *P. fluorescens* (EP-5) was clearly a top performing isolate as it showed higher activity of defense related PAL enzymes. With regards to formulations, talc was best suited for both *P. fluorescens* and (Pf-4) *P. putida* (RFP-13) isolates with 12 x 10^7 and 10 x 10^7 cfu/g respectively up to 300 days of storage. It is essential to work out the compatibility of bioagents with other insect pest and disease management chemicals since the bioagents are to be integrated as one of the inputs and practiced in agro-ecosystem approach. Among fungicides, *P. fluorescens* (EP-5) and *P. putida* (RP-46) isolates were compatible with Hexaconazole, Tricyclazole and Propiconazole, but were incompatible with Isoprothioline. The isolates were compatible with Carbofuran and Imidacloprid, whereas incompatible with Fipronil and Buprofezin. Further the isolates were compatible with plant products such as neem seed kernel extract. Among the fungal bioagents, *Trichoderma* spp. are a ubiquitous, abundantly available, naturally occurring and widely distributed fungi. In the genomic era, *Trichoderma* is investigated in detail with respect to identification of >200 mycoparasitic genes, deciphering the role of cell wall degrading enzymes, secondary metabolites, peptibols, volatile organic compounds such as alcohols, ketones, alkanes, pyrones, stimulants of plant growth, pharmaceutical and biofuel use, terpenoids compounds etc. A lucid account of their isolation, characterization, molecular identification of species, bioefficacy, identification of climate resilient isolates in terms of temperature tolerant (T_{33}, T_{41}, T_{46}, T_{49} and T_{50}), salinity tolerant (T_{10}, T_{1}, T_{41}, T_{4} and T_{5}), compatible with pesticides (T_{45}, T_{36}, T_{38}, T_{41},T_{44} T_{48}, T_{25} and T_{21}) has been presented in this paper. The deduced amino acids structural superimposition of Tatub-2 of 1NTG-2 with T_5 and 2NTG-2 with T_5 gene indicated 37 and 183 residues respectively. Synonymous and non-synonymous substitution of amino acids could be the reason for mutation and Carbendazim tolerance. The present day trend is to adopt IPM schedule where in the various components of fungicides, insecticides, bio agents and other inputs were integrated and operated to use in the same ecosystem.

JF Dastur Memorial Award Lecture

AL (03): The continuous challenges of citrus greening disease and its impact on global citrus industry

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Citrus greening, a devastating disease of citrus, is caused by a phloem limited,Gram negative, unculturable bacterium *Candidatus* Liberibacter asiaticus (*C*Las). Its taxonomical classification is based on 16S rRNA gene sequence and grouped into alpha subdivision of proteobacteria, genus *Candidatus* Liberibacter in the family *Rhizobiaceae*. It is transmitted by the Asian citrus psyllid vector, *Diaphorina citri*. The typical disease symptom includes leaf yellowing along the veins and blotchy mottling which sometimes resembles to zinc and iron deficiency symptoms. The disease mainly diagnosed through symptom expression, biological indexing and different PCR based molecular diagnostic techniques viz. PCR, multiplex PCR, real time PCR using sets of bacterium-specific primers targeting 16S rDNA, 16S/23S intergenic regions, ribosomal protein genes and *omp* genes. Recently, more simpler and cost-effective loop-mediated isothermal amplification (LAMP) andrecombinase polymerase based isothermal amplification combined with lateral flow assay (HLB-RPA-LFA) technique have been developed for detection of *C*Las. All the infected samples yielded specific amplification products, sizes of which were found similar to that amplified from '*Ca.* Liberibacter asiaticus'.Variability studies based on the tandem repeats at hyper variable genomic locus CLIBASIA_ 01645 reveals that the Indian populations of '*Ca.* L. asiaticus' is more diverse than other reported populations of China and USA. All these developed diagnostic techniques are being used routinely for implementing citrus budwood certification with the annual production target of five lakhs disease-free nursery plants for the citrus growers of the country. For effective control of the disease, aqueous formulations of inhibitor molecules *viz.*2S albumin (a plant based protein; ~12.5 kDa), Nano-Zinc Oxide (Nano-ZnO; ~ 4.0 nm diameter) were trunk-injected to HLB affected Mosambi plants and the dynamics of pathogen load was assessed using TaqMan-qPCR assay in every 30 days after treatment (DAT) for 120 days inside screen house. It was found that 2S albumin-Nano- ZnO formulation performed the best among all the treatments decreasing CLas population by 96.2%, 97.6%, 95.6%, and 97% of the initial bacterial load at 30, 60, 90, and 120 DAT, respectively. Further field evaluation of the technology involving more number of field infected citrus plants is in progress.

Sharda Lele Memorial Award

AL (04): Epidemiology and management of Phytophthora diseases of tomato and bell pepper in North Western Himalayas

S.K. Gupta

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Tomato (*Solanum lycopersicon* L.) and bell pepper (*Capsicum annuum* L.) are major solanaceous vegetable crops of mid hills of North Western Himalayas which are grown during April to September and fruits are transported to the northern plains where they fetch remunerative prices. With the onset of monsoon rains these crops are severely infected with different diseases of fungal, bacterial and viral nature of which *Phytophthora* diseases are very important. Occurrence of buckeye rot (*Phytophthora nicotianae* var. *parasitica*), late blight (*Phytophthora infestans*) in tomato and leaf blight and fruit rot (*Phytophthora nicotianae* var. *nicotianae* and *P. capsici*) in bell pepper have been recorded. Fruiting in these crops coincides with the onset of monsoon rains and inoculum of these pathogens is splashed from soil to the foliage through rain splashes, thus causing rotting of fruits. Keeping in view the importance of the crops and diseases incited by *Phytophthora* spp., present studies were carried out to identify the critical epidemiological parameters for the initiation and development of these diseases and their management through cultural, host resistance, chemical alone and their integration. The genome size of *P. nicotianae* var. *parasitica* is 82 Mb. Cultural, morphological and genetic variability among 23 isolates of *P. nicotianae* var. *nicotianae* revealed that the colour of mycelium varied from white to creamy or dirty white and the appearance of the mycelium was fluffy or suppressed and dry or slimy. The dendrogram produced from computerized cluster analysis of the DNA fingerprints revealed a great deal of heterogeneity among isolates as expected after DNA banding pattern analysis of gel image. Both pathogens survive in the form of oospore and chlamydospore in soil for more than one year in ordinary field conditions. Rainfall has been found to be positively correlated with the incidence of these diseases which not only help in maintaining higher levels of relative humidity but also help in dispersal of inoculum. Due to the soil borne nature of these pathogens and the infection caused by the rain splashed inoculum, single management practice is not enough to keep these diseases below economic threshold level. In tomato, cherry tomato (*Lycopersicon esculentum* var. *ceresiformae*) was found resistant under natural epiphytotic conditions where as in bell pepper line “Dark Green” was found resistant against 18 isolates of *P. nicotianae* var. *nicotianae* collected from different parts of Himachal Pradesh. Cultural practice like staking of plants, collection and destruction of infected fallen fruits and leaves, proper drainage of the field and wider spacing have been found effective. Among fungicides, both non-systemic and systemic were found effective in managing these diseases. Recently available Strobilurin fungicides alone and in combination with non-systemic fungicides have also been found effective in keeping the ravages of these diseases in check. Induction of resistance through abiotic elicitors was effective for the management of these diseases. Two foliar sprays of acibenzolar-S-methyl and â-aminobutyric acid was very effective in reducing the disease incidence and disease index of fruit rot and leaf blight in bell pepper. These treatments also significantly increased the fruit yield. Integration of cultural and chemical methods is more suitable for the management of these diseases. Application of pine needle mulch on the field floor alone and in combination with the sprays of metalaxyl + mancozeb (0.25%) on mulch and foliage resulted in significantly lower disease levels followed by sprays of copper oxychloride (0.3%) both on mulch and foliage and increased the fruit yield.

A.K. Sarbhoy Memorial Award Lecture

AL (05): Fungal epiphytes toendophytes: A cryptic and potential resource for biodiversity, bioremediation and bioactive compounds

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Fungi appear to external part of plants and animals and produce symptoms are known as epiphytes. Variety of symptoms may be produced by different epiphytic fungi which reduce either the yield or may damage the parts which it affects. But endophytic fungi reside inside healthy plant tissues without causing any detectable symptoms. Exploiting the potential of non-conventional resources for microbial diversity and microbial products is necessity of time for continuous and sustainable development. Diversity of fungal endophytes is relatively untouched and alternative resource that could be used to microbiology and biotechnology for resolving the better solutions to a wide range of problems. Varied environmental settings, cause different stresses to plant systems like drought, salt and temperature, including many diseases which are matter of concern. In animal systems, diseases such as malaria, multi/or extremely drug resistant bacteria, cancer, parasitic protozoans, non-curative diseases, and pathogenic fungi are important problems. The above mentioned problems existing with crops and society require intensive approach for the attainment of novel and more effective agents that have the attribute to be developed into new commercial products. Natural products are often produced by microbes and may have specific functions in nature. The abundance of microbial biodiversity is as yet largely unknown, and the defined microbes representing but perhaps a small fraction of the potential, and as such, the search and identification of novel biotopes that may provide unique and useful products, will likely be a successful endeavor. Perennial plants are found to harbor novel endophytic fungal biotopes. These endophytes have been largely unexplored and undermined for their potential to produce novel natural products for commercial use. However, the process from discovery to production is complex. The utilization of endophytic fungi and their functional metabolites on an industrial scale begins with intelligent screening of endophytes, and then requires growth of the microbe(s) and subsequent scaling up for fermentation, as well as optimization of many other necessary factors. The isolation and characterization of bioactive substances from culture filtrates is done using bioassay guided fractionation and spectroscopic methods. Some examples of novel natural products produced by endophytic microbes that have been successfully produced on an industrial levels includesazadirachtin, rohitukin, podophyllotoxin, taxol, pestacin, terrin, munumbicin, isopestacin, pseudomycin, jasmonic acid, torryanic acid, javanicin, terrin and piperine to name a few. The endophytic biodiversity, their role in alleviatingdifferent abiotic stresses from plants, potentiality and epigenetic modulation of endophytesfor discovering the novel and cryptic natural products active against different diseases representing to both humans and plants will be discussed. The role of fungal hydrophobins would be the future approach to elucidate its attributes.

S.N. Das Memorial Award lecture abstract

AL (06): Our understanding about phytoplasma research scenario in India

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Since the first report of existence of phytoplasma disease in 1874 in India, now more than 150 plant species are reported to be infected with phytoplasmas. The causal organism was known as mycoplasma like organisms (MLOs) till 1994 and thereafter was named as phytoplasmas. There are currently 36 groups of phytoplasmas are known worldwide, out of which ten groups are reported in India on the basis of 16SrRNA gene sequence comparison. The phytoplasma diseases are well documented from all parts of the country and aster yellows group (16SrI) is the most prevalent and widespread group followed by 16SrII, 16SrVI, 16SrXI and 16SrXIV groups. Sesame phyllody, brinjal little leaf, sugarcane grassy shoot, sandal spike, coconut root wilt, areca nut yellow leaf and many ornamentals maladies are the major phytoplasma diseases in India causing serious economic losses. Nearly a dozen of leafhopper and planthopper species were reported as natural vectors and more than 30 weed species as natural reservoirs of phytoplasmas. Numerous new phytoplasma strains on several crops have been identified in India during last decade, which revealed that phytoplasmas are more diverse than thought. Very recently two full draft genome sequence of 16SrXI (sugarcane grassy shoot) and 16SrXIV (Bermudagrass white leaf disease) have been deposited in GenBank from India which open-ups the possibilities of studies on functional genomics. Mixed infections of phytoplasmas and viruses have also been emerging as serious problems in several crops and are responsible for more synergistic losses. Since last two decades, nested PCR assays has been successfully used to detect phytoplasmas strains in diseased plants and insect vectors by utilizing 16S rRNA, 16Sr- 23S rRNA spacer region and several multilocus gene specific primers (*sec A, tuf, gyrA, gyrB, dnaB, groEL, imp, rp, SP11, SAP24, leu C, gyrA, gyrB, dnaB*). However, new developed isothermal amplifications methods (LAMP & RPAs) for sensitive and quick detection of phytoplasmas are little attempted in India and needs to be explored for identification of Indian phytoplasma strains. Multiplex PCR system has also been developed to detect the phytoplasma in one cycle utilizing nested PCR primers and multilocus gene specific primers in one PCR cycle. Some essential metabolic pathways are completely lacking and some are substantially reduced in phytoplasma infected plants, and hence it is difficult to draw a clear picture of the regulation of metabolic processes in them. Very little attempt has been made to study metabolic interaction in phytoplasma host plants and insects in India. Some efforts in last decade has been made to elucidate the host responses at biochemical, genomics, proteomics and metabolomic levels for understanding the host-pathogen interactions and more concentrated efforts needs to be emphasized that will help formulate strategies for controlling phytoplasma diseases. Presently the suggested effective management practices in India are pruning infected portions, growing resistant varieties, heat therapy, use of tertracycline, control of insect vectors and natural host reservoirs. However, none of them have completely proved successful. Future approach on developing resistant genotypes, development of inoculation techniques for phytoplasma screening of genotypes, culturing of phytoplasmas, full genome sequencing of major phytoplasma strains and RNA interference needs to be strengthened for a better understanding and management of these peculiar microbial pathogens.

D.P. Misra and R.N. Pandey IPS Women Scintes Award

AL (07): Chickpea wilt: Variability of Foc isolates in Central India

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Chickpea (*Cicer arietinum* .L) is one of the world most important cool season grain legume globally grown in over 40 countries (Anwar *et al*. 2009). It is the best suited crop largely grown in rainfed environment in *Rabi* season throughout the nation and most vulnerable to climate change. The crop suffers from various seed, soil and air borne pathogens in different stages of crop growth, out of which seed and seedling rot (*Sclerotium rolfsii*) under soybean-chickpea, paddy-chickpea cropping system, vascular wilt (*Fusarium oxysporum* f. sp. *ciceri*) dry rot rot (*Rhizoctonia bataticola*) are major one specially in central and southern part of the country. Fusarium wilt is the most important disease of chickpea which occurs from seedling to pod formation stage and causes annual yield loses of 10-60% annually (Jalali and Chand 1992). Plant pathogens inspite of sound management technology still result losses due to climate as well as pathogenic variability. Since more than three decades there is a shift in cropping pattern in chickpea as it has shifted from highly productive state from north India to rainfed areas in central and southern India. Attempt has been made to manage the disease through identification of broad based wilt resistant genotypes by rigorous screening in wilt sick plots (AICRP Chickpea project). But, due to variability in isolates of wilt pathogen satisfactory results yet to achieve for locating consistent multiple race resistant genotype of chickpea under multilocation evaluation test against Foc. Considering the facts, survey of chickpea field was conducted in four states of central India *viz* Madhya Pradesh, Chhattisgarh, Gujarat and Maharashtra (under wilt net project) covering 240 locations. One hundred twenty isolates of *F. oxyspotum* f. sp. *ciceri* were isolated from collected chickpea wilted plant.The isolates were studied in respect to cultural, morphological and pathological characterization and grouped. Out of 46 grouped representative isolates reaction of 14 chickpea differential genotypes studied against 24 isolates of Foc. from Madhya Pradesh, 6 isolates from Chhattisgarh, 8 from Gujarat and 8 from Maharashtra states under artificial inoculation using soil inoculation method (2 % w/w) led to conclusion that reaction of differential genotypes against test isolates from each state were highly variable. Based on the reaction of differential genotypes the isolates could be grouped into three pathogenic races alongwith new variants. The race picture existing in state are M. P. (Race-2, 4), Chhattisgarh (Race-2, 4, 5), Maharashtra and Gujarat (Race-2). Existences of races in the chickpea wilt pathogen warrants for multirace or multi-variant resistance in chickpea. Evaluation of identified 26 donors against 8 races/variants selected from four states indicated that Foc. Isolates not only differ in their virulence but also behaved differently in their reaction. JG 315 and Vishal were found resistant to the races / specific races (2, 4, 5 and 1new variants) indicating the broad based host resistance to *F. oxysporum* f.sp. *ciceri.* However, BCP 91 was found resistant with all the isolates except I-77. The genotypes L550, PG 5, GG 2, DCP 92-3, CPS 1, Vijay, PBG 1, K 850 and H-82-2 susceptible to highly susceptible against these races. Virulence of the isolates does not have an important role in identification of resistance against wilt in chickpea genotypes. The genotypes having resistance against 8 isolates of *F. oxysporum* are of great value, may be used as donors in breeding for wilt resistance. In respect to molecular characterization seven isolates from 4 states of central India could be grouped into three clusters by both RAPD and SSR primers whereas it could be grouped into 2 main clusters by ITS-RFLP primers. Indicating prevalence of 2-3 variants of Foc in Central India.

M. J. Narsimhan Academic Merit Award Contest

M.J.N. (E) 01: Molecular characterization of an old world *Begomovirus* infecting chilli in North Bengal

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Begomovirus (Geminiviridae) are plant infecting single stranded DNA viruses known to evolve very fast. *Begomovirus* typically have genomes consisting of two separately encapsidated genomic components, known as DNA-A and DNA-B. The DNA-A component contains six ORFs coding for *av1*(Coat Protein), *av2* (Pre-Coat Protein), *ac1* (Replication Associated protein), *ac2* (Transcription activator protein), *ac3* (Replication Enhancer Protein), *ac4* (Unknown) in both orientations that play major roles in viral replication, infection, establishment and symptom development. In the present study we have analyzed the DNA-A sequence of 302 begomoviruses reported in the database from different countries following the list of International Comittee on Taxonomy of Viruses(ICTV). Phylogenetic analysis of the sequences was performed which revealed two major evolutionary distinct groups mainly Old World and New World viruses. From the analysis of the genomic components constituting DNA-A from both viral groups it was evident that OW viruses have six gene i.e. *av1, av2, ac1, ac2, ac3, ac4* whereas New World viruses doesn't contain av2 in any case and are also devoid of ac4 very often. Our results demonstrated that the coat protein in Old World viruses generally possess Nuclear Localization Signals (NLS) which is missing in New World coat proteins. North Bengal is known for production and export of different types of chilli. This crop is highly affected by leaf curl virus which is prevalent in this area and occurs every year in chilli growing season. But information about the leaf curl virus of this region has not been documented till date. We have confirmed the presence of begomovirus in chilli with symptoms of leaf curl infection by PCR with begomovirus specific primers. All the six genomic components of begomoviral DNA-A were amplified using gene specific primers which suggest that this virus is a monopartite virus Old World virus. The amplified *av1* gene product was sequenced and protein sequence was derived from nucleotide sequence which has shown the presence of strong Nuclear Localization Signal at N-terminal of protein. Phylogenetic analysis of this chilli infecting begomovirus was performed with available sequences to understand the evolutionary pattern of the virus. The result clearly indicates that this begomovirus infecting chilli in the North Bengal region is a new recombinant strain of Pepper leaf curl Bangladesh virus and Tomato leaf curl Joydebpur virus.

M.J.N. (E) 02: Population structure analysis of *Ralstonia solanacearum* in West Bengal, India and influence of crop rotation on its survival in the rhizospheres of various crops

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R. solanacearum is a destructive phytopathogenic bacterium that causes wilt of several economically important crops and ornamentals. *R. solanacearum* has been categorized into five races and six biovars based on host range and sugar utilization ability. Fegan and Prior (2005) proposed a new hierarchical classification scheme to partition strains of *R. solanacearum* into four taxonomic levels: species, phylotype, sequevar, and clone. The knowledge of diversity of strains of *R. solanacearum* species complex within a geographical area is of paramount important for providing the foundation of a successful breeding and integrated management programme. Presentlyscanty or no systemic information is available over the genetic diversity and distribution of diverse strains of *Ralstonia solanaceraum* in West Bengal. Since bacterial wilt is a monocyclic disease, crop rotation could be very effective in reducing initial inoculum, and thereafter may delay disease development. Moreover, soil physico-chemical and biological factors, soil temperature and moisture at different depths and rhizodeposition of different hosts and non-hosts crops ultimately influenced the survival ability of *Ralstonia solanacearum* in an environment or ecosystem. In the context mentioned above, the present research programme was framed for diversity analysis of *Ralstonia solanacearum* and identification of suppressant crops against *Ralstonia solanacearum*. In the present investigation, 36 strains of *R. solanacearum* were collected during 2016 to 2018 from across the thirteen different vegetable growing districts under five different Agro-climatic zones (ACZ) of West Bengal. Variable bacterial wilt severity was recorded during survey conducted in five Agro-climatic Zones (ACZ) of West Bengal. The strains were identified as phylotype I by multiplex polymerase chain reaction and further divided into sequevars based on polymorphisms in the endoglucanase (egl) gene. Bacterial wilt of bottle gourd incited by *R. solanacearum* was first time reported from India. Two new biovars (6 and 7) along with biovar 3 have been found to be prevalent under West Bengal conditions. Genetic diversity and AMOVA analysis of ERIC PCR results revealed *R. solanacearum* strains of ACZ 3 to be genetically distant from the rest ACZs. Two season crop rotational experiments were conducted to determine the effects of crop rotation on *R. solanacearum* population and aubergine bacterial wilt incidence in wilt conducive plots at C-Block Farm, BCKV, Kalyani, Nadia during 2017-19. Cereals, leguminous, brassicaceous, solanaceous and malvaceous vegetables commonly grown in this area were included in different sets of rotation experiments. A two-season rotation under two year rotational system on highly infested soil resulted percent reduction of bacterial wilt incidence to 86.3 %, 65% and 65% in Maize-Maize-Aubergine, Okra-Maize-Aubergine and Sorghum-Maize-Aubergine system, respectively as compared to Aubergine-Aubergine-Aubergine rotation scheme. qRT-PCR was conducted to monitor the dynamicsof *R. solanacearum* population using soil DNA extracted from crop rhizosphere and the result revealed that the population of bacterial wilt pathogen was recorded in a declining trend in cereal based crop rotation system. Illuma-Hiseq sequencing illustrated the increase in Firmicutes and Actinobacteria at phylum level and Bacillaceae, Burkhloderiaceae, Paenibacillaceae and Streptomycetaceae in family level in Maize-Maize-Aubergine, Okra-Maize-Aubergine and Sorghum-Maize-Aubergine system as compared to Aubergine-Aubergine-Aubergine rotation scheme. Cluster tree based on Unifrac approach clearly delineated that rhizosphere of Aubergine mono-cropping system was genetically less diverse and distant from beneficiary microflora enriched rhizospheres with Maize-Maize-Aubergine, Okra-Maize-Aubergine and Sorghum-Maize-Aubergine under two year rotation system. Maize, sorghum and okra were identified as suppressant crops and can be used as good rotation crop at two season rotation in Aubergine based cropping system for management of bacterial wilt of Aubergine.

M.J.N. (NE) 03: Post transcriptional gene silencing using Coat protein gene specific dsRNA molecules against cognate Potato Virus Y (PVY) infecting potato crop of Assam

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Viral Double-stranded RNA (dsRNA) is the trigger for induction of the Post transcriptional gene silencing (PTGS) as a antiviral defense mechanism in plants. dsRNA when exogenously applied, was proven as a potent means for virus control. It is hypothesized that the exogenously applied dsRNA mimics the viral RNA intermediate, which is involved in viral replication, and thereby triggers RNAi. Based on these concepts of RNAi in plants, coat protein (CP) gene of Potato virus Y (PVY) was targeted, in such a way that the plant virus was unable to replicate in the plant cytoplasm. In the present study, we aimed at investigating whether exogenous application of dsRNAs corresponding to the viral genes of PVY could suppress viral titters in potato. The specific objectives of the study was to develop a dsRNA construct for PVY resistance in Potato and a proof of concept studies for PVY silencing in potato using dsRNA assay strategy. For performing this experiment PVY infected potato leaf tissue samples were collected from some potato growing locations of Jorhat district and PVY was successfully detected by two-step Reverse Transcriptase PCR (RT- PCR). Two methods of dsRNA production were successfully employed in this study. In the first method, using a two-step PCR followed by *in vitro* transcription protocol. In the second method, large scale production of PVY coat protein gene specific dsRNA was produced using *E. coli* with T7 RNA polymerase. The expression of PVY coat protein in the vaccinated and non-vaccinated plants was analysed by conventional semi-quantitative PCR. Results signified that, when dsRNA exogenously applied on the leaves of the potato along with virus PVY, the viral replication was reduced. Further results revealed the height of the vaccinated plants were enhanced, whereas non-vaccinated plants showed stunted growth and had non-reproductive growth habit. In conclusion, our results revealed that the exogenous application of crude extract of bacterially-expressed dsRNA molecules derived from PVY coat Protein gene, caused considerable reduction in PVY infection and allowed a better vegetative plant growth. *Enterobacter cloacae, Pantoea ananatis, Pseudomonas psychrotolerans, Pseudomonas monteilii, Acinetobacter bayliyi, Pantoea vagans, Pseudomonas stutzeri* were found effective against *Xanthomonas oryzae* pv. oryzae. This study culminated in identification of potential bacterial communities for bacteriome transplantation on rice phyllosphere for mitigation of foliar diseases.

M.J.N. (NE) 04: Exploring actinomycetes and endophytes of rice ecosystem for management of bacterial blight of rice

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Endophytic microbes and rhizospheric *Streptomyces* of rice (*Oryza sativa* L.) plants were explored to develop a biocontrol strategy for the management of bacterial blight (BB) disease caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). *In-vitro* studies revealed that promising endophytic microbes (EB8 and EF2) and rhizospheric *Streptomyces* (S2 and S15) could inhibit the growth of BB pathogen effectively. The treatment combination of endophytic and rhizospheric microbes (EB8+S2+S15) showed highest (58.71%) suppression of the BB pathogen. Various plant growth promoting characteristics such as production of IAA, hydrogen cyanide, siderophore production, zinc, phosphorus and potassium solubilisation were estimated for most of the endophytes and rhizospheric *Streptomyces*. These effective endophytes and rhizospheric *Streptomyces* found *in vitro* were further tested *in planta* for their efficacy in managing BB of rice by applying as seed treatment, root treatment, soil treatment and spray application. The BB incidence was significantly reduced (66.03 to 86.27%) when the plants were treated with all the combinations of effective microbes (Control= 0.00%). The phenol content (1.75 to 2.52%) of the treated plant leaves was assayed to be at higher concentrations (Control= 1.05%). Moreover, few antibiotics produced by the effective *Streptomyces* sp. were recorded at higher peaks of retention time, *viz*., Pyrisulfoxin B, APHE 4, Kanamycin C, Nitracidomycin B, Clavulanic acid, Neothramycin A, Nitracidomycin A and Furaquinocin E.

M.J.N. (DZ) 05: Understanding the etiology of leaf crinkle disease in Urdbean (*Vigna mungo* L.) using conventional and RNA- seq approaches

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Vigna mungo (L.) Hepper, (Blackgram) is an important leguminous crop of Indian subcontinent. It is severely affected by various diseases, among which uncharacterized Urdbean leaf crinkle disease (ULCD) is one of most important. Present study was carried out on epidemiology and etiology of the disease by various approaches from conventional to deep sequencing techniques. A significant effect was observed on seed characteristics. Reduction in seed index was observed to be 23.7 % to 26.1% in diseased plants compared to healthy while only 58% germination was observed for diseased seeds. Temperature range 30–35°C was found to be most favorable for symptom development and non-linear beta model study revealed central India and northern India are prone to severe and low leaf crinkle disease during kharif and summer season respectively. In present study, the rate of seed transmission was found upto 100%. To find out the association of earlier reported viruses viz.,CPMMV, SoYMMV and GBNV, a large number of symptomatic samples were tested using electron microscopy, ELISA and RT-PCR, but could not find a consistent association of any of these viruses even on severely symptomatic samples. Next generation sequencing using Illumina platform of small RNA and transcriptome of seed transmitted glasshouse samples followed by Sequence alignment with geneBank revealed that none of the reads were matching with any of the known plant viruses including the ones which were already reported (CPMMV, SoYMMV and GBNV). However, most of the reads were matching with viroids sequences in all symptomatic samples. The consensus sequences identified from reads matching viroids had extensive secondary structures, high G-C content and the conserved domain, which is signature evidence of association of viroids. Few of the reads were also aligning with viroids from healthy samples, but were insignificant. Thermal inactivation point was observed between 70°C and 75°C. The high thermal inactivation point due to extensive secondary structures and seed transmission are characteristic of viroids. Thus our findings strongly point to viroid etiology of the disease. In response to pathogenic infections, physiological changes are often observed in plants. In the present study, differential gene expression has been studied. Transcriptome analysis revealed that a total of 727 genes were found to be differentially expressed out of which 460 were up-regulated and 267 were down-regulated. Out of total up-regulated genes 74 genes were of unknown functions while 42 genes with unknown function among down-regulated genes. It is evident from our study that no virus association with ULCD, every possibility of association of viroid which needs further validation and characterization.

M.J.N. (DZ) 06: Comparative analysis of spermosphere and phyllosphere bacteriome of rice and their effect on foliar pathogens, *Magnaporthe oryzae* and *Xanthomonas oryzae* pv. *oryzae*

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Rice is aprimary staple food which feeds billions of people predominantly in Asia. With the current estimation of increase in human population, the yield has to be doubled or tripled to meet the growing demand. The major constraints to rice production are its biotic stresses such as blast disease caused by *Magnaporthe oryzae* and bacterial leaf blight caused by *Xanthomonas oryzae* pv. *oryzae*. Current method of disease management exploits host resistance and agrochemicals. While host resistance is short lived, the agrochemicals are not acceptable in international trade due to chemical residues on the product of commerce. In order to develop an alternative or supplementary ecofriendly option for disease management, bacterial flora naturally occurring on the phyllosphere and spermosphere of rice was explored. The phyllopshere and spermosphere bacteriome of basmati and non basmati rice cultivars, namely PB1 and VLD85 were analysed using metagenomic and traditional cultivation based methods. While the culturable bacteriome was analysed on nutrient agar and M9 media, the total bacteriome was estimated by sequencing ribosomal V3-V4 conserved region using Illumina HiSeq Platform. Bacteriome of adaxial and abaxial surface of phyllosphere as well as bacteriome of blast lesion were also studied. Bacterial species like *Pseudomonas fulva* and *Pantoea agglomerans* were found dominating in cultured bacteriome of both the surfaces and *Methylobacterium platani* were found in high numbers in native bacteriome of phyllosphere of two cultivars. On blast lesion, two species were exclusively found namely *Paenibacillus lautus* and *Pantoea septica*. *Pseudomonas oryzihabitans* and *Flavobacterium acidificum* were found dominant in cultured and native spermosphere of basmati cultivar whereas *Pantoea ananatis* and *Flavobacterium acidificum* were found in non basmati cultivar in high numbers. A total of 189 bacterial isolates were obtained from the two surfaces of the phyllosphere and spermosphere. BOX PCR based DNA fingerprinting of isolates revealed 104 distinct bacterial isolates among the collection that was glycerol preserved for long term storage. The isolates were further species identified by comparing 16S rDNA sequences with four public databases like NCBI, SILVA, RDP and EMBL. Among the 104 species, 36 different species of bacteria were evaluated for their potential to suppress two important foliar pathogens of rice, *Magnaporthe oryzae* and *Xanthomonas oryzae* pv.*oryzae.* Nineteen isolates were found highly antagonistic against blast fungus by showing up more than 50% inhibition, several isolates displayed antagonism against bacterial blight pathogen. *Pantoea dispersa*, *Pantoea agglomerans*, *Pseudomonas parafulva*, *Pantoea ananatis*, Acinetobacter *baumannii*, *Enterobacter cloacae*, *Pantoea vagans*, *Pantoea deleyi* were found effective against *Magnaporthe oryzae. Pseudomonas parafulva* BG1, *Chryseobacterium cucilis, Pantoea anthophila, Enterobacter cloacae, Pantoea ananatis, Pseudomonas psychrotolerans, Pseudomonas monteilii, Acinetobacter bayliyi*, *Pantoea vagans, Pseudomonas stutzeri* were found effective against *Xanthomonas oryzae* pv. *oryzae.*This study culminated in identification of potential bacterial communities for bacteriome transplantation on rice phyllosphere for mitigation of foliar diseases.

M.J.N. (SZ) 07: Epidemiology, variability and management of purple blotch of onion caused by *Alternaria porri* (Ellis) Cifferi

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Onion (*Allium cepa* L.) literally called to be queen of kitchen is an important commercial vegetable crop grown throughout the world for domestic as well as export purpose. The crop suffers from various biotic and abiotic stresses. Among the biotic factors hindering the production purple blotch caused by *Alternaria porri* (Ellis) Cifferi is a major threat causing huge crop loss under field conditions. Intensive roving survey conducted in ten major onion growing districts of Karnataka revealed that, the mean maximum severity in Gadag (55.91 %) followed by Chitradurga district (52.29 %) during *kharif* 2017-18 and 2018-19. Thirty different *Alternaria* isolates showed variability with respect to cultural, morphological and pathogenic traits. For the molecular confirmation full length ITS rDNA region was amplified using ITS1 and ITS 4 primers for the isolates of *Alternaria* spp. The DNA amplicon was observed at the region 580 bp. Based on rDNA sequence comparison, the isolates were confirmed as *A. porri* and *A. alternata* respectively. Out of 30 isolates only fast growing ten isolates were sequenced and were deposited in the Genbank for which the accession numbers were obtained. Variability of twenty four *A. porri* and six *A. alternata* isolates were studied by using ten Inter Specific Sequence repeats (ISSR) primers *viz*., ISSR-1 to 10. All the thirty isolates showed polymorphic and distinguishable banding pattern. Epidemiological studies revealed positive correlation of purple blotch with maximum temperature and rainfall. Real time and lead time equations computed at weekly intervals, showed the increase in the severity of the disease at third date of sowing in *kharif* during both the seasons. Study on estimation of rhizosphere colonization using organics as food base revealed that the treatment amended with farm yard manure had the highest number of colony forming units (cfu's) with a comparatively high vigour index of seedlings. The antagonist isolated during rhizosphere population estimation at 40 and 80 days after sowing were identified as *T. harzianum*, *B. subtilis* and *P. fluorescens* by various morphological and biochemical tests. In the study on *in vitro* efficacy showed bio agents, *T. viride* and *P. fluorescens* commercial botanicals perfekt,plant extracts *E. globules* and *A. sativum* and fungicides *viz*., mancozeb, difenconazole, hexaconazole and propiconazole (tebuconazole 50 % + trifloxystrobin 25 %), (hexaconazole 4 % + zineb 68 %), (fluopyram 17.7 % + tebuconazole 17.7 %) and (carboxin 37.5 % + thiram 37.5 %) to be significantly superior in inhibiting the mycelial growth of *A. porri.* Management trials during both the years revealed seed treatment with *T. harzianum* @ 10 g/kg, furrow application of enriched *T. harzianum* (*T. harzianum* 1 kg + vermicompost 100 kg) @ 250 kg/ha followed by spray of (tebuconazole 50 % + trifloxystrobin 25 %) @ 0.5 g/l was proved to be significantly superior in terms of reduction in the disease and increasing in the bulb yield.

M.J.N. (SZ) 08: Molecular characterization and management of viral diseases of capsicum (bell pepper) under protected cultivation in Dharwad, Karnataka

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Capsicum (*Capsicum annuum* L. var. *grossum* Sendt.) a member of family *Solanaceae*, is commonly known as sweet pepper, bell pepper and Shimla mirchi. Under protected cultivation, capsicum is widely grown due to higher productivity and economic feasibility. However, diseases of viral nature affect production significantly, both in terms of yield and quality. Survey conducted during *rabi* 2017 and 2018 in seven districts of Karnataka under protected cultivation revealed that highest mean incidence (27.92%) of leaf curl disease in Dharwad, mild mottle disease(27.61%) in Belagavi andmosaic disease (21.39%) in Chikkaballapur districts were recorded.Virus infected capsicum plants exhibit symptoms of curling, cupping, puckering, mosaic, reduced plant growth and bushy appearance, chlorotic rings on leaves and fruits. Leaf curl symptomatic capsicum plants were associated with begomovirus, *Chilli leaf curl virus* (ChiLCV) and *Tomato leaf curl virus* (ToLCV) were confirmed by PCR ~200 bp. Upon PCR amplification with CP genes of ChiLCV and ToLCV were amplified at ~500 bp and ~510 bp respectively. Sequencing results of ChiLCV and ToLCV isolates infecting capsicum in Dharwad were found to be (>98%) identical to the previously reported ChiLC-Papaya-New Delhi and ToLC-Karnataka viruses. This is the first report of ChiLCV and ToLCV isolates associated with leaf curl symptoms on capsicum in Karnataka.Mosaic and mottling symptoms were associated with *Cucumber mosaic virus* (CMV), *Pepper mild mottle virus* (PMMoV), *Tobacco mosaic virus* (TMV) and were confirmed through RT-PCR, which amplified the CP-gene of CMV ~381 bp, PMMoV ~730 bp and TMV ~481 bp respectively. Rings on leaves and fruits were associated with *Groundnut bud necrosis virus* (GBNV) amplified ~830 bp by PCR. Coat protein gene of CMV infecting capsicum matched (95-97%) with previously reported Chilli-Turkey (KY973676) and Banana-Sikkim (KT447515). While CP-gene of PMMoV shared (99%) homology with PMMoV-Bell pepper-Himachal Pradesh (KJ631123). This is the report of PMMoV on capsicum from Dharwad, Karnataka. The transgenic capsicum (var. DMC-14) was developed by *in planta* transformation methodusing *Agrobacterium tumefaciens*pHAB531 construct carrying ChiVMV-CP. Out of 16 T_0 transgenic plants only two plants were found to be positive for PCR and GUS activity. Out of 13 T_1 transgenic plants, only seven plants showed positive for PCR and GUS activity.Fourteen hybrids were screened against capsicum viral diseases, the results revealed that none of them were resistant. However, six hybrids were moderately susceptible to leaf curl disease. Hybrids Arka Gaurav and Arka Basanti, recorded moderately resistant reaction to mild mottle disease. While eight hybrids showed moderately susceptible reaction to mosaic disease.Results of integrated viral disease management revealed that lowest leaf curl disease (22.57%), mosaic and mottling (8.15%), least infestation of whiteflies (6.45%) and aphids (1.11%) recorded in treatment with spraying of NSKE (0.4%), spinosad (0.03%) + azoxystrobin (0.05%), nimbecidine (0.5%) + fipronil (0.1%), nimbecidine (0.5%) + propargite(0.1%), thiomethoxam (0.05%), diafenthiuron (0.025%) at 15 days interval of each spray recorded significantly higher yield of 4.77 t/500 m^2 with 3.72 benefit cost ratio, compared to control (2.50 t/500 m^2 with 1.60 benefit cost ratio).

M.J.N. (CZ) 09: Studies on storage rot of ginger in Assam and its management with botanicals

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Post-harvest deterioration is the most important cause of loss of ginger during storage due to rotting, resulting in considerable loss to farmers as well as traders. The investigation was carried out to study the pathogens associated with storage rot of ginger and management of the disease with botanicals. Survey under different agro-climatic zones of Assam revealed that altogether three fungi and one bacterium were associated with the disease. The microbes have been identified as *Fusarium redolens, Fusarium oxysporum, Pythium aphanidermatum* and *Ralstonia solanacearum* based on morphogenetic characterization. In the study of management of disease with botanicals, ten botanicals (*Acorus calamus, Allamanda cathertica, Allium cepa, Allium sativum, Curcuma longa, Datura wrightii, Lasia spinosa, Laurus nobilis, Ocimum sanctum* and *Piper betle*) were tested against the pathogens. Aqueous extracts (20%) of *Allium sativum, Allamanda cathertica* and *Laurus nobilis* significantly inhibited the growth of fungal pathogens whereas only *A. sativum* was inhibited the bacterial growth. These three most effective botanicals were further tested at four different concentrations (5, 10, 15 and 20 per cent) and exhibited highest inhibition of 92.22, 94.44 per cent and 11.6 mm against *F. oxysporum*, *P. aphanidermatum* and *R. solanacearum* respectively at 20 per cent concentration. The efficiency of botanicals (20%) was also evaluated *in vivo* and the lowest disease index of storage rot and weight loss of rhizome was recorded with *A. sativum* with 46.38 and 44.85 per cent respectively.

M.J.N. (CZ) 10: Characterization of *Papaya ring spot virus* pathotype P from mid-hills of Meghalaya

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Papaya (*Carica papaya* L.) is an important fruit crop grown widely in tropical and subtropical regions.In the world India ranks first in papaya production with 5988.8metric tons(Indian Horticulture Database-2017-18).Among the viruses infecting papaya, *Papaya ringspot virus* (PRSV) is the major constraint to papaya industry worldwide. The survey conducted in mid-hill Meghalaya during April to June, 2015.Presence of PRSV was confirmed through reverse transcription polymerase chain reaction (RT-PCR) using viral genome sequence specific primers for CP (>1kb) and HC-Pro (850 bp) gene. RT-PCR assay detected PRSV infection in 38 of 53 samples collected from surveyed locations with an average incidence of 71.7%.The representative PRSV-P (Umiam isolate) was maintained in healthy papaya seedlings by standard sap inoculation method and typical symptoms of PRSV infection expressed within 21–24 days of post inoculation. Studies on the physical properties of PRSV-P Umiam isolate revealed that dilution end point of the virus was 10^{-2}, longevity in vitro of the virus was 18 h at room temperature (25 ± 2°C) and thermal inactivation point of virus was in between 50°C-55°C.In host range studies, among the cucurbitaceous hosts, pumpkin (*Cucurbita pepo*) alone exhibited chlorotic lesions on leaves within 20–25 days' post inoculation indicating narrow host range of PRSV-P (Umiam). Molecular characterization of PRSV-P Umiam isolate revealed that Partial CP gene shared maximum nucleotide (~95%) and amino acid (~98%) identity with PRSV isolates reported from northern and eastern India. Whereas, the Partial HC-Pro gene of PRSV-P Umiam isolate shared maximum nucleotide identity with American isolate and maximum amino acid identity with PRSV-W isolate reported from India. During phylogenetic analysis based on partial CP, the PRSV-P (Umiam) from Meghalaya clustered with the same isolates from north and east India. Overall, the present study indicated that the PRSV isolate occurring in mid-hill Meghalaya might be introduced from plains of India.

M.J.N. (MEZ) 11: *In- vitro* and *In-vivo* evaluation of different bio-agents against *Fusarium oxysporum* f. sp. *lycopersici*

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Tomato (*Solanum lycopersicum* L.) ranks first amongst all the fruits and vegetables as a source of vitamins, minerals and phenolic antioxidants. Tomato production is constantly threatened by biotic constraints, mainly fungal diseases among which Fusarium wilt of tomato caused by *Fusarium oxysporum* f.sp. *lycopersici* causes serious economic loss. Application of fungicides is commonly used to effectively control the disease, although they are undesirable due to environmental consequences. In this connection, the use of bio-control agents serves as a suitable alternative to chemical approach. Hence, an investigation was carried out to test the effect of different bacterial and fungal bio-agents against *Fusarium oxysporum* f.sp. *lycopersici. Trichoderma harzianum*, *Bacillus subtilis* and *Pseudomonas fluorescens* were tested *in-vitro* for their antagonistic activity against *Fusarium oxysporum* f.sp*. lycopersici.* The antagonistic potentiality of *Trichoderma harzianum* was determined by dual culture technique that resulted in 25.4% inhibition of the growth of *F.oxysporum* f.sp. *lycopersici* in presence of bio-control agent (*T. harzianum*). Antagonistic activity of bacterial bio-control agents was determined through Well Diffusion Technique and results revealed maximum Zone of Inhibition (ZOI) with *Bacillus subtilis (*29.9 mm) followed by *Pseudomonas fluorescens* (25.6 mm).The effect of *T. harzianum, B.subtilis*, *Pseudomonas fluorescens* and systemic fungicides against *F.oxysporum* f.sp. *lycopersici* was tested in glasshouse and field conditions. The seedling treatment with a combination of 2% *T. harzianum* and 0.2% Carbendazim recorded better biometrics of tomato crop (root-shoot length, yield, vigour index), germination% (86.70% in glasshouse,77.73% under field conditions) and significantly reduced wilt incidence (13.33% in glasshouse, 22.27% under field conditions) as compared to single application of bio-agents or Carbendazim or of combinations of bacterial and fungal bio-agents.

M.J.N. (NZ) 12: Genetic association of MLB disease with field screening of maydis leaf blight resistance by using SSR markers

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In maize the major fungal foliar disease called maydis leaf blight (MLB) or southern corn leaf blight (SCLB) is a serious and widespread disease which causes substantial yield losses worldwide. The information on the aspects of the study of genetic nature of resistance of the diseases is scanty and aid of molecular markers may help in selection and adoption of breeding approaches suitable for improving yield, quality and disease resistance. Therefore, the present study has been planned with the objective to find the associated molecular markers with the resistant gene of maydis leaf blight and to determine the genetic nature of MLB disease. The experimental material comprised of six generations (P1, P2, F_1, F_2, BC_1 and BC_2) was carried out at CCS Haryana Agricultural University, Regional Research Station, Karnal, during 2013 to 2016 harvesting season to study the infection caused by maydis leaf blight on maize and detect the resistance parents and hybrids using artificial inoculation conditions using standard procedure of disease rating scale of 1-5. Eight inbred lines, out of which four inbred lines (HKI 209, HKI 1332, HKI 325-17AN and HKI 488-1RG) were susceptible and four inbred lines (HKI 1128, HKI 163, HKI 164D-4-(O) and HKI 193-2-2) were resistant to maydis leaf blight on the basis of disease reaction in the field were used to generate sixteen crosses *viz*., HKI 209 x HKI 1128, HKI 209 x HKI 163, HKI 209 x HKI 164D-4-(O) **,** HKI 209 x HKI 193-2-2**,** HKI 1332 x HKI 1128, HKI 1332 x HKI 163, HKI 1332 x HKI 164D-4-(O) , HKI 1332 x HKI 193-2-2 , HKI 325-17AN x HKI 1128 , HKI 325-17AN x HKI 163 **,** HKI 325-17AN x HKI 164D-4-(O), HKI 325-17AN x HKI 193-2-2**,** HKI 488-1RG x HKI 1128, HKI 488-1RG x HKI 163, HKI 488-1RG x HKI 164D-4-(O)**,** HKI 488-1RG x HKI 193-2 during Kharif 2013 to obtain 16 F_1s by using Line x Tester mating design. These F_1s were advanced by part of seeds from each of the six parental inbred lines and their resultant F_1 hybrids were planted in the field during *rabi* 2013-14 to produce F_2, BC_1 and BC_2 generations. F_2 generation of each cross was produced by selfing the F_1 plants while BC_1 and BC_2 generations were developed by back crossing each F_1 hybrid with its respective male and female parents. Futher after selfing and crossing the experimental material comprised of six generations (P1, P2, F_1, F_2, BC_1 and BC_2) of the sixteen crosses were evaluated both for disease severity in the field and molecular studies were undertaken to find out the genetic nature of MLB disease, as well as to find associated markers to resistant genes. Frequency distributions of disease severity of F_2 plants of the crosses in the field condition were found to be continous and thus indicated that inheritance of maydis leaf blight was governed by polygenes or by quantitative inheritance (Sharma et al., 2017). Molecular markers (SSR) were also used to screen the plants of six generations for resistance and susceptibility and to see the association of DNA marker with field studies. For this, fresh young leaves were collected and DNA of each parental line was isolated using CTAB procedure. PCR amplification conditions were optimized after qualitative and quantitative estimation of DNA. A total of 43 SSR primers were used to screen eight parental genotypes on the basis of their disease reaction for polymorphism and then analyzed F_2 and backcrosses of each of the sixteen crosses, with the polymorphic primers to detect segregation pattern and association of DNA markers for maydis leaf blight resistance. Out of 43, 37 primers showed amplification in all parents under study, however, 5 were monomorphic *viz.,* p-umc2253, p-umc1525, p-bnlg1732, p-bnlg2241and p-umc1159 and 32 were polymorphic. The six primers *viz.,* p-umc1500, p-umc1250, p-umc1622, p-umc1641, p-umc1184, p-bnlg2248 did not show amplification. All F_2 plants and 10 backcross plants were individually genotyped for these 32 SSR markers. The numbers of alleles confirm the wide genetic base of the maize varieties and the number of alleles at each locus ranged from 2 to 4. The overall size of PCR amplified products ranged from 105 bp (p-umc1380, p-bnlg1712, p-umc1020 and p-umc2158) to 230 (p-umc1086). The molecular size difference between the smallest and the largest allele at a SSR locus varied from 5 bp (p-bnlg1064) to 50 bp (p-bnlg1496). The polymorphic information content (PIC) value ranged from 0.36 (p-umc1812) to 0.84 (p-phi085). It has been observed that there was a strong association between field results for inheritance of maydis leaf blight and SSR marker studied due to high similarity between the two in all the crosses. The field results have shown that inheritance of maydis leaf blight is governed by more than two genes which were also confirmed by SSR marker analysis. The ratio obtained on the phenotypic and genotypic level was same i.e. which revealed that maydis leaf blight resistance is governed by quantitative inheritance or polygenes. However, the SSR markers which have been used for the study are validated for maydis leaf blight resistance but further needs to be validated whether or not these markers are responsible for maydis leaf blight resistance.

M.J.N. (NZ) 13: Antagonistic activity of endophytic bacteria against pathogenic fungi *Fusarium oxysporum* f. sp. *ciceris,* incitant of chickpea wilt

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Endophytic bacteria have been found virtually in every plant, where they colonize internal tissues of their host plant. The world's third most important annual legume crop, chickpea (*Cicer arietinum*) generally gets affected by fusarium wilt caused by *Fusarium oxysporum* f.sp. *ciceris.* In present study, attempts were made to retrieve the endophytic bacteria from roots of chickpea cultivars as potential biocontrol agent against incitant of chickpea wilt. Twenty bacterial isolates were retrieved and characterized on the basis of morphological and biochemical properties. All the endophytic bacterial isolates were evaluated for their*in vitro* activity against test fungus *Fusarium oxysporum* f. sp. *ciceris* and other biocontrol activities *viz.,* siderophore production and HCN production. Amongst the bacterial isolates retrieved, isolate CHE17 and CHE19 exhibited antagonistic activity against test fungus *Fusarium oxysporum* f. sp.*ciceris* and were siderophore producer also but only isolate CHE17 showed positive reaction for HCN production. Bacterial colonies of isolate CHE17 were whitish, circular, smooth and raised while that of isolate CHE19 were baby pink, smooth, flat and shiny. On the basis of biochemical character *viz.,* indole production, MR, VP, Citrate, motility, starch hydrolysis and gelatin utilization, two isolates *viz.,* CHE 17 and CHE 19 were similar to *Bacillus* sp. and *Serratia* sp respectively.

APS Travel Award Contest

APS (DZ) 01: Transcriptomic and metabolomic approaches to unravel the antagonistic mechanism of *Chaetomium globosum* against *Bipolaris sorokiniana*

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Nature has bestowed us with plenty of worthy microbes. Among these, *Chaetomium globosum* Kunze, has been recognized as internationally emerging biocontrol fungus. It has a great potential as a biological control agent which mycoparasitize a various plant pathogen and also produce antifungal metabolites suppressing the growth of pathogenic fungi. However, their biosynthetic pathway and molecular mechanism of biocontrol activity is not yet been elucidated. Here, we integrate metabolome and transcriptomic analyses of *C. globosum* strain Cg2 during interaction with phytopathogen *Bipolaris sorokiniana* to explore gene expression pattern and associated antifungal volatile and non-volatile metabolites. RNA-seq generated 40.07 Gbp for downstream analyses. In total, 265,377,816 clean reads were generated, and gene expression levels were calculated using FPKM (fragments per kilo base of exon model per million mapped reads). The data suggested that, a total of 14366 (log2FC and pval 0.01) differentially expressed genes (DEGs) that mainly participated in various biological functions such as biosynthesis of secondary metabolites, hydrolytic enzymes, putative fungistatic metabolites, carbohydrate and protein metabolism related and signaling genes. Among them 7145 were exclusively upregulated and 7221 were downregulated. Further, Gas chromatography–mass spectrometry (GC-MS) showed that C. globosum strain Cg2 produces variety of antifungal secondary metabolites such as 1-dodecene, 1-tetradecane, 1-ocatdene, hexadecane, trans-limonene oxide, n-tetracosanol-1,1-heptacosanol, tris (2,4-di-tert-butylphenyl) phosphate and phenol, 4-(2,2,3,3-Tetramethylbutyl)-, which may be involved in the antagonisms. This work indicates that the biocontrol agent has produced a number of compounds to inhibit the growth of pathogen. The current studies provide comprehensive gene expression and metabolite profile leading to better understanding of molecular mechanism of *Chaetomium globosum* against plant pathogens.

APS (DZ) 02: Unravelling the virome of Indian grapevines (*Vitis vinifera* L.) through comparison of mRNA and sRNA viromes

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Virome analyses using mRNA and sRNA poolsfor NGS have routinely been used for reliable detection of plant viruses and viroids. To compare the efficiency of both these nucleic acid pools in identification of viruses/ viroids and genome reconstruction, a comparative study was performed using the publically available mRNAome and sRNAome datasets of three Indian grapevine cultivars. Twenty three viruses and viroids were identified from two tissues (fruit peels and young leaves) of three cultivars among which 11 grapevine viruses and viroids were identified for the first time in India. mRNA based approach identified more acellular pathogens than sRNA based approach across cultivars except for three viruses and a viroid which were identified by the latter approach in one of the cultivars, irrespective of the assemblers and tissues (one or more) used. Further, the mRNAomeidentified and reconstructed nearly similar number of viruses/viroids which was on par with the whole transcriptome. Through *de novo* assembly of transcriptomes followed by mapping against reference genome, we reconstructed 19 complete/ near complete genomes of identified viruses and viroids. Detection of large number of viral variants in this study ascertained the quasispecies nature of viruses. Three recombination events detected in two viruses and phylogenetic analyses using reconstructed genomes suggested the possible introduction of viruses and viroids into India from several continents through the planting material. The whole genome sequences generated in this study can serve as a resource for reliable indexing of grapevine viruses in quarantine stations and certification programmes.

APS (CZ) 03: Studies on Cercospora leaf spot of greengram in relation to weather, host plant resistance and disease management

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Greengram, *Vigna radiata* (L.) Wilczek, is a short duration legume crop cultivated primarily for their dry seeds.It is affected by fungi, bacteria, viruses, nematodes and also abiotic stresses. Among the fungal diseases, Cercospora leaf spot is most common. Leaf spot disease of greengram incited by *Cercospora canescens*(Ellis and Martin) is an important disease in mungbean growing areas. Studies on Cercospora leaf spot of greengram were carried out during 2015-16. Disease progression with weather parameters, screening of greengram genotypes, morphological and biochemical analysis in resistant and susceptible greengram genotypes, Cercospora leaf spot relationship with other foliar diseases, influence of different solid media on mycelial growth and sporulation and management of the disease with fungicides were studied. *Cercosporacanescens* identity was confirmed by cultural features and measuring the conidial dimensions. Multiple regression analysis revealed that minimum temperature and evening relative humidity were significant and negatively correlated with disease index (PDI). Age of the crop was significant and positively correlated with disease index (PDI). Per cent disease incidence and Per cent disease index of Cercospora leaf spot showed neither positive nor negative significant correlation with powdery mildew and *MYMV* disease in both *kharif* and *rabi* seasons during 2015-16. All these three foliar diseases acted independently without any adverse affect on this. Out of 61 genotypes screened under field conditions during *kharif* and *rabi* 2015-16, Greengram genotypes KMP 44, GAYT 575, COGG 912, GAYT 586, BASANTI, KMP 39, KMP 24, MH 901, AKM 9910, SATYA, RMP-15-6 and RMP-15-7 showed resistant reaction. Stomatal frequency was more in susceptible genotypes (182.83 to 199.36 per mm^2) and lower in resistant genotypes (74.10 to 86.56 per mm^2). Total phenols (0.95 to 0.99 mg/100 mg) and total proteins (1.94 to 1.99 mg/100 mg) were high in Cercospora leaf spot disease resistant genotypes compared to susceptible genotypes. Whereas, total sugars (7.56 to 7.72 mg/100 mg) were high in Cercospora leaf spot disease susceptible genotypes compared to resistant genotypes. Among different solid media used for mycelial growth of *Cercospora canescens*, Potato dextrose agar (PDA) supported maximum mycelia growth but failed to support sporulation. Greengram leaf extract agar supported both mycelial growth and sporulation. Highest inhibition of radial growth of *C. canescens*over control was observed with 0.1% propiconazole (89.83%) followed by 0.15% hexaconazole + captan (87.06%). Complete inhibition of spore germination was observed with 0.1% propiconazole and 0.15% hexaconazole + captan followed by 0.05% trifloxystrobin + tebuconazole. Significantly lowest PDI was recorded with 0.1% propiconazole (17.24) followed by 0.15% hexaconazole + captan (21.10) with decrease in PDI over control of 71.13 and 65.40 respectively. Significantly highest yield (10.53 q ha^{-1}) and best benefit cost ratio (2.59) was recorded with propiconazole (0.1%) followed by hexaconazole + captan (0.15%) and trifloxystrobin + tebuconazole (0.05%) which were on a par as per yield concerned.

APS (CZ) 04: Studies on late leaf spot disease of groundnut (*Phaeoisariopsis Personata* Berk. and Curt.)

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Groundnut (*Arachis hypogaea* L.) is one of the world's major oil seed crop belongs to the family fabaceae. Foliar fungal diseases (early leaf spot, late leaf spot, rust, Alternaria leaf spot) are major yield limiting factors in groundnut production and productivity. Of the foliar fungal diseases, early leaf spot and late leaf spots together are popularly known as "Tikka" disease in India. Late leaf spot (LLS) caused by *Phaeoisariopsis personata* (Berk. and Curt.) was more destructive and occurs late, *i.e.,* during flowering time and, causes severe defoliation and reduces both haulm and pod yields. Present investigation entitled, "Studies on late leaf spot disease of groundnut (*Phaeoisariopsis personata* Berk. and Curt.)" includes study of morphological and biochemical parameters *in vitro* in selected genotypes in relation to late leaf spot of groundnut and influence of weather parameters on groundnut late leaf spot disease development, under different dates of sowings were studied and observations were carried out with prevailing weather conditions at Agricultural College Farm, Bapatla, Guntur. Six groundnut genotypes were selected and categorized into resistant (Kadiri Harithandra), moderately resistant (ALR-3, JCG-8, GPBD-4) and susceptible (Narayani and K-6). Morphological characters and biochemical parameters were estimated in selected groundnut genotypes. Morphological characters such as leaf area was highest in susceptible genotype Narayani (3362.50 mm^2), highest leaf thickness was observed in resistant genotype Kadiri Harithandra (271.55 µm), the highest trichome density was observed on abaxial surface of leaf compared to adaxial surface. On abaxial surface numbers of trichomes were significantly high in resistant genotype Kadiri Harithandra (170.59 per mm^2)

Technical Session

Session 1
Taxonomy of Plant Pathogens

Keynote Papers

KN (S 01) 01: Biodiversity, taxonomy of plant pathogens and disease diagnosis

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Agriculture has shown phenomenal growth after green revolution. In recent past due to biotechnological applications, development of disease resistant varieties, application of plant protection measures, IPM, and also farmers commitment, there has been food security. However, growing population in India requires around 40 to 50 per cent more food production. Around 32% crop losses have incurred due to plant pathogens. Identification, morphotaxonomy characterization and conservation of plant pathogens is an important aspect which has to be dealt on priority basis. The fungal taxonomies have dwindled in their number and not many are available to identify the plant pathogens. There is a need to train the youngsters in this area. Identification and diagnosis of plant pathogens in the process of early infection can help for the disease management. In recent times, molecular tools have been developed besides serological, biochemical, and other technologies. All these are aimed at proper identification of plant pathogen and disease identification in shortest time. Farmer is interested in rapid detection of the disease and its control. Therefore, this is the challenging area in the field of plant pathology.

KN (S 01) 02: The biology and evolution of rust fungi

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In terms of species numbers, the rust fungi (Pucciniales) are an incredibly successful lineage. Together, the more than 7000 described species form the largest known monophyletic group of plant pathogens. All are obligate parasites of vascular plants including agricultural, forest and ornamental crops resulting in billions of dollars of damage worldwide each year. An intriguing aspect of rust biology is that many species are heteroecious, i.e., require alternation between two unrelated hosts in order to complete their life cycle. Whether the character of heteroecism is ancestral or derived within the rusts has never been satisfactorily resolved. Most classical treatments of rust classification were based on the hypothesis that “primitive” hosts (e.g., ferns) harbored “primitive” rusts (e.g., *Uredinopsis*, *Hyalopsora*) that alternate on members of the Pinaceae. However, alternative hypotheses of rust evolution have proposed various short-cycled primarily tropical rusts as ancestral, with the defining characteristic of heteroecism thus being derived within the group. Molecular studies based on rDNA genes have since disproved the fern rust hypothesis, but the second hypothesis remains. This study analyzes loci from multiple genes and taxa selected from all known families to resolve the base of the rust fungi and infer ancestral characters including the origins of heteroecism for the order.

Invited Papers

I (S 01) 03: Cryptic speciation in fungal species complexes: Current insights

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The term ‘species complex’ is suggestive to cover groups of or-ganisms or lineages that are taxonomically closely related or even difficult to distinguish. However, no clear definition of the category ‘species complex’ exists so far and some clarity in the use of the term is urgently needed. Morphologically indistinguishable species that have been revealed by molecular phylogenetic methods, and ultimately only recognised by their DNA sequences, are referred to as cryptic species. The importance of cryptic species is that they may have significant differences in the severity of diseases they cause, host range and geographic distribution. It is these differences that are of concern to many biosecurity agencies of the country. There has been a rapid increase in the number of cryptic species of plant pathogenic and biocontrol fungi discovered in recent years with the widespread use of DNA sequence-based techniques. The best-known ‘species complexes’ in the kingdom Fungi are in the genera *Fusarium, Aspergillus and Trichoderma* where ‘species complexes’ were introduced as an alternative to the subgeneric ‘sections’ in which the older phenotypic sections did not match with phylogeny. The current species complexes in above fungi are monophyletic, together encompass all species known in the respective genera, and hence such species complexes can be viewed as taxonomic categories. However, in other cases viz. Colletotrichum and Beauveria ‘species complex’ just describes a selected group of entities that are difficult to distinguish from each other and classification of such groups is poorly resolved. Therefore, cryptic speciation of fungal species complexes of *Fusarium, Trichoderma, Colletotrichum* are being studied through multi locus sequence typing (MLST) at Indian Type Culture Collection, New Delhi which is oldest culture collection in India (WDCM, registration number 430). The combined data of morphological and and phylogenetic analysis suggested the occurrence of 5 cryptic species viz.,. *Trichoderma. afarasin, T. afroharzianum, T. atrobrunneum, T. inhamatum* and *T. rifaii* in *T.harzianum complex,* seven cryptic species viz., *Fusarium falciforme, F. petroliphilum, F. keratinoplasticum, F. metavorans, F.solani* f. sp. *pisi*, FSSC 5 and FSSC 21 in *F.solani* complex and 6 cryptic species viz., *C. siamense, C. fructicola, C. endophytica, C. asianim, C. aotearoa* and *C*. *kahawae* subsp. *ciggaro* in *C. gloeosporioides* species complex.

I (S 01) 04: Relevance of a new fungal family to accommodate important plant pathogenic genera *Diporthella* and *Kamalia* under Diaporthales

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A leaf spots inducing fungal taxon was isolated from natural symptoms collected from Himachal Pradesh, India. This isolate was studied in detail and found interesting based on morphological characters of asexual-morphs, cultural characteristics and phylogenetic analyses of the partial nuclear ribosomal 28S large subunit (LSU) and internal transcribed spacer (ITS) rDNA sequence data. Combined phylogenetic analysis using nuclear ribosomal DNA (ITS and 28S partial) nested the present isolate in a unique, distinct, and well-supported monophyletic clade in the phylogenetic tree. Our isolate formed a sister clade with the genus *Diaporthella.* A new genus, *Kamalia* was erected to accommodate this type species isolated from the living leaves of *Mallotus* *philipensis*. However, possibility to erect a new legitimate family to accommodate two genera of diaporthalean fungi, *Diaporthella* and the other one, newly established genus which is being referred to *Kamalia,* as presently both are placed in incertis sedis. It was found that the present isolate shows nearly 88% identity with the known isolates of Diaporthales on the basis of ITS gene region. The family is typified by *Diaporthella*. To evaluate the validity of each taxon and to clarify the phylogenetic relationships within this family, sequences from ITS-5.8S nrDNA (ITS) and LSU were also conducted. Monophyly of the family and that of each genus were strongly supported by analyses based on a combined dataset of the two regions (ITS+LSU). Results obtained would be discussed in detail during presentation.

Oral Papers

O (S 01) 05: Genus *Cercospora* in India

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Cercospora Fresen. is one of the most importance genera of plant pathogenic fungi in agriculture and is commonly associated with leaf spots. The genus is a destructive plant pathogen and a major agent of crop losses worldwide as it is nearly universally pathogenic, occurring on a wide range of hosts in almost all major families of dicotyledonous, most monocotyledonous families, some gymnosperms and ferns. The information regarding *Cercospora* leaf spots in India is scattered and mainly based on Vasudeva's compilation in Indian Cercosporae. Therefore, a study was conducted which provides an update that includes synonyms, morphological descriptions, illustrations, host range, geographical distribution and literature related to the *Cercospora* species present in India. This will benefit mycologists, plant pathologists and quarantine officials who need to study this group of fungi. The present study represents a compilation of 489 species of *Cercospora* associated with 603 of host plants collected from several states in India between 1894 and 2018 and deposited in Herbarium Cryptogamae Indiae Orientalis (HCIO), New Delhi. Fifty eight plant species were found infected with *C. apii* majorly belongs to the families of Asteraceae, Convolvulaceae, Euphorbiaceae, Fabaceae, Lamiaceae, Leguminosae, Polygonaceae, Solanaceae and Urticaceae. Partial nucleotide sequence data for ITS region was analysed for all species. Results from this study indicate that members of the genus *Cercospora* vary regarding host specificity, with some taxa having wide host ranges, and others being host-specific. Several collections could not be resolved to species level due to the lack of reference cultures and DNA data for morphologically similar species. Further collections from other countries are needed to resolve the taxonomy of some species complexes occurring on various plant hosts in India.

O (S 01) 06: Occurrence of Mycosphaerellaceae (Ascomycota) in medicinal plants of Madhya Pradesh

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The present paper is a continuation of a series of comprehensive taxonomic treatments of cercosporoid fungi (formerly *Cercospora s. lat.*), belonging to Mycosphaerellaceae (Ascomycota). The significance of vegetation as a chief source of therapeutic agents has unspecified greater importance during the recent years because of the extraordinary revitalization in use of plants for health care throughout the world. This has resulted in the large-scale exploitation of some medicinal plants as raw material for pharmaceuticals. Fungal invasion of medicinal plants causes two damages in many ways, first it reduces yield (roots, stem, leaves and seeds) of the plants and secondly reduces the quality of the product as fungal invasion releases toxins and break up the constituents of plants (Mukherji and Bhasin, 1986). During 2005-2015 periodical survey of different places of Madhya Pradesh (Balaghat, Satna, Mandla, Katni, Chitrakoot, Seoni, Narsinghpur, Bilaspur) and the neighborhood of Jabalpur were made within a radius of about 40 km. The correct identity of the medicinal plant is important to protect their medicinal value from the damage. Therefore, a study was undertaken to record new fungi for the country/state using flora of Madhya Pradesh. In the present research paper twenty-one Cercosporoid (Mycosphaerellaceae) were recorded in medicinal plants are enumerated for the state as new host records. *Passalora ajrekari* (Syd.) U.Braun (*Jatropha curcas* Linn. *Pseudocercospora blumeae* (Thumen) Deighton (*Blumea lacera* DC), *Cercospora asteracearum* (*Blumea lacera* DC.), *Cercospora apii s.lat* (*Diplocyclos palmatus* L. Jeffery), *Pseudocercospora cocculi* (Syd.) Deighton [*Cocculus hirsutus* (Linn.) Diels], *Passalora dioscoreae* (Ellis& G.Martin) U.Braun (*Dioscorea sp*.), *Cercospora apii s.lat*. (*Erythrina suberosa* Roxb.), *Cercospora apii s. lato* (*Oscimum officinalis* Linn.), *Acarocybella jasminicola* (Hansf.) M.B.Ellis (*Jasminum arborescens* Roxb.), *Cercospora lantanae-indicae* Munjal, Lall & Chona (*Lantana camara* Linn.), *Cercospora apii s.lat*.[*Abuliton indicum* (Linn.) Sweet], *Cercospora apii s.lat*. (*Mentha arvensis* Linn.), *Pseudocercospora nyctanthes* (Roy) U. Braun.(*Nyctanthes arbor-tritis* Linn.), *Cercospora apii s.lat*. [*Operculina turpethum* (Linn.) Silva Manso], *Pseudocercospora pogostomonis* (Singh & Kamal) U.Braun. (*Pogostemon plectranthoides* Desf.), *Cercospora ranjita* (S.Chowdhury) Deighton (*Gmelina arborea* Linn.), *Cercospora ricinella* Sacc.& Berl. (*Ricinus communis* Linn.), *Pseudocercospora subsessilis* (Syd. & P.Syd.) Deighton (*Azadirachta indica* A.Juss.), *Cercospora ternateae* Petch. (*Clitoria ternata* Linn.), *Cercosporella tinosporae* (Lacy & Thirum.) Deighton [*Tinospora cordifolia* (Willd.) Hook. f. Thoms], *Pseudocercospora vitis* (Lev.) Speg. (*Vitex negundo* Linn.), *Pseudocercospora withaniae* (Syd.& P.Syd.) Deighton (*Withania somnifera* Dunal.) and *Cercospora sp*. (*Abroma augusta* Linn.f, *Elephantopus scaber* Linn, *Hyoscyamus niger* Linn and *Paederia foetida* Linn.)

O (S 01) 07: Study of storage fungal association and their effect on seed quality of groundnut *Arachis hypogea* in Gorakhpur, UP and adjacent areas

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We are living in the time of extensive research programmes to improve various crops to support the rapidly growing human population with the result a number of high yielding varieties have been developed to feed the mankind. Groundnut is one of them. These high yielding crops should reach the farmers in good condition. Thus proper storage and distribution of seeds becomes more important. Groundnut is an oil yielding crop, therefore it is more vulnerable as it looses its viability very soon. Properly maintained good quality seeds are very important as they have comparatively long shelf life. Though, the initial seed quality and storage environment are important to prolong the shelf life of seeds, but fungal pathogens play a major role in deteriorating the seed quality. In this study effect of fungi on seeds during storage has been studied. According to study around 25% world crops are affected by fungi. In India 82% of ground nut is utilised for oil, whereas 12% is used as seed. This 12% portion should be properly taken care of as they transmit disease as they carry a number of pathogens which get associated either in the field or in the post-harvest conditions. It was observed that the most common mould in this area is *Aspergillus* which is the main cause of aflatoxin contamination. Some other fungi are *Alternaria* sp.,*Curvularia, Rhizopus, Macrophomina, Penicillium* and *Fusarium* etc. These fungi cause discolouration, rotting, sinking, necrosis and loss in germination.

O (S 01) 08: Investigations on etiology of streak and stunting disease of wheat in Central India

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During survey of wheat experimental fields at ICAR-IARI Regional Research Station, Indore (Madhya Pradesh), India, a total 151 genotypes of durum as well as bread wheat exhibiting symptoms of chlorosis with defined chlorotic streaks, mild to complete yellowing of leaves, stunting, bushy growth, yellowing of spikes and drying of infected clumps were recorded in the months of October to March every year from 2015 to 2018. The disease incidence was more in durum wheat genotypes (1.7 to 30%) as compared to bread wheat genotypes (1.3 to 11.22%). The possibility of association of any fungal, bacterial and viral pathogens was ruled out whereas, confirmation of phytoplasma associated through molecular biology assays was confirmed. Presence of phytoplasmas was confirmed in all the symptomatic samples from selected 31 durum and bread wheat genotypes using nested PCR assays using universal primer pairs (P1/P7 and R16F2n/R16R2n). BLAST analysis and phylogenetic relationship of 16S rDNA sequences of wheat streak and stunting phytoplasma strains confirmed association of 16Sr XI group in 11 and 16Sr XIV group in 20 wheat genotypes. *In silico* RFLP analysis through *i*PhyClassifier tool further grouped the wheat streak and stunting phytoplasma isolates into 16Sr XI-B and 16SrXIV-A subgroups. During the course of survey of wheat fields, phytoplasma strains belonging to rice yellow dwarf (16SrXI) subgroup B were confirmed in two weed species (*P. hysterophorus* and *C. gynandra*), however, four weed species (*C. dactylon*, *D. sanginalis, E. hirta* and *R. minima*) were identified as natural host of bermuda grass white leaf phytoplasma (16SrXIV-A). Thirteen planthopper and leafhopper species feeding on wheat plants were collected and identified from wheat fields out of which, *Sogatella furcifera*, *Exitianus indicus* and *Balclutha rubrostriata,* were found associated with phytoplasma strains of 16SrXIV-A subgroup and *Sogatella kolophon*, *Cofana unimaculata* and *Maiestas sp.* were found positive for phytoplasma strains belonging to 16SrXI-B subgroup. The identification of similar phytoplasma strains from wheat, weeds and hoppers (16SrXI and 16SrXIV group) showed 99% sequence identities among respective groups and strains of phytoplasma strains of 16SrXI and 16SrXIV group indicating the possibility of potential role of these hoppers and weeds species in secondary spread of wheat streak and stunting phytoplasma strains in nature.

O (S 01) 09: A new report of disease-complex caused by *Meloidogyne enterolobii* and *Fusarium oxysporum* f.sp. *psidii* on guava in district Ratlam of Madhya Pradesh, India

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Guava (*Psidium guajava* L.) is an important fruit crop in our country and known as poor men‘s apple which is highly prone to soil borne root invaders in early stages, recently identified in district Ratlam of Madhya Pradesh. Root knot nematode, *Meloidogyne enterolobii,* not only by itself but also causing havoc through predisposing the host for secondary attack by wilt fungus *Fusarium oxysporun* f.sp. *psidii* causing ‘disease-complex’ with synergistic effects on the common host guava(Cv VNR vihi). Severely infested guava plants showed small leaves, leaf browning, leaf drop, stunted growth whereas roots are distorted by multiple galling leading to sudden death of tree. During survey it was experienced with closer interaction of local growers that they have never seen such kind of root disease in their fields and this is for the first time when they are facing serious loss in productivity from 45% to 85% in Guava crop,CV. VNR vihi.Being a transplantable crop, farmers are purchasing saplings from VNR nurseries possibly infected thus harboring this soil borne pathogen or introducing to new uninfected area. The farmers' hidden enemies in soil associated with guava roots are capable of killing the host plants within two months after the onset of symptoms. These heavily infested orchards selected for further investigation particularly for safe and cost effective management through application of sustainable components.

O (S 01) 10: Phylogenetic analysis and species identification of *Bipolaris-Curvularia-Exserohilum* complex

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The species belonging to genera *Bipolaris*, *Curvularia* and *Exserohilum* are important seed-borne plant pathogenic fungi, which cause diseases mostly in Poaceae family. These genera have frequent nomenclatural changes, as morphology is not clearly distinct. We investigated the phylogenetic status of the seed borne fungi of these genera using ITS gene sequences. In this study, seven isolates of *Bipolaris*, 10 isolates of *Curvularia* and 4 isolates of *Exserohilum* were isolated from different hosts' species belonging to Gramineae, Solanaceae, Fabaceae and Brassicaceae during seed health testing of indigenously collected or multiplied and imported germplasm. The ITS region of the above isolates were amplified, sequenced and constructed phylogenetic tree using MEGA7 software. The phylogenetic trees formed two major clusters; one is having *Exserohilum* belong to one published species *E. rostratum* while other cluster having strains of *Bipolaris* and *Curvularia*. The strains of *Bipolaris* and *Curvularia* further grouped into separate sub-cluster. The strains of *Bipolaris*, in this study belong to three published species, including *B. maydis, B. sorokiniana* and *B. oryzae* while strains of *Curvularia* belong to five published species, including *C. hawaiiensis, C. spicifera, C. trifolii, C. lunata* and *C. verruculosa*. Our findings reveal that ITS gene sequencing can distinctly confirm identity of all the species of three genera.

O (S 01) 11: Characterization of aflatoxigenic *Aspergillus flavus* associated with aflatoxin B1 (AFB1) production of maize kernel in India

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Mycotoxin-producing fungi directly impact on the yield and quality of agricultural produce. *Aspergillus flavus* is one of the major producers of aflatoxin B1 (AFB1) mycotoxin in maize. Early detection and quantification of aflatoxin B1 producing *A. flavus* is indispensable to mitigate maize loss. With this aim, three different detection method (PCR, qPCR and HPLC) were deployed to screen highly toxigenic and atoxigenic isolates of *A. flavus*. Analysis of four isolates of *A. flavus* by PCR revealed possession of all the six toxigenic genes (*aflO, aflP, aflQ, aflM, aflS* and *aflD*) where as *aflO*, *aflP* and *aflQ* were most prevalent in all the isolates. In qPCR, seven isolates tested representing 5 different maize growing agroclimatic zones of India, expressed *nor-1* gene. In 2 isolates, higher mean expression levels was noticed. In HPLC, aflatoxin B1 (AFB1) production capacity of all the isolates was tested in culture media. About 65% of the *A. flavus* isolates produced aflatoxin

B1 (between 43.87 to 0.88 µg/g). This study exhibited that the highly toxic isolate observed from the sample collected from Hyderabad, where maize crop is growing year round, followed by nagaon's sample from Assam, Therefore these location will need extra care during post harvest condition to minimize the risk of aflatoxin in storage.

O (S 01) 12: Morpho-molecular characterization of *Diplodia* spp. associated with apple canker disease in India

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Apple (*Malus* × *domestica* Borkh) is one of the commercially grown fruit in temperate regions of India. In recent years, the incidence of apple cankers disease is increasing and assuming an epidemic in most of the apple growing parts of Kashmir. During 2017-18, canker disease incidence was observed in all the apple growing regions surveyed, with characteristic symptoms of canker disease. In order to characterize the pathogen and species associated with the disease, 40 infected diseased samples were collected during 2017-18 from different apple growing regions of J&K. The symptoms observed were sunken brown elliptical lesions having series of concentric rings, girdled the affected branch and large tree trunks. Out of 40 samples, 20 isolates representing north, centre and south Kashmir were maintained for morpho-molecular characterization. The cultural characteristics revealed that the colonies were fluffy, irregular margin having dark centre and reached 20-30 mm after 7 days on PDA at 25ºC. The pycnidia immersed in the culture medium, became partially erumpent, produced after 20-25 days. Conidiogenous cells were hyaline, smooth, cylindrical, somewhat swollen at base and measured about 9"17 × 2"5 µm, producing a single apical conidium. Conidia initially hyaline and later becomes pale brown, aseptate, few developing a central transverse median septum, smooth, thick walled, oblong to ovoid, apex and measured 20.0-28.0 x 9.0-14.5 µm. Based on morphological characters, the fungus was identified as genus *Diplodia*. To confirm the identity of genus and species at the molecular level, internal transcribed spacer region (ITS) and elongation factor (EF1) gene was amplified. Amplicon of 550 bp from ITS was amplified from all 20 isolates and sequence analysis showed maximum similarity (97-99%) with two species*, D. bulgarica* and *D. seriata*. To further validate the ITS results, elongation factor (EF1) gene with an amplicon size of 300 bp was amplified from both the isolates of *D. bulgarica* and *D. seriata*. The sequence result further confirmed the species identity and showed sequence similarity 97-98% with *D. bulgarica* and *D. seriata*. All the generated sequences were submitted to NCBI GenBank and accession numbers were recieved. The Phylogenetic analysis based on both the genes clustered the two species in two different clusters along with the isolates from other regions of world of same species. The pot experiment was conducted with three replication to confirm the pathogenicity on two-year-old potted plants of apple cv. Red Delicious. The symptoms of canker on stem of the inoculated plants were similar to those observed in the field after 30 days of inoculation. In conclusion two species were identified and to the best of our knowledge, among the two species *Diplodia bulgarica* is new report from India.

O (S 01) 13: Subgroup level identification of phytoplasma strain associated with sugarcane white leaf disease in Sri Lanka

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Sugarcane white leaf disease (SCWLD) is one of the major sugarcane diseases in the Asian continent caused by phytoplasmas. SCWLD occurred in all sugarcane growing areas in Sri Lanka and causing severe economic losses. But, so far no finer taxonomic classification of SCWLD phytoplasma strain in Sri Lanka has been attempted. Therefore, the objective of the present study was to identify the group and sub-group of the sugarcane white leaf phytoplasma (SCWLP) strain in Sri Lanka and also to identify whether weed grasses as alternative host of SCWLP responsible for natural transmission of the disease. DNA was extracted from fourty SCWLD infected sugarcane plants representing all major sugarcane growing varieties and areas of Sri Lanka and symptomatic weeds showing white leaf (*Urochloa distachya* and *Cynodon dactylon*) in sugarcane fields. PCR assays were performed using universal primer pair P1/P7 followed by nested primer R16F2n/R2. Amplicons of ~1.2 kb were consistently amplified from all the symptomatic samples of sugarcane plants and weeds in nested PCR assay. However, no amplification was observed with any of the asymptomatic sugarcane and weed samples. Pair wise sequence comparison and phylogenetic relationships of 16S rDNA sequences of sugarcane white leaf phytoplasma (SCWLP) strain revealed 99% sequence identity of SCWLP isolates with '*Candidatus* Phytoplasma oryzae'. However, the 16S rDNA sequences of the weeds (*U. distachya* and *C. dactylon*) phytoplasma isolates showed 99% sequence identity with '*Candidatus* Phytoplasma cynodontis' strains. Further virtual RFLP analysis with *i*Phyclassifier tool using 17 restriction enzymes allowed affiliation of the SCWLP strains with 16SrXI-B subgroup and in weeds phytoplasma strain with 16SrXIV-A subgroup with a similarity coefficient of 1.0. Based on the sequence comparisions results of the *16S rRNA* gene, SCWLP strains were identified as *Ca.* P. oryzae (16SrXI-B sub-group). However, the identified phytoplasma strain from weeds in the present study could not match with SCWLP phytoplasma strains, indicating that they were not real natural reservoir of SCWLP in Sri Lanka. Further studies on epidemiology of SCWLD along with identification of natural reservoirs is in progress.

O (S 01) 14: Distribution, identification of ambrosia beetle (*Euwallacea fornicatus*) and fungal associates causing decline or sudden death of Tree bean (*Parkia timoriana*) in the North-Eastern India

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Extensive mortality of tree bean (*Parkia timoriana*) trees has been observed in the Northeastern India since 2002. During 2019, an area-wide survey was conducted in all tree bean trees growing groves of North eastern regions, i.e. Manipur (77 sites), Mizoram (52 sites), Meghalaya (2 sites), Tripura (1 site) to determine the distribution and abundance of *E. fornicatus*, to identify different populations of bark beetles and their fungal associates, and to assess the extent of damage to tree bean trees. We show that the tree bean mortality is due to a vascular wilt disease caused by an undescribed *Fusarium* sp. that is a fungal symbiont of *Euwallacea fornicatus* (Coleoptera: Curculionidae: Scolytinae), a southeast Asia origin ambrosia beetle commonly known as tea shoot hole borer (TSHB). Trees affected by the disease exhibit gradual wilting or sudden death symptoms that include a black discoloration of the sapwood, excessive gummosis, emission trash, emission of rotten odour from infected wood. Visual inspections detected significant damage and decline incidence recorded in tune of 47.62 to 64.69% in in all tree beans growing regions. The most dominant ambrosia beetle, *E. fornicatus* were captured in 130 of the 132 sampled sites. A sample of 100 beetles from three different states (Manipur, Mizoram and Meghalaya) were identified as *E. fornicatus*, which is genetically distinct from the species causing damage in the region. Ten prominent fungal associates were also isolated and DNA based identification was performed: *Fusarium euwallaceae, F ambrosium, F. oxysporum, Lasidiodiplodia theobromae, L. pseudotheobromae, Clonostachys rosea f. rosea, Nectria pseudotrichia, Phialemononiopsis cornearis*, *Neofusicoccum parvum* and *Cylindrocladium* species. The *Fusarium* isolates were the most abundant and frequently found fungus species associated with adult ambrosia beetles and lesions surrounding the beetle galleries. More deep research is needed to determine the potential threat *E. fornicatus* and its fungal associate-*Fusarium*sppor other fungal symbiontspose to the tree bean trees in agroforestry system and natural ecosystems in the North eastern region.

O (S 01) 15: A new host record of *Passalora* on bottle gourd from India

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Fungi are ubiquitous in extreme habitats such as tropical to polar region,which are characterized by its own vast diversity .It has been divided into two broad division: the Myxomycota and Eumycota . The Eumycota includes five division viz: Mastigomycotina, Zygomycotina, Ascomycotina, Basidiomycotina and Deuteromycotina. The sub-division Deutromycotina is reprouducing only asexually, is a dustbin group which has been in state of flux from the beginning. This sub-disivison Deuteromycotina includes three distinct classes Blastomycetes, Hyphomycetes and Coelomycetes. The foliiclous hyphomycetes consist of *Cercospora* complex almost all the generic segregates have their root in monophyletic Mycosphaerella teleomorph, which is one of the largest genera of Ascomycetes. These seggreates of *Cercospora* complex fall into two groups: The Dematiaceous and Non Dematiaceous. The former group are represented by *Cercospora* and are collectively called *Cercosporoids* and the latter represented by *Ramularia*, are collectively called *Ramularoids*. The Cercosporoid fungi consist of no. of fungi .in which the *Passalora* is one of them. *Passalora* was the first genus introduced for cercosporoid hyphomycetes by Fries 1849 on the type species *Passalora bacilligera* (Mont. & Fr.) A new record of *Passalora* is described which is based on the presence of largest conidiophores and the differences in conidial size & shape. This record occurs on *Lagenaria siceraria* (Curcurbitaceae) from forest of Orchha of Bundelkhand region in M.P. (India).The description and illustration made with the help of pertinent literatures. Upon critical examination and comparision of morphotaxonomic features of those allied taxa a new record of the geneus Passalora was found. The holotype of specimen deposited in AMH ,Pune and isotype has been kept in Departmental Herbarirum for further reference.

Poster Papers

P (S 01) 01: Morpho-molecular characterization of *Colletotrichum* species isolated from different hosts in Himachal Pradesh

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The genus *Colletotrichum* constitute one of the important groups of fungal plant pathogens causing anthracnose/ fruit rot and/or die back in number of plant species. It causes economic damage to crops in tropical, subtropical, and temperate regions both at pre and post harvest seasons. In this study, an attempt was made to characterize different *Colletotrichum* species associated with crop plants of Himachal Pradesh using morpho-molecular traits. The disease samples showing anthracnose/necrotic symptoms collected from different areas were first microscopically observed for association of target pathogen species. The fungal cultures raised on PDA, purified by single spore isolation were multiplied on Mathur's media favoring maximum sporulation. The data recorded on various morpho-cultural characteristics of fungal isolates using standard identification keys revealed the association of *C. truncatum* with soybean, *C. orbiculare* with cucumber, *C. nymphaeae* with guava, *C. coccodes, C. capsici* with chilli, *C. gloeosporioides* with chilli and banana and *C. lindemuthianum* with common beans. Conidial shape and size revealed significant differences within and between the species. rDNA analysis of the different *Colletotrichum* species observed in this study showed maximum homology with the sequences of referral isolates of respective species. Two isolates, Cs-1 and Cs-2 from soybean exhibited maximum homology with *C. truncatum*, whereas banana isolate (Cba-1) resembled with *C. gloeosporioides.* Two isolates Cch-1 and Cch-2 from chilli resembled with referral sequences of *C. coccodes* and *C. capsici*, respectively. The study indicated that wide prevalence of *Colletotrichum* species on different cultivated crops in the state.

P (S 01) 02: Studies on variability and yield evaluation of paddy straw mushroom collected from different areas of Chhattisgarh

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A detailed study of available native isolates of this mushroom from different locations was done to identify an isolate with high biological efficiency. A survey was conducted to explore the native isolates of *Volvariella* sp. 20 isolates were collected isolated and purified on PDA from 7 (seven) districts (Dhamtari, Balodabazar, Raipur, Balrampur, Bemetara, Raigarh, Bilaspur and Janjgir-champa) of Chhattisgarh. The habitat, substrate, minimum and maximum temperature, GPS data of the isolate collected were recorded and compared. Adetailed study was done to characterize the isolates both morphologically and microscopically. The fruiting body size of the isolates varied in diameter from 8 cm (VV- 13) to 18 cm (VV-08). The cultural studies of different isolates were done on PDA media.The mycelia growth of VV-22 was found to be fluffy and thick whereas it was sparse and thin in VV-13. A detailed study of VV-08,Dhamtari(20^{0}51’24"N 81^{0}38’45"E) was done. The mycelia growth of VV-08 was fluffy and thick with 60 mm maximum radial growth observed after 5 days.The period required for spawn run and pinhead initiation was significantly less (11 days and 5 days respectively).The Biological efficiency of VV-08 was recorded 22.10% under open cultivation under mango orchards.

P (S 01) 03: New record of *Diplodia* sp. on *Aglaonema commutatum* and its *in vitro* efficacy with fungicides and bioagents

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Aglaonema commutatum commonly called as Chinese evergreen is an economically important foliage ornamental plant. Recently, the plants were found severely infected with a leaf blight disease and was found wide spread in newly developing suckers. Symptoms on the leaves appeared as water soaked lesion with light brown necrotic area bordered by a dark brown wavy margin. Pathogen was isolated on potato dextrose agar medium (PDA) and pathogenicity was established under laboratory conditions on live plant. Black, erumpent, dot like pycnidia, 80.8 – 200.8 ì wide appeared on the necrotic area of the infected leaf. Morphological characters revealed that conidia was initially ovoid to ellipsoid, hyaline, single celled, 16.1–28.4 x 12.2–16.5 ì and on maturation, turned two celled, dark brown with size 22.2 – 28.2 x 12.6 – 17.3 ì. Based on morphology and cultural characteristics, the pathogen was confirmed as *Diplodia*. Efficacy of different fungicides at different concentration and bioagents against *Diplodia* was assessed under *in vitro* conditions. A total of six fungicides (azoxystrobin 0.1%, carbendazim 0.1%, copper hydroxide 0.2%, mancozeb 0.25%, cymoxanil (8%) + mancozeb (64%) at 0.25% and hexaconazole 0.2%) and two bioagents (*Trichoderma asperellum* and *Pseudomonas fluorescens*) were tested. Results showed that carbendazim 0.1% and cymoxanil (8 %) + mancozeb (64%) at 0.25% were found to be the most effective with a percent inhibition of 90.77 and 90 per cent respectively. However, among the bioagents, only *Trichoderma asperellum* could inhibit the growth of the pathogen by 72.2 per cent.

P (S 01) 04: Standardization of media of *Trichoderma asperellum* for commercialization of biocapsules with and without adjuvants

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Present day agriculture encourages the use of biocontrol agents as an alternative to chemical fungicides because of its safety to humans, environment and nonpathogenic organisms. *Trichoderma* sp., a very effective biocontrol agent meant for plant disease management is known to promote plant growth and induce biotic and abiotic stress tolerance in plants. The ability of *Trichoderma* to sense, invade and destroy other fungi has been the major trait behind their commercial success as biopesticides. Commercialization of biopesticide products is primarily hindered due to poor shelf life. This limitation can be addressed by improving the shelf life of the organism through standardization of media of *Trichoderma asperellum* with adjuvants. Hence, a study was conducted to check the effectiveness of adjuvants on population of *Trichoderma* in different media. The culture was grown in potato dextrose (PD) broth and Trichoderma selective medium (TSM), with and without adjuvants. Both media were supplemented each with a sugar source (mannitol 3% and trehalose 15mM), wetting agent (PVP 2% and PEG 0.25%), adhesive (glycerol 3%, CMC 1% and liquid paraffin 1%) and surfactant (tween-80 0.5%). Twelve different combinations of these additives were used in both media and thereby standardized for maximum conidial production. The population of bioagent was studied at monthly intervals. Results showed that trehalose in combination with polyethylene glycol (PEG), glycerol, tween 80

and polyvinylpyrrolidone (PVP), glycerol, tween 80 in potato dextrose broth were the best, where the population of the bioagent was observed as 19 × 1016 and 10.66 × 1016 respectively at 60 days after inoculation (DAI). Also it was observed that all the treatments in potato dextrose broth showed higher population of the bioagent when compared with the treatments in TSM. From the study it is clear that both media along with additives could enhance the shelf life of *Trichoderma asperellum*.

P (S 01) 05: Pitting disease caused by *Pyricularia angulata*- an emerging threat to banana cultivation in Kerala

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A severe outbreak of a fruit disease of banana was noticed by the end of South-West monsoon during August-September 2019 in Ernakulam and Thrissur districts of Kerala. The fruits of banana varieties like Nendran and Robusta showed severe symptoms of numerous depressed brown coloured spots on all the fruits of bunches which were nearing maturity. These lesions on the fruits were initially brown pinhead sized spots of 0.1-0.2 mm diameter expanded to sunken, black, 0.5-0.7 mm diameter lesions surrounded by purple halo. Apart from fruit infection, spots also appeared on peduncle, petioles, pseudo-stem and leaves. The symptoms on the leaves started as small water-soaked lesions, later turned to tan brown to black, 0.5-2 cm diameter spots, often surrounded by an yellow halo, followed by chlorosis and necrosis of leaf lamina. The pathogen was isolated on Potato Dextrose Agar medium and the morphological along with cultural characters of the fungus were studied. The fungal colony appeared off-white initially, later turning to gray and took 15-20 days for complete growth on a 9 cm diameter Petriplate. The growth appeared greyish brown on the undersurface of the plate. The conidia of the fungus were hyaline to light brown, obclavate, two septate with a small truncate hilum at the base and measured 18.2-25.5 µm in length and 5.4-7.7 µm in breadth. Based on the cultural and morphological characters, the fungus was tentatively identified as *Pyricularia* sp. The pathogenicity was then proved by inoculating the pure culture of the fungus on mature fruits of banana var. Nendran as well as on the leaves of tissue culture derived seedlings. The identity of the pathogen was further confirmed at species level through molecular characterization of the ITS r-DNA region of the fungal genome. Total DNA of the fungus was isolated, followed by PCR amplification using universal primers of ITS (ITS-1F and ITS- 4R) specific to ITS region. The sequencing and *in-silico* analysis was carried out. The homology search of the sequence in NCBI database using BLASTn analysis showed 99 per cent homology with *Pyricularia angulata*. This confirmed the etiology of pitting disease affecting banana cultivation in the state of Kerala as *Pyricularia angulata.*

P (S 01) 06: First report of *Fusarium equiseti* causing crown and root rot of cucumber in India

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Cucumber (*Cucumis sativus*) is one of the most important crop belonging to the family cucurbitaceae. During survey of cucumber growing areas of Solan district of Himachal Pradesh, the crop was found infected with a root and crown rot fungus showing yellowing and wilting of leaves. Specimens of infected plants were brought to the laboratory and isolations were made from root, crown and stem portion using standard procedure on PDA and kept at 25^{0}C for 7 days. White, aerial and floccose growth of colonies appeared after 2-3 days which later on turned to yellowish to buff brown in colour after 7 days. Macroconidia, 3-7 septate with tapered and elongated apical cell and prominent foot shaped cell were observed after 6 days in culture, measuring 20.5 to 50.5 x 3.4 x 6.0 µm in size. Chlamydospores were thick, intercalary, abundant in chains or clumps, ellipsoidal or globose measuring 5.6x 8.4 µm in diameter. On the basis of morphological characters, fungus was identified as *Fusarium equiseti* (Corda) Sacc. and its identity got confirmed from ITCC, New Delhi. For DNA-based molecular identification of the fungal isolate, total genomic DNA of the fungus was isolated and PCR amplification of the ITS region of 5.8S ribosomal DNA was performed with primer combinations ITS1 and ITS4. The BLAST result showed maximum 98.8% nucleotide sequence identity with the ITS sequence of *Fusarium equiseti* (MK713371). Therefore, on the basis of morphological and molecular characterization, fungus was identified as *Fusarium equiseti* (Corda) Sacc. To confirm pathogenicity of the isolated fungus, 21 days old seedlings of cucumber var. KH-1 was inoculated with 50 ml of conidial suspension (1 x10^7 conidia/ml). Symptoms of yellowing of leaves were observed 14 days after inoculation followed by necrosis and wilting. The seedlings died after 20 days of inoculation, from which *F. equiseti* was re- isolated thereby, confirming Koch's postulates. To the best of our knowledge, this is the first report of *F. equiseti* causing crown and root rot on cucumber in India.

P (S 01) 07: Isolation and identification of thermophilic fungi in *Agaricus bisporus* mushroom compost

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Thermophilic fungi are small assemblage in Eukaryota that have a unique mechanism of growing at elevated tempreture extending upto 60 to 62°C.Thermophilic and thermotolarent fungi were isloted from *Agaricus bisporus* compost prepared by long term method of composting at various depth ranges upto 10 – 45 cm for compost sample collection.For isolation two techniques were used-Dilution plate technique and Waksman's direct Inoculation Method. Procedure involved four different medias such as Emerson's modified Yeast Starch Agar (YpSs), Czapek Dox Agar (CZA),Yeast Glucose Agar (YGA) , Potato Dextrose Agar (PDA) and incubated in 42°C and 28°C in moist chambers. Isolated fungus were confirmed by microscopic examination of the culture at 10x, 40x and 100x magnification using light microscope. Fungi were identified on the basis of their colonial and morphological characteristics. Seven species of thermophilic fungi were isolated viz., *Absidia corymbifera,Chaetomium senegalensis, Myceliophthora fergusii, Humicola fuscoatra, Humicola insolens,Thermomyces lanuginosis,Scytalidium thermophilum.*Thermotolerant fungi were also being isolated viz., *Aspergillus niger, A. glaucus, A. terreus, A. flavus, A. fumigates, A. nidulans, A. granulosus.* Thermophilic fungi representative isolates were purified in YpSs media which were successfully sub-cultured at 42°C to 50°C . The culture were stored at 4°C for further works.

P (S 01) 08: First report of *Curvularia lunata* causing flower and fruit rot of dragon fruit in India

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Dragon fruit Hylocereus *undatus* (Haworth) Britton & Rose, is a promising and remunerative intercrop in coconut gardens in Kerala because of the optimum weather factors and soil condition available under Kerala condition. A flower and fruit rot disease observed in white-fleshed dragon fruit from ICAR-CPCRI, Kasargod, Kerala was studied to identify the causative agent. The symptoms included water-soaked, olive to black powdery spots to coalescing soft rot in the later stages in both flowers and fruits. The diseased fruits were then isolated for the fungal pathogen. The pathogen of this disease was identified as *Curvularia lunata* and its pathogenicity was confirmed by satisfying Koch's postulates. To confirm this, the molecular identification and phylogenetic analysis using two gene sequences, internal transcribed spacer (ITS) amplified with ITS1 and ITS4 primers and beta-tubulin gene primers were thus employed and the fungal pathogen of rot disease on the dragon fruits was confirmed as *C. lunata*. To our knowledge, this is the first report of *C. lunata* causing flower and fruit rot in dragon fruit from India.

P (S 01) 09: Pathological and molecular approaches for the identification and nomenclature of *Albugo candida* pathotypes of Indian origin

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White rust disease of rapeseed-mustard is caused by the fungus *Albugo candida.* The obligate and highly variable nature of the pathogen pose a challenge in the proper identification of *A. candida* pathotypes/races. In India, a comprehensive study on the identification of *A. candida* pathotypes/races is lacking. Therefore, in this study characterization and identification of 33 *A. candida* isolates of Indian origin has been done on the basis of molecular and host differential studies. Molecular characterization using ITS and COX2 gene yielded 1250bp and 650bp bands while, maximum parsimony tree showed 15 and 13 clusters from 33 *A. candida* isolates respectively. On the basis of pathogenicity reactions on 19 host differentials on *B. juncea* cultivar (out of 7) and on different *Brassica* spp. 03 major groups have been identified as Group Ia was pathotype of *B. juncea,* Group Ib was pathotype of *B. juncea* cv. Cutlass, Group Ic was pathotype of *B. juncea* cv. Donskaja, Group Id was different *B. juncea* pathotype that showed disease reaction on *B. oleracea*, Group Ie was *B. juncea* pathotype that showed disease reaction on *B. carinata* cv. Kiran. Group II was pathotype of *B. rapa* var. Toria, Group III was pathotype of *B. rapa*. Finally, from 33 *A. candida* isolates a total of 21 pathotypes have been identified on the basis of combined grouping of pathogenicity reactions on host differentials and ITS and COX2 gene sequence analysis. A new nomenclature has been given as per the International standard, in which 15 pathotypes were designated as AC2-1 to AC2-15 which showed more virulence to *B. juncea*, similarly, 06 pathotypes were named as AC7-1 to AC7-6 which showed virulence to *B. rapa*. This pathotype identification of *A. candida* could be utilized for the selection and deployment of resistant cultivars in major mustard growing areas.

P (S 01) 10: Pestalotiopsis twig blight of Thuja: Alarm bell for ornamental landscape gardens

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Thuja orientalis Linn. (Family- Cupressaceae) is an evergreen shrub/tree growing to a height of 10 -60 feet. The plant is monoecious in nature with flat scale like leaves and resin glands containing essential oils. Thuja leaves are well known for their antimicrobial and medicinal properties. Apart from its medicinal value Thuja spp. is an inevitable component in landscape gardens throughout world. The improved awareness in landscaping has intensified planting of Thuja as important ornamental foliage in home as well as public gardens. Recently there were increased reports on severe incidence of leaf blight of Thuja spp. in Kerala. The infected plants showed twig blight, which initiated from the leaf tips as light yellow to brown discolouration. Further advancement of infection resulted in blighting and death of entire twigs. Blighted twigs were dotted with pin head sized black fungal fruiting bodies. On isolation, the pathogen in potato dextrose agar medium yielded whitish mycelium with crenate edges and denser on older parts of the colony. The colony showed clear diurnal zonation of mycelium and black acervuli at the centre. The pathogen was tentatively identified as *Pestalotiopsis* spp. based on colony morphology and conidial characters. Pathogenicity was established by detached leaf method. Conidia were fusiform, straight or slightly curved and five celled, hardly constricted at septa. Middle three cells were coloured with thick walls. The apical and basal cells were cylindrical to obtuse, thin walled and colourless. Two to three apical appendages were present and the base appendage of the conidia was hyaline, straight with a prominent beak. Conidia measured 23.53 – 27.55 x 5.55- 7.08 µm.

P (S 01) 11: New report on detection of Phytoplasma in crown chocking disease of arecanut in India

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Areca nut (*Areca catechu*) is an important commercial crop cultivated in many countries across the world. In recent years, crown chocking (Hidimundige) has become a severe problem in major Arecanut growing areas of Karnataka especially in plain regions. Once it appears it not only reduces the growth and productivity of the palm, but it also kills the plant with in one or two years from the appearance of first symptom. Initially infected plants produce dark green color leaves and as the disease progresses the leaves get shortened due to hypoplasia and hypotrophy of the cells resulting in bunchy appearance of the crown. Leaflets of the affected leave fail to unfold properly showing fan-like appearance and such leaves become crinkled and brittle. Apart from this, reduced inter nodal length and tapering of stem at the apex, with complete arrest of production of new leaves leading to appearance of barren stem with a pointed tip. Affected palms become unproductive and even if they produce bunches are small and malformed. Infected plant roots are blackened and poorly developed; such roots were short and brittle in nature and failed to produce the feeder roots. To find out the etiology of this disease, effort was made to prove the association of various biotic agents such as fungi, bacteria, nematode etc.,by researcher. But their effort became futile.The symptoms appeared on infected plant leaves resembles phytoplasma symptoms found in other phytoplasma infected plants. Apart from symptomatology, diagnosis of its association was also detected though molecular methods. DNA was isolated from collected leaf samples and subjected to PCR amplification with 16S rDNA of the Phytoplasma by nested PCR with P1/P7 and R16F2n/R16R21 primers. Approximately 1,800 bp and 1,200 bp size products were amplified in first round

PCR and nested-PCR respectively. The identity was confirmed by sequencing the PCR product and obtained sequence is analyzed by NCBI program similarity index and confirmed it is a phytoplasma . The current study proved the association of Phytoplasma with crown choking disease in areca nut. To our knowledge, this seems to be first report of the association of Phytoplasma with the areca nut crown choking disease in India.

P (S 01) 12: Emerging diseases of arecanut in Karnataka

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Arecanut (*Areca catechu*) is an important commercial crop cultivated in many countries in the world. Successful cultivation of arecanut is becoming very difficult as crop suffers from various biotic and abiotic stresses resulting huge loss to the growers. Some of the important biotic stresses includes, Koleroga / Mahali / Fruit rot disease caused by *Phytophthora meadii*, Basal stem rot / Anaberoga- *Ganoderma lucidum*, Inflorescence die back / button shedding - *Colletotrichum gloeosporioides* and Lethal yellowing- Phytoplasma. In recent years, there have been significant Changes with respect to occurrence of diseases in different parts of Karnataka. Mostly due to severe drought appeared between 2014-15 to 2018-19 and heavy rain fall in the year 2019 -20. These uncertainties influencing the emergence of new diseases in severe form as well as their spread to new areas. In the advent of climate change new diseases have emerged and created panic among the arecanut growers and to the areca industry too. One such disease is Leaf stripe or rot - *Xanthomonas campestris* pv. *arecae* that attacks during seedling stage of the plant with the age group between 1-6 years resulting poor crop stand as well as death of plants. This disease is more severe in maidan and semi malnad regions of karnataka *viz*., Davanagere, Shivamogga and Chikkamagaluru districts with a mean maximum incidence of 27.91 per cent in Davanagere district, followed by Shivamogga with 24.99 per cent. Management practices using bactericidal revealed, highest per cent disease reduction in Kasugamycin (0.3%) treated plots with 81.74 which was closely followed by Copper oxy chloride + Streptocycline treated plots (80.95 %). Apart from this, in recent years Crown chocking (Hidimundige) problem also becoming very severe in plain regions of Karnataka. Wherein it not only reduces the growth and productivity of the palm but, it also kills the plant within one or two years from the appearance of first symptom. The first symptom appear as reduced intermodal length followed by severe reduction in the size of leaves, such leaves appears dark green in color compare to normal green of healthy leaves. As the problem continues the crown attains a rosette shape. The leaflet's become brittle with distorted margins and fall down in quick succession. The reduced inter nodal length (1 to 2cm) and tapering of stem at the apex is also very common in affected plants. The affected palms remain mostly unproductive and continue to live for few years. The bunches and nuts if at all produced are small and malformed. Roots turn black and poorly developed; such roots were short and brittle in nature and fail to produce the feeder roots. And now recently during this *kharif* season, because of heavy rain fall Koleroga / Mahali / Fruit rot disease caused by *Phytophthora meadii* which was not reported from plains regions of Karnataka appeared to be serious threat to arecanut farmers in getting expected yield leading to heavy loss. So effort is needed to evolve new management strategies in combating the problem and to address the impacts of climate change on arecanut diseases to mitigate the threats to future production.

P (S 01) 13: Morpho-molecular identification of guava wilt pathogens and their management through biocontrol agent *Aspergillus niger*

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Guava is an important fruit crop, widely grown under subtropical and tropical climate but mainly wilt disease is a major one because it results in complete mortality of the infected plants. It is a soil borne, complex disease associated with many pathogens predominantly caused by *Fusarium oxysporum* f. sp. *psidii*. Therefore, a survey was conducted to collect the wilt infected guava plants. Fifty diseased plant of severely affected field were collected from eight states of India. Thirty five Isolates were examined based on morphological observation and PCR amplification was done to confirm using *Fusarium* specific translation elongation factor 1 (*tef-1*) primers. The amplified products of 650 bp were sequenced for thirty two isolates out of thirty five morphologically identified isolates. The sequences was subjected NCBI Blast and confirmed the four species of *Fusarium viz*, *F. oxysporum* f.sp. *psidii, F. solani, F. verticillioides* and *F. chlamydosporum.* Pathogenicity was confirmed by inoculating *F. oxysporum* f.sp. *psidii* and *F. solani* individually to the six month old air layered plant (var. Allahabad safeda) through stem hole technique and soil incorporation method. Management of guava wilt is not successful because of its complex etiology. Chemicals found ineffective under field condition so an alternative, eco-friendly and effective management strategy is required to manage the disease. Therefore *Aspergillus niger* were selected as a biocontrol to test against guava wilt pathogen, *F. oxysporum* f.sp. *psidii* in the present study. Eleven isolates of *A. niger* were collected from the Indian type culture collection (ITCC), ICAR- IARI, New Delhi. Isolates were evaluated under both *in-vitro* and *in-vivo.* Dual culture, Volatile and Non-volatile methods were performed under *in-vitro* study, isolates AN-1, AN-2, AN-3, AN-5, AN-6, AN-7 and AN-11 were found effective in controlling the pathogen*. In-vivo* studies were conducted in pot containing 6 month old air layered plant (var. Allahabad safeda) under pre and post inoculation trials. Overall AN-2, AN-3, AN-4, AN-6 and AN-11 were found potential bio-control agents against guava wilt pathogen *F. oxysporum* f.sp. *psidii.* These isolates need to be evaluated in the form of formulation in larger area for the eco-friendly management of guava wilt.

P (S 01) 14: Addition to new records of *Cladosporium* from India

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The genus *Cladosporium* was established by Link (1815) to accommodate a hyphomycetous fungus genus producing single to branched conidiophores and hyaline, branched conidia. This genus *Cladosporium* is cosmopolitan found usually as saprobe, colonizing a variety of organic substrates of plant origin as well as weak parasites. A number of species are economically important as these cause blasoom, blights, head and leaf moulds, damage to the inflorescences, fruits and vegetable rots, shot holes, leaf spots, as well as important pathogens of stored grains. This fungus infect the plant leaves and degrade photosynthetic yield on one hand and biproductivity on the other hand. This communication devoted to description and illustration of new records that foliar fungi *viz*. *Cladosporium atriella* on *Azadirechta indica* Adr. (Meliaceae), *C. fulvum* on *Solanum melangenum*. L. (Solanceae) and *C. colocasiae* on *C. colocasia antiquerum* L. (Araceae) respectively. New records have been described on the basis of morphological features.The holotype deposited in HCIO, New Delhi and corresponding isotype in Mycological herbarium of the college for the further reference.

P (S 01) 15: A new sett rot disease of sugarcane caused by *Sclerotium rolfsii* Sacc.

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Sugarcane (*Saccharum officinarum* L.) is important case crop. Sugarcane is grown in16m ha in 79 countries of world. India stand first in area 3.93mha and production 167mt. In Gujarat during 2017-19 sugarcane area under 182000 ha cultivation. In South Gujarat is major sugarcane area due to fertile land and irrigation facility. This crop is suffering many fungal diseases. *Sclerotium rolfsii* Sacc. is an important soil borne disease. During survey of sugarcane diseases in South Gujarat, Bardoli Baben sugar factory growing single eye bud in nursery. Due to continuous rain and high humidity soil borne *Sclerotium rolfsii* severally infected to sugarcane setts, hence severe mortality of sugarcane single eye bud was reported. Infected plant was initially yellowing and then after wilting due to *Sclerotium rolfsii.* Planting of Co-11015 variety at Badoli sugar factory nursery during *Kharif* 2019. Looking to observation of sugarcane bud germination after 11 days most of single eye buds setts were found poor germination and near by infected setts white fungus mycelium was observed after five to six days brown colour sclerotia of this fungus also observed. Infected buds were not successfully germination and reduced germination percentage of sugarcane setts. Germinated setts become yellowing and wilting. Isolation of fungus from infected single eye bud through standard technique of isolation on potato dextrose agar medium. White thread like mycelium with fast growth of fungus was observed on PDA medium. After six days of isolation, initially white sclerotia are develop on PDA medium and then after sclerotia become brown colour. Sugarcane setts was first time reported rotting due to *Sclerotium rolfsii*. The repeated isolation from the infected tissue revealed the presence of *Sclerotium rolfsii*. The pathogenicity was proved. This is the first report of *Sclerotium rolfsii* cause sett rot of sugarcane.

P (S 01) 16: A new stem rot disease of beggarweed (*Desmodium triquetrum* L.) caused by *Sclerotium rolfsii*

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The stem rot of groundnut (*Arachis hypogaea* L.) caused by *Sclerotium rolfsii* Sacc. is an important soil borne disease. Its occurrence has been reported from several countries including India. *Sclerotium rolfsii* is a polyphagous plant pathogen. Aycock (1966) in his monograph “Stem rot and other diseases caused by *S. rolfsii”* listed more than 500 plant species belonging to 100 families as the host of this fungus. The *Sclerotium rolfsii* (ITCC No. 5543/03) was used for host rage study in pot experiment was conducted at department of plant pathology, Junagadh Agricultural University, Junagadh. The host range study was carried out by soil inoculation method. Ten plants of the each crop and weed were grown in pots (15" x 15" x 10") filled with sterilized soil previously inoculated with *S. rolfsii*. Similarly ten plants of same plant species were also grown in the pot without inoculum which, served as check. All these plants were provided to humid conditions in net house. The observation of disease incidence was recorded up to the maturity of plants. The disease appears in 30 to 45 d old plants of *Desmodium triquetrum* L. The infected stem area became water soaked and discoloured. White fungal growth and brown sclerotia were observed on infected stem. Infected plants became withered and died. The repeated isolation from the infected tissue revealed the presence of *Sclerotium rolfsii*. The pathogenicity was proved. This is the first report of *S. rolfsii* cause stem rot of *Desmodium triquetrum* L.

P (S 01) 17: Occurrence of leaf spot of ridge gourd caused by *Didymella* sp. in Himachal Pradesh

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Ridge gourd or sponge gourd (*Luffa acutangula)* is popularly known as 'Turai'. It is a ridged and dark green vegetable with white pulp inside. It is extremely rich in dietary fibre and enriched with all the vital elements that include Vitamin-C, zinc, iron, riboflavin, magnesium, thiamine and traces of another minerals. It has also been found to have antioxidant, antimicrobial and antifungal properties. During routine crop surveys in July-August, 2019, a characteristic leaf spots observed in ridge gourd vines grown at Research Farm, Department of Entomology, Dr YS Parmar University of Horticulture and Forestry, Nauni. Leaf spots were round or triangular, particularly those at the leaf margins, or sometimes rhomboid and were dark brown in colour. The centre of spots often was a lighter shade of brown than the surrounding portion. Leaf spots frequently displayed alternating rings of dark and light brown necrosis, which corresponded to diurnal periods of pathogen growth when leaves are wet with dew. Old leaf spots had a defined margin and had shredded in some lesions. Diagnostic signs were the pycnidia and pseudothecia of the pathogen that formed readily in leaf spots. Pseudothecia were dark brown to black and usually were slightly immersed in the host tissue. Pycnidia were tan when young and became brown with age. They usually were slightly larger than pseudothecia. The pathogen was isolated from infected tissues onto PDA medium in pure culture and its pathogenicity was proved by artificial inoculation. On the basis of the cultural and morphological characters of the fungus, it was identified as *Did uymella* sp. This constitutes the first report of *Didymella* sp. infecting ridge gourd in Himachal Pradesh.

P (S 01) 18: Detection of seed mycoflora of pigeonpea by seed health testing methods

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An investigation was conducted to detect the associated seed mycoflora in pigeonpea. A total of 5 varieties of pigeonpea seeds were collected from Agriculture Research Station, Badnapur. Standard agar plate methods and modified PDA method were used for detection of seed mycoflora of pigeonpea seeds. Across the two methods adopted, a total of ten fungal genera including *Aspergillus niger, Aspergillus flavus, Rhizopus stolonifer, Macrophomina phaseolina, Fusarium oxysporum* f. sp*. udum, Alternaria alternata, Botrytis cinerea, Aspergillu ssp., Trichoderma* sp. and *Cladosporium* sp. with the seeds of pigeon pea were detected. The fungi detected were identified based on their cultural and morphological characteristics. Among the ten fungal species detected the occurrence of *A. niger* was observed (57.75, 53.58, 37.32, 35.20 and 32.67%, respectively) in cultivars ICP-8863, ICP-2376, BSMR-736, BDN-708 and BSMR-853, followed by the fungi *A. flavus* (31.10, 17.15, 16.33, 14.60 and 12.05%, respectively) in cultivars ICP-8863, BSMR-736, BSMR-853, BDN-708 and ICP-2376 in Standard agar plate method. In modified PDA method maximum frequency of *Botrytis cinerea*was observed (55.00, 52.50, 30.00 and 25.80%, respectively) in var. BSMR-736, BSMR-853, ICP-2376 and ICP-8863, followed by the fungus *A. niger* (40.10, 37.45, 32.50 , 10.00 and 0.00, respectively) in the cultivars ICP-2376, ICP-8863, BDN-708 and BSMR-736, Per cent infectivity of seed mycoflora varied across the methods adopted and varieties tested. The highest per cent infectivity of 57.75% was observed with the fungus *A. niger* on ICP-8863 in Standard agar plate methods. In modified PDA method the highest per cent infectivity of 55.00% was observed with the fungus *Botrytis cinerea* on BSMR-736.

P (S 01) 19: Multilocus gene specific characterization of '*Candidatus* Phytoplasma asteris' (16SrI-B) associated with phyllody and flat stem diseases of marigold in India

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Symptoms of phyllody and flat stem were observed in the marigold fields at Laxmibil, Sepahijala district of Tripura and University campus, Gorakhpur, Uttar Pradesh, respectively in 2018. Two symptomatic samples each of marigold phyllody (MP), marigold flat stem (MFS) and asymptomatic marigold plants were collected and DNA was extracted. The ~1.2 kb DNA fragment of *16S rRNA* gene was amplified from symptomatic MP and MFS samples using phytoplasma universal primer pair P1/P7 and nested primer pair F2n/R2. BLASTn search comparison of 16S rDNA sequence and phylogenetic analysis revealed that MP and MFS phytoplasma isolates had 99% 16S rDNA sequence identity with the '*Candidatus* Phytoplasma asteris'- related strain. Virtual RFLP analysis of F2n/R2 primed 16S rDNA sequences of MP and MFS phytoplasma isolates using *i*PhyClassifier online tool with 17 selected restriction enzymes confirmed the association of '*Ca.* P. asteris' subgroup B. The association of 16SrI group was further confirmed by utilizing multilocus genes *rp*, *sec*Y and *tuf* specific primers to 16SrI group. Our study suggests that *rp, sec*Y and *tuf* gene could be used for specific detection of 16SrI group phytoplasma strains.

P (S 01) 20: Taxonomy and morphology of Zygomycetous fungi

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Zygomycetes is a diverse fungal class of the phylum Zygomycota found worldwide. There are over 1050 species known in which only one percent of the species described. The zygomycetes is a small, ecologically heterogeneous, paraphyletic or polyphyletic group of mostly terrestrial in habit, living in soil or on decaying plant or animal material and in aquatic ecosystem. Zygomycetous fungi are the source of enzymes, organic acids and alcohals. Some of them are used as bio-control agents while others form symbiotic relationship with plants. Attempts were made to characterize the zygomycetous fungi of India with the help of their morphology characters. Twenty isolates were collected from different host and were analyzed based on macro-morphology viz., growth rate, colour and texture of the colony and micro-morphology viz., branching pattern of Sporangiophores, Columella, shape and size of Sporangia, and aplonospores. Based on these morphological characters, the isolates were described in detail into eight different genera viz., *Absidia, Circinella, Cunninghmella, Mucor, Rhizopus, Syncephalastrum,Thamnostylum,* and *Gongronella* along with the well defined illustrations.

P (S 01) 21: A new fruit rot disease of okra (*Abelmoschus esculentus*)

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A severe fruit rot problem was observed on okra (*Abelmoschus esculentus*) during August 2019 grown in open conditions in the farmer's fields of Thrissur and Kasaragod districts of Kerala state. The rot appeared as water-soaked lesions on fruits, starting from the tip. These water-soaked areas later got covered with white thread like mycelial growth advancing in a radial pattern. The mycelia produced minute pinhead like structures which later developed into pinkish sclerotial bodies of 1-3 mm diameter. The rotting advanced deeper into the fruits leading to complete decay of fruits along with immature seeds. In advanced stage, the fruits were completely covered with the fungal mycelia especially under high humid conditions. The rotting further spread to fruit stalk and stem. Infection on stem resulted in wilting of branches in isolated patches. The pathogen was isolated on Potato Dextrose Agar medium, brought into pure culture and morphological and cultural characters were studied. The colony of the fungus appeared white in colour and developed creamish pink globular to irregular sclerotial bodies within 7-10 days. The pathogenicity of the fungus was proved on detached fruits. Based on the morphological and cultural characters, the pathogen was tentatively identified as *Sclerotium* sp. The identity of the pathogen was further confirmed at species level through molecular characterization of ITS r DNA region of the fungal genome. The total DNA of the fungus was isolated and carried out PCR amplification using universal primers specific to ITS region (ITS 1F and ITS 4R) which yielded amplicons of size 450-500 bp. The sequencing of amplicons followed by homology search in NCBI database using BLASTn analysis showed 99 per cent homology with *Sclerotium rolfsii*. It is concluded that the fruit rot of okra is caused by *Sclerotium rolfsii* Sacc. and this disease could be an emerging threat for okra cultivation in the state.

P (S 01) 22: Morphology and phylogeny based diversity analysis of agricultural important cryptic species of *Fusarium solani* species complex in India

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Members of the *Fusarium solani* Species Complex (FSSC) have been known to cause disease of several agricultural important crops. Nevertheless, the taxonomic status of such an important group of fungi is still very confusing due to very limited morphological distinction and many new species as well as lineages have been elucidated recently. Interestingly, most of the new taxa have been discover under temperate and sub-tropical climate. Therefore, the present study were to identify cryptic species of FSSC recovered from different plant sources in India. In the present study, 75 isolates belonging to the FSSC were examined base on morphological features and selected for molecular studies using translation elongation factor-1 (TEF-1á). Based on morphological features and phylogenetic analysis all the isolates were classified into seven described cryptic species viz., *Fusarium falciforme, Fusarium petroliphilum, Fusarium keratinoplasticum, Fusarium metavorans, Fusarium solani* f. sp. *pisi*, FSSC 5 and FSSC 21. The data obtained from morphological and molecular studies shows sufficiently supported each other. The phylogenetic tree base on TEF-1á dataset clearly distinguished closely related species and distinctly separated all morphological taxa. This study found that *Fusarium falciforme* is the most dominant cryptic species of *Fusarium solani* species complex present in India which contribute alone more than 58% with causing disease to diverse agricultural crops.

P (S 01) 23: First report of Phaeosphaeria leaf spot of maize from Karnataka, South India

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In India about ten major foliar diseases have been reported to affect the maize crop. *Phaeosphaeria* leaf spot on maize was reported as emerging disease in many countries besides certain areas of northern India. Intensive roving survey in Karnataka revealed that *Phaeosphaeria* leaf spot disease was appeared in moderate to severe form in maize growing areas of Karnataka state, for the first time in south India. The disease was noticed for the first time during rainy season of 2019 in maize fields at Dharwad, Karnataka state. The initial infection on leaves was observed during second fortnight of September and disease progressed during October. Disease severity suddenly increased during October first fortnight after heavy rainfall. At tasseling to dough stage severe leaf necrosis was noticed and affected large active photosynthetic leaf area which later had impact on reduced cob size and shrivelled grains. In the early stage of infection symptoms were characterized by small dark green water soaked lesions on leaf which are in varied shapes like circular, oval, elliptic, slightly elongate to oblong measuring 0.3 to 2.0 cm in diameter. Lesions found scattered over the leaf surface and had chlorotic appearance, which later turned pale green, straw-colored, bleached and finally necrotic. These lesions coalesce become irregularly shaped and resulted in necrosis of entire leaf. Disease was favoured by high rainfall and moderate temperatures. Humidity levels above 80 per cent and low night temperatures aggravated disease severity. Based on the morphological and cultural characters, the pathogen was identified as *Phaeosphaeria maydis* (Henn.) Rane, Payak and Renfro. Further studies were initiated. Hitherto disease was not reported from south India, Hence the present finding is the first report of the *Phaeosphaeria* leaf spot of maize caused by *Phaeosphaeria maydis* (Henn.) Rane, Payak and Renfro from Dharwad, Karnataka state in South India.

P (S 01) 24: Morphological, cultural and molecular characteristics of *Bipolaris maydis* causing southern corn leaf blight disease

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Maize is an important food crop as rice and wheat globally. Losses caused by biotic stresses in maize are substantial and southern corn leaf blight (SCLB) or maydis leaf blight (MLB) is important among them. The leaf samples were collected from infected maize growing areas of district Panchmahal and Dahod, Gujarat in 2017. A total of 5 fungal isolates were examined for morphological, cultural and molecular properties and based on the results, the 5 isolates were identified as *Bipolaris maydis*. Conidia were olivaceous brown, spindle-shaped with tapering to round ends and bipolar germination. Cultural characteristics showed that variation existed among the isolates in colony growth and colour. Mycelia growth rates of the isolates were significantly different on potato dextrose agar (PDA), corn meal agar (CMA) and potato sucrose agar (PSA) media, growth on CMA was faster than on PSA and PDA. The number of septa ranged from 5-7 to 7-11 representing isolates BM2 and BM3, respectively. Similarly, conidial length varied from 31.75 µm to 60.54 µm for isolates BM2 and BM3, respectively. The pathogenic variability tested on GM-6 corn variety, showed that isolates BM1 and BM3 were more aggressive while isolate BM5 was less aggressive among the isolates tested. Both morphology and molecular results showed that, the isolates were identified as *Bipolaris maydis*. The findings of this study will serve as a baseline for future studies.

P (S 01) 25: Influence of anatomical, biochemical and meteorological variants on incidence of grape anthracnose

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Grape anthracnose caused by *Gloeosporium ampelophagum* (Pass.) Sacc. is a serious disease affecting several grape cultivars. The present investigation was carried out at the Fruit Research Farm of Punjab Agricultural University, Ludhiana for three consecutive years (2015-16 to 2017-18) to screen five grapevine cultivars (H 516, Pusa Navrang, Beauty Seedless, Flame Seedless and Perlette) against anthracnose and to investigate its relationship with weather, disease, and host-related factors. The Percent Disease Index (PDI) was calculated on the basis of 0-5 rating scale and the anatomical, physiological & biochemical characteristics of healthy and anthracnose infected leaves of grapevine cultivars were evaluated. Pearson correlation coefficients were computed between PDI and stomatal length, width & index. A significant positive correlation of PDI is being reported with stomatal length ($r = 0.685^{**}$), stomatal width ($r = 0.584^{**}$) and stomatal index ($r = 0.883^{**}$). Pearson correlation coefficients that were generated for establishing the correlation between the PDI and biochemical parameters revealed a highest pearson correlation coefficient between PDI and chlorophyll b ($r = -0.886^{**}$) followed by total soluble phenols ($r = -0.846^{**}$). The influence of weather parameters on development of anthracnose in the region was also worked out. The regression equation explains, if rains coupled with high humidity favour the primary infection of the crop.

P (S 01) 26: *Leucas aspera* and *Crotolaria juncea*: New hosts recorded for 16Sr II-D subgroup Phytoplasma in Karnataka

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Leucas aspera is considered as a weed as well as an important medicinal plant that is used in the preparation of medicinal formulations. *Crotalaria juncea* is a commercial fibre yielding crop. A recent survey revealed the symptoms of phyllody, excessive shoot proliferation and stunted growth which are typical of Phytoplasmal association on these host plants. The total genomic DNA was isolated from the leaves of the symptomatic samples followed by PCR amplification using P1/P6 and R16F2n/R16R2 primer pairs. Results showed amplicons of 1.5 kb and 1.25 kb corresponding to the 16SrRNA gene region on 1.2% agarose gel. The amplified PCR products were purified, sequenced from both the strands and the resulting sequences were assembled. The sequence homology search using nBLAST revealed the maximum nucleotide identity with phytoplasma strains of 16SrII group i.e., "*Candidatus* Phytoplasma aurantifolia" with a per cent homology of 99.35% and 99.84% respectively. The sequences under study were aligned along with the reference sequences retrieved from NCBI-GenBank using CLUSTAL W and a phylogenetic tree was constructed by Neighbour-Joining method where they formed a separate clade with the reference sequences of subgroup 16SrII-D. The virtual RFLP patterns generated using PhyClassifier tool also justified with that of Phytoplasma associated with *L. aspera* and *C. juncea* Phyllody belonged to 16Sr II group, subgroup D with a similarity co-efficient of 1.00 in comparison with reference strain Y10097. So far no reports are available on the phyllody disease of *L. aspera* and *C. juncea* caused by 16SrII-D group Phytoplasma from India. This constitutes the first report on occurrence of Phytoplasma with two new hosts in India.

P (S 01) 27: Microbial profiling of microbiome affecting drought tolerance in rice

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Rice one of the major staple foods typically cultivated in flooded soil, resulting in oxic and anoxic zones within the rice rhizosphere select for specific physiological groups of microbiota. It results in compartment specific restructuring of rice root associated microbiomes. Such microbiome shows the greatest diversity of bacterial species. In the present investigation, soil samples collected from rhizosphere, rhizoplane and endosphere of one drought tolerant (Dagaddesi: D) and one drought susceptible rice genotype (MTU1010: M) under two conditions (irrigated: D1/M1 and drought: D2/M2) was used for cultivation dependent and cultivation independent isolation of microbiome. Simultaneously DNA extracted from soils were subjected to metagenomics analysis for the identification of bacterial and fungal community. The Ion 16S Metagenomics Kit used two primer pools to amplify seven hypervariable regions (V2, V3, V4, V6, V7, V8, and V9) of bacterial 16S rRNA for bacterial community identification. For fungal community DNA amplification, the spacer ITS1 region of the rRNA gene was amplified using ITS1- ITS2 primer set. *Sphingomonas* sp. and *Lysobacter pocheonensis* is abundant in all the four samples and *Rhodanobacter lindanicias* is present in all except D1. Similarly *Nocardioides* sp. is present in all except M1. In rhizosperic DNA of MTU1010 under stress condition the abundance of *Lysobacter pocheonensis* substantially increases as compared to control condition. Where as in case of rhizosperic DNA of Dagaddeshi (stress), abundance of *Sphingomonas* sp. is enriched as compared to that in control irrigated condition. We could observe differential abundance in bacterial species with respect to rice genotypes as well as experimental conditions. Similar data was observed at family level, phylum level as well as OTU level abundance also. Documentation of species makeup of rice phytobiome in adverse condition and transcriptome analysis will provide brief understanding as how rice plants shape the microbial community composition to boost its health.

P (S 01) 28: A new rust on *Albizia*

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The taxonomic history of *Albizia lebbeck* is somewhat convoluted. *A. lebbeck* is a species of *Albizia*, widely cultivated and naturalized in other tropical and subtropical regions. *A. lebbeck* is an astringent, also used by some cultures to treat the eye, flu, gingivitis, lung problems, pectoral problems, is used as a tonic, and is used to treat abdominal tumors. The bark is used medicinally to treat inflammation. During the exploration of the rust flora, leaves of *Albizia* found infected with the rust fungi were collected and specimen was deposited at division of Plant Pathology, IARI, New Delhi (HCIO no. 46661). Looking to the importance of the pathogen these infected leaves brought into the laboratory for microscopic examination and on the basis of spore morphology the pathogen identified as *Sphaerophragmium acaciae* (Cooke) Magnus of the family Sphaerophragmiaceae.

P (S 01) 29: Some Myxomycetes from Telangana state, India

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Myxomycetes are commonly known as slime molds and are classified under phylum myxomycota of Kingdom Protista. Around 2000 species are reported from the world, and about 200 species are known from India. Check list of slime molds of India indicates need of systematic surveys of diversified habitats for documentation of myxomycetous taxa. The present investigation adds additional information on 30 myxomycetes collected from diversified habitats of some forest localities of Telangana state. In the present study, wood supported the maximum presence of mixomycetous taxa followed by litter and bark. This study enriches the data on myxomycete floristics of India. This report form new additions to Telangana state, India.

P (S 01) 30: Cultural characteristics of Alternaria spp. on different media

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An experiment was conducted to evaluate different media namely Oat meal agar, Richard's agar, Potato Dextrose Agar, Carrot agar, Rose Bengal agar, Asthana & Hawker's agar and Czapek's Dox agar. The Nine isolates of *Alternaria* spp. collected from various fields of JNKVV and evaluated for their colony characters under laboratory conditions. The indicated that all the nine isolates differed from each other in terms of mycelial growth, sporulation, colony colour, zonation and irregular and smooth margins**.** Growth of Alternaria spp. on different media, incubated for 48, 96, 144 and 192 h, favored the colonization and sporulation. The growth of fungi was tested under culture. Out of seven different media tested Potato dextrose agar (PDA) supported better sporulation, while oat meal agar and carrot agar were found suitable for colonization, whereas, Richard's agar, Asthana & Hawker's agar, Czapek's Dox agar and Rose Bengal agar could not support colonization and profuse sporulation.

Session 2
Plant disease diagnostics

Keynote Papers

KN (S 02) 01: Role of disease diagnostics in tropical tuber crops plant health management

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Tropical tuber crops are energy rich and staple food for millions of people across the globe and they have potential for overcoming the climate change problems. Like other crops, these group of crops also attacked by different groups of plant pathogens and among them the diseases caused by viruses are most important, as they are carried through infected planting material (setts / tubers) from one season to next season and lead to substantial loss in yield and quality. They belong to different virus groups viz., Potyvirus, Begomovirus, Carlavirus, Badnavirus, Crinivirus etc. Primary spread of these causal agents is through infected propagating material and secondary spread in the field occurs through vectors like whitefly or aphids or by other means. In cassava, so far twenty nine different viruses have been reported around the world; however, in India only two viruses viz., *Indian cassava mosaic begomovirus* (ICMV), *SriLankan cassava mosaic begomovirus* (SLCMV) are prevalent. About 20 different viruses are known to infect sweet potato world over, however only sweet potato feathery mottle caused by *Sweet potato feathery mottle virus* (SPFMV) and leaf curl disease caused by *Sweet potato leaf curl virus* (SPLCV) are prevalent in India at present. The yam mosaic is also commonly present in many of the yam growing areas and occurrence of *Yam mosaic virus* (YMV), *Yam mild mosaic virus*(YMMV), *yam chlorotic necrosis virus* (YCNV),*Cucumber mosaic virus* (CMV) *and Dioscorea alata bacilliform virus* (DaBV) were confirmed in India. The virus infecting elephant foot yam and taro has been identified as *Dasheen mosaic virus* (DsMV) based on next generation sequencing. Different diagnostic techniques like ELISA, DIBA, PCR / RT-PCR, qPCR, LAMP were standardized for detection of ICMV / SLCMV from cassava plants. Polyclonal antiserum against the DsMV has been produced by expressing the coat protein gene of the virus in bacterial expression vector and validated with large number of field samples. Lateral flow device for detecting DsMV infection elephant foot yam also succeeded. Our continuous research efforts depicted the diversity among the viruses infecting tropical tuber crops at genomic level and variation in symptom expression. *In vitro* tissue culture techniques namely meristem/shoot tip/nodal culture combined with thermo or chemotherapy for virus elimination in cassava, sweet potato and yams have been standardized.

KN (S 02) 02: Advanced molecular diagnostics for plant pathogenic bacterial detection

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The elimination of disease-causing microbes from the plant/seed/food is a primary goal to maintain the health of both plants and animals including humans and this presentation deals with the overall techniques available for detection of bacterial pathogens. Microbiological safety of seed/plant/food has become an important concern of consumers, industry, and regulatory agencies. Currently available methods are often unsuitable for use in industrial laboratories because of lack of sensitivity, complex to perform and require specialized expertise to operate in addition to expensiveness. Bacterial pathogens are diverse in their nature and keep causing major health problems in plants and humans worldwide. The elimination of disease-causing microbes is a primary goal in the globe. Identification of pathogens in a short period of time is still challenging to the scientific field. Now-a-days conventional methods are replaced by advanced methods like Biosensors, Nucleic Acid-based Tests (NAT), different PCR-based techniques used in molecular biology to identify specific pathogens of seed/plant/food. Molecular techniques in pathogenic detection are very promising alternatives to classical cultures, biochemical and serological identification and typification methods. Pathogenic bacteria like, *Ralstonia solanacearum, Xanthomonas axonopodi* pv. *vesicatoria*, *X. campestris* pv. *campestris, X. oryzae* pv*. oryzae*; and food-borne pathogens like, *Bacillus cereus, Staphylococcus aureus, Escherichia coli, Salmonella* spp., were used in the present studies for the development of molecular diagnostics. Pathogens are detected in contaminated samples that cause always diseases in plants/humans in any one or the other way. The low level of contamination by major pathogens requires specific sensitive detection platforms and the present area of hot research looking forward to new nano-molecular techniques make them suitable for the development of assays with high sensitivity, comparatively in less time, and portability. With the sound of these, we in the present study attempted to develop the diagnostic methods for seed/plant/food-borne pathogen detection by rapid, sensitive, accurate, and affordable, which can replace the conventional methods *viz.,* PCR-SSCP, multiplex PCR, colony PCR, LAMP assay and finally MALDI Biotyper. The techniques developed in the present study are useful for international sanitary surveillance of seed/plant material exchanges. The possible use of these advanced molecular diagnostics was discussed in the present research.

KN (S 02) 03: Diagnosis to discovery of plant viruses: An Indian scenario

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Viral diseases pose great economic loss in different field and horticultural crops. Detection and identification of virus plays important role in managing viral diseases. Diagnosis of viruses is often attempted by conventional serological and PCR based detection assays. Serological assays have been standardized for a large number of viruses using antibodies/conjugates available commercially or produced in house by using recombinant coat proteins. Similarly PCR or variants of PCR including multiplex PCR have been standardized for several plant viruses infecting different crops. These methods have been used in identification of viruses, in screening of resistance against viruses, indexing of vegetative propagated crops as well as certification of tissue cultured plants under National Certification System. PCR based assays are more sensitive than ELISA but they are laborious, time consuming and require well equipped laboratories and skilled manpower. To overcome the complexities of PCR based virus detection, a novel and rapid isothermal recombinase polymerase amplification (RPA) assays have been developed for DNA as well as RNA viruses which can be easily performed in less than 30 min using a very small amount of crude sap extract at a constant low temperature (37°C-42°C) or even at room temperature dispensing the use of expensive thermal cycler. RPA is superior to other isothermal amplification techniques such as loop mediated isothermal amplification (LAMP). For parallel detection of multiple infections of viruses in crops, DNA microarray chip has been developed. Using DNA chip several new reports of viruses and viroids have been made in India. Next generation sequencing (NGS) is a novel unbiased and hypothesis-free testing of plant samples to discover viruses and viroids. RNA-sequencing (RNA-seq) of plant material has been used for identification of several viruses/viroids in field and horticultural crops. These methods are complex, require skills and may be expensive but are highly useful for quarantine and biosecurity.

Invited Papers

I (S 02) 04: Association of two novel viruses with chlorotic fleck disease of ginger

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Chlorotic fleck disease of ginger, the causal virus of which is unknown so far is an important production constraint of ginger in India and other parts of the world. In the present study two new RNA viruses were discovered in chlorotic fleck affected plant by the virome analysis using high throughput sequencing of small RNA (sRNA) and transcriptome. The high throughput sequencing results were verified through reverse transcription polymerase chain reaction (RT-PCR) using total RNA from infected plant and primers designed to the contigs that hit both viruses. The cloning, sequencing and phylogenetic analysis of complete genome of one of the viruses considered to be a new member of the family Tombusviridae while partial genome analysis of the other virus considered being a new member of the genus Ampelovirus (Family: Closteroviridae). Therefore the tentative names corresponding to these viruses are ginger chlorotic fleck associated tombusviridae virus (GCFaTV) and ginger chlorotic fleck associated ampelovirus (GCFaAV). A reliable RT-PCR and SYBR Green-based real-time RT-PCR assays were developed for the detection of both viruses in plants that would aid in the identification and propagation of virus-free ginger plants. The viral population analysis in the field infected plants showed that both viruses more or less occur in equal concentration.

I (S 02) 05: Early detection of blister blight disease in tea based on hyperspectral reflectance data

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Blister blight disease caused by *Exobasidium vexans* Masee is a threat to tea (*Camellia sinensis* (L.) O. Kuntze) in Sri Lanka incurring direct crop loss in fields in harvesting and severe shoot dieback in fields recovering after pruning. Early detection and accurate estimation of the disease is important for precision disease management. This study aimed at (i) non-destructive sensing and estimating blister blight disease severity in canopies of TRI 2024, TRI 2025 and CY 9 tea cultivars employing hyperspectral reflectance data and (ii) evaluating informative spectral regions. The hyperspectral data were collected from 10 cm above tea canopies with different levels of disease infection with a hand-held PSR 1100f Spectroradiometer with a spectral range of 320 – 1100 nm visible to near-infrared (VNIR). Single leaf reflectance measurements with a leaf clip and reflectance measurements of artificial canopy made of sampled tea shoots were also taken under laboratory conditions. Spectral region 740 – 1000 nm of NIR was sensitive to blister blight. As blister blight progressed through translucent stage, mature blister stage and necrotic spot stage, spectral reflectance decreased by an average of 2%, 16% and 32% respectively, in comparison to those of healthy leaves. Spectral signatures acquired under field conditions and from artificial canopies also decreased by 30% in comparison to healthy canopies. Principal Component Analysis (PCA) of spectral data differentiated blister blight infection form healthy canopies. These results suggest a possibility of low-cost, low-altitude aerial imaging using a small UAV or airborne hyperspectral imaging for early identification and estimation of blister blight for precision management and plant protection activities.

I (S 02) 06: A few important diseases of the north-eastern region of India: Their diagnostics and management

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Rice, citrus, large cardamom, ginger, orchids and vegetables are major crops grown by the farming communities in the North-Eastern sub-Himalayan region (NER) of India which suffer substantial losses due to one or more virus and virus-like diseases in addition to few fungal and bacterial diseases. With the spread of modern high yielding rice varieties, *tungro,* the most important viral disease of rice, has become potential menace to the rice production not only in Assam but in the whole of NER. Earlier the disease was noticed only in winter rice, but of late, its occurrences have also been observed in summer rice and autumn rice. A progressive increase in the disease incidence is observed from August onward which reaches its peak in October and November and declines thereafter. In general, there is very low *tungro* incidence from January to July. Screening of the *tungro* isolates against rice differentials has indicated presence of strains. Orange (*Citrus reticulata* Blanco) accounts for 90% of the area under citrus cultivation. Once it was a flourishing cash crop of NER but since early 1960s, citrus decline has incurred enormous losses to the growers. Declining orange orchards of the region have been found to have incidences of a number of virus and virus-like diseases of which *tristeza* and *huanglongbing* are considered to be the most important ones. Earlier *tristeza* was thought to play primary role in causing citrus decline but widespread incidence of *huanglongbing* in the decline-affected orange orchards has been confirmed during the last two decades. Large cardamom (*Amomum subulatum* Roxb.) is a commercial spice crop grown extensively in the humid, sub-tropical, semi-evergreen forests of the Eastern sub-Himalayas. The crop is affected by three different virus diseases, of which two, *viz*., *chirke* and *foorkey* diseases are of major concern to the large cardamom growers. Substantial progress has been made in characterization of the viruses causing these two diseases. Blight, a devastating fungal disease, has been reported to occur in large cardamom plantations since 1999 which turned epiphytotic within a period of five years. The disease appears generally with the advent of the pre-monsoon showers and progresses rapidly during the rainy season (June to August). The affected large cardamom clumps exhibit burnt-up appearance. Investigations have revealed association of *Glomerella cingulata* (*Colletotrichum gloeosporioides*) with the disease. Five different viruses namely, Cymbidium mosaic *potexvirus*, Odontoglossum ringspot *tobamovirus*, Calanthe mild mosaic *potyvirus*, Groundnut bud necrosis *tospovirus* and Orchid fleck *rhabdovirus* have been found to affect cultivated orchid genera and species. Chayote (*Sechium edule* L.) yellow mosaic, mosaic diseases of *bhoot jalakiya, dalley khorsani* and beans, okra yellow vein mosaic, tomato leaf curl and rhizome rot complex of ginger are a few important diseases affecting vegetable crops. In most of the vegetatively propagated crops, greater emphasis has to be laid on production and use of disease-free planting material and rigorous monitoring of the disease incidence.

I (S 02) 07: Molecular characterization and real time PCR based diagnosis of flag smut of wheat

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Flag smut caused by *Urocystis agropyri*, is an important seed and soil borne diseaseof wheat. For analyzing genetic variation among *U. agropyri* isolates, 50 different isolates of *U. agropyri* representing five different states (Punjab, Rajasthan, Himachal Pradesh, Uttrakhand and Haryana) of India were collected and their genetic characterization was performed. Comparative analysis of internal transcribed spacer (ITS) regionof collected isolates and their phylogenetic analysis with global isolates revealed clear demarcationbetween Indian and global isolates representing USA, Australia, Ukrain and China. Further attempts have been made to monitor and quantify the occurrence of this fungus by devising diagnostic tool based on real-time PCR. A pair of ITS primers (UAITSF1/UAITSR1) was designed to amplify a specific 548-bp DNA fragment from all the isolates of *U.agropyri*.The developed primers were highly specific for *U. agropyri*, as no amplification signal was produced in other related and unrelated wheat pathogens.The detection limit of the developed marker was 0.1 ngìl^{-1} of DNA from *U. agropyri*. Moreover, developed SYBR Green I real-time PCR assay was also successfully validated onartificially as well as naturally *U.agropyri* infected wheat seedlings.This method allows highly efficient, rapid and accurate differentiation of the pathogen from related pathogens.

Oral Papers

O (S 02) 08: Production of recombinant coat protein of *Banana bract mosaic virus* for development of serological detection assays

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Banana bract mosaic disease which accounts for about 40% yield loss annually in Kerala, is caused by *Banana bract mosaic potyvirus* (BBrMV). The characteristic symptom is mosaic of dark brown and red colour on the bract after which the disease and causative agent is named. Almost all the cultivars of banana succumb to the disease resulting in malformed bunches weighing less than half of normal ones. Early detection of the virus is very important not only to check the spread of the virus through infected planting material but also for uninterrupted international germplasm exchange. Serological method, enzyme linked immunosorbent assay is most widely preferred for virus indexing as it is economical and reliable. However, the sensitivity and specificity of the method depends upon the quality of antiserum used for detection. Partially purified virus preparation tends to have antibodies against the plant proteins which considerably reduces the titre. Recombinant coat protein (CP) overexpressed and purified from a bacterial host is the answer to this problem. In the current study the CP gene segment present at the 3' terminal region of the viral genome amplified by RT-PCR was cloned into expression vectors, pRSET-C and pGEX-4T-2. Recombinant BBrMV CP expressed using pRSET-C was insoluble whereas, it was in the soluble fraction when expressed from pGEX-4T-2. The GST-fusion protein was purified by GSH sepharose affinity column chromatography and western blot analysis was performed using anti GST antibodies. The GST tag was cleaved from the purified protein by incubation with thrombin at room temperature overnight. The protein concentration was quantified using Bradford's assay. 360ug/mL of protein was purified from 1L of culture. The purified untagged CP will be used for raising polyclonal antisera in New Zealand white rabbit. The antiserum obtained after booster dose of CP will be checked for its ability to detect the virus in various field samples.

O (S 02) 09: Identification and characterization of viruses infecting flower crops in India

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Virus diseases are of great economic importance in flower crops as most of them are propagated vegetatively. Many viral diseases cause significant losses in the quality of the flower making it unfit for export and viruses are very difficult to control. Recent advancement in the molecular biology have provided new tools for the identification of viruses. In this study genome sequence based detection and characterization have been employed successfully for identification of viruses infecting Gladiolus, Tuberose, Jasmine and Amaryllis. Plant samples showing characteristic symptoms of virus infection such as mosaic, mottling, streak, ring spot and yellow mosaic were collected and preliminary tests were conducted through Electron Microscopy by leaf dip method. The results indicated the presence of isometric, flexuous and bullet shaped particles in the infected leaf samples of Jasmine, where as in Gladiolus, Amaryllis and Tuberose only flexuous filamentous particles were observed. For molecular identification of these samples, total DNA and RNA was isolated and PCR and RT-PCR was performed using CMV, *Badnavirus* and *Potyvirus* specific primers. The DNA fragment was further processed and used for cloning and sequencing. Nucleotide sequences of the obtained amplicons were determined and compared with sequences present in the NCBI database using the BLAST algorithm. Results revealed the presence of *Tuberose mild mottle virus* in Tuberose, *Bean yellow mosaic virus* in Gladiolus, *Amaryllis potyvirus* in Amaryllis and CMV and *Badnavirus* in Jasmine. The virus-specific sequence information generated in this study can subsequently be used to develop PCR-based detection methods. Since most of the ornamentals and flower crops are propagated through bulbs and the mother stock once infected, act as a source for disease spread in successive generations. Therefore detection and certification of virus-free propagation material is imperative for production of quality flowers.

O (S 02) 10: Citrus huanglongbing associated *Candidatus* Lberibacter asiaticus in North East India: Genetic characterization and development of simplified diagnostics

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Huanglongbing (greening) is a devastating disease of citrus causing huge economic losses worldwide. North East India is a major citrus grove known for large number of economically important citrus species and their wild relatives. However, the systematic studies on the prevalence and characterization of huanglongbing (HLB) disease were lacking from this region. Present study reports the results of systematic surveys carried out in different citrus groves of North East India (Manipur, Nagaland, Tripura, Mizoram, Arunachal Pradesh and Sikkim). Out of the 336 samples collected, 198 samples were tested positive for HLB (58.93%) in PCR using specific primers targeting 16S rDNA. For the partial 16S rDNA sequences of HLB-associated *Candidatus* Liberibacter asiaticus (CLas) isolates exhibited genetic divergence up to 2.3% among them, up to 3.4% compared to CLas isolates from other parts of India and up to 9.8% with the CLas isolates from other parts of

the world. For the outer membrane protein (OMP) gene sequences, CLas isolates from North East India exhibited genetic divergence up to 7.1% among them. Concatenated multi-locus sequence analysis (16S rDNA and OMP gene sequences) indicated the overall concurrence with the OMP gene based diversity. Genetic diversity in the CLas strains based on tandem repeat numbers (TRN) profiling in CLIBASIA_01645 loci of CLas was also studied. The TRN in HLB-associated CLas strains varied from 0-21 and a novel repeat motif was also identified. In the citrus cultivated on hilly terrains of NE India, the CLas genotypes with TRN5 and TRN9 were most frequent (total frequency of 36.36%) and TRN9 was present in all HLB-infected citrus cultivars in all the states. The region-wise distribution of CLas varied; nevertheless Class II (TRN>5d"10) genotypes were prevalent in the citrus groves of India. A simplified template preparation using crude sap extract of plants in isothermal recombinase polymerase amplification (RPA) was developed for the detection of huanglongbing-associated *Candidatus* Liberibacter asiaticus. Developed RPA assay could detection the target pathogens up to 10^{-7} of crude sap dilution and was as sensitive as bench mark PCR. The developed assay was validated using large number of field samples and found highly robust.

O (S 02) 11: Pokkah boeng of sugarcane- an emerging disease in India

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Sugarcane, an important agro-industrial crop, is cultivated under tropical and subtropical regions around the world. Sugarcane crop remains in the field for 12-14 months and is affected by various fungal, bacterial, viral and phytoplasma diseases. Among them, pokkah boeng caused by *Fusarium* species complex is becoming a serious fungal disease on the basis of its rapid spread during last few years, posing new threat to sugarcane cultivation in most of the sugarcane growing areas of the world including India. This disease reduce the quality of the harvested crop mainly among varieties with high sugar yields and sugar production depending upon the variety up to 41- 65%. Now this disease has become a matter of concern as it is spreading rapidly in India having monoculture of single variety and due to lack of effective management strategies. Use of resistant varieties is the most effective measure for its management. Sixty eight varieties of sugarcane were screened against pokkah boeng disease under natural conditions at RRS CCSHAU Karnal. Forty seven varieties showed resistant reaction (0-4.76%) and ten varieties showed moderately susceptible reaction (5.26-7.89%) against pokkah boeng disease. Six varieties exhibited susceptible reaction (10.52-19.56%) and five varieties exhibited highly susceptible reaction (20.93-47.3%) against pokkah boeng disease. Predominantly cultivated variety Co 238 in North-West zone showed the highest disease incidence. For the management of pokkah boeng overnight cane soaking with carbendazim 0.1% and three foliar sprays with carbendazim 0.1% at 15 days interval were found most effective in checking the the pokkah boeng disease which gave highest disease control of 76.95% and 69.38% in Co 0238 and CoS 8436, respectively.

O (S 02) 12: Identification of charcoal rot disease in soybean using laser biospeckle activity

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Soybean (*Glycine max* L.) is a leading oil seed crop in the world. Owing to climate change, its production is challenged by incidence of several diseases. Among them, charcoal rot is the most devastating diseases of soybean caused by *Macrophomina Phaseolina*. *M. phaseolina* is mostly facultative saprophytic in term of plant pathogenic nature, which leads to easy break down of resistance and create difficulty in screening of genotypes. Expression of charcoal rot symptom is highly depends on environmental conditions which also leads difficulty in screening of soybean genotypes. Hence, there is a need of robust and automatic technique for detection and quantification of pathogens for screening large number of soybean varieties. In this work,we developed a prototype based on laser biospeckle activity (BA) which can detect or quantify *M. phaseolina.* Two contrast soybean genotypes JS 9041 (moderate resistance) and AMSMBS-18 (susceptible) were inoculated with *M. phaseolina* (Jabalpur isolate MP 10) through cut stem technique on 15 days old plant. Both uninoculated and inoculated plants were exposed to expanded laser light (wavelength = 632.8 nm) for biospeckle analysis. Backscattered light generates a speckle pattern which depicts physiochemical property of soybean stem surface. Subtraction average based image processing technique was utilized to quantify inoculation density of *M. Phaseolina* from speckle patterns. BA of AMSMBS-18 is significantly higher (2.57×10^3) as compare to JS 9041 (2.05×10^3) after 10 days of inoculation. At day to day interval, BA is also recorded higher in AMSMBS-18 as compared to JS 9041. Diseases severity is also increasing in both varieties according to biospeckle activity. The biospeckle activity was found to be strongly correlated with the disease severity ($R=0.88$, $p<0.01$) of infected soybean plant. This result indicates that the techniques can be used for screening of soybean genotypes against charcoal rot disease.

O (S 02) 13: Characterization of *Rhizoctonia solani* isolates from rice-potato cropping sequence from Uttar Pradesh in India

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The black scurf & stem canker of potato and sheath blight of rice caused by *Rhizoctonia solani* is an important disease and caused significant losses of economic yield in potato and rice crops in India. Generally, rice-potato and maize-potato cropping sequences are following in major potato growing areas. It is well known that different AGs (Anastomosis groups) of *R. solani* are infecting potato and rice crops. However, variability in different isolates of *R. solani* infecting in rice-potato cropping sequence is not known. The 40 isolates of *R. solani* (20 from rice and 20 from potato) were collected from rice-potato cropping sequence during Kharif 2017 & *Rabi* 2018 from different districts of western Uttar Pradesh and diversity was studies on morphological, cultural, pathological and genetic levels. The results revealed that *R. solani* isolates were highly divers on morphological and cultural parameters. Rice isolates were fast growing than potato isolates and produced more number of sclerotia. On pathological diversity, it was observed that potato isolates were more pathogenic on potato host while rice isolates on rice host. Only some isolates of *R. solani* were showed cross infectivity in both the crops. The SSR (Simple Sequences Repeats) co-dominant markers were used to analyze genetic diversity. Four polymorphic markers (SSR1, SSR2, SSR4 and SSR5) were used for genotyping of *R. solani.* All the *R. solani* isolates from potato amplified three alleles (143,155,175bp with SSR1 & 183, 200, 255bp with SSR4) while isolates from rice amplified two alleles (153,175bp with SSR1 & 193, 245bp with SSR4) with SSR1 and SSR4 markers. However, with SSR2 and SSR5 marker four alleles were amplified in both the potato and rice isolates. It is observed that isolates from rice-potato cropping sequences are highly variable and they may cause more economic loss in future due to cross–infectivity of the both the crops. Therefore, we have to re-look disease management practices especially in rice-potato cropping sequences.

O (S 02) 14: Non-structural protein based recombinant polyclonal antibodies for specific detection of *Watermelon bud necrosis virus* in plants and thrips vectors

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Watermelon bud necrosis virus (WBNV) causing bud necrosis disease (BND), is an emerging threat for watermelon cultivation. Besides WBNV, few recent reports suggest the occurrence of GBNV also on watermelon. Both the viruses are known to induce indistinguishable symptoms leading to confusion in the symptom-based diagnosis. This, in turn, would affect the accuracy in evaluating watermelon genotypes and identification of resistant stocks/cultivars. The development of high throughput and species-specific methods are required for routine and accurate diagnosis of BND. Although the polyclonal antibodies (pAbs) raised to recombinant nucleoprotein (N) of GBNV is available, it lacks the ability for differential and specific detection. Besides, the antibodies raised to N-protein can only indicate the mere presence of the virus and fail to confirm whether the virus is biologically active in its host or not. In this study, the recombinant antibodies are produced against a truncated (243bp) region of Non-structural (NSs) protein unique to WBNV by cloning in a bacterial expression vector pET-28a+. The recombinant protein expressed in the *E. coli* strain BL21 (DE3) through the induction with 1mM IPTG and incubation at 37°C at 200 rpm for 4 hrs was confirmed based on western blot analysis against commercial anti-His antibodies. The gel-purified protein was used as an immunogen to raise the pAbs. The resultant pAbs when evaluated at different dilutions revealed that the pAbs were working well at 1:1000 dilutions. The pAbs react specifically with only WBNV infected (plant & thrips) samples, but not those infected with GBNV. This anti-WBNV NSs antiserum is the first of its kind in the world with regard to the pAbs specific to WBNV, that too against NSs protein. This antiserum will have an immense significance in evaluating the watermelon genotypes for resistance to WBNV as well as in the virus-vector relationship studies.

O (S 02) 15: Identification and rehabilitated from fungal disease affected plants

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Plant disease has become a major threat to global food security. Plant diseases contribute 10– 16% losses in the global harvest of crops each year. Plant disease affects the quality of fruits, vegetables, grains, legumes and causes heavy losses in production so we are Identification of the plants disease (FUNGAL) and its preventing the major losses in the yield and quantity of the agriculture product. (Stage-1) The studies of the plants diseases mean the studies of visually observable patterns seen on the plant health monitoring and disease detection for sustainable agriculture. It requires tremendous amount of work, expertise in the plant disease and also excessive processing time. Hence image processing is used for the detection of plant diseases it involves the steps like image acquisition, image pre-processing image segmentation, feature extraction and classification after completion of disease identification process (stage-2) terminating the disease cells by injecting flow of electrons to conduct small amount of electricity through plant inside on affected area of roots, stems, leaves. The shock does not seem to harm the plants. It gives rehabilitate to the plant and also this method may be a factor and less expensive way of cell incitement of plants production. Finally this terminology stands for terminating plant disease without chemical which harmful to both humans and plants finally cultivating healthy agriculture.

Poster Papers

P (S 02) 01: Detection of *Tobacco streak virus* (TSV) causing latent infection in strawberry

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Strawberry, one of the most complex among the crop plants, harboring eight sets of chromosomes (2n=8x=56) derived from four diploid ancestors (x=7), having a genome size of ~240 mb is one of the important emerging fruit crops of Himachal Pradesh. With the increase in cultivated area, virus disease incidence is also increasing in the recent past. Many viruses are reported to inflict strawberry crop producing variety of symptoms which vary with the virus species involved, prevailing environment and the host variety. Association of five viruses viz. *Tobacco streak virus* (TSV), *Strawberry Latent ring spot virus* (SLRSV), *Strawberry mild yellow edge virus* (SMYEV), *Tobacco Ring Spot Virus* (TRSV) and *Raspberry Ring Spot Virus* (RRSV) were observed in strawberry plantations. The serological assay of different plant samples with latent infection indicated the presence of *Tobacco streak virus* (TSV); however, the ELISA results were not consistent so, an attempt was made to detect this virus using PCR based method. The total RNA was isolated from leaf samples using RNA isolation kit. cDNA was synthesized by using reverse transcriptase enzyme following manufacturer's instructions. The RT-PCR performed using TSV specific primer pair generated an amplicon of ~750 bp size, typical of TSV cp gene in different samples. The comparison of ELISA vs. RT-PCR for the detection of this virus revealed that RT-PCR based protocol is more reliable for its routine diagnosis.

P (S 02) 02: Effect of different growing media on different varieties of Oriental lilium (*Lilium orientalis*) under shade net in Allahabad agro-climatic conditions

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The present investigation was undertaken in the Department of Horticulture, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad during winter season (2016-2017). Factorial completely randomized design of experiment with three replications was carried out to assess the performance of five Oriental lilium varieties viz. Cobra Red, Signum, Yelloween, Sorbonne and Justina grown in different media compositions of vermicompost, coco peat and sand in different compositions. The study revealed that all varieties performed satisfactorily with respect to several parameters related to growth, flowering, bulblet and bulbil production. Maximum growth was observed in medium containing equal proportion of vermicompost: coco peat: soil (1:1:1, v/v) and maximum bulbil production was recorded in vermicompost: coco peat: soil (2:1:1, v/v). Maximum plant height (77.40cm), number of leaves (82.80), early flowering (55.7days) grown in media containing vermicompost: coco peat: soil (1:1:1, v/v) and bulbils production (5.93) grown in media containing vermicompost: coco peat: soil (2:1:1, v/v) observed in Yelloween. Maximum bud diameter (41.10mm), bulblet (6.24) recorded in Sorbonne variety grown in media containing vermicompost: coco peat: soil (1:1:1, v/v). Maximum bud length(132.50mm) flower diameter (299.90mm) and pedicel length(131.47mm) observed in Justina with media containing vermicompost: coco peat: soil (1:1:1, v/v). Maximum stalk diameter (6.83mm) in Cobra Red and early bud initiation (28.93 days) observed in Signum with media containing vermicompost: coco peat: soil (1:1:1, v/v).

P (S 02) 03: Mfpmt: A machine learning-based forecasting system for powdery mildew disease in tomato plant

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Plant disease detection based on weather conditions is seeking attention from various agricultural scientists. A standardized range of weather conditions of a particular area play a crucial role in the productivity of any crop. However, an inadequate change in weather conditions may result in development of a disease in plant which in turn reduces its yield and quality. For instance, humidity, leaf wetness, global radiations, wind speed, and temperature are the most critical meteorological factors for the development of powdery mildew in tomato plants. Powdery mildew is one of the most severe diseases found in tomato plant caused by a fungus named *Leveillula taurica*. In this study, a machine learning-based forecasting system for powdery mildew disease in tomato plant (MFPMT) has been developed using a well-known approach named as random forest algorithm. The proposed model shows accuracy up to 93.24% in the early detection of tomato powdery mildew disease. A real time version of the proposed model can be used by agricultural experts to take preventive measures in the most sensitive areas that are prone to powdery mildew disease based on the weather conditions. Hence, timely intervention would help in reducing the loss in productivity of tomato crop which will further benefit the global economy, agricultural production, and the food industry.

P (S 02) 04: DNA barcode and multiplex PCR based identification and detection of *Alternaria alternata, Fusarium oxysporum* f. sp. *ciceris* and *Rhizoctonia solani*

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The exchange of germplasm has immense importance for their use in developing high yielding varieties and has a risk of introduction of new exotic pathogens or races/pathotypes/biotypes. Consistent and highly reliable detection is required to check the introduction, spread and management of pathogens based on DNA barcoding and molecular markers. Universal internal transcribed spacer (ITS) region based DNA barcodes were developed for identification of *Alternaria alternata, Fusarium oxysporum* f. sp. *ciceris,* and *Rhizoctonia*

solani and submitted to the Barcode of Life Data System (BOLD). ITS region based markers namely, BAA2aF & BAA2aR for *A. alternata* and BRS17cF & BRS17cR for *R. solani* were developed with 400bp and 200 bp amplicons, respectively. Whereas COX I region based marker FOCox1F & FOCox3R was developed for *Fusarium oxysporum* f. sp. *ciceris* with amplicon size of 150 bp. All the markers proved to be highly specific and sensitive and able to detect up to 0.0001 ng template DNA using qPCR. The highly sensitive, specific and reliable conventional and multiplex PCR assay was developed for diagnosis of these pathogens simultaneously.

P (S 02) 05: Identification and molecular characterization of *Xanthomonas citri* subsp. *citri* causing citrus canker in *Citrus* species

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Citrus canker caused by a gram-negative bacterium *Xanthomonas citri* subsp*. citri* (Xcc), is one of the most devastating and widespread disease affecting several species of citrus including acid lime, grapefruit, lemon etc. globally. In this study, the different samples of acid lime and grape fruit cultivars showed symptoms of citrus canker were isolated and characterized at molecular level. The citrus canker symptomatic leaf samples of acid lime was collected from research field, Indian Agricultural Research Institute, New Delhi, India and used for the isolation of Xcc on Nutrient agar medium at 28°C. The gDNA was isolated from different isolated cultures of Xcc by CTAB method and 16S ribosomal RNA gene primers were used to characterize the cultures of Xcc by PCR and DNA sequencing. The in-silico analysis of 16S rRNA gene of Indian isolate of *X. citri* subsp. *citri* showed 97% homology with other accessions of *X. citri* subsp. *citri* submitted in NCBI database. Additionally, these molecular characterized isolates of Xcc was maintained on Yeast glucose calcium agar (YGCA) medium at 28°C and the pathogenicity test was performed to develop the same symptoms of citrus canker disease on acid lime to check their pathogenicity. Furthermore, these characterized isolates will be used for the study of resistance mechanism of *X. citri* subsp. *citri* in citrus species.

P (S 02) 06: A simplified recombinase polymerase amplification assay for rapid detection of *Candidatus* Liberibacter asiaticus associated with Hunaglongbing disease in different citrus cultivars

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Citrus greening (huanglongbing; HLB) is one of the devastating bacterial diseases of citrus worldwide. HLB is caused by the phloem limited, gram negative, non-culturable, alpha-proteobacterium, '*Candidatus* Liberibacter asiaticus'. Currently, polymerase chain reaction (PCR) and real time PCR have been routinely used for the detection of '*Ca*. L. asiaticus'. However, these detection methods are expensive; require well equipped laboratories, non-user-friendly and unsuitable for on-site pathogen detection. In the current study, we have successfully developed an isothermal amplification method i.e. recombinase polymerase amplification (RPA) for rapid detection of '*Ca*. L. asiaticus' from infected citrus samples that dispenses the use of thermocycler. The assay was standardized for '*Ca*. *L. asiaticus'* detection by designing specific primer pair from the conserved outer membrane protein (OMP) gene and was optimized for temperature and reaction time using purified DNA and crude plant extracts. The best RPA results were achieved at an isothermal temperature of 37°C for 30 min. A total of 130 symptomatic and asymptomatic leaf samples (leaf midrib) of different citrus cultivars were evaluated and the pathogen associated with HLB was efficiently detected by RPA using crude sap as template. Similar results were obtained with conventional polymerase chain reaction (PCR) using purified DNA as template. To dispense the use of PCR, a rapid protocol for detection of '*Ca*. L. asiaticus' infections from crude leaf extract by RPA was developed. Thus, the RPA assay has greater potential to provide an improved on-farm detection of '*Ca*. L. asiaticus' infected plants for the farmers, disease surveyors and mobile plant pathology laboratories.

P (S 02) 07: Leaf blight of Hibiscus: An add-on to Phytophthora diseases in Kerala

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*Hibiscus rosa-sinensis*is an important candidate in ornamental gardening with its picturesquely coloured flowers. The plant has gained importance due to its use as a flowering hedge in landscapes. Phytophthora diseases are of major concern in plantation crops, spices and other important crops of Kerala with the onset of monsoon, as the fungus spreads rapidly in favourable environmental conditions. Hibiscus was reported to have infected with severe leaf blight and leaf fall during the monsoon season in Kerala. The symptoms appeared on leaves as water soaked lesions surrounded by yellow halo initiating from apical portion. The lesions later enlarged in size covering entire leaf lamina and the leaves turned yellowish and brownish black within 3 -5 days .The affected leaves abscised prematurely. Pathogen was isolated on potato dextrose agar (PDA) medium, characterized culturally, morphologically and pathogenicity established with standard protocols. On PDA, the fungus produced irregularly fluffy white mycelium in a rosette pattern. Sporangiophores irregularly or sympodially branched. Sporangia broadly ovoid or obpyriform to spherical of dimensions, 37.26- 57.74 x 24.16 - 41.12 µm with a conspicuous papillae. Based on cultural and morphological studies, the pathogen was identified as *Phytophthora* spp. The environmental relative humidity of > 90 % prevailing during monsoon is the major predisposing factor apart from high soil moisture which favours the spread of the fungus.

P (S 02) 08: Detection of *Macrophomina phaseolina* through loop mediated isothermal amplification assay

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A loop-mediated isothermal amplification (LAMP) technique was employed to develop a simple method for the detection of *Macrophomina phaseolina* in diseased plants of maize (*Zea mays*). Six sets of primers were designed for targeting the conserved region of *M. phaseolina* and were successfully detected in the LAMP technique. The assay was optimised to amplify fungal DNA under isothermal condition at 63 °C for 60 min. LAMP amplification products were detected by visual examination using nucleic acid stain indicating a ladder-like appearance on a 2% agarose gel. The LAMP products were visualized by presence or absence of turbidity and staining directly in the tube with nucleic acid stain dye allows easy detection which is similar to the analysis by gel electrophoresis. Further tests indicated that the LAMP assay was more sensitive and faster than the conventional PCR. However, reaction was not observed in the tissues of healthy plants by either in LAMP or PCR. Although both the LAMP and the PCR methods were capable of detecting *M. phaseolina* in infected tissues of maize, the LAMP method would be more useful than the PCR method for detection of *M. phaseolina* infection in maize and other host plants because it is more rapid, simple, accurate method. In contrast with conventional PCR and real-time PCR assays, expensive thermocycling equipment was not necessary which makes LAMP much more efficient and cost effective. Further validation of LAMP assay was carried out with field samples for detection of *M. phaseolina*.

P (S 02) 09: Identification and characterization of *Dickeya zeae* a causal agent of bacterial stalk rot disease in maize

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Maize is the third largest field crop after wheat and rice in the world. Globally maize occupies an area of 184 million hectares, with a production of 1016 million tonnes and productivity of 5.5 tonnes per ha. India ranks fourth next to USA, China and Brazil in maize production in the world with an area of 9.51 million hectares and annual production of 24.3 million tonnes. Maize production is constrained by a number of insect pests and diseases. Among diseases, bacterial stalk rot caused by *Dickeya zeae* has emerged as one of the most important disease in kharif sown maize crop during the recent years. Maize plants showing symptoms including premature withering and wilting, collapse of stems and unusual odour with slimy and soft. The infected plants were collected from farmers' fields of maize at Ludhiana (Punjab), Pantnagar (Utharakhand), IARI field (Delhi) and six districts of Telangana during kharif season 2019. The pathogen strains were isolated from infected maize stem and leaf sheath on a semi-selective CVP (Crystal Violet Pectate) Medium. Those strains formed characteristic deep pits on CVP medium were subjected to biochemical (Gram staining, 5% salt tolerance test, growth on NA at 37^{f} ˜C test and sensitivity to antibiotics test). All the pathogen isolates were grown individually in liquid Kings B medium for 24 h and bacterial suspension was adjusted to approximately 10^{8}-10^{9} cells/ml and tested for pathogenicity on susceptible varieties. The bacterial isolates that fulfilled Koch's postulates were used for molecular analysis. All the isolates should amplification at expected fragments of 420 bp and 1500 bp by PCR using primers corresponding to a virulence gene pelADE and a ribosomal gene 16SrDNA.

P (S 02) 10: Passion fruit - Another victim of wilt pathogen, *Ralstonia solanacearum* (Smith) Yabuuchi *et al.*

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Passion fruit (*Passiflora edulis* Sims.) is a perennial, woody vine crop which is valued for its fruits with unique flavour and high market value. Recently, this crop is being cultivated widely by many farmers in Kerala. During the month of May 2019, sudden wilting of entire vines of passionfruit was observed in Manjapra region of

Ernakulam district, Kerala with an incidence of 35 - 40 per cent. Purposive sampling surveys were conducted to assess the incidence in other locations and it revealed the presence of the disease in Thrissur district too. The plants of all ages were infected but more incidence was observed in fruiting plants. This highlights the importance of the disease which leads to complete yield and crop loss to the farmers. The most prominent symptom is the rapid wilting of the entire vines while the leaves remained still green. Within few days of infection, the entire plant was wilted and dried, spreading the infection to nearby vines. *In situ* ooze test carried out using the stem of the infected plants showed positive result. The isolation of the bacteria carried out on nutrient agar produced smooth, round, off white colonies with mucoid appearance. When grown on Tetrazolium Chloride medium specific to *Ralstonia,* typical fluidal white coloured bacterial colonies with reddish pink centre were produced. Gram staining test revealed that the bacteria was gram negative and rod shaped. Based on the morphological and cultural characters, the pathogen was tentatively identified as *Ralstonia solanacearum*. The pathogenicity of the isolate was proved by inoculating into passionfruit seedlings which expressed typical wilt symptoms and on isolation yielded the same bacteria. Identity of the pathogen was further confirmed through molecular characterization. Genomic DNA was isolated using NucleoSpin® Tissue Kit (Macherey-Nagel) following manufacturer's instructions. DNA was then subjected to PCR amplification using primer specific to 16s r RNA region of the bacterial genome which yielded an amplicon of size 1.5 KB.Sequencing and *in silico* analysis revealed that the isolate showed maximum homology of 97 per cent with *R. solanacearum*. Thus, confirmed the etiology of bacterial wilt disease of passionfruit as *Ralstonia solanacearum* (Smith) Yabuuchi *et al.* A perusal of literature revealed that this might be the first report of passion fruit (*Passiflora edulis* Sims.) as a susceptible host to bacterial wilt pathogen *R. solanacearum* from India.

P (S 02) 11: Molecular variability of *Magnaporthe grisea* infecting finger millet (*Eleusine coracana*)

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Finger millet (*Eleusine coracana)* commonly known as Ragi is one of the most important millets crop and largely grown in India. Ragi is affected by many diseases. Among them, blast disease (*Magnaporthe grisea*) is causing major yield loss to the crop. The symptoms of blast on ragi are much similar to the rice. Spindle shaped lesions of varying sizes are formed on leaves. These are usually greyish-green in the center with a yellowish margin, but later the central portion turns whitish and gradually disintegrates. Large oval or elongated brown spots occur on the leaves and often the neck below the ear head is attacked, resulting in failure of grain set or shrivelled seeds. Severity of blast on finger millet depends on the climatic conditions the fungus is known to prefer low temperature (less than 20°C) with high humidity, rainfall and low light for outbreaks. Moderate temperatures between 21 °C to 29 °C with more than 80 per cent mean atmospheric relative humidity during reproductive period favoured the disease development. Fourteen isolates of *M. grisea* were used to study their variability through RAPD analysis using random primers**.** RAPD analysis of twenty random primers amplified DNA fragments with different sizes. The RAPD pattern obtained for these isolates with different primers were defined by the presence or absence of bands. Each RAPD pattern was compared with each other and euclidean distance matrix was calculated for all the 14 isolates of *M. grisea.* The relationship among the isolates was represented as dendrogram using UPGMA. The isolates divided into two main group were further subdivided into clusters. Among the isolates, Mg13 isolate was grouped under group I and remaining 13 isolates were grouped under group II. The Mg13 isolate was placed in group I with approximately 78 per cent similarity coefficient between them and the isolates in group II. Group II divided into several clusters with 79 per cent similarity and so on. Overall, all the isolates significantly differed from each other.

P (S 02) 12: Association of causal agents in boll rot complex of cotton in Northern Karnataka

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Cotton (*Gossypium* spp. Family: Malvaceae) is one of the world's leading agricultural crops which is wide spread, plentiful and economically produced and ranks first among the fibres. It is not only a source of natural fibre but also a protein and oil source in animal feed and an excellent source for pharmaceutical uses. Karnataka ranks sixth in area with 5.65 lakh hectares and fourth in production with 19.0 lakh bales of lint with the productivity of 572 kg/ha (Anon., 2018). Cotton is vulnerable to many biotic and abiotic stresses which accounts for its low yield potential and in turn the high cost of production. Fusarium wilt, Verticillium wilt, Alternaria blight, angular leaf spot, boll rot and leaf curl are the major diseases which are responsible for loss of yield and quality parameters in cotton. Cotton boll rot complex is a disease condition where the associations of many pathogens influence the appearance and quality of matured cotton bolls. Experiment was conducted to know the association of pathogens and found that, pathogens such as *Alternaria macrospora, Fusarium oxysporum* f. sp. *vasinfectum, Exserohilum rostratum, Colletotrichum gossypii, Phoma* sp., *Trichothecium roseum, Aspergillus niger, Nigrospora oryzae* and *Rhizopus stolonifer* were found to be associated in causing boll rot complex disease of Bt.cotton and were identified on the basis of pathogenicity, morphological and molecular studies. Injection infiltration method was found better over spray inoculation technique for artificial inoculation of pathogens to prove the pathogenicity. The typical symptoms produced as a result of artificial inoculation of boll rot pathogens indicates that majority of organisms can gain entry into the host tissues with the aid of insect damage and can also penetrate through the boll surface (Bagga, 1970; Luke and Pinckard, 1970).Morphological and molecular characterization revealed that the fungal pathogens namely, *Alternaria macrospora, Fusarium oxysporum* f. sp. *vasinfectum, Exserohilum rostratum, Colletotrichum gossypii, Phoma* sp., *Trichothecium roseum, Aspergillus niger, Nigrospora oryzae* and *Rhizopus stolonifer* are associated in causing boll rot complex of cotton in northern Karnataka.

P (S 02) 13: Molecular characterization and genome organization of *Tomato mosaic virus* (ToMV) infecting tomato

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Viral diseases are part of the limiting factors to tomato (*Solanum lycopersicum* L.) cultivation which imparts huge economic loss by reducing both quality and quantity of yield. Among these, *Tomato mosaic virus* (ToMV) is one of major devastating viral diseases of tomato. The molecular characteristics of the full length genome of ToMV isolated from major tomato growing area of Andhra pradesh has been done through PCR followed by its sequencing. The complete genome of the ToMV-BG encoding four Open Reading Frames(ORFs). Based on the homology of translated and untranslated regions with other ToMV strains, the 5 proximal ORF1 encodes 126.7 kDa products that terminates in an amber codon which may read through to produce a 184.4 kDa replication-associated protein (ORF2). ORF 3 encodes for 28.8 kDa movement protein and ORF4 encodes for 17.4 kDa of the coat protein. Comparative sequence analysis of the ToMV-BG with ToMV isolates and other tobamoviruses has indicated that it is closely identical to ToMV strains from Egypt (AHM) and had sequence nucleotide identity of 41.8 to 84.0% with other tobamoviruses, whereas 98.0 to 98.8% with different ToMV isolates. The phylogenetic analysis of ToMV-BG isolate showed three main clades with a high bootstrap support results that relationship of ToMV-BG with ToMV isolates from Egypt (AHM), USA (Jasmine), Zimbabwe, India and the rest of the world.

P (S 02) 14: Characterization of *Leaf curl virus* infecting chilli crop in North Bengal

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Plants are often exposed to various environmental stresses which adversely affect the plants at physiological and cellular levels. Biotic stresses are results of attack from different potential microbial pathogens including viruses. Begomoviruses (Family- Geminiviridae) are major group of plant infecting viruses which cause severe damage to vegetable production. Being the leader in vegetable production, West Bengal has already become the hotspot of begomoviral infection which is a serious threat to our vegetable production. North Bengal (especially Terai region) is famous for chilli production. But chilli crop in this region is highly affected by begomoviruses. Begomoviruses typically have genomes consisting of two separately encapsidated genomic components, known as DNA-A and DNA-B. The DNA-A component contains six Open Reading Frames (ORFs) in both orientations that encode proteins which play major roles in symptom development, viral replication and infectivity, whereas the DNA-B component encodes two genes for viral movement and nuclear shuttling. These viruses are white fly-transmitted and produces symptoms like yellowing, mottling and inward curling of the leaves. Severe infection affects the growth and yield of chilli plant. The symptomatic presence of chilli leaf curl virus was assured by visualizing the typical symptoms followed by PCR based detection system. PCR protocol was carried out using begomoviral gene specific primers. Cloning and sequencing was done for the PCR products of the begomoviral genomic components. Based on the sequencing result and BLAST analysis it can be postulated that a new recombinant strain of begomovirus with 92.46% and 97.19% similarity with Pepper leaf curl Bangladesh virus (NC_004192.1) and Tomato leaf curl Joydevpur virus (EF194765.1) is in emergence. Besides characterization of the viruses, we have analyzed some defense as well as stress responsive enzymes like PPO, POD, CAT, PAL, Chitinase, Beta 1,3 glucanase to assess the extent of physiological stress which the plant is going through. The Phenyl Propanoid Pathway (P-P-P) which is the main defensive pathway of plants was also well elucidated for healthy as well as infected samples by HPLC techniques. Data were collected from healthy as well as infected plant during the infection period at 15 days interval and the result showed significant difference between healthy and infected plants in oxidative stress, accumulation of phenolics and cell death.

P (S 02) 15: Molecular characterization of virus complex associated with chilli leaf curl disease in Maharashtra

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Chilli is a widely cultivated crop, which is an almost crucial ingredient of Indian food and many other countries. Chilli leaf curl disease has been a major limitation to its crop cultivation and production, especially in tropical and subtropical parts of India, mostly Maharashtra, Telangana, Madhya Pradesh and Chhattisgarh. In year 2016, epidemics of chilli leaf curl disease have been a serious problem observed in various main chilli-growing districts of Maharashtra including Yavatmal. The severity of chilli leaf curl disease was so much that forced the farmers to completely abandon the crop mid way and produce alternative crops which ultimately resulted in drastic reduction of area and production of major chilli growing regions of Maharashtra. Chilli has been reported to be infected by several begomoviruses, namely Chilli leaf curl virus, Tomato leaf curl New Delhi virus and Tomato leaf curl Joydebpur virus. Consequently the present study aims to describe the association of a distinct begomovirus species and a betasatellite which will give a limelight to prevent the crop losses as well as spread of this chilli leaf curl disease in Maharashtra and central India. Leaf samples showing typical leaf curl disease symptoms like leaf curling, leaf distortion, leaf crinkling and yellow leaf margins were collected from widely separated areas of Maharashtra. This investigation observed that the size of leaves and branches were reduced noticeably and such plants bear only a few flowers and fruits. Sixteen infected samples were screened by using polymerase chain reaction with coat protein, movement protein and beta satellite specific primers. The infected samples showed amplification with respective expected sizes and supports the causes of the infection are begomoviruses. Further characterization of these begomovirus complex at sequence level and development of *Agrobacterium* based screening method for checking the resistance in chilli genotypes against chilli leaf curl disease is under progress.

P (S 02) 16: Recombinase polymerase amplification-based assay for field-level identification of *Thrips palmi*, a vector of tospoviruses

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Thrips palmi (Thysanoptera: Thripidae) is one of the important vectors transmitting seven tospoviruses. It is predominant tospovirus vector in Southeast Asia and has spread throughout Asia during the recent decade. It has been introduced in America, Africa, and Australia and considered as a quarantine pest in Europe. Identification of *T. palmi* at an early stage is crucial in formulating appropriate pest management strategies. Since morphological identification of *T. palmi* based on adult stage needs taxonomic expertise and time-consuming, there is need to develop rapid and reliable identification tools independent of developmental stages. Here, we report a field-level assay for rapid identification of *T. palmi* based on recombinase polymerase amplification (RPA). The RPA assay included three core enzymes *viz*. recombinase, single-stranded DNA binding protein and strand-displacing polymerase. Three pairs of RPA primers were designed based on 32 polymorphism at Internal Transcribed Spacer 2 region of *T. palmi*. Out of three pairs of primers tested, one pair (AG117 and AG118) efficiently discriminated *T. palmi* without any cross-reactivity with other predominant thrips species. The assay was standardized by ridding of routine nucleic acid extraction procedures and thermal cycling. This assay could be completed within 30 min at 37^0 C temperature. The assay was further simplified by using fluorescent as well as colorimetric dyes thus eliminating the gel-electrophoresis steps. The presence of *T. palmi* could be visualized by fluorescence signal or change in colour from violet to sky blue. In this assay no other sample manipulation such as thermal or chemical melting is required to initiate amplification. This rapid, field-level assay for diagnosis of *T. palmi* could be used in quarantine by non-taxonomic experts and will be helpful in developing suitable pest management strategies against thrips vectors and tospoviruses as well.

P (S 02) 17: Detection and identification of viruses associated with orchids from Sikkim and Darjeeling hills and molecular characterization of four isolates of *Odontoglossum ringspot virus (ORSV)*

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Orchid is a major floricultural crop worldwide and valued for cut flowers, potted plant and herbal medicine. Virus diseases are major constraints in orchid production and more than 58 viruses have been recorded on orchids so far. A survey was conducted at different orchid growing areas of Sikkim and Darjeeling Hills of West Bengal in 2018 and collected 44 samples of orchids with variable symptoms. Samples were examined under electron microscopy and rigid rods, flexuous rods; bullets shaped particles and enveloped quasi-spherical particles were observed in different samples. Subsequently, based on the particle morphology, double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) was performed for Odontoglossum ringspot virus (ORSV), Cymbidium mosaic virus (CymMV), Orchid fleck virus (OFV), Calanthe mild mosaic virus (CalMMV) and Groundnut bud necrosis virus (GBNV). DAS–ELISA results revealed the presence of CymMV, ORSV, GBNV and CalMMV. Similarly RT-PCR test using specific primers confirmed the presence of ORSV, CymMV, GBNV and CalMMV. No amplification of OFV was found in any of the samples. Cloning of coat protein gene of ORSV in four species of orchids (*Phaius tankervilleae* from NRCO Sikkim, Cymbidium hybrid (Baltic Glacier Mint Ice and SHOL-2 from CDC Rumtek, and *Epidendrum* from Everest nursery Kalimpong) showed 100% identity in nucleic acid sequences among themselves and more than 99% with other ORSV isolates available on GenBank. Present study showed that coat protein sequences of ORSV in India and elsewhere are highly conserved and proved that ORSV might have entered in Sikkim and Darjeeling Hills from other countries.

P (S 02) 18: Survivability of *Bacillus subtilis* in different liquid bioformulation for the management of foliar diseases of tomato

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Increase in soil fertility, plant growth promotion and suppression of phytopathogens are the targets of the use of potential bioformulation that containing bacterial antagonists leads to the development of eco-friendly environment. A liquid bio-formulation using different constituents and a suitable microorganism namely *Bacillus subtilis* has been developed to control fungal and bacterial diseases of tomato crops to replace pesticides. This liquid bio-formulation in addition to facilitates long shelf life, zero contamination, no need of carriers, convenience of handling, storage and transportation has easy to use with irrigation. The liquid bio-formulation was tested and compared for viability as well as its inhibitory characteristics against *Alternaria solani, Phytophthora infestans* and *Xanthomonas euvesicatoria* which cause the foliar diseases of tomato. Using the liquid bio-formulation the bacterial cell viability tests were carried out by plate count method for every month. The cell viability of *Bacillus subtilis* retains *Pseudomonas fluorescens* and *B. amyloliquefaciens.* This indicates that the formulation upto nine months showed better support for the viable cells. Moreover, the liquid bioformulation increased the tomato fruit yield compared to untreated control under glasshouse and field conditions.

P (S 02) 19: Diagnosis and management of *Clavibacter michiganensis* susbsp *michiganensis*; the cause of bacterial canker of tomato

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Tomato (*Solanum lycopersicon* L.) is severely affected by different bacterial diseases amongst them the bacterial wilt and canker disease of tomato caused by *Clavibacter michiganenis subsp michiganensis (Cmm)* is of utmost importance as the pathogen is showing its spread to several uninfected states of India. In the present study survey was carried in tomato growing areas in the lesser and outer Himalayan tomato growing belt of Himachal Pradesh and Uttarkhand, for identifying the location of pathogen spread. *Cmm* was isolated from different regions of Uttarakhand and Himachal Pradesh. Five different tomato growing regions in Uttarakhand and nine tomato growing regions in Himachal Pradesh are surveyed to assess the spread of disease and it was observed that the extent of the disease spread was very high in Himachal Pradesh with a mean disease incidence of 33.59% and disease severity of 27.71% while in Uttarakhand the spread of disease was observed in restricted areas and the recorded disease incidence was 5.55% while the recorded disease severity was 4.52%. The isolates of the test bacterium were established by biochemical, physical and morphological characterization and the sequence of most virulent isolate was submitted to NCBI with an accession no. of MH321815. For the management of disease, PBAT-1 (biocontrol agent), Streptomycin sulphate (antibiotic), BTH (prophylactic spray) and SA (protective spray) were found to be most effective in controlling the further spread of the pathogen.

P (S 02) 20: Development of nucleic acid based rapid diagnostic assays against wheat pathogens

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Diseases are main constrain in wheat production. Early detection of diseases is imperative for timely disease management. Molecular markers are fast reliable and robust and one needs unique stable regions for development of molecular diagnostics. The present study established phylogenetic relationship and multiple sequence alignment among different wheat pathogens based on different conserved regions i.e., internal transcribed spacer (ITS) regions, translation elongation factor 1á (*TEF-1á*), *â- tubulin* gene and glyceraldehyde 3- phosphate dehydrogenase (*GAPDH*) gene. The intergeneric variability among different pathogens was in range of 5-30% while, intrageneric was 2-24%. The polymorphism among them varied from few nucleotides (5 to 50) to large number of nucleotides (100-250 bp), which enabled identification of the many species specific stable unique regions. Visualization of extent of variability among different pathogens at different loci opened the access for selecting appropriate diagnostic markers. In present study we developed different diagnostic markers as polymerase chain reaction (PCR) based markers for detection of seed borne pathogens as *Tilletia indica*, a quarantine pathogen and *Fusarium graminearum,* a primary cause of Fusarium head blight (FHB), of small cereals and producer of the mycotoxins deoxynivalenol, nivalenol, and zearalenone in infected inflorescence and grains of wheat. These markers detected pathogens at as low as 10-100pg of DNA. LAMP based assay had also been developed for *T. indica.* LAMP assay was found superior to PCR or real time PCR as it was cheaper, less time consuming, does not require thermocycler and agarose gel electrophoresis. It detected as little as 100fg of DNA. Further, to resolve the problem of mixed fungal infection involving many pathogens there is a need of simultaneous detection of causal organisms. A macroarray, which is based on reverse line blot hybridization, had been developed for simultaneous detection of seven wheat pathogens viz., *Bipolaris sorokiniana, Tilletia indica, T. caries, Fusarium graminearum, Alternaria alternata, A. triticina* and *Ustilago tritici segetum* using ITS region and for three species of *Puccinia* using *â-tubulin* gene. This study has opened a wide horizon in the field of detecting wheat pathogens.

P (S 02) 21: Characterization of bacterial blight of anthurium in Karnataka

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Anthurium is the second largest tropical cut flower crop cultivated throughout the tropics as well as in temperate regions. The anthurium cut flower production is hampered by numerous fungal, bacterial and viral diseases. Among them, bacterial blight incited by *Xanthomonas axonopodis* pv. *dieffenbachiae* is one of the most serious and devastating disease. The survey for the incidence of bacterial blight of anthurium in different polyhouses of Karnataka revealed that the highest of 46 per cent was in Makonahalli village of Mudigere Taluk of Chikkamagaluru district and lowest of 16 per cent was in Bavikere village of Thirtahalli Taluk (Shivamogga).Six different isolates were collected from the different poyhouses. With regard to morphological variation, the isolates varied in their morphology on the different solid media used for screening but yeast extract dextrose calcium carbonate supported good growth of all the isolates. Temperature of 30ºC was optimum for the growth of all the isolates. Among the isolates, four isolates of *X. axonopodis* pv. *dieffenbachiae* required pH 6.0 for maximum growth and two isolates required pH 5.0 for maximum growth. The growth of all the isolates decreased as the pH of the medium gradually increased to 8.0. Molecular detection using 16S-rRNA species universal primers amplified with a fragment size of approximately 700bp. *In vitro* screening of different bactericides revealed that gentamycin, was highly effective as compared with others.

P (S 02) 22: Deep learning based assessment of disease severity in grape plant

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Indian economy highly depends on the overall agricultural productivity, with agriculture being the most significant sector and major contributor in terms of GDP as well as employment. Diseases in crops not only hampers the total yield and its quality, the excessive use of chemicals for their treatment produces substantial amount of residue, which leads to environmental pollution. In order to optimize the agricultural output, use of agrochemicals should be minimized. This can be achieved, if the severity stage of a disease is known, so that a recommended amount of pesticide is applied, under the observation of agronomists and botanists. In this study, the authors have implemented two popular CNN models, namely SqueezeNet and ResNet50, for evaluation of disease severity (early, middle, final) in leaf blight disease, affecting the grape plant. Colored images of healthy as well as diseased leaf images were selected in each category from the PlantVillage dataset. It is an open repository of more than 50,000 leaf images of 14 crops and 26 diseases, labelled and categorized into 38 plant - disease pairs. Three color image enhancement techniques namely Image adjust using function *imadjust*, histogram equalization, Contrast-limited adaptive histogram equalization (CLAHE) were first applied to the selected images and used for training the models separately. Performance measures viz. accuracy, mean Recall, mean Precision, mean F1-score and loss were recorded for comparison. SqueezeNet achieved the highest accuracy of 84.02% with *imadjust* approach, 83.51% with CLAHE technique, 81.96% with histogram equalization and 83.25% with original images. Similar performances was observed with ResNet50 architecture, achieving the highest accuracy of 80.41% with *imadjust* approach. The implementation was done on a Windows workstation, using MATLAB R2018b, equipped with GTX1060 6GB GPU.

P (S 02) 23: Molecular detection of *Tomato chlorotic dwarf viroid* infecting tomato (*Solanum lycopersicum*) in India

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Tomato chlorotic dwarf viroid (TCDVd) is a member of the genus *Pospiviroid,* family *Pospiviroidae*. It was first identified on naturally infecting Tomato plants in Canada and in some ornamental species from Europe and Asian countries. Tomato plants showing typical viroid symptoms such as stunting, leaf curling and epinasty were sampled from tomato cultivated fields in Mysore district, Karnataka state (India). Low molecular weight RNA was extracted from the suspected tomato plants by lithium chloride method. The RNA samples were subjected to RT-PCR using the universal primer pairs Pospi1-RE/Pospi1-FW for the detection of *Posiviroids*. The expected amplicon (200bp) was amplified and the PCR product was purified and sequenced directly. PCR product was cloned in to pGEM®-T Easy vector and sequenced. Further direct sequencing of the amplicon revealed 97% and 95% identity to the *Tomato Chlorotic Dwarf Viroid* (TCDVd) in the GenBank with Accession No AB329668.1 and EF26530.1 from Japan and Netherland isolates respectively. The viroid infected tomato sap was mechanically infected to healthy tomato seedlings at two leaf stages. Seedlings showed leaf curling and reduction in plant growth after 45 days of post inoculation. The presence of pospiviroid from tomato *(Solanum Lycopersicum)* was identified as TCDVd and further studies are in progress for the amplification and sequence of full length TCDVd. To the best of our knowledge, this is the first report of TCDVd occurring on Tomato in India.

P (S 02) 24: Confocal microscopy: Its potential uses in plant pathological research

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Confocal Laser Scaning Microscopy (CLSM) has, of late, become an important tool in several scientific spheres namely biological, biomedical and material sciences. The technique involves imaging fluorescently-labelled specimens with significant three dimensional structures and generates information from a well-defined optical section rather than from entire specimen, thereby eliminating the out of focus glare and increasing the contrast, clarity and detection sensitivity. A laser is used to provide the excitation light which passes through a pinhole aperture and reflects off a dichromatic mirror. These mirrors scan the laser across the sample. Dye in the sample fluoresces and the emitted light gets descanned by the same dichromatic mirror. The emitted light passing through the pinhole is measured by a detector, *i.e*., Photo-multiplier tube and produces an image. CLSM was invented by Marwin Minsky in 1955 specifically for studying neural network in the living tissue which now provides novel and better understanding of cellular structure and processes, *modus operandi* of microbes and pathogenesis at cellular and sub-cellular level. Use of fluorescent probe permits localization of substrate without interference with each other. It is possible to examine a field of cells *in vitro* or *in vivo*. Now a days, many fluorescent probes are available from various manufacturers which are designed to recognise specific biological macromolecules (a protein, nucleic acid), or to localize within a specific structural region. Thus, CLSM is a tool of choice to identify the phenotype of a cell in conjunction with its co-expression of other marker or proteins. It also produces improved images of unstained specimen that reflects enough light to produce contrast image in bright field. It is useful in studying physiology of host-pathogen interaction by (i) Localization of various proteins, including proteins associated with fungi, bacteria and viruses, (ii) Characterization of structural proteins; (iii) Characterization of fungal spores; (iii) Microbial live/dead cell counts. Fluorescent molecules in confocal microscopy also allows to locate and visualize a wide range of live and fixed specimens (through point to point illumination), including immuno-labelling, imaging in live cells, ion dynamics, cell division, apoptosis, necrosis, membrane potential endocytosis, multiple labelling, exocytosis, membrane fluidity, protein trafficking, signal transduction, and enzymatic activity.

P (S 02) 25: Incidence and effect of burl disease associated with mango germplasm

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Mango (*Mangifera indica L*.) isthe most economically important fruit of India which suffers by wide range of disease and disorders that diminishes mango fruit yield and quality. “Mango burl” disease is one of them that isminor and recently reported disease in India. Earlier there is no report about burl incidence and its effect in western part (Gujarat) of India therefore; the study was conducted in 2017-2018. During the study major mango growing district of Gujarat state were surveyed for burl incidence and nearly two hundred mango germplasm were screened on the basis of burl appearance or morphological characteristic. Morphologically burl is an uncontrolled outgrowth and abnormal swelling, usually occurs on main trunk and primary branches, but sometimes it can be seen on the whole plant.Plant samples were also collected and further processed in laboratory for pathogen identification. Samples were inoculated in Hofers bacterial media and white creamy colony was appeared after 24hr of inoculation. The isolated bacterium was *Agrobacterium tumefaciens* confirmed morphologically by gram staining. For the confirmation of burl development, isolated bacterial colonies were inoculated in two mango germplasm in *In-vitro* condition and 33.33% disease incidence was observed. Naturally, 20% disease incidence was observed during survey and maximum incidence percent was observed in ArkaArunaBadami model and MahmoodVikarabad whereas Mallika, Amarpali and Dasahari were found free from burl disease. Langra and Rajapurigermplasm observed as minimum incidence percent comparative to ArkaAruna and MahmoodVikarabad but found highly susceptible germplasm from western part (Gujarat) of India.

P (S 02) 26: Multiplex polymerase chain reaction for simultaneous detection of begomovirus and satellite molecules associated with cotton leaf curl disease in India

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Cotton leaf curl disease (CLCuD) is a major constraint in cultivation of cotton (*Gossypium hirsutum*) in entire Northwest (NW) India. The CLCuD is caused by whitefly *Bemisia tabaci* transmitted begomovirus and associated betasatellite and alphasatellite molecules. A quick, sensitive and effective multiplex polymerase chain reaction (mPCR) assay was developed in this study for the simultaneous detection of the CLCuD-begomovirus and associated betasatellite and alphasatellite molecules. Different primer sets for each viral component were designed based on the retrieved nucleotide sequences of CLCuD-begomovirus and associated satellite molecules from the GenBank. Primer blast was carried out to check the specificity of the primer to amplify the target viral sequences. The specific pair of primers designed for each single virus component was evaluated for its sensitivity and specificity using both a component-specific PCR that amplified that virus component as well as the mPCR assay. Three specific pairs of primers were identified, which in combinations amplified simultaneously the complete CP gene (771bp) of the CLCuD-begomovirus, the complete âC1 gene (363 bp) of the betasatellite and the partial Rep gene (440 bp) of the alphasatellite in mPCR assay. The component-specific amplified products produced by these assays were identified based on their desired amplicon sizes. The identities of the viral components were confirmed by cloning and sequencing the amplicons obtained in the mPCR. The mPCR assay was validated using naturally CLCuD-infected cotton plants which were collected from the cotton fields of Haryana, Punjab and Rajasthan states of NW India. This assay will be useful for the epidemiological monitoring of the viral components associated with CLCuD in India.

P (S 02) 27: Studies on *Pestalotiopsis* leaf spot of some selected minor fruits grown in Nadia district of West Bengal

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Minor fruits, grown in most parts of world, are well known for their good nutritional and medicinal values, maintaining health, livelihood and nutritional security for many people in developing countries by minimizing food gaps during periods of drought or scarcity. Though the minor fruit crops are attacked by fungal, viral, bacterial and nematode diseases, but fungal diseases are most important. Of the fungal pathogens, *Pestalotiopsis* is known to attack a number of crop plants grown in the world and causes their considerable economic loss. But very limited works have been done on this fungal genus, attacking minor fruits grown in the state of West Bengal, and particularly on its occurrence, symptom development and cultural characteristics. Present attempts have been made to study the symptom, time of occurrence, causal organism and pathogenicity testing of the disease and cultural characteristics of pathogens isolated from minor fruit crops namely Mahuwa (*Madhuca longifolia*), Persimmon (*Diospyros kaki* Thunb.), Sapota (*Achras sapota* Linn.), Barbados cherry (*Malpighia glabra* L) and Water apple [*Syzygium aqueum* (Burm.f.) Alston]. The *Pestalotiopsis* spp. isolated from these hosts were positive for pathogenicity testing at their respective hosts and later grown in six growth media *viz.* Potato Dextrose Agar (PDA), Czapek Dox Agar (CDA), Czapek Dox Agar with 0.1% Yeast Extract (CDAYE), Oat Meal Agar (OMA), Richard's Agar (RA) and Malt Extract Agar (MEA) and incubated for 9 days for studying radial growth and its growth rate. On Barbados cherry, leaf spot pathogen was isolated and identified as *Pestalotiopsis*. Maximum radial growth was observed in RA medium (av. 8.875 cm) and minimum growth in CDA medium (av. 6.625 cm) whereas the same trend in highest growth rate was noticed at RA medium (0.037cm/ hour) and lowest at CZA (av. 0.028 cm/ hour). From the leaf spot of water apple, *Pestalotiopsis* sp. was isolated. Full plate radial growth (9.0 cm) of the fungus was noticed in RA medium (av. 8.45 cm) followed by PDA medium and minimum was recorded in MEA medium (av. 6.025 cm). The growth rate of this fungus was documented highest in RA medium (av.0.038 cm/day) and lowest in Malt Extract Agar (av. 0.025 cm/day). In case of leaf spot of sapota, causal pathogen of this crop was recognized as *Pestalotiopsis* sp. and maximum growth of it was recorded in PDA medium (av. 8.9 cm) followed by RA medium (av. 8.77cm) and minimum growth was found in MEA medium (av. 6.625cm). The growth rate of this fungus was observed highest in RA medium (av.0.036cm/hr) and lowest in MEA medium (av. 0.028cm/hr). On Madhuca, the leaf spot pathogen was identified as *Pestalotiopsis olivaceae* assumed to be the first report on Madhuka from West Bengal. The same six different culture media were tested for radial growth. Radial growth of this fungus was recorded highest in CDA medium (av. 8.8 cm) whereas the same was lowest in MEA medium (av. 6.05 cm). The average growth rate of this fungus was found highest in CDA medium (av. 0.037cm/hr) and lowest in MEA (av. 0.025cm/hr).

P (S 02) 28: Comparison of amino acid sequence profiles and 3-D structural prediction of coat protein of sweet potato *Feathery mottle virus* (SPFMV) reveal strain variation

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Sweetpotato Feathery Mottle Virus (SPFMV) under potyviridae family is the most widespread disease in sweetpotato (*Ipomoea batatus L.*) across the world and causes differential symptoms of feathery mottle and degeneration of leaves and deformed root. The present study highlights the enhanced molecular resolution and 3-state prediction of amino acid of coat protein of seven SPFMV strains. Viral coat protein (CP) derived from an isolate (Gene bank Accession No.HM035545 and poly protein ID D6R1L4_9POTV) BCKV, India showed close relationship with RC (Russet Crack) strain and diverged from the strains 4C, EC,S, O and K1 of SPFMV. Protein Feature View of PDB entries mapped with watermelon mosaic virus (WMV) Polyprotein (PF00767) to a UniProtKB sequence S480335 and predicted structural similarities for the SPFMV strains in PDB ID 5ODV for WMV. Analysis of Nuclear Localization Signal (NLSs) and its prediction of CP sequences unveiled the key amino acids in the corresponding amino acid sequences of SPFMV strains required for systemic infection, viral particle formation and insect transmission and showed typically rich in arginine and lysine residues. SPFMV, BCKV isolate revealed a significant correlation between clustering of the viruses and geographical origin and sequence variation in coat protein gene of SPFMV in different subcontinents of the world is an interesting natural mutational phenomenon compared to the conserved coat protein domain of several plant viruses instead. Phylogenetic studies of polyprotein of SPFMV, BCKV isolate showed evolutionary compatibility with other viral taxa and a motif Asp-Ala-Gly (DAG) with the nucleotide sequence GATGCGGGA (nt 31-39) was found at the N-terminal region of coat protein (CP) gene of BCKV are same to other isolates and highly conserved domain which is required for aphid transmissibility. About 20 amino acids downstream from the DAG motif, there is a potential trypsin cleavage cited that is conserved in all potyviruses.

P (S 02) 29: A novel technique for growing *Hypsizygus ulmarius* in bottles

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A study was conducted for exploring the possibilities of discarded chemical bottle (bottle of 2.5 L) of 30 cm and 16 cm width made of sintered glass for cultivation of *Hypsizygus ulmarius*.The neck of the bottle was cut by binding a thread soaked in kerosene oil near the neck region. The thread was ignited and once the entire thread encircling the neck was inflammable the bottle was sprinkled with water and as a result the neck of the bottles was removed. These bottles were utilized for cultivation of oyster mushroom. The bottle was primarily washed with calcium carbonate and clean water. Wheat straw was sterilized with bavistin and formalin one day prior of bottling. On the day of filling the bottles wheat straw was allowed to dry in shade for removal of excess moisture, thereafter the substrate was filled in sterilized glass bottles @ 0.8-0.9 Kg/bottle (wet basis). Spawning was done by layer method. After spawning the bottles were covered with polythene and tied by rubber or thread. Spawned bottled was kept in growing room at temperature 25°C.Complete spawn run was observed after 12 days of spawning; pin head formation was observed after 14 days of spawning ;fruiting body observed in 16-18 days of spawning.The total weight of harvested mushroom was 575 grams per bottle with Biological Efficiency of 143%.

Session 3
Population genetics and pathogen diversity

Keynote Papers

KN (S 03) 01: Plant virus threats to SDGs in sub-Saharan Africa: Progress and lessons from the case study on banana bunchy top virus

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Increasing and sustaining crop productivity per unit area is one of the main requirements to achieve Sustainable Development Goals (SDGs), particularly SDG1 (no poverty) and SDG2 (zero hunger). However, in sub-Saharan Africa (SSA) average yields falls far below the global average and there is major variation across regions and seasons. Furthermore, annual crop production increase in many countries in SSA is mainly due to increase in area harvested. Diseases caused by several endemic (e.g. cassava mosaic, maize streak and yam mosaic) and emerging (e.g. banana bunchy top, cassava brown streak and maize chlorotic mottle) viruses are among the major contributing factors for poor production and high yield gap. For instance, the *Banana bunchy top virus* (BBTV, genus *Babuvirus*), responsible for the most devastating "bunchy top" disease, reduces production to near zero in affected plantations. This virus introduced into African continent in 1920s has spread to 15 countries and pose as a serious threat to banana production in 3.7 million ha. The virus has a six-circular single-stranded DNA genome and has been inadvertently spread through the movement of infected planting material. The banana aphid (*Pentalonia nigronervosa*) that occur in all regions of banana production is the natural vector responsible for secondary spread of virus acquired from the introduced contaminated planting material. In the absence of durable host resistance, management strategies for BBTV involving quarantine, eradication and clean seed programs have not been effective in containing the virus spread. Based on the status of occurrence, different countries in SSA have categorized BBTV as endemic, emerging or invasive threat. This presentation based on the BBTV case study, enlists challenges to control endemic, emerging and invasive virus threats in SSA, and provides an updated status on the impact ofBBTV threat to banana production in SSA;knowledge on virus diversity and host-virus interactions; advances in diagnostics, including use of ICTs, remote sensing and machine learning for virus disease surveillance; effectiveness of control interventions based on containment and clean seed production programs; and concludes with lessons and recommendations for effective virus disease control and its significance to achieve SDGs in SSA.

KN (S 03) 02: *Citrus tristeza virus is* a major biological stress causing citrus decline in India and its management strategies

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Citrus tristeza virus (CTV), an *Toxoptera citricidus* transmitted closterovirus destroys millions of citrus trees worldwide including India. The virus contains flexuous filamentous particles (2000 x 11 nm), +ve sense ssRNA (~19.3kb with 12 ORFs encoding 19 proteins) genome. CTV infects most of the cultivated citrus causing symptoms like decline, yellowing, growth cessation/stunting and stem pitting with poor fruit yield and quality. CTV is a century old problem and killed > one millions tree in India. CTV occurs in all the citrus growing geographical zones and infects all the commercial citrus and its relatives. The overall disease incidence 26.3-60% in India has been estimated; where 47-56% in Northeast, 36.3% in Central, 36-50% in South and 16-60% in North-Northwest India. A total of 114 CTV isolates (19 from Central India, 56 from Northeast, 21 from South and 18 from North India) were characterized based on sequencing 5'ORF1a and CP gene. Indian isolates are extensive diverse showing 78-99% nt identity falling into at least seven different genotypes. A decline inducing CTV strain, namely Kpg3 of the Darjeeling hills of Northeast India was identified and its complete genome (19253nt: HM573451) was sequenced for the first time in India. The Kpg3 is a recombinant and genetically related to Israel severe CTV isolate VT. Based on the 32 half genome (8.4 kb, ORFs 2-11), four Indian CTV isolates B5 (Bangalore: HQ912023), D1 (Delhi: HQ912022), G28 (Assam: KJ914661) and Kat1 (Vidarbha: KJ914662) were characterized based on sequencing analysis. They had 89-99% nt identities among them. Genomes of Indian, Asian and International isolates were also analysed and compared. The Asian isolates fell into six, whereas the Indian isolates into four genogroups. Indian isolates D1, Kat 1 and Kpg3 grouped together (Kpg3Gr). The B5 isolate is a new and the G28 is distinct isolates/strains. The recombination phenomenon is the major factor for evolution of diversified CTV in India. Codon usage biasness (CUB), negative selection and gene flow also play major role for evolution of CTV variants. Bud wood and shoot tip grafting for developing disease free citrus planting materials are very much important. CTV-free mandarin plantlets was developed and supplied to the farmers of in many areas of India. For development of transgenic resistant citrus, several anti-sence (RNAi) and hairpin (ihp-RNAi) gene constructs targeting CP (p25) and suppressor (p23) gene of CTV were made in pBinAR and pRNAi-GG. Agrobacterium-mediated transformation protocol was developed using epicotyl explants of citrus seedlings. Regeneration efficiency of transformed plant was 1.38% at 2.0 mg/l BAP in MS medium. Mild cross protecting strains (MCPS) were identified through *in silico* CUB analysis using the CP and p23 gene sequences of CTV available in our laboratory and MCPS is being evaluated by challenging with severe CTV isolates through biological indexing.

Invited Papers

I (S 03) 03: Population dynamics of *Phomopsis* vexans causing die back and fruit rot disease in brinjal and its management under temperate ecology of Kashmir, India

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Morphological studies of isolates revealed variations in size and shape of pycnidia, shape, size of á and â conidia and formation of guttulae in á-conidia. Average size of á-conidia varied from 4.01 × 1.25 to 14.12 × 4.09 µ while as â-conidia ranged from 15.39 × 0.65 to 35.57 × 1.07 µ. Pycnidial size varied from 144.47 × 410.67 to 534.89 × 321.19 µ. Majority of the isolates took 10 to 20 days to produce sporulating pycnidia on PDA with marked differences in pycnidial density however, some isolates produce sporulating pycnidia in less than 10 days. In most of the isolates pycnidia were randomly distributed in the colony however, distribution of pycnidia in concentric rings was also found in some isolates. The effect of temperature, pH, carbon and nitrogen sources on the mycelial growth and fructification of *Phomopsis vexans* were studied in the laboratory. The isolates produced best mycelial growth and fructification at 25^{o}C and at pH 5.5. Disaccharides among the carbon sources and nitrate form among the nitrogen sources proved best for both mycelial growth as well as fructification. On the basis of disease reaction expressed by different brinjal lines, Pusa Purple Long (PPL) was found to be most susceptible to PV$_{1}$, PV$_{11}$, PV$_{16}$, PV$_{17}$ and PV$_{21}$ isolates of *P. vexans* while as SK-BL-01 was found to be least susceptible to the said isolates. Role of temperature in the interconversion of á and â-conidia was studied under both field and laboratory conditions and it was found that lower temperature (10-15^{o}C) favoured the formation of â-conidia while as the higher temperature (25-30^{o}C) produced á-conidia. Host range studies on tomato, chilli, capsicum and okra revealed that only tomato acts as a host for the said pathogen. The pathogen *P. vexans* overwintered as mycelium and pycnidia on infected leaves, twigs and fruits and also in infected seeds. The viability of spores as well as per cent survival gradually decreased with increase in storage period in both seeds and infected plant parts. Further, the viability and per cent survival was more at ground surface than at increasing depths and these values were more on stem than on leaves and fruits. *In vivo* evaluation of different treatments revealed that soil amendment with vermicompost @ 7 q ha^{-1} and seed treatment with carbendazim 50 WP @ 2 g kg^{-1} seed proved most effective in nursery against damping off and leaf blight. The present investigation revealed that soil amendment with vermicompost @ 7q ha^{-1}, soil amendment with *T. harzianum* @ 5kg ha^{-1}, carbendazim 50 WP @ 0.1% as root dip and carbendazim 50 WP @ 0.1% as foliar spray proved to be highly effective against leaf blight, stem blight and fruit rot under field conditions.

I (S 03) 04: Pathogenic and genomic variability reveals adoptive evolution in Indian isolates of *Xanthomonas oryzae* pv. *oryzae*

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Xanthomonas oryzae pv. *oryzae* (*Xoo*) is a serious pathogen of rice causing bacterial leaf blight (BLB) disease. Resistant varieties and breeding programs are being hampered by the emergence of highly virulentstrains. An understandingof diversity within *Xoo* population is required for identifying the *Xa* genes that are to be deployed for development of resistant rice cultivars. Among 1214 isolates of *Xoo* collected from 20 different states of India, 12 major pathotypes were distinguished based on their reaction towards eleven*Xa* genes (*Xa1*, *Xa3*, *Xa4*, *xa5*, *Xa7*, *xa8*, *Xa10*, *Xa11*, *xa13*, *Xa21, Xa23*). The vast majority of the assayed *Xoo* isolates were incompatible with one or more *Xa* genes. Whole genome sequencing and analysis of 100 *Xoo* isolates revealed the clustering of Indian isolates along with other Asian isolates, distinct from African and US *Xoo* isolates. Indian *Xoo* population consists of a major clonal lineage and four minor but highly diverse lineages. Further analysis revealed that the major lineage, L-I is youngest and of recent origin compared to remaining minor lineages that seems to have originated much earlier in the past. This study provided unprecedented insights into the origin of *Xoo* lineages in India and its relationship with those present worldwide. The information generated in this study is being utilized for development of BLB resistant cultivars, and will be further useful in efforts towards building sustainable solution against this pathogen.

I (S 03) 05: Assessment of genetic diversity and population structure of *Ustilaginoidea virens* isolates, causing false smut disease of rice

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False smut caused by *Ustilaginoidea virens* is one of the most emerging diseases of rice in the world because of its adverse effect on quantity as well as quality of the produce. The false smut fungus shows a high degree of variability in the field and limited information is available on its genetic diversity and population structure in India. Twenty-nine (29) polymorphic RAPD (15) and SSR (14) markers were used to investigate the genetic diversity and population structure of 63 false smut isolates collected from eastern and north-eastern states like Assam, Bihar, Punjab, Odisha, Meghalaya, Tamilnadu and West Bengal. The markers yielded a total of 140 alleles and number of alleles per locus varied from 2 to 8. The similarity coefficients based on the combined RAPD and SSR data, ranged from 0.37 to 0.97 indicating moderate genetic differences among isolates. Phylogenetic analysis showed that all isolates were divided into three clad with a similarity coefficient of 0.706. Population structure analysis was done and K value equal to 2, indicating that the optimal number of subpopulations was two with few admixtures. The AMOVA results supported the presence of genetic diversity and the highest percentage of variation (82%) was within populations and 12% among populations of *U.virens* isolates. Mantel test showed that genetic distance between the isolates is increasing with the increasing geographic distance. The results in this study imply that geographical environments influence genetic variation. The high level of genetic diversity within isolates represented an extreme case of genetic differentiation, which was probably attributed to migration and partially to the intrinsic nature of *U. virens*. The findings definitely would help to understand the genetic diversity of *U. virens* from east and north-eastern India and would show the way to develop appropriate management strategies and developing false smut resistant variety through molecular breeding.

Oral Papers

O (S 03) 06: Morpho-pathological and molecular diversity analysis of *Alternaria brassicae* isolated from *Brassica juncea* collected from various locations of India

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Alternaria blight isone of the important disease of *Brassica* oilseed crops caused *by Alternaria brassicae,* which causes losses in yield upto 47%. Till date no resistance source to Alternaria blight available world over and chemical control measures are only options to managed this disease. Present investigation was conducted to study on morpho-pathological and molecular diversity among the isolates of *A. brassicae* collected from Brassicas. Diseased leaves samples were collected from various locations and Alternaria fungi were isolated on potato dextrose agar and radish agar media using aseptic conditions. Fungus was purified by single spore method. Observations were recorded on colour and morphology of colony and its conidia. Results indicates that twelve isolates of *A. brassicae* were purified and characterized. All isolates were confirmed as *A. brassicae* on the basis of morphological and molecular data.Variation was recorded among all isolates on the basis of colour and morphology of colony and its conidial characteristics. Every isolate was designated as Ab-1 to Ab-12. Mycelia colour was different among different isolates ranging from olivaceous green to black. Kinetic growth of isolate Ab-1 was smooth and slow, while rest of the isolates were fast grown.Diversity among isolates were found in spore morphology in respect to conidial length, width and number of horizontal and vertical septa. Variations in conidial length (25.1 um -142.5 um)and width(7.5 um -18-6 um) among isolates was recorded. However, average number of horizontal and vertical septa was ranging from (3-8.6) and (0-3), respectively. Specifically, maximum conidial length (142.5um) and transverse septae (9 nos) was recorded in isolate Ab-1, while max conidial width recorded in Ab-7 (18.7 um). Minimum conidial length (25.1 um) and width (7.5 um) was observed in isolate Ab-6. Colour variations were also recorded in conidia as yellow (Ab-7), black (Ab-6) and all other isolates were brown. Pathogenic reaction showed that isolate Ab-1 was highly virulent while other isolates were exhibited pathogenic variations. Molecular data indicated clear-cut variation among each isolates. It is concluded that substantial diversity was found in *A. brassicae* isolates in India.

O (S 03) 07: Prevalence of rice root knot nematode a serious threat to basmati rice production in western Uttar Pradesh

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Basmati rice is pride of India, being cultivated in limited area of India such as Western Uttar Pradesh, Haryana,Punjab, Himachal Pradesh, Uttrakhand, J&K. and some part of Delhi. In which Western Uttar Pradesh play very important role in basmati rice production since last few years. In India, area under basmati rice cultivation is approximatly44.86 million hectare with total production of 5.64 million tonnes.Basmati rice is affected by many fungal bacterial,viral and nematode diseases. Among the nematode, rice root knot nematode disease is one of the most economically important disease of rice. It has been reported to cause significant yield losses in many regions of rice growing areas. To know the status of this nematode in Western Uttar Pradesh, survey was conducted during kharif 2014 and 2015 in rice growing area of the region. In this survey rice fields from 200 villages of 18 district of Western U.P. falls under the jurisdiction of SVPUA&T, Meerut were

surveyed. Through the surveyit was observed that due to continuous following rice- wheat cropping system by the farmers, rice root knot nematode problem is emerging as a serious threat to rice production particularly for basmati rice. Frequency of occurrence of rice root knot nematode infestation in different surveyed area was recorded from 50-90%. Highest frequency of occurrence 90% in Ghaziabad and minimum 50% in Bagpat, G.B.Nagar, Bareilly, Rampur and Shahjahanpur districts was recorded. Maximum disease incidence 88% in Ghaziabad and minimum38% was recorded in Shahjahanpur district. Maximum disease severity 3.68 % was recorded in Ghaziabad and minimum 0.8% in Saharanpur district was observed.

O (S 03) 08: Unveiling the taxonomic identity and genetic diversity of *Colletotrichum gloeosporioides* species complex causing anthracnose in different fruit crops

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Colletotrichum sp. cause anthracnose disease in several plant species in tropical and temperate regions. In the present study a total of 30 isolates of *Colletotrichum* spp. were isolated from plant samples showing anthracnose symptoms. The isolates were characterized based on morphology and typified into 3 major groups based on their morphological characters in culture media. Molecular analysis based onglyceraldehyde-3-phosphate dehydrogenase (GAPDH) sequence,resolved the isolates as *C. siamense, C. fructicola, C. endophytica, C. asianim, C. aotearoa* and *C. kahawae* subsp. c*iggaro* belonging to the *C gloeosporioides* species complex. To study diversity of the *C. gloeosporioides* species complex population, the isolates were grouped into 4 geographical cluster i.e. Delhi, Rahuri, West Bengal and North East. 12 ISSR primers were used to study the population diversity and 11 primers generated scorable polymorphic band of 100-1300 bp with average PIC value of 0.27. The genetic diversity was high in NE population with polymorphism (78.75%). The genetic distance was high (0.129) between Rahuri and WB populations. The degree of genetic differentiation among population was 0.09 and gene flow was estimated at 2.45 within population of *Colletotrichum* cryptic species. Population stratification was reflected through the UPGMA dendogram, which consisted two main subdivision. Group 1 consisted mixture of isolates from all over the geographical region and Group 2 consisted only population from NE region. The present study indicated presence of admixture between isolatesfrom all over the geographical region.

O (S 03) 09: Pathogenicity and anastomosis of *Rhizoctonia bataticola* causing dry root rot of chickpea

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Dry root rot caused by *Rhizoctonia bataticola* (Taub.) Butler [Pycnidial stage: *Macrophomina phaseolina* (Tassi) Goid] is a soil borne fungal pathogen. Keeping in view the importance of the disease due to change in climatic conditions, studies were conducted on distribution of the disease, cultural, morphological, pathological and molecular diversity. The experiment was conducted at Department of Plant Pathology CSA, Kanpur. In the present studies, fifty isolates of *R. bataticola* were isolated disease sample of dry root rot of chickpea from different regions of Uttar Pradesh. Those isolates were analyzed for cultural and morphological variability. Significant differences were detected among fifty isolates in their radial growth, colony colour, pigmentation, margin type, growth pattern, aerial hyphae, sclerotial size and shape. Six isolates among fifty were producing dark red colour pigment on PDA & other media. Seventeen isolates showing black colour colony, sixteen were giving olive colour and remaining seventeen showing gray colour on PDA media. On the basis of pathogenicity there are thirty two isolates which are highly virulent and others are less virulent. Anastomosis is also found in some isolates. On the basis of their sclerotial size, twenty two isolates were classified as large sized, eighteen as medium sized, and the remaining ten isolates as small sized sclerotia. These cultural and morphological variations in among different isolates are very useful in study of diversity of *R. bataticola*.

O (S 03) 10: Characterisation and biodiversity study of *Trichoderma* community in crop rhizosphere of Southern Rajasthan, India

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To investigate the biodiversity of Trichoderma we conducted first survey of soil inhabiting Trichoderma in agricultural fields in seven districts of southern Rajasthan, India. We collected a total of 284 samples. Seventy four isolates were obtained including eight species viz. *Trichoderma harzianum, T. asperellum, T. brevicompactum, T. longibracheatum, T. ghanense, T. hamatum, T. atroviride* and *T. erinaceum*. Their phylogenetic positions are determined by sequence analysis of combined partial sequence of Internal Transcribed Spacer (ITS) region and translation elongation factor (Tef) 1- á. Morphology and culture characteristics are observed, described and illustrated in detail. The isolates collected were screened against *Sclerotium rolfsii*, *Rhizoctonia solani* and *Fusarium* spp. by confrontation assay and selected most potential isolates. Among all the isolates antagonistic activity exerted by *T. harzianum* isolates were relatively more potent ($P<0.05$) than that of other isolates. These selected isolates were studied for production of chitinase, gibberellins and IAA. These isolates were also studied for production of volatile and non volatile compounds. The ability of induced systemic resistance against *S. rolfsii* in tomato plant was evaluated and studied chitinolytic and â 1, 3-glucnase activity. The *T. harzianum* isolates BThr4 and BThr29 showed highest chitinolytic activity (26.22 mg/ml and 20.38 mg/ml) and â 1,3-glucnase activity by BThr29 (284.62 µg/ml).

O (S 03) 11: Characterization, virulence and cross-infectivity of *Fusarium* spp. on cucurbits

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Surveys were done and 30 isolates of *Fusarium* spp.were isolated from wilted muskmelon plants collected from different fields in the districts of Rajasthan, Haryana, Uttar Pradesh, Uttarakhand, Laddakh and Delhi. The *Fusarium* isolates were characterized at species level and their morphology was studied. Interestingly, it was found that along with the suspected species *Fusarium oxysporum,* various other species of *Fusarium* were alsofound to be associated with the wilted muskmelon plants viz., *F. solani*, *F. palladoroseum* and *F. verticilloides*. Pathogenecity test was conducted to check virulence of the isolates of *Fusarium* spp. onsusceptible muskmelon cultivar viz., Kashi Madhu under net house condition. Pathogenecity test proved the virulence of *Fusarium* isolates on muskmelon with varying degree of response. Pathogenecity test also proved formae specialis (f. sp.) of *F. oxysporum* as *melonis* and *F. solani* as *cucurbitae*. Inoculum method was standardized and soil inoculation method was found superior to root-dip inoculation method. The plants showed mild to severe wilting within a few days depending on the virulence of the pathogen. Disease index was recorded and the isolates were categorized as highly virulent, moderately virulent or less virulent on the basis of their virulence. 11 isolates were found highly virulent, 16 were moderately virulent and 3 were less virulent. *F. oxysporum* f. sp. *melonis* recorded higher disease index than other species of *Fusarium*. Cross-infectivity test of theisolates was conducted on cucumber and bitter gourd through soil inoculation and root-dip inoculation method to check the infectivity of forma specialis of *Fusarium* on other cucurbit hosts. The results of cross-infectivity test revealed that 2 muskmelon isolates were highly virulent on cucumber and bitter gourd, and 8 isolates did not cross-infectand were categorized as non-pathogenic. The remaining isolates were found either less virulent or moderately virulent on cucumber and bitter gourd.

O (S 03) 12: Diversity, epidemiology, resistance and management of *Fusarium* wilt in chickpea

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Chickpea (*Cicer arietinum* L.), is a rabi season pulse crop in India is affected by killer disease Fusarium wilt that limits the productivity at large, the losses to the tune of 12-15% and in severe case yield loss upto100%. Seventy isolates of *Fusarium oxysporum* f. sp*. ciceris* (Foc) causing chickpea wilt representing 13 states and 4 crop cultivation zones of India were analyzed for their virulence on a set of chickpea differential cultivars for three years. Based on differential responses, the isolates were grouped into six races/pathotypes of the pathogen. Translation elongation factor-1α (TEF-1α), α-tubulin, internal transcribed spacer (ITS), COX-1and RBP2 genes were used to determine the genetic diversity of 70 isolates of *Foc*. Growth Index is the product of temperature and moisture indices in climax for the future distribution. In the soil moisture index is negatively correlated with disease index and pathogen population. For the further projection we had taken the consideration of the pathogen population present in the rhizosphere soil of resistant and susceptible cultivars. In the present study, one hundred and forty six plants of F_2 generation of chickpea derived from the cross between BGD 72 (moderately wilt resistant both 30 DAS and 60 DAS) and WR 315 (early and late wilt resistant) were phenotyped for wilt reaction. Marker assisted Backcross (MABC) population grown under field conditions were used for genotyping purpose. Three STMS primer (TA59, TA96 and TR19) were utilized in present study to characterize chickpea genotypes against race-4 resistance. Twenty one isolates from different species of *Trichoderma* including Pusa 5 SD and TH-3 were evaluated against *Fusarium oxysporum* infecting chickpea, out of which 9 isolates of *Trichoderma* (Pusa- 5SD, T-32, TH-3, ITCC 7856, T-15, T-16, T-19, ITCC 7838 and T-13) showed more inhibition under *in vitro* conditions.

O (S 03) 13: Virulence diversity among isolates of *Colletotrichum graminicola* causing anthracnose of sorghum

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Studies were carried out to monitor the virulence diversity among ten isolates of *C. graminicola* infecting foliage of sorghum collected from different localities in Uttarakhand, India. Virulence of the isolates was tested on ten selected lines under field conditions. Plants were whorl inoculated with conidial suspension (1×10^3 conidia/ml) of each isolate at 15- and 30 days after sowing. Observations were taken at boot leaf emergence and 50% flowering using 1 – 9 scale based on percent leaf area infected. Symptoms and disease severity on different lines varied with the isolates indicating existence of diversity among the isolates. On the basis of virulence (Per cent disease index) and symptoms on foliage, seven pathotypes viz. P1-P7 were distinguished.

O (S 03) 14: Molecular characterization and management of viral diseases of capsicum (bell pepper) under protected cultivation in Dharwad, Karnataka

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Capsicum (*Capsicum annuum* L. var. *grossum* Sendt.) a member of family *Solanaceae*, is commonly known as sweet pepper, bell pepper and Shimla mirchi. Under protected cultivation, capsicum is widely grown due to higher productivity and economic feasibility. However, diseases of viral nature affect production significantly, both in terms of yield and quality. Survey conducted during *rabi* 2017 and 2018 in seven districts of Karnataka under protected cultivation revealed that highest mean incidence (27.92%) of leaf curl disease in Dharwad, mild mottle disease(27.61%) in Belagavi andmosaic disease (21.39%) in Chikkaballapur districts were recorded.Virus infected capsicum plants exhibit symptoms of curling, cupping, puckering, mosaic, reduced plant growth and bushy appearance, chlorotic rings on leaves and fruits. Leaf curl symptomatic capsicum plants were associated with begomovirus, *Chilli leaf curl virus* (ChiLCV) and *Tomato leaf curl virus* (ToLCV) were confirmed by PCR ~200 bp. Upon PCR amplification with CP genes of ChiLCV and ToLCV were amplified at ~500 bp and ~510 bp respectively. Sequencing results of ChiLCV and ToLCV isolates infecting capsicum in Dharwad were found to be (>98%) identical to the previously reported ChiLC-Papaya-New Delhi and ToLC-Karnataka viruses. This is the first report of ChiLCV and ToLCV isolates associated with leaf curl symptoms on capsicum in Karnataka.Mosaic and mottling symptoms were associated with *Cucumber mosaic virus* (CMV), *Pepper mild mottle virus* (PMMoV), *Tobacco mosaic virus* (TMV) and were confirmed through RT-PCR, which amplified the CP-gene of CMV ~381 bp, PMMoV ~730 bp and TMV ~481 bp respectively. Rings on leaves and fruits were associated with *Groundnut bud necrosis virus* (GBNV) amplified ~830 bp by PCR. Coat protein gene of CMV infecting capsicum matched (95-97%) with previously reported Chilli-Turkey (KY973676) and Banana-Sikkim (KT447515). While CP-gene of PMMoV shared (99%) homology with PMMoV-Bell pepper-Himachal Pradesh (KJ631123). This is the report of PMMoV on capsicum from Dharwad, Karnataka. The transgenic capsicum (var. DMC-14) was developed by *in planta* transformation methodusing *Agrobacterium tumefaciens*pHAB531 construct carrying ChiVMV-CP. Out of 16 T_0 transgenic plants, only two plants were found to be positive for PCR and GUS activity. Out of 13 T_1 transgenic plants, only seven plants showed positive for PCR and GUS activity.Fourteen hybrids were screened against capsicum viral diseases, the results revealed that none of them were resistant. However, six hybrids were moderately susceptible to leaf curl disease. Hybrids Arka Gaurav and Arka Basanti, recorded moderately resistant reaction to mild mottle disease. While eight hybrids showed moderately susceptible reaction to mosaic disease.Results of integrated viral disease management revealed that lowest leaf curl disease (22.57%), mosaic and mottling (8.15%), least infestation of whiteflies (6.45%) and aphids (1.11%) recorded in treatment with spraying of NSKE (0.4%), spinosad (0.03%) + azoxystrobin (0.05%), nimbecidine (0.5%) + fipronil (0.1%), nimbecidine (0.5%) + propargite(0.1%), thiomethoxam (0.05%), diafenthiuron (0.025%) at 15 days interval of each spray recorded significantly higher yield of 4.77 t/500 m^2 with 3.72 benefit cost ratio, compared to control (2.50 t/500 m^2 with 1.60 benefit cost ratio).

Poster Papers

P (S 03) 01: Occurrence of mating types of *Phytophthora capsici* Leonian causing Phytophthora blight of capsicum in North Western Himalayas

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Phytophthora blight of capsicum caused by *Phytophthora capsici* Leonian has emerged as one of the major problem both in open field and protected environment causing root rot, crown rot, fruit rot and leaf blight symptoms in the disease syndrome. The pathogen is an oomyceteous organism and known to reproducing sexually through oospores which are important means of survival and pathogenic variability. Sexual reproduction in *P. capsici* requires the presence of two compatible mating types (A1 and A2). Hence, the knowledge of presence of mating types in a given area is of prime importance to explore the disease management through host resistance, so present study was carried out to know the occurrence of mating types in capsicum growing areas of Himachal Pradesh. Twenty single sporangium culture of the *P. capsici* isolateswere used to determine the mating types by paired culture technique on carrot agar medium. Oospores formation was observed in 19 isolates when paired with opposite mating type, however one isolate (Pc-9) was self fertile as it induced oospores formation in its pure culture. On the basis of average diameter of oospores of eight *P. capsici* isolates were characterised as A1 mating type while eleven isolates were placed in A2 mating type. Over all frequency of mating type A1 and A2 of *P. capsici* were 40 and 55 per cent, respectively. However, five per cent self-fertile or homothallic population were also prevalent. Different isolates were observed to form variable number of oospores with low to high frequency. Formation of oospores in this pathogen probably indicates their role in disease recurrence and existence of variability in the population.

P (S 03) 02: Poacic acid: a novel plant-derived bioactive compound elicits systemic immunity against pearl millet downy mildew disease

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Downy mildew of pearl millet is caused by the biotrophic, oomycete *Sclerospora graminicola* (Sacc.) Schroet., remains the most widespread disease of pearl millet causing huge economic losses. Poacic acid (PA), a diferulate found in lignocellulosic hydrolysates of corn and other grasses, was isolated and tested for its efficiency to induce systemic resistance against the pearl millet downy mildew disease. PA at 250 µg/ml concentration for 3 h treatment time was found to be optimum for seed treatment. Seed treatment with PA showed the least downy mildew incidence of 17.7% and 15.4 % under greenhouse and filed conditions respectively. The nature of resistance induced by PA was found to be systemic which was demonstrated by maintaining spatial and temporal separation of the inducer and the challenger. In addition, PA did not have any effect on the release of zoospore from sporangia, zoospore mobility and zoospore germination either. Histological studies showed that PA treatment increased cell wall reinforcement mechanisms like the callose, lignin and H_2O_2, NO, HRGPs accumulation and hypersensitive reaction. Rapidity and intensity of expression defense enzymes glucanase, PAL, POX, PPO, LOX and the defense protein HRGPs was significantly increased in PA treated seedlings compared to the control. High levels of POX, PPO, PAL, glucanase, HRGPs, PR-1, and PR-5 gene activities were substantially induced in PA treated pearl millet seedlings which correlated with high levels of resistance to downy mildew disease. At a broader applied level, PA is found to be a potential new resistance elicitor for managing the destructive effects of downy mildew disease on pearl millet and other important agricultural crops.

P (S 03) 03: Occurrence and distribution of sesame Alternaria leaf blight disease in different Agro climatic zones of Maharashtra state

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Sesame is considered to be a drought resistant crop. It is capable of withstanding a high degree of water stress and disease attack compared to other cultivated plants. But due to climate change, as like other crops sesame is also suffer from many diseases. Among these Alternaria blight caused by *Alternaria sesami* (Kawamura) is one of the most widely spread disease. A roving surveywas conducted to record sesame Alternaria blight disease intensity during two *Kharif* seasons (2014-15 and 2015-16), covering 234 and 240 sesame crop fields of nine agro climatic zones of the Maharashtra state in India respectively. The results of the survey indicated that overall disease intensity was comparatively higher during *Kharif* 2015-16 season compared to that of *Kharif* 2014-15. The average blight disease intensity during *Kharif* 2014-15 was maximum in Central Maharashtra Plateau Zone (39.58 %) followed by the zones *viz*., Western Maharashtra Plain Zone (37.28 %), Central Vidarbha Zone (35.19 %) and Western Maharashtra Scarcity Zone (32.67 %). In rest of the zones surveyed, the disease intensity was ranged from 21.83% (Western Ghat Zone) to 27.94 %(SubMountain Zone). This variability may be due to the climatic factors like rainfall pattern, relative humidity, temperature, wind velocity etc. The pooled data of the year *Kharif*, 2014-15 and 2015-16 revealed that the disease intensity was maximum in Central Maharashtra Plateau Zone (37.99 %) followed by the zones *viz*., Western Maharashtra Plain Zone (36.21 %), Central Vidarbha Zone (34.27 %) and Western Maharashtra Scarcity Zone (31.06 %); whereas, it was minimum in the Western Ghat Zone (20.24 %) and North Konkan Coastal Zone (21.82 %).

P (S 03) 04: Morphological and cultural characterization of *Sarocladium oryzae* from different regions of Telangana and Andhra Pradesh states

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The major feature of sheath rot disease is rotting and discolouration of sheath, leading to chaffyness and sterility of resulting grains. For many years sheath rot considered as a minor, but it is recently gained momentum and became wide spread. Total of 17 isolates were collected from different regions of Telangana and Andhra Pradesh. Diversity in cultural and morphological characters of *S. oryzae* was studied in five different media at room temperature 27±1°C. The observations on radial growth of the fungus at 10 days, 20

days and 30 days after inoculation and colony characters and sporulation of the fungus were recorded. The isolates vary significantly in morphology from one region to other. The colour of the fungal growth of isolates varies from white to pale orange. Mycelium growth varies with fluffy, flat and circular. The isolate Kakinada showed the maximum radial growth (8.07 cm) and the isolate Vizianagaram showed the minimum radial growth (6.10 cm). From Telangana, the isolate DRR showed the maximum radial growth (7.90 cm) and the isolate Adilabad showed the minimum radial growth (6.97 cm). The fungus *Sarocladium oryzae* taking more than 35 days to fill the entire Petri plate. The effect of different culture media on the growth of fungi differed significantly. At 30 days after incubation maximum radial growth of *S. oryzae* was recorded on Oat meal agar (8.63 cm), which was found to be significantly superior to all other media. The least radial growth was recorded in Cornmeal agar (5.77 cm). Sporulation also showed greater variation in different media, ranging from excellent to poor sporulation. Excellent sporulation was recorded on Potato dextrose agar media and poor sporulation was recorded in Cornmeal agar medium. The size of the spore varies from 1.3 -1.9µm width and 3.6 - 4.8 µm length.

P (S 03) 05: Diversity of grapevine viruses present in different cultivars of IARI orchard

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Grapevine (*Vitis vinifera* L.) is one of the most commercially important fruit crops of the world. Among all the fruits, grape occupies first position in terms of area and production in the world. In India it is grown over an area of 1.23 MHa with an annual production of 2.82 MT. Maharashtra is the leading grapes producing state with production of 2.05 MT in the year 2014-15. The country has the distinction of achieving the highest productivity of grape in the world, with an average yield of 20 to 25 tonnes/ha in 2012-13 (APEDA). Among biotic stresses, viruses cause substantial yield losses in term of both quantity and quality of berries. Nearly 70 viruses and other infectious sub-cellular obligate parasites, collectively referred to as graft-transmissible agents (GTAs), have been documented in grapevines. However, in India only few studies have been carried out on grapevine viruses. Grapevine leafroll-associated viruses 3 and 1 (GLRaV-3 and GLRaV-1) are reported to be associated with grapevine leafroll disease in India. India has wide variety of cultivars of grapevine and all of them have different susceptibility level to different grapevine viruses. Survey of IARI grapevine orchard were carried out during 2017-18 and total of 8 samples (2 greenhouse + 6 field) were tested against 5 different viruses like GLRaV-1, 3, 4, GVF and GRSPaV through RT-PCR. Results from RT-PCR data has shown that greenhouse samples were infected with GLRaV-1, GLRaV-3 and Grapevine virus- F (GVF). Among the field samples GLRaV-1 was present in two samples, GLRaV-3 in three samples, GVF in one sample, GRSPaV in one sample and GLRaV-4 was absent in all the samples.

P (S 03) 06: Current situation and status of rice false smut disease in South Gujarat

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Roving surveyed of farmers field conducted during Kharif-2014 to 2017 for false smut disease of rice in 50 villages of ten talukas viz., Vyara, Dolwan, Songadh, Mandvi, Mahuva, Vansda, Pardi, Waghai, Netrang and

Dediapada represented all districts of South Gujarat and conclude that overall tillers infection was observed in ranged from 0.56-10.00 percent (3.03%) and grain infection was observed in ranged from 0.64-2.75 percent (1.38%). Disease severity and percent disease index also observed in ranged from 0.89 -46.57 and 0.27-5.55 percent in Dediapada and Vansda taluka respectively. However percent grain weight and grain yield loss was also observed in ranged from 2.58-14.08 (overall 6.80%) and 0.020-2.354 (0.492%) percent in Dediapada and Vansda taluka respectively. The false smut disease of rice has attained a major status in Vansada taluka and recorded the maximum loss up to 28.098 percent in hybrid cultivar. Moreover, tillers infection, grains infection, disease severity, PDI and grain yield loss were more observed in hybrid rice cultivars when regular rainfall occur from panicle initiation (pre-heading) to dough stage with low deep water condition. Favorable condition for false smut of rice disease development was found more suitable in Vansda taluka of South Gujarat.

P (S 03) 07: Characterisation of new 16SrII-C subgroup phytoplasma associated with chickpea stunt disease using mutlilocus gene specific primers

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Chickpea (*Cicer arientinum*) is one of the important pulse crop in the world and India ranks first in the world in respect of production of 7.17 million tonnes (about 75%) as well as acreage of 8.35 Mha. Severe stunting and phyllody symptoms were observed in chickpea fields at Proddatur and Jammalamadugu mandals of Kadapa (Dist) of Andhra Pradesh during Nov-Dec 2018 with an incidence of 20-30 per cent. An investigation was carried out to identify and characterize the phytoplasma association with the chickpea stunt disease. Total DNA from symptomatic and non-symptomatic chickpea plants was extracted and PCR assay was performed. Amplicons of 1.2 kb were consistently amplified in most of the symptomatic chickpea plants in nested PCR assays utilising primer pairs P1/P7 and primers R16F2n/R16Rn. The 16Sr DNA sequence of (Chickpea stunt phytoplasma) CpSP isolate revealed 100% sequence identity with those of 16SrII-C phytoplasma. Three multilocus gene specific primers, *imp* (IMPIIF2 /IMPIIR1), *tuf* (TUFIIF2/TUFIIR1) and *secY* (SECYF1(II)/SECYR1(II) were employed to further confirm the 16SrII-C subgroup phytoplama associated with CpSP samples. Amplicons of 717bp, 1094bp and 1700bp were consistently obtained with *imp*, *tuf* and *secY* gene specific primers, respectively in all the symptomatic chickpea stunt samples. The 16Sr RNA and the three multilocus gene sequence comparative analysis of the CpSP isolate confirmed the association of 16SrII-C subgroup with CpS disease. Our results revealed that all the three multilocus genes specific primers could be alternatively utilised for authentic identification and characterization of chickpea stunt phytoplasma at subgroup level.

P (S 03) 08: Identification and characterization of Ca. Phytoplasma ziziphi with witches broom disease in *Ziziphus oenoplia*in Karnataka, India

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Ziziphusoenoplia also known as jakhal jujube or small fruited jujube is a spiny, evergreen small tropical fruit tree species belonging to ber family (Rhamnaceae). During a survey in the adjoining forests of College of

Forestry, Sirsi, Karnataka (N 14º36’31" and E 74º50’40"), the jujube trees exhibited witches’ broom symptoms. An investigation was carried out to identify the association of phytoplasma with the jujube witches’ broom (JWB) disease in the present study. Total DNA was extracted from leaf veins of symptomatic jujube plants using CTAB method and PCR assay was performed using 16S rRNA gene specific primer pairs P1/P7 and 3F/3R. Amplicons of ~1.3 kb were consistently amplified from all the symptomatic plant samples in nested PCR assays, however, no amplification was observed with any non-symptomatic samples. A BLASTn similarity search analysis of 16Sr RNA sequences of JWB strain revealed that it shared 99.93% sequence identity with those of ‘*Candidatus* Phytoplasma ziziphi’ related. Virtual RFLP and phylogenetic analysis revealed that the phytoplasma sequences amplified from JWB phytoplasma strain is more closely related to *Ca. P. ziziphi* subgroup 16SrV-B with a similarity coefficient of 0.91. But a little difference in restriction profiles with restriction enzymes *Alu*I and *Hae*III of 16SrV-B subgroup reference strain (Acc No. AB052876) suggested that it may be a new subgroup strain under 16SrV group, which needs further investigation with real RFLP analysis.

P (S 03) 09: Molecular genetics, pathogenic and symptomatological diversity in population of *Mycogone perniciosa* on the cultivated button mushroom *Agaricus bisporus*

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The fungus *Mycogone perniciosa* is a major pathogen of common button mushroom *Agaricus bisporus*. Wet Bubble infection has been reported in various *A. bisporus* production areas around the world. In severe cases the impact of this disease may leads to the permanent phasing out of cultivation of *A. bisporus*. The objective of this study were to examine genetic variation, morphological, physiological dissimilarities and diversity among the different isolates of *Mycogone perniciosa* collected from different parts of Haryana, Punjab and Himachal Pradesh mushroom farms. The genetic variability was investigated by using random amplification of polymorphic DNA. The symptoms induced by different isolates of *M. perniciosa* varied from thick stipe to sclerodermoid having brown amber coloured droplets and internal browning. While symptoms variation observed among the isolates of *M. perniciosa* were compared with morphological, physiological and genetic variability of the isolates, KSN and BSN2 produced fluffy, even, very feathery and brown in colony colour was recorded fastest growing. These two isolates *viz.,* KSN and BSN2 were highly diversed from rest of isolates of the *M. perniciosa* showing wide genetic distance.The highest pair wise genetic similarity *i.e.*, 92.0 per cent was observed between sub cluster isolates RSN and BSN1 followed by 85.0 per cent genetic similarity between isolates KSN and BSN2 of major cluster B. In future it is likely these two isolates of *Mycogone perniciosa* can be used in the screening programme of strains of *Agaricus bisporus.*

P (S 03) 10: Pathogenicity and virulence of entomopathogenic fungi *Beauveria bassiana* and *Metarhizium anisopliae* against *Spodoptera litura*

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Entomopathogenic fungus are the alternate form of insects and pests management, with lower cost and longer run. It's reduces the use of chemical pesticides due to their wide host range and effectiveness. The entomopathogenic fungus act as parasite of insects and kills or seriously disables themdifferent insects and these are potentially the most versatile biological control. Entomopathogenic fungi (EPF) are naturally occurring organisms which are perceived as less damaging to the environment. EPF was isolated from naturally infected insects cadavers and soil by Galleria bait methods. Their pathogenicity and virulence was determined against the *Spodoptera litura* of Soybean at different 10^7, 10^8 and 10^9 conidial concentration under laboratory condition on third and fourth larval instar. All the isolates were found pathogenic to larvae. Isolates Bb1, Bb3 and Bb16 recorded 100% mortality of larvae after 96 HAT at 1×10^9 conidial concentration ml-^{1} while Bb4 was least effective (32.44%) when pathogencity were determined. In virulence study mean mortality per cent was maximum in isolates Ma2 (70.83%) and Bb3 (68.34%) against third instar larvae while against fourth instar it reduces. The mortality per cent of *Spodoptera litura* were increases (36.12 to 46.59 and 62.78%) when concentration of *Beauveria* isolates increases and for *Metarhizium isolates* 50 to 61.71 and 88.83 per cent mortality increases respectively.

P (S 03) 11: Identification and molecular characterization of tomato *SlNPR* gene family

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Plants have evolved numerous strategies to defend themselves from potential threat of pathogen and pests. Such defense responses are mainly mediated through SA, JA and ET dependent signaling pathways. Crosstalk between these phytohormones eventually fine tunes the defense response to curtail the ingress of pathogen. Several transcription regulators and co- regulators are implicated in transcriptional regulation of such interconnected defense signaling network. One such co-regulator is the non-expressor of pathogenesis-related gene 1 (*NPR1*) which is implicated in SA-mediated systemic acquired resistance (SAR) and modulating cross talk between SA and other phytohormones. In this study we identified and characterized tomato *SlNPR1*, homologous to Arabidopsis *AtNPR1* and its four paralogs and arbitrary assigned identifiers as *SlNPR2, SlNPR3, SlNPR4 and SlNPR5.* Phylogenetic analysis showed that SlNPR-1 belongs to the clade containing AtNPR-1 and AtNPR BTB, SlNPR3 and SlNPR4 was grouped in the same clade with AtNPR3 & AtNPR4. SlNPR2 was grouped in clade containing AtNPR BOP1 and AtNPR BOP2. SlNPR5 was not grouped into clade containing AtNPR. Comparative promoter analysis of *SlNPR1* and its paralog genes revealed over representation of various cis- elements which respond to phytohormones like SA, JA and ABA and also biotic stress. Time course expression profiles of *SlNPR1* and its four paralogs was carried out in response to exogenous application of phytohormons SA, JA, ABA and foliar pathogen *Alternaria solani* and also in tomato mutant lines impaired in SA, JA and ABA signaling pathway with or without pathogen application. Results indicated differential expression of *SlNPR1* and *SlNPR1* like genes in the all treatments examined. Further, functional characterization

of *SlNPR1*, homologous to *AtNPR1* was done by generating transgenic *SlNPR1* overexpressed and RNAi silenced lines. Overexpression of *SlNPR1* led to increased susceptibility towards *A. solani* wereas silencing resulted in reduction in disease severity. Expression analysis of SA & JA associated defense genes in transgenic lines altered for *SlNPR1* expression showed their differential expression. In conclusion, our study suggested role of tomato *SlNPR1* and *SlNPR1* like genes during tomato- pathogen interaction which may help breeders to formulate novel strategies to improve disease resistance.

P (S 03) 12: Diversity analysis of important *Phomopsis* species using morphological characters and molecular marker.

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The genus Diaporthe is a well known pathogen infecting wide range of agiculturally important crops. They cause important diseases such as damping off, blight, fruit rot and canker resulting in yield loss upto 15-30%. Twenty isolates of different Phomopsis species from different part of India and abroad were collected and analysed for morphological, cultural and molecular variation. The population showed variation in various morphological characters such as colony colour, zonation, growth rate, conidia size and shape. Majority of isolates were fast (>14mm/ day) and medium (11-14mm/ day) growing with aerial, subaerial and submerged colony. Size of alpha condia ranged from 3.5-6.5 x 2.5- 4.2 µm, whereas size of beta conidia ranged from 13.54-19.68 x 1.34-1.9 µm. Three species namely P. phaseolorum, P. vexans and Phomopsis sp. produced both types of conidia. Since morphological characters were insufficient to distinguish species, molecular characterization was used as tool to analyse diversity within the genus and identify upto species level. ITS1-5.8-ITS4 region of the isolates were amplified and they showed 95-100% similarity. Phylogenetic tree was constructed and analysed that the isolates belonging to same geographic region representing same or different species clustered together indicating high level of sequence similarity. Translational Elongation Factor (EF-1?) region was also amplified and sequences showed 90-95 % similarity. Phylogenetic tree constructed grouped the isolates belonging to same geographic region into same cluster indicating sequence similarity. Thus, to resolve the Phomopsis species complex single genomic region will not be sufficient, more genomic region need to be explored. However, ITS region proved suitable for genetic diversity analysis of the pathogen.

P (S 03) 13: Genetic and phenotypic characterization of *Alternaria* species reveals association of highly virulent *Alternaria alternata* in early blight of tomato

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Early blight of tomato is caused by fungal pathogen belong to *Alternaria* species. A total of 90 isolate of *Alternaria* representing three locations from north India were isolated. The isolates were characterized by adopting polyphasic phenotypic and genotypic tools. Pathogenicity test performed on tomato cultivar, Pusa-Ruby, revealed 69 among the 90 isolates were found to be pathogenic with 38 of them were rated highly pathogenic and 21 were non-pathogenic under green-house condition. Colony and conidia characteristics were analysed for morpho-grouping of the isolates which resulted into 11 broad clusters. Species identify was confirmed by sequence comparision of three housekeeping genes such as *ITS, ß-tubulin and cyt-B* and one major allergen gene *alt a 1* with NCBI and *Alternaria* whole genome database. Molecular analysis revealed association of prevalence of two species *Alternaria alternata* and *A. tenuissima* in early blight of tomato. Out of eleven isolates, ten were confirmed as *Alternaria alternate* and one as *Alternaria tenuissima.* Phylogenic tree was also constructed using Maximum likelihood method using partial sequences of housekeeping genes. Four *Alternaria* spp. *i.e. A. alternata* ATCC 11680, *A. brassicicola* ATCC 96836, *A. solani* BMP 0185, and *A. tenuissima* BMP0304 were used for comparison. *ITS, ß-tubulin* and *cyt-B* gene sequence based analysis generated identical phylogenic tree depicting *A. alternate* and *A. tenuissima* in one cluster. However, *alt a1* gene sequenced could make sub-clusters within *A. alternata* and *A. tenuissima* clade indicating its intraspecific discriminatory potential. The present study confirmed that *A. alternata* and *A. tenuissima* were independently capable of causing early blight on tomato.

P (S 03) 14: Diversity and cultural studies of *Termitomyces* spp. from Chhattisgarh

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Termitomyces is a wild mushroom growing in symbiotic association of termites (*Odontotermes* spp., *Macrotermes* spp.). The diversity of *Termitomyces* species occurring in Chhattisgarh was studied. Termite mounds were identified bearing different species of *Termitomyces* and their GPS data was recorded using GPS receiver (Garmin etrex model). Macro-morphological characters cap size, colour of the cap and pseudorrhiza presence, annulus presence, pseudorrhiza colour, size,spore prints were recorded. The spore print colour varied from light pink to dark brown. Some species of *Termitomyces,* namely, *T. microcarpus*, *T. eurhizus*, *T. clypeatus*,*T. striatus*,*T. bulborhizus, T. globulus*, *T. heimii* were identified based on macro morphological characteristics and documented. Pure cultures were isolated from the asexual fruit bodies growing on or near the termite mounds by tissue culture techniques on Potato Dextrose Agar. Further cultural studies were conducted on five different media Potato Dextrose Agar (PDA), Wheat Dextrose Agar (WDA), Hagem Modess (HM), Malt Extract Agar (MEA) and Potato Sucrose Agar (PSA) and incubated at 28°C in total darkness. Radial growth on WDA was 77.3 mm, on PDA 44.6 mm, on PSA 43.3 mm, on MEA 64.0 mm, on HM 51.3 mm. After one month maximum radial growth was observed to be on WDA media. Fungus comb bearing sporodochia isolated from termitarium were kept in a box to induce growth using wheat extract at 26-28°C. After 3 days of incubation erected white mycelium with tiny pinheads were observed that turned greyish on maturity.

P (S 03) 15: Identification and characterization of *Rhizoctonia solani* isolates of rice from India

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Thefungus *Rhizoctonia solani* is a plant pathogen which causes sheath blight disease in rice. It is a major soil-borne pathogen which has a very broad host range in infecting crops worldwide besides rice. Sheath blight is one of the most economically important diseases of rice and has been reported from all rice growing regions of the world. The sheath blight disease is responsible for major grain yield and quality losses of rice crop.This study aims to identify and characterize the different *R. solani* isolates causing sheath blight disease in rice. Total of 89 isolates of *Rhizoctonia* spp. were obtained from the different states of India which were Jammu & Kashmir, Uttar Pradesh, Uttarakhand, Tripura, Bihar, Telangana, Haryana, Sikkim, Tamil Nadu, Madhya Pradesh and others. The isolates were characterized morphologically and also on the basis of internal transcribed spacer (ITS) region amplification. The (ITS) based identification of these isolates was done which indicated that 85.89% of these isolates were *R. solani.* The phylogenetic tree of these isolates were constructed based on neighbour joining method which classified them into three categories of *Rhizoctonia* spp. *viz*. *R. solani, R. oryzae sativae* and *R. oryzae*. The information generated will be helpful for the devising of future management strategies against these pathogens.

P (S 03) 16: Characterization and pathogenicity of *Fusarium* spp. incitant of potato dry rot in Punjab

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Total twenty four (F1- F24) *Fusarium* isolates collected from different cold storages situated at different locations like Hoshiarpur, Jalandhar, Ludhiana, Kapurthala, Sangrur, Gurdaspur, Rupnagar, SBS Nagar and Moga districts of the Punjab state were analyzed for species identification and virulence pattern. Highest disease incidence was recorded in district Jalandhar district where dry rot incidence varied from 3.3 to 90.0 percent followed by Hoshiarpur district where disease incidence was in the range of 22.5-50.0 percent.Fusarium isolates were characterized on the basis of radial growth, colour and pattern of growth, size and septation of micro, macro conidia and chlamydospore formation (Leslie and Summerell 2006). Isolates F1 to F11 were identified as *Fusarium avenaceum* whereas F16, F18 to F24 were identified as *F. culmorum* and F12 to F15 and F17 were identified as *F. sambucinum* based on their morphological and cultural characteristics. Dendogram was generated based on their morphological and cultural characteristics like colony colour, type of mycelium, pigmentation, growth rate per day (mm) and size of macro-conidia & micro-conidia (µm) of each Fusarium isolates by using PAST 3.25 and were grouped into three clusters. Cluster I, II and III contained 5, 8 and 11 isolates respectively. Further accurate identification was confirmed by using internal transcribed spacer (ITS) species specific primers (Fcoer, Fsulp, JIA and Fco1). The DNA of eight isolates (F16, F18 to F24) got confirmed the presence of *F*. *culmorum* with a single amplified product of 592 bp. The DNA of eleven isolates (F1 to F11) confirmed the presence of *F*. *avenaceum* with a single amplified product of 294 bp. *F. culmorum* were produced maximum average rot volume (8.12 cm^3) as compared to *F*. *avenaceum* (4.37 cm^3) and *F. sambucinum* (2.12 cm^3) at 4°C*. F*. *culmorum* wasmore virulent as compared to *F*. *avenaceum* and *F. sambucinum*, causing significantly larger lesions compared with that of the other species at both 4°C and 10°C storage temperatures.

P (S 03) 17: Virulence spectrum and genetic diversity of *Rhizoctonia solani*, the incitant of banded leaf and sheath blight of maize

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Forty-five *Rhizoctonia* isolates collected from major maize growing areas of Punjab were analyzed for species identification, anastomosis group, genetic diversity, and virulence pattern. The hierarchical cluster analysis differentiated four morphological quantitative traits into six major groups (M1-M6). Group M1 had nine isolates with the highest mean number of sclerotia per plate (131.13), moderate level of sclerotial diameter (2.2 mm), hyphal width (6.72 µm) and colony growth rate per day (33.3 mm). Group M5 had eight isolates with lowest colony growth rate per day (31.9 mm) and hyphal width (5.78 µm). Seven inbred lines and four hybrids were evaluated against all isolates under artificial condition. Nine main groups (V1-V9) were identified from the hierarchical cluster analyses using Mahalanobis coefficient. Highest disease severity (63.66 %) and maximum virulence index (20.90 %) were observed in group V9 isolates, whereas lowest were observed in group V8. Identification of the fungal species using internal transcribed spacer (ITS) species-specific primers confirmed the presence of *R. solani* (100%) with a single amplified product of 0.55 kbp and mixed infection of *R. oryzae-sativae* (18.18%) with amplified product of 1.2 kbp. PCR amplification revealed all isolates belonged to AG1-IA with a single amplified product of 0.3 kbp. Genetic variation that was analyzed by using 27 inter simple sequence repeat (ISSR) primers. The genetic structure of the isolates revealed a high degree of polymorphism (PIC value ranging from 0.82 to 0.92), clustering the pathogen population into four major groups. The maximum and minimum numbers of fragments were obtained from primer R28 and R15.

P (S 03) 18: Characterization of *Villosiclava virens* causing false smut of rice and its bio-control in India

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False smutof rice is caused by *Villosiclava virens* (Tanaka) on rice was first described by Cooke in Tamil Nadu in 1878. It has become a serious pathogen in almost all the rice growing areas of the world. Diseases incidence of 10-20% and 5-85% respectively has been reported from Punjab and Tamil Nadu on different rice cultivars. Morphological characterization of*V. virens* isolates from PB showed creamy dull white, grey black, fluffy mycelium, undulated, compact, ring pattern growth of colonies. Spores were, circular to ovate, echinulated, double walled. While, the isolates from Delhi and UP showed creamy dull white-grey, cottony, undulated colonies. Spores were circular to ovate, highly echinulated, double walled, mass of spores covered with silvery membrane. The conidia (3-5µm) of *V. virens*were globose to irregularly rounded and ornamented with prominent spines (200-500nm). A greenhouse trial was conducted to standardize the inoculation technique in false smut of rice (CV. Swarna) during the 2018 Kharif season by using syringe and spray inoculation methods at boot, early flowering and grain filling stages of the crop. Syringe inoculation of spore suspension (4X10^6) of *V. virens* at early flowering stage of the rice crop was most successful method in producing the disease as compared to the spray method. Syringe inoculation produced 10.0% disease incidence and 0.4% disease severity at early flowering stage of the crop respectively. The disease was not produced at boot and grain filling stages of the crop by either method. A set of 25 novel actinomycetes was evaluated for its antifungal activities against *V. virens*using dual culture technique under *in vitro* conditions. Ninteen actinomycetes showed disease inhibition in the range of 7.6-58.9% under *in vitro* conditions.

P (S 03) 19: Prevalence of major viruses in apple nurseries and their serological detection

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Viruses pose a serious threat to apple cultivation all over the world as infection resulting from viruses and related pathogens are limiting factor in the production of certified planting material in apple.Himachal Pradesh is well known as “Apple state” of country and apple plays a pivotal role in economy of growers of Himachal Pradesh. Viruses, however, have emerged as a major hindrance in its commercial cultivation. Surveys were conducted during 2018-2019 in apple nurseries of Solan district of Himachal Pradesh for the presence of four major viruses namely ApMV (apple mosaic virus), ACLSV (apple chlorotic leaf spot virus), ASPV (apple stem pitting virus), ASGV (apple stem grooving virus) and additionally PNRSV (prunus necrotic ring spot virus) on the basis of symptoms exhibited by leaves at nursery stage. Based on visual symptoms, percentage of incidence was found to range between 1.99 percent to 17.61 percent. These viruses, being latent in nature cannot be assessed by symptoms alone. Thus, ELISA based serological detection proved to be a quick and reliable method to confirm the presence of apple viruses. DAC and DAS ELISA resulted in the detection of ACLSV, ApMV, ASPV and ASGV in plants marked on basis of visual symptoms. However, ACLSV was found to be the most prevalent among all viruses. Detection of viruses at early stages of plant growth is the key factor in developing a clean stock programme leading to production of virus indexed plants and these studies will help in the production of virus indexed planting material of apple for developing a sound certification programme.

P (S 03) 20: Isolation and characterization of *Pseudomonas fluorescens* isolates from different rhizospheric soils of Latur district of Maharashtra

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Pseudomonas fluorescens used as a biocontrol agent in agriculture. Pseudomonads belong to PGPR, play a major role in plant growth promotion, induced systemic resistance, biological control of pathogens. In this study to collect rhizospheric soil sample from different crops *viz*. tomato, chilli, brinjal and pomegranate from different locations in Latur district. *Pseudomonas fluorescens* was successfully isolated on King’s B Agar medium. Ten isolates were coded according to the place of collection and crop name. These isolates were subjected for cultural and biochemical characterization. Colour of colony varied from yellowish, light yellow and yellowish white with high, medium and weak fluorescence under UV light, respectively. Colonies were circular, convex, smooth, glistening with entire margin. The bacteria was non-spore forming and motile rod shape. Cultural and morphological characters of different isolates studied on seven medias viz., (King’s B medium, Nutrient agar medium, Potato dextrose agar, Yeast peptone agar, Yeast extract agar, Czapeak’s dox agar Richards synthetic agar) revealed the variation in respect of colony characters such as colony colour, colony shape, cell shape, nature, elevation, margin and texture. The test bacteria were Gram-negative and showed positive reactions to Catalase oxidation and KOH test. Starch hydrolysis tests positive for eight and negative for two isolates. All isolates were able to solubilize phosphate. Ten native strains were identified as a *Pseudomonas fluorescens*.

P (S 03) 21: Colonial, biochemical and molecular diversity among different isolates of bacterial panicle blight pathogen in the regions of Northern India

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The bacterial panicle blight (BPB) caused by *Burkholderia glumae,* is an emerging disease of rice which has recently come out as a menace in rice-growing areas of northern India. Considering the importance of crop and continuous spread of the disease, present research was initiated to decipher the prevalence and characterization of the *Burkholderia* sp. in different regions of northern Indiaduring the year 2017-2018 and 2018-2019. The findings revealed that symptomatic and asymptomatic seeds and infected plant parts collected from different geographical regions of northern India mostly, including states *viz.* - Uttarakhand, Haryana, Uttar Pradesh, Bihar and Assam exhibited symptoms of BPB on infected leaf, leaf sheath, base of boot leaf and panicles. A total of 28 bacterial isolates were recovered out of which only 21 isolates were found pathogenic on rice under glass house conditions. Colony characters revealed that 6 different coloured colonies *viz.* - White (glistening), Creamy white (smooth), Creamy (smooth), Creamy yellow (smooth), Pale yellow and (smooth), Shiny yellow (flattened) were present among the isolates. Biochemical studies revealed that the pathogenic isolates were positive for gelatin liquefaction, KOH Solubility and catalase test while negative for starch hydrolysis, oxidase reaction and arginine dihydrolase test. Molecular characterization of the isolates on the basis of their 16S rDNA sequences confirmed that (14) *Burkholderia glumae,* (5) *B. gladioli* and(2) *B. plantarii* were recovered from the infected samples and thus, showed the prevalence of different *Burkholderia* sp. causing BPB in the regions of northern India. Under the oil immersion lens of compound microscope (100X) through gram staining the bacterial isolates were found to be gram negative absorbing red colour of the counter stain and rod shaped with round ends.

P (S 03) 22: Occurrence, distribution and isolation of entomopathogenic fungi from Chhattisgarh

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Growing demand for reducing chemical inputs in agriculture and increased resistance to insecticides has provided great impetus to the development of alternative forms of insect-pest management. Microbial control of crop pests offers environmentally acceptable strategies with lower cost and longer run effect. The Entomopathogenic fungus that act as a parasite of insects and kills or seriously disables them, comprise a diverse group of over 90 genera with approximately 750 species, reported from different insects and these are potentially the most versatile biological control agents due to their wide host range. Entomopathogenic fungi are naturally occurring organisms which are perceived as less damaging to the environment. Their occurrence and distribution are widely distributed in diverse habitats (aquatic, forest and non forest). An extensive survey was conducted during Kharif and Rabi season of 2017-18 and 2018-19 on different crops grown in different regions of Chhattisgarh and collected naturally infected insect cadavers and also soils samples from forest, non forest and cultivated lands. The purpose of this work was to isolate different entomopathogenic fungi, identify them and study the taxonomy & biodiversity of local isolates. The entomopathogenic fungi was isolated from insect cadavers and soil samples using Galleria bait method and identified as *Beauveria bassiana, Metarhizium anisopliae, Nomuraea rileyi* and *Aspergillus flavus* from different insects of Soybean, Groundnut, Mustard and Pigeonpea. The favourable time for collection of EPF was 1st week of September to 2nd week of October for Soybean, Groundnut and Rice crops whereas 2nd week of September to last week of December from sugarcane crop, November to December was ideal for Pigeonpea crops insects which are infected by entomopathogenic fungi.

P (S 03) 23: Characterization and genetic diversity of *Ralstonia solanacearum* causing bacterial wilt of brinjal

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Occurrence of bacterial wilt disease in brinjal crops was noted in 8 states of India as Meghalaya, Odisha, West Bengal, Jharkhand, Uttarakhand, Himachal Pradesh, Jammua & Kashmir and Karnataka with high disease incidence. Maximum incidence of disease was found in rainy season from July to October up to 60% whereas low about less than 10% in summer season (April to June) of the crop. Thirty eight isolates of *R. solanacearum*were isolated from brinjal crops from these states and they produced typical white colour fluidal colonies with pinkish in center and irregular in shape. A phylogenetic tree was generated by comparing 1049 nucleotides of *hrp*B and they showed 100% sequence similarity with *hrp* Bgene of *R. solanacearum*. This tree revealed four phylogenetically distinct groups. Cluster A showed the similarity 100% with 18 isolates of *R. solanacearum* along with the reference strain *R. solanacearum* Y45. Cluster B showed the 100% similarity but divided 2 sub groups. Genetic diversity of 38 isolated was studied using combined fingerprinting data generated by BOX, ERIC and REP PCRswhich showed that isolates were grouped into two distinct clusters. All the isolates of *R. solanacearum* biovar 3 showed 27 DNA types at 75% similarity coefficient which was separated into different clusters. Cluster 1 was further divided into distinct 24 subgroups at 75% similarity coefficient. This technique helped to discriminate between biovar 3 of *R. Solanacearum.*

P (S 03) 24: Cultural characterization and yield evaluation of different strains of *Hericium erinaceus*

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Hericium erinaceus is an edible, medicinal mushroom belonging to Hericiaceae, Basidiomycota. It can be easily distinguished by its thin tendrils protruding from a white rubbery center. The experiments was conducted to explore the role of different temperatures, media, and pH on growth and biomass of two strains(HE-5 and HE-8) of *Hericium erinaceus* and yield attributing performance of 9 strains (HE-01, HE-02,HE- 03, HE-04,HE-05,HE-06, HE-07,HE-08 and HE-09) on wheat straw.There was significant difference observed in radial growth, fresh and dry mycelia weight of HE-5 and HE-08 on different media under study. The highest radial growth (80.80mm), fresh mycelia weight (4.56gm) and dry mycelia weight (0.24gm) of HE-08 was noticed on potato dextrose agar medium and potato dextrose broth. Temperature significantly influenced the radial growth and biomass of HE-5 and HE-08. Significantly highest radial growth(88.60mm) , fresh (4.37gm) and dry mycelia weight(0.25gm) of HE-08was recorded at 24°C.The radial growth(69.20mm), fresh(4.24gm) and dry biomass (0.22gm) production of HE-08 was more at pH 6 than other tested pH. The period required for spawn run and pin head initiation was significantly less (17 days and 4.2 days) and highest yield tested (183.60 gm/ 500 gm dry substrate), biological efficiency (36.72%) observed on HE-08 strainamong the different strains of *Hericium erinaceus*.

P (S 03) 25: Molecular diagnosis and phylogenetic analysis of phytoplasma infecting chickpea in Dharwad, Karnataka

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Chickpea plants showing phytoplasma symptoms were observed in the research plots at University of Agricultural Sciences, Dharwad Karnataka. The typical symptoms of phyllody include proliferation of shoots resulting in sterility of flowers, compact growth at the shoot (bushy appearance), leaf curling/ cupping, yellowing, phloem necrosis, swollen veins and dieback. Affected plants were scattered in the field and were more easily spotted at flowering and podding time. The flowers developed abnormal green structures (phyllody) instead of normal flowers. At the time of crop maturity when the healthy plants were drying the diseased plants in the field were conspicuously green. The causal agent of the phyllody disease was identified based on symptoms, amplification of 16S rDNA of the phytoplasma by nested PCR with primers P1/P7 and R16F2n/R16R2 and 1,800 bp and 1,200 bp size products were amplified in first round PCR and nested-PCR respectively. The PCR product was sequenced, partial sequence was submitted to NCBI and received the accession number (MN453609) and compared with the reference phytoplasma sequences collected from the database (NCBI). 16S rDNA sequences of Dharwad chickpea phytoplasma shared the highest nucleotide identity of (>98%) with Periwinkle phyllody16SrII-E (EU096500). This study indicated the association of 'Candidatus Phytoplasma aurantifolia' the 16SrII-E group infecting chickpea from Northern Karnataka.

P (S 03) 26: Studies of root rot of vegetable clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] caused by *Rhizoctonia solani*

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Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.], is an important legume crop and mainly grown under rainfed conditions in arid and semi arid regions of tropical India during *Kharif* and *Zayad* seasons. Diseased samples were collected from Horticulture Farm, S.K.N. College of Agriculture, Jobner. Isolation of the pathogen was made from rotted roots of clusterbean and purified by hypal tip method. The pathogenicity of the fungus was proved by soil inoculation technique. The pathogenic fungus was identified as *Rhizoctonia solani*. Maximum mycelium growth was recorded at temperature 30^{0}C, RH 100 per cent and pH 6.5, independently. Among five fungicides tested by Poisoned Food Technique, carbendazim was found most effective in inhibiting mycelial growth followed by carbendazim +mancozeb. Seed application of carbendazim was found most effective in reducing disease incidence in field followed by carbendazim+mancozeb. Under dual culture technique, *T. harzianum* showed highest inhibition of mycelial growth of the pathogen in comparison to *T. viride.* Seed-cum-soil application of *Trichoderma harzianum* was found most effective in reducing disease incidence. Among five organic amendments tested under field conditions, neem cake showed highest disease control followed by castor cake. Out of seven cultivars, screened for resistance, none of the cultivars was found resistant against root rot pathogen. However, M-83, Neelam-51, Neelam-81 and Ronak-51 were found moderately susceptible.

Session 4

Host pathogen interaction and plant immunity

Keynote Papers

KN (S 04) 01: Molecular basis of red rot resistance in sugarcane: Understanding regulatory mechanism through NGS approach

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Sugarcane, a major cash crop grown in the tropics and sub-tropics around the globe for sugar, ethanol and its byproducts. In India, the crop is grown in different states accounting for 18.72% of global cane production and it stands second, after Brazil, a major sugarcane producer. Different biotic stress factors such as fungi, viruses, bacteria and phytoplasma seriously affect crop production and productivity in sugarcane. Among them red rot caused by the fungal pathogen *Colletotrichum falcatum* Went is a dreadful disease accounting for severe yield losses to the farmers and loss in sugar recovery in sugar mills. The polypoid sugarcane genome makes the resistant mechanism difficult to understand. Our previous studies deciphered host resistance mechanism and identified different genes involved in sugarcane defence responses during pathogen invasion especially on early defence signaling cascades. We made further studies on microRNAs that play a crucial role in gene regulation by posttranscriptional modification to understand miRNAs and their regulatory targets involved in resistance mechanism against the invading red rot pathogen in sugarcane. Through NGS platform six small RNA libraries were constructed from resistant (Co 93009) and susceptible (CoC 671) cultivars at different time intervals after pathogen inoculation. The results showed early response of various genes involved in biological, molecular and cellular functions. Differential expression of various miRNA families viz., miR444, miR164, miR166, miR167, miR162, miR5568, miR818, miR395 and miR6227 was found during the host-pathogen interaction. Subsequently, miRNA target analyses identified genes involved in Ca^+ signaling pathways, auxin signaling, HR response, ubiquitination pathway, ER stress responsive pathways, phenylpropanoid biosynthesis pathway, hormone signaling pathways and host defence response during *C. falcatum* infection process. Our results identified various functions of sugarcane miRNAs and their respective target gene transcripts involved in the host defence response against the red rot pathogen.

KN (S 04) 02: RNAseq analysis of rice infected by *Xanthomonas oryzae* pv. *oryzae* relative to a T3SS-deficient mutant reveal the differential expression of immune responsive genes involved in host-pathogen interactions

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Bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) is a destructive disease of rice worldwide. The causal bacterium Xoo subverts the rice innate immunity through secreting T3SS- effectors. The genetics of resistance to BB via *R*-genes is extensively studied but the comprehensive understanding on rice proteins involved in T3SS-effectors mediated interaction is yet to fully investigated. Here we analysis the transcriptome profile of rice cultivar from Northern India infected with predominant Indian Xoo race 4 relatives to avirulent Xoo (a functionally impaired T3SS mutant of Xoo) at early (2-6 hpi) and late (16-24 hpi) hours of infection. Transcriptome analysis showed a total of 925 differentially expressed genes (DEGs) associated with various physiological activities. Out of total DEGs, 118 genes were up-regulated and 167 genes were down-regulated in early responsive category. In late responsive category, 431 genes were up-regulated and 209 genes were down-regulated. KEGG pathway analysis revealed that the DEGs are involved in hormone signalling, plant defense and cellular metabolism. In addition, we have also identified many differentially expressed transcription factors, sweet genes, peroxidises and disease resistant genes. Some selected DEGs involved in defense response and plant pathogen interactions were validated through quantitative real-time PCR and showed similar expression confirming the consistency of the transcriptome data. Altogether our study unravels the rice transcripts that are differentially participate to favour the pathogen leading to BB. This study would certainly lead to identify the novel rice targets that are being targeted by Xoo during BB pathogenesis, which could further be exploited in disease resistance programme.

Invited Papers

I (S 04) 03: Fusarium head blight of wheat-variability in pathogens and resistant sources

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India harvested record wheat production of 102.19mt from an area of 29.50mha during 2018-19. *Fusarium* head blight or head scab of wheat caused by *Fusarium spp*. has emerged as most important wheat diseases worldwide in 21st century. Presently, FHB is a minor disease in India but can cause significant yield loss if rain occurs during mid anthesis. *Fusarium graminearum* is known to produce mycotoxins which affect human and animal health. Extensive disease survey undertaken in Himachal Pradesh and Tamil Nadu (Wellington) during 2010-19 revealed the dominance of *F. graminearum* causing head blight of wheat in India. Pathogenic variation among *Fusarium* spp./isolates have been studied by inoculating on a set of wheat varieties under artificially inoculated conditions. Genetic variation among *F. graminearum* isolates have been detected with microsatellite and RAPD markers. Evaluation of more than 5000 wheat lines (indigenous germplasm, released varieties and exotic lines) during 2001-2019 could identified resistant lines to head scab pathogen. During 2017-18 crop season, out of 250 lines (indigenous and CIMMYT lines) evaluated under artificially inoculated conditions at IARI, New Delhi, only 40 lines showed moderate resistance to head scab pathogen, *F. graminearum*. Since most of popular cultivars grown in India are susceptible to head scab, so there is a need to screen more indigenous and exotic wheat lines for incorporating head scab resistance in popular wheat cultivars possessing resistance to other diseases.

I (S 04) 04: Influence of silicon in counteracting rice disease management

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Rice (*Oryza sativa* L.) is the important cereal crop grown in India contributes 40% of total food grain production and cover 42% of the total cropped area. Food security has been a major concern in India to fulfill the nutritional needs of the people, numerous attempts are being made to defeat hunger. Since ages, the use of pesticides is thought of as an immediate solution to increase crop productivity but this strategy is leading to a drastic environmental stresses faced both by man and plants. Fungi are known to cause 55 diseases in rice, 43 of which are seed borne or seed-transmittable. The three most important pathogens in rice are *Pyricularia grisea, Drechslera oryzae* and *Xanthomonas oryzae* often kills seedlings or plants at the tillering stage and may largely destroy the panicles. The disease causes yield loss as high as 70–80% when predisposition factors (low temperature, relative humidity higher than 85–89%, presence of dew and excessive nitrogen fertilization) favour epidemic development. So the need of the hour is to rely on eco-friendly approaches so as to be in harmony with nature. One of such approach is use of Silicon (Si) in our agricultural practices to combat various a biotic and biotic stresses as Silicon is continuously gaining serious attention since last few years due to its abundance and non-hazardous nature. Rice in particular, is affected by the presence of Si, with diseases such as blast, brown spot and sheath blight becoming more severe on rice plants grown in Si-depleted soils. Among rice diseases, blast is recognized as the most devastating one. Silicon fertilization has been reported to be efficacious in controlling and mitigating rice blast severity due to mechanical barrier and physiological roles in disease resistance. Si-mediated resistance against pathogenesis associated with the accumulation of phenolics and phytoalexins as well as with the activation of some PR-genes. In context of biotic stresses, Silicon provides resistance to plants against diseases either due to an accumulation of absorbed Silicon in the epidermal tissue, or expression of pathogenesis-induced host defense responses. A better molecular understanding of Si uptake in plants is important to maximize the benefits derived from Silicon fertilization. The present research topic compiles many aspects helpful to generate a better understanding required for the optimal utilization of Si to promote sustainable development and climate-adapted cropping.

I (S 04) 05: Importance of sugars in virulence of a rice pathogen *Xanthomonas oryzae* pv. *oryzae*

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Xanthomonas oryzae pv. *oryzae* (*Xoo*) is the causal agent of bacterial leaf blight of rice, one of the most serious rice diseases worldwide, especially in tropical and sub-tropical Asian countries. The type III secretion system (T3SS) plays important roles in the *Xoo*-rice interactions. Through the system, dozens of proteins, so called effectors, are directly secreted from bacterial cells to rice cells. The effectors suppress the rice immune system or induce plant susceptibility to the pathogen, resulting in successful bacterial colonization and multiplication in plants. In the last decade the contribution of TALEs (transcriptional activator-like effectors) on bacterial virulence have been reported. The effectors activate transcription of rice susceptibility-related genes, including sucrose transporter genes, called *Sweet*. In a Japanese *Xoo* strain MAFF311018, at least two TALEs activating rice *Sweet* genes are produced, and the mutant lacking the two TALE genes completely loses virulence. Components of T3SS are encoded in the clustered *hrp* genes. The expression of *hrp* genes is strictly regulated; it is generally induced under the *in planta* condition, but not under culture conditions except for certain nutrient poor media, so-called *hrp*-inducing media. Several factors have been shown to be involved in regulation of *hrp* gene expression. Among them, we have found that xylose and a transcriptional regulator XylR, which regulates the expression of xylan/xylose metabolism-related genes, play a key role in *hrp* regulation in *Xoo*. Xylan is a major component of rice cell walls. XylR represses the transcription of xylan/xylose metabolism-related genes by binding to the promoter region of target genes, but, in the presence of xylose, the regulator detaches from the promoter, enabling the genes to be expressed. Simultaneously, XylR suppresses the expression of *hrp* gene expression by decreasing the accumulation of a Hrp regulator, named HrpX. Inactivation of XylR by xylose allows an abundant accumulation of HrpX, resulting in highly expression of *hrp* genes followed by highly secretion of effectors via T3SS. Lesion lengths were shorter than rice leaves inoculated with the strain producing the mutated XylR that is not responsive to xylose than those with the wild type. The results indicate the importance of xylose in virulence of *Xoo*, and it is likely that the bacterium utilizes xylose not only as a nutrient but also as an inducer for virulence-related genes, *hrp*. Thus, it is likely that “sugars” are ones of important factors for virulence of *X. oryzae* pv. *oryzae*.

I (S 04) 06: Death and defense - dynamic regulation during stress and functional analyses of tomato metacaspases

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The functioning of metacaspases- the caspase homologs in plants, in perceiving stress cues and executing its downstream signaling is still an enigma. The identification of the stress-responsive substrates of these cysteine proteases is fundamental in investigating how alteration of the metacaspase and its targets can affect the stress response in plant. Our experiments have identified 8 putative metacaspase genes (*MC*s) in the tomato genome, designated as *MC1-MC8*, of which *MC1* and *MC5* transcripts were observed to be differentially regulated upon different biotic stresses- *Alternaria solani*, *Pseudomonas syringae,* and ToLCNDV. Comparison of the metacaspase activity in the protein isolates of virulent and avirulent *A. solani* infected leaves revealed that the metacaspase activity was significantly higher in the samples infected with the virulent pathogen, thus underlining their significance in biotic-stress response. Quantitative GUS reporter assays revealed that *MC1* promoter activity was upregulated upon *Alternaria solani* infection and modulation of the promoter activity was probably brought about by the interactions with biotic stress-responsive transcription factors. Transient overexpression of MC1 and MC5 into leaf tissues caused increased accumulation of H_2O_2 and enhanced expression of ROS generating enzyme transcripts, supporting the fact that they are involved in pathogen triggered PCD. Bacterial overexpression of MC5 led to the autocatalytic processing of the protein which was validated by western blot analysis. Purified MC5 cleaved synthetic fluorogenic tri/tetrapeptides with Lys and Arg specificity. MC5 was observed to be most active at an acidic pH range of 5-6, its proteolytic activity was independent of Ca2+ and drastically inhibited by cysteine protease inhibitors, thus establishing their identity as cysteine dependent endopeptidases. Further, to decipher the targets of these metacaspases under physiological conditions, a metacaspase-cleavable reporter assay and comparative proteomics-based approach using control tomato plant and CRISPR-Cas9 knockdown transgenic line is also in progress.

Oral Papers

O (S 04) 07: Physiological race profiling of *Fusarium oxysporum* isolates infecting eggplant (*Solanum melongena* L.)

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Fusarium oxysporum inciting vascular wilt is one of the major limiting factors for successful cultivation of brinjal. Despite its significance, no reports on its physiological races worldwide. Also, lack of reports on resistant cultivars in India. Development of resistant varieties could have been hampered by lack of knowledge on the physiological races of the fungus. Hence, to characterize the pathogenic fungus, fungal isolates representing 10 locations and preserved as laboratory collections were characterized. These were characterized based on their cultural, and morphological characteristics and their identities were confirmed by sequencing of ITS region and translation elongation factor 1-alpha (EF-1α) gene. Pathogenicity was established in a susceptible cultivar under artificial inoculation conditions in a polyhouse. In assessing their genetic variability using Inter Simple Sequence Repeat, the fingerprints showed genetic variability among the isolates. Effector (Secreted In Xylem, *SIX*) gene screening of the pathogenic ones discriminated them as race 2 isolates. In bioassays employing *I-2* cultivars (267), these race 2 isolates incited no or low vascular wilt incidence confirming their physiological race. This knowledge on physiological race may enable development and deployment of resistant cultivars for commercial cultivation.

O (S 04) 08: Procedures for race analysis in *Blumeria gramins* (DC) Speer (Syn. *Erysiphe graminins* DC) f. sp. *tritici* by designing host differentials of *Triticum* species

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Among biotrophic pathogens, the frequent changes in varieties and cultivation practices favoured powdery mildew pathogen to become major threat for commercial cultivation of wheat in India. This particular disease results yield loss (30%) and seedling loss (upto 100%) in India. Wheat cultivars having race-specific resistance genes provide immunity, thereby exert a strong selection pressure on pathogen population but often results in development of new pathotypes or races with matching virulence genes. Different 'R' genes were identified in wheat and regional specific races of *Puccinia* spp. are well known in India. However, races of powdery mildew pathogen are not studied so far. Owing to Nilgiri hills is hot spot for the biotrophic pathogens of wheat, we utilized this natural epiphytotic conditions for races analysis in populationof *B. graminis* f. sp. *tritici*. Genetic stocks of *Triticum* spp. were imported from CIMMYT and other sources. Test pathogen was cultured artificially on tender seedlings under aseptic conditions. We also standardized a rapid method for mass culturing method of *Bgt*conidia and about 250 isolates of *Bgt* are maintained. Selected isolates were used for genetic analysis using genomic DNA and submitted partial genome sequences. The phenotypic responses of *Pm* genes in isogenic lines of *T. aestivum* were evaluated under a exclusive environment of this pathogen. In order to profile races in *Bgt* population, three set of host differentials were identified and grouped as 0, A and B sets. The standard mathematical formula on decanary value was followed with slight modifications. Uniform number in

all three differentials set was maintained and each value was denoted with first letter of test pathogen (BGT). Five representative isolates were race analysis and interestingly, distinct infection and virulence pattern were identified with this new procedure. Five isolates namely N16, Nanj-1, No.59, CPM-10 and No54 had values as B62G0T108, B190G0T68, B62G2T104, B254G2T454 and B126G4T76 and distinguished the isolates of different locations. Therefore, this new set of procedures supported with genomic data could be as first model to be followed for the race analysis in wheat powdery mildew pathogen.

O (S 04) 09: Differential expression pattern of pathogenicity inducing effector genes in *Xanthomonas axonopodis* pv. *punicae* with pomegranate

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Pomegranate is a premier export intended crop in India. Of late, bacterial blight disease in pomegranate is causing significant yield loss. The disease causing bacteria *Xanthomonas axonopodis* pv. *punicae* (Xap) secretes type III effector proteins to suppress the pathogen associated molecular pattern (PAMP)-triggered plant immunity (PTI) and fosters the disease. The role and induction of *effector* genes during host-pathogen interaction in pomegranate Xap is not known. In this context, an attempt was made to identify the expression profile of ten putative effectors (pathogenicity-related genes) during host-pathogen interaction. These candidate pathogenicity-related genes were identified through *in silico* analysis, which includes seven genes with putative type III secretion system (XopAK, XopV1, XopP, XopN, XopR, HpaP and HrpB), and one each of a general secretory pathway gene (GspH), a lipase family protein gene (Abhydrolase) and a serine/threonine kinase gene (PKc). The PCR-based amplification confirmed the homology between *in silico* and *in vivo* analysis of selected candidate effector proteins. Expression analysis through real-time quantitative PCR showed the induction of candidate pathogenicity-related genes during infection. The XopN, Abhydrolase and PKc gene were highly induced on an interaction between host-pathogen, than pathogen alone. The expression of these effector genes in the host during different time points of infection provided significant insight to deciphering the virulence mechanism of Xap. Unidentified and potentially new virulence factors were reported, which could be subverting host cell resistance processes.

O (S 04) 10: Development and utilization of *Soybean yellow mottle mosaic virus* infectious clone for understanding the seed transmission nature in French bean

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Soybean yellow mottle mosaic virus (SYMMV) is a newly identified species in the genus *Gammacarmovirus,* belongs to subfamily *Procedovirinae* with in the family *Tombusviridae*. SYMMV was initially reported from South Korea and North America in soybean plants exhibiting bright yellow mosaic symptoms followed by in

India from mungbean, soybean and urdbean plants showing mottling, mosaic and puckering symptoms. The complete SYMMV genome (~4kb) from mungbean was initially amplified and cloned in pJET 1.2 cloning vector. This SYMMV genome was restricted from pJET 1.2 and ligated to pHANNIBAL vector to utilize CaMV 35S promoter and OCS terminator with the replacement of intron region. The complete cassette consisting of 35S-SYMMV-OCS terminator was subcloned in pORE O4 open series binary vector. The recombinant clones used for infectivity assay through agro-inoculation showed the symptoms of chlorotic blotches with delay but indistinguishable from mechanical sap inoculation. The leaf tissue harvested from agro-inoculated French bean plants were used to sap inoculate fresh French bean plants to study the seed transmission nature of SYMMV. Seed harvested from mechanical sap inoculated French bean plants showed higher absorbance values in DAC-ELISA with SYMMV polyclonal antisera and amplification corresponding to replicase, movement and coat protein region of SYMMV. The relative accumulation of SYMMV was higher in pod walls, immature seed and stamens and stigma of mechanical sap inoculated French bean. Progeny assays through grow out method with infected seed revealed the seed transmission nature of SYMMV at the rate of 73.33% in French bean. Mechanical sap inoculation of progeny seedlings on French bean cv. Pusa Parvati produced the characteristic symptoms of SYMMV. The results obtained from this study demonstrate that SYMMV is seed borne in nature and can be transmitted to next generation seedlings. This is the first report of seed transmission nature of SYMMV in French bean.

O (S 04) 11: miR398: An integrator of biotic and abiotic stress signaling in tomato

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Cu/Zn Superoxide Dismutase (SOD) is one of the enzymatic repertoires of the stress responsive cellular singling cascade involved in the elimination of superoxide radicals. miR398 targets a crucial stress responsive SOD in tomato as observed by transcriptomic analyses of *Alternaria solani* infected plants followed by 5’-RLM-RACE experiments. To further validate, a target reporter construct was designed which showed decreased activity upon transient over expression of miR398 precursor in tomato plant. Mutation of the target site abolished this decrease, confirming the miRNA-target interaction. Heat stress or pathogen infection during heat exposure also dampened miR398 expression with a concomitant increase in SOD levels, suggesting, miR398-Cu/Zn SOD interaction works in the interface of biotic and abiotic stress signaling. In accordance, miR398 promoter activity was adversely affected in both *Alternaria* and heat stresses, whereas, the promoter activity of the SOD gene remained unaltered. Activity gel assays indicated increased protein level accompanied the increase in SOD transcript level during these stresses. Thus, our studies proved that miR398-mediated post-transcriptional regulation is key determinant for maintaining active SOD level during stresses. In order to understand the biological significance of this interaction, miR398 knockout tomato lines have been developed and we are in the process of generating plants with abolished target site in the SOD gene. Overall, these studies highlight the role of a small RNA in integrating biotic and abiotic stress signaling in plant.

O (S 04) 12: Seed biopriming with microbial inoculant triggers local and long distance defense responses against *Rhizoctonia solani* causing banded leaf and sheath blight in maize

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Plant growth promoting rhizobacteria, *Pseudomonas aeruginosa* strain MF-30 isolated from maize rhizosphere was characterized for several plant growth stimulating attributes. The strain MF-30 was also evaluated for antifungal properties against *Rhizoctonia solani* under *in vitro* conditions and found to have the higher mycelial growth suppression in the culture suspension (67.41%) followed by volatile organic compounds (62.66%) and crude extract (51.20%) in dual plate assay. The endophytic and epiphytic colonization ability was tested using Green fluorescent protein (*gfp*)-tagging strain. Visualization through confocal scanning laser microscope clearly indicated that strain MF-30 colonize the root and foliar parts of the plants. Further, the effects of seed bio-priming with *P. aeruginosa* MF-30 was evaluated in the induction and bioaccumulation of defense-related biomolecules, enzymes, natural antioxidants, and other changes in maize under pot trial. This not only provided protection from *R. solani* but also ensure growth promotion under pathogenic stress conditions in maize. The maximum concentration of hydrogen peroxide (H_2O_2) was reported in the root and shoot of the plants treated with *R. solani* alone (8.47 and 17.50 mmol mg^{-1} protein, respectively) compared to bioagent, *P. aeruginosa* MF-30 bio-primed plants (3.49 and 7.50 mmol mg^{-1} protein, respectively). Effects on total soluble sugar content, total protein, and total proline was also found due to inoculation of *P. aeruginosa* MF-30. The activities of anti-oxidative defense enzymes phenylalanine ammonia lyase (PAL), ascorbate peroxidase, peroxidase, and superoxide dismutase, and catalase increased significantly in the plants bio-primed with *P. aeruginosa* MF-30 and subsequent foliar spray of culture suspension of MF-30 compared to pathogen alone inoculated plants. qRT-PCR analysis revealed that seed bio-priming and foliar application of *P. aeruginosa* MF-30 significantly increased the expression of PR-1 and PR-10 genes with the simultaneous decrease in the disease severity and lesion length in the maize plants under pathogenic stressed conditions. A significant enhancement of shoot and root biomass as compared to control ($p< 0.05$) was recorded in MF-30 bio-primed plants. Significant increase in growth, antioxidant content and decreased disease severity in the *P. aeruginosa* MF-30 bio-primed plants suggests the possibility of an eco-friendly and economical mean of achieving antioxidants rich, healthier maize plants.

O (S 04) 13: Evaluation of effects of *Rhizoctonia solani* double stranded RNA on disease severity in *Zea mays*

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Banded Leaf and Sheath Blight (BLSB) disease on maize caused by *Rhizoctonia solani* f. sp. *sassakii* (*Thanetophorous cucumeris*, Frank) has been of serious concern due to its devastating disease potential causing 40-70% yield losses. The symptoms show variability on the same genotype grown in different locations. In the last three decades fungal double stranded RNA elements have been the subject of considerable research because of their potential *adverse effects* on pathogenicity of the fungus, and the prospects of utilizing them in biocontrol schemes against the host fungus. The present study was undertaken to screen the population of *R. solani* for presence of hypo/hyper virulence and to examine the effect of the dsRNA on disease severity in *Zea mays*. Total 108 isolates of *Rhizoctonia spp* were screened for presence of double stranded (ds) RNA using specific primers for presence or absence of dsRNA of interest. Only 28 isolates showed the presence of dsRNA of interest. A partial occurrence of 3.5 kb fragment was detected in 10 isolates. However; only 2 isolates carried a combination of 6.4 kb and 2.3 kb dsRNA. Only the isolates with presence of partial or complete dsRNA sequence were screened for further studies. Only one isolate *RsP-Lck* showed the presence of 2.1kbp length partial sequence of M2 dsRNA. The ten *Rhizoctonia* isolates, *viz.; RsU-1, RsU-2, RsU-3, RsU-4, RsU-5, Rs-U-6, RsM-Bth, RsM-Krl, RsR- Ymn, and RsHr-Srs* were used as donors for examining the transmission of virulence. Isolates *RsR-Sms, RsR-Lck, RsMh-Khp, RsW-1, RsW-2*, *RsP-Del, RsP-Ghz, RsP-Var*, *RsUp-Lck, RsM-Bhv* were used as recipients. Colony morphology on PDA could not be used as a reliable indicator to differentiate the hypovirulent isolates. The variation in virulence among the hypovirulent isolates was relatively small. Pathogenicity tests were conducted on 10 *Rhizoctonia* isolates *viz.*; *RsR-Sms, RsR-Lck, RsMh-Khp, RsW-1, RsW-2*, *RsP-Del, RsP-Ghz, RsP-Var*, *RsUp-Lck, RsM-Bhv* which have acquired partial/complete dsRNA fragments, on anastomosis with hypovirulent strains. The presence of one or two lesions with no characteristic banded pattern on sheath indicated that each of the isolates was poorly pathogenic. The electron microscopy revealed that none of the dsRNAs are encapsidated as virus-like particles. The study revealed that dsRNAs affected the virulence pattern of the disease. The reduced severity of symptoms and disease progress further opens the prospects of use of these isolates of fungus for cross-protection against severe isolates.

Poster Papers

P (S 04) 01: Effect of salicylic acid on biochemical constitutes of chilli against fruit rot pathogen *Colletotrichum capsici*

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Chilli (*Capsicum annuum* L.) is vernacularly known as “*Mirchi*”. It occupies an important place in daily diet and can be used in a variety of ways. Chilli fruits are used as pickles, sauces, ketchup, essence, oleoresins and is an inevitable ingredient in Indian dishes. A field experiment was conducted at Horticulture Farm, SKNCOA, Jobner during 2015-16 and 2016-17. In this study, four different varieties *viz*., Pusa Jwala, Pusa Sadabahar, Pusa Dipti and Amulaya and three germplasm NU-7078, NP-46A and G-S of chilli were raised and transplanted in third week of July. Roots of seedlings of chilli were dipped in hundred ppm solution of salicylic acid for 30 minute before transplanting and same concentration of salicylic acid was also sprayed on all varieties before flowering and PDI was noted 90 DAS. The peroxidase was increased maximum (28.95%) in infected plants of Pusa Sadabahar variety followed by Pusa Depti (20.59%), NP-46A (19.35%), Amulya (18.18%) and minimum in Pusa Jwala (9.09%) as compared to healthy ones. Minimum disease intensity was recorded in Pusa

Sadabahar (7.93%), as it also resulted in maximum increase in peroxidase. While higher per cent disease intensity was recorded in Pusa Jwala (43.4%), which resulted in minimum increase in peroxidase. The polyphenol content was increased maximum (23.68%) in infected plants of Pusa Sadabahar variety followed by Amulya (20.69%), NP-46A (17.14%) and it was found minimum in Pusa Jwala (13.04%) as compared to healthy ones. Phenol content was increased maximum (23.53%) in infected plants of Pusa Sadabahar variety followed by NP-46A (20.45%), G-S (14.29%), NU-7078 (12.50%) and it was increased minimum in Pusa Jwala (12.00%) as compared to healthy ones.

P (S 04) 02: *In silico* analysis of *Xanthomonasoryzae*pv. *oryzae*XopF effector and its two cognate interactors in rice to explore new targets for bacterial blight resistance

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Bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) is a most destructive rice disease that adversely affects crop productivity. Xoo secrets various effector proteins directly into rice cells through a specialized *hrp*-encoded type three secretion system (TTSS). The effectors play important role in suppressing the plant immunity and thus detailed analysis of these effectors would be useful to explore durable resistance strategies. Functional annotation using predict protein tools showed that XopF has 23 protein binding, 1 polynucleotide and many macromolecule binding regions. It does not have any disulphide bridge and transmembrane helices and has helix (49.32%), loop (49.62%) and strand (1.06%) confirmation. Further, this protein has exposed (51.13%), buried (41.60%) and intermediate (7.26%) regions. We identified the XopF interacting proteins in rice using Y2H system involving cDNA library as pray and XopF as bait. The sequenced interactors showed >99% homology with chloroplastic photosystem I (PSI) reaction centre subunit V (PSI-G) (Accession No. XP_015611871) and cyclophilin II (Accession No. GQ848065). The PSI-G is a 141 amino acid protein and is localized to chloroplast membrane. This protein is involved in electron transport and is crucial for the stability of photosystem I (PSI). STRING analysis validated the facts that XopF interacts with PSI and light harvesting complex. Another protein, the cyclophilin II encodes for a 172 amino acid protein. It interacts with heat shock protein 81-2, pre-mRNA processing factor 19, protein BUD31 homologs and SNW/SKI-interacting protein B. Apart from their native functions; both proteins contribute in plant defense response against bacterial pathogens. Molecular docking of XopF with PSI-G and cyclophilin II identified the important amino acid crucial for interaction. Further functional characterization of these rice interactors in BB development is in progress. This insight will be useful in exploring strategies for disease resistance by targeting the host proteins.

P (S 04) 03: Elucidation of the role of uncharacterized and hypothetical pathogenicity genes of *Colletotrichum orbiculare* in cucumber and chilli anthracnose

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Uncharacterised and hypothetical pathogenicity genes of *Colletotrichum orbiculare* and inciting anthracnose of cucumber are poorly annotated but could be potential antifungal targets in anthracnose control. Hence, to associate them with specific functions in fungal–host interactions for exploitation in anthracnose control, two fungal isolates, CUCO-MT and CHCC-MU of cucumber and chilli, preserved as laboratory collections were recharacterized using their cultural, and morphological characteristics and their identities were confirmed by PCR amplification of their ITS region and sequencing. Pathogenicity of the isolates was established in the polyhouse under artificial inoculation conditions. The fact that the uncharacterized genes of *C. orbiculare* are putative pathogenicity genes, six genes (ENH87679, ENH89286, ENH86880, ENH81967, ENH78781 and ENH87556) constitutively expressing in a minimal medium and identified among 51 randomly selected ones from *in silico* analyses of *C. orbiculare* genome were tested for *in planta* expression in cucumber (cv Pusa Uday) and chilli (cv. Pusa Sadabahar) upon inoculation with *C. orbiculare* (CUCO-MT) and C. capsici (CHCC-MU) isolates, respectively. Two genes, ENH87556 and ENH87679 were identified to be the potential ones for expressing in both the hosts all the time indicating that the genes are not redundant and may function under stress conditions. In phylogenetic analysis, these two genes aligned in different clusters indicating no homology among themselves. These genes could therefore be potential molecular targets for anthracnose control in cucumber and chilli upon validation by functional analysis.

P (S 04) 04: *In vivo* studies of banana endophytes from Assam for suppression of *Fusarium oxysporum* f. sp. *cubense* (Foc) inciting panama wilt of banana

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Pannama wilt of banana is a major constraint in banana production worldwide. Existence of different races (Race 1, 2, 3, 4) threatening the banana cultivation. Foc1 infects Gross michel, Foc 2 infects bluggoe, Foc 3 infects heliconia and Foc 4 infects cavendish cultivars. To date Foc4 has caused serious crop loss in Asia, Australia, and Africa. As the pathogen is soil inhabitant cultural and chemical approaches does not give a considerable reduction in the disease, however increased public concern over the hazardous effects of pesticide residues will also suggests us there is a urgent need to think about novel methods of plant disease management such as endophytes. Endophytic microorganisms (Fungi, bacteria & actinomycetes) are those that inhabit the interior part of the plants, especially in leaves, branches, root and stem, without any harmful effect to the host. In present study banana samples (leaf, pseudostem, root) samples were collected from different agroclimatic zones of Assam. Bacterial endophytes were isolated by following standard protocols. A total of 320 endophytes are obtained and they are categorised based on colony morphology and evaluated against Foc by dual culture technique. Three bacteria showed 60 per cent and above inhibition and other bacteria showed less than 40 per cent inhibition. Three endophytes (2 fungi and 1 bacteria) were further evaluated for their efficacy *in vivo* and positive correlation with biometrical parameters of the plants were observed. The disease development was also evaluated by area under disease progress curve (AUDPC). Banana plantlets pre-treated with UH EF +AAU EF+UH EB (Combination treatment) gave the lowest AUDPC of 99.09 units2 with epidemic rate of 0.02 units d-1. The challenge inoculation of the promising endophytes to the banana plant has shown an increase in activity of peroxidase (POD), Polyphenol oxidase (PPO) and Phenyal alanine ammonia lyase (PAL).

P (S 04) 05: Identification of source of resistance in cauliflower against *Xanthomonas campestris* pv. campestris

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Black rot, caused by *Xanthomonas campestris* pv. *campestris* (Xcc) is one of the most important disease of crucifer crops. In India, 3 different races of Xcc were identified on the basis of host specificity and pathogenicity characteristics. The objective of this study was to identify the resistant genotypes of cauliflower. The 356 genotypes of cauliflower (*Brassica oleracea*) were screened against 3 Indian races of Xcc i.e. race 1, 4 and 6 by bacterial inoculation and the pathogenicity test at Indian Agricultural Research Institute, Farmers field, New Delhi. Three young leaves of 30-day-old plants were inoculated using small scissors that had been dipped in a suspension from a 48-h-old culture of Xcc grown on Nutrient agar medium at 28 °C. The black rot disease reaction was recorded 15 days after pathogen inoculation. The pathogenicity analysis of Xcc is based on the disease score i.e. 0 to 9. The disease score analysis revealed that only 10 out of 356 genotypes of cauliflower having moderate resistance towards Xcc race 1, 4 and 6 respectively. Additionally, field analysis elucidated the pathogenicity profile of these three races in India and reveals the dominance pattern in order as Race 1 > Race4 > Race6. The scientific outcome of this study will be used in breeding to develop resistant varieties and increase the farmer's land yield & income.

P (S 04) 06: VIGS mediated functional validation of differentially expressed rice transcripts induced by virulent strain of *Xanthomonas oryzae* pv. *oryzae* causing bacterial blight of rice

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Virus-induced gene silencing (VIGS) is a plant virus based reverse genetics tool for rapid and high throughput transient silencing of plant gene(s) in dicot as well as monocot plants. The Rice tungro bacilliform virus (RTBV)-derived VIGS system (RTBV-VIGS) are frequently used to study the gene function in rice. In this study, we have validated the function of *rpm1* gene upon infection with a virulent Indian strain of *Xanthomonas oryzae* pv*. oryae* (Xoo). It is an important gene that encodes a NBS LRR protein localized to the plasma membrane and confers resistance against *Pseudomonas syringae*. A short fragment of 300bp for optimum silencing was selected based on SGN VIGS tool and cloned into pGEM-T easy vector. The fragment was excised by restriction digestion with *Pac*I and *Mlu* and further sub-cloned into RTBV vector. The RTBV vector, VIGS control (RTBV-PDS) and the silencing construct (RTBC-RPM1) were transformed into *Agrobacterium tumefaciens* strain EHA 105. The grown agrobacterium cultures were infiltrated into 20 days old rice plants (cv. PB1). The infiltrated plants were kept at plant growth chamber at 28^{0}C and humidity >80% and continuously observed for the development of silenced phenotype. The validation of *rpm1* and *pds1* silencing was analyzed through quantitative real time PCR. The mock (buffer infiltrated) and silenced plants was infected with Indian Xoo race 4. The validation of disease related events in mock and silenced plants is in progress.

P (S 04) 07: Pathogenicity and anastomosis of *Rhizoctonia bataticola* causing dry root rot of chickpea

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Dry root rot caused by *Rhizoctonia bataticola* (Taub.) Butler [Pycnidial stage: *Macrophomina phaseolina* (Tassi) Goid] is a soil borne fungal pathogen. Keeping in view the importance of the disease due to change in climatic conditions, studies were conducted on distribution of the disease, cultural, morphological, pathological and molecular diversity. The experiment was conducted at Department of Plant Pathology CSA, Kanpur. In the present studies, fifty isolates of *R. bataticola* were isolated disease sample of dry root rot of chickpea from different regions of Uttar Pradesh. Those isolates were analyzed for cultural and morphological variability. Significant differences were detected among fifty isolates in their radial growth, colony colour, pigmentation, margin type, growth pattern, aerial hyphae, sclerotial size and shape. Six isolates among fifty were producing dark red colour pigment on PDA & other media. Seventeen isolates showing black colour colony, sixteen were giving olive colour and remaining seventeen showing gray colour on PDA media. On the basis of pathogenicity there are thirty two isolates which are highly virulent and others are less virulent. Anastomosis is also found in some isolates. On the basis of their sclerotial size, twenty two isolates were classified as large sized, eighteen as medium sized, and the remaining ten isolates as small sized sclerotia. These cultural and morphological variations in among different isolates are very useful in study of diversity of *R. bataticola*.

P (S 04) 08: Potential of antagonism and antibiosis by *Trichoderma* spp. strains native to Madhya Pradesh against different plant pathogenic fungi

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Trichoderma spp. are economically important fungi as sources of industrial enzymes, plant disease biocontrol agents, good plant growth promoters and as inducer of resistance in plants against invading pathogens through limited colonization of plant roots. *Trichoderma* spp. are a rich source of secondary metabolites (SMs). Based upon analytical reports, *Trichoderma* spp. are prolific producers of SMs (natural products), with the structures of more than 100 compounds reported which include low-molecular-mass non-polar compounds such as pyrones, terpenoids, steroids and polyketides. Members of the genus are prominent producers of a subgroup of peptaibiotics known as peptaibols. This vast potential of *Trichoderma* spp. to produce numerous types of metabolites is reflected in the genomes of the three species. Hundreds of such compounds are known to be produced by *Trichoderma* spp., many with anti-microbial, anti-proliferative and plant growth/ defense promoting properties. It is thus important to make best (and safe) use of these economically important fungi by exploring the secondary metabolite production and antibiosis capability of different isolates of *Trichoderma.* In the present investigation, a repository of 40 isolates of *Trichoderma* were firstly evaluated for their antagonistic potential against *Rhizoctonia bataticola*, *Helminthosporium graminea* and *Alternaria solani* and subsequently selected isolates were evaluated for antibiosis activity against *Pythium* sp. by extracting acetone soluble metabolites. Isolate T_{21} showed its maximum inhibition capacity against *R. bataticola* (48.39%) and *Trichoderma* isolate T_6 showed its maximum inhibition capacity against *Helminthosporium graminea*

(45.45%) and *Alternaria solani* (54.82%). Further, All the selected isolates showed differential activity of antibiosis in bioassay against the test pathogen. However, isolate T_6 and T_{23} showed maximum inhibition in growth of *Pythium* spp using acetone soluble metabolites. However, a set of eight isolates namely T_5, T_{12}, T_{15}, T_{21}, T_{25}, T_{33}, T_{34} and T_{36} effectively parasitized the 100 % sclerotia of *S. rolfsii* under *in vitro* conditions. In this way, different native isolates of *Trichoderma* exhibited differential activity of antagonism and antibiosis which needs to be further evaluated under field conditions before their successful use in plant disease management.

P (S 04) 09: Effect of PGPF in the induction of resistance in chilli (*Capsicum annuum* L.) against *Colletotrichum capsici* (Syd.)

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PGPF (plant growth promoting fungi) are the native fungi that harbours naturally in the soil which have the potential to promote growth and control phytopathogens. Chilli is a chief crop consumed as spice across the world specially in India. Anthracnose disease of chilli is one of the deleterious disease causing huge yield losses to farmers thereby affecting Indian economy. In the current study, total of 70 rhizospheric fungi isolated and based on plant growth promoting property and pathogenicity, 5 PGPFs were selected and screened for growth promotion and protection against *C. capsici* under greenhouse conditions. Five potential fungi evidenced resistance by elevating defense related enzymes activity (PAL, POX, GLU, CHI) and also enhanced deposition of defensive cell wall materials such as lignin and callose upon infection with *C. capsici* than the control. Thus, PGPF can be used as potential source in control of anthracnose pathogen.

P (S 04) 10: Morphological and biochemical variability in green gram genotypes with reaction to Cercospora leaf spot disease

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Greengram or Mungbean [*Vigna radiata* (L.) Wilczek], is an important leguminous crop of South and Southeast Asia. In India the total production of greengram is 14 lakh tonnes from an area of 34.4 lakh ha with a productivity of 406 kg ha^{-1}. In Andhra Pradesh (A. P) it is grown in an area of 2.78 lakh ha producing 1.94 lakh t with a productivity of 696 kg/ha (Directorate of Economics & Statistics, Government of A. P, 2013). It is cultivated preceding crop to rice in Nagarjuna sagar project (NSP) right canal dryland areas and tank fed areas in Guntur and Prakasham districts. Greengram suffers from many diseases caused by fungi, bacteria, viruses, nematodes and also abiotic stresses. Among the fungal diseases, Cercospora leaf spot is of common occurrence throughout Asia. The present *in vitro* experiment was conducted at Agricultural College, Bapatla, Guntur, Andhra Pradesh to evaluate the stomatal frequency, level of total sugars, total proteins and total phenols in resistant and susceptible greengram genotypes against Cercospora leaf spot disease. Number of stomata per mm^2 was found higher in susceptible genotypes (199.36 mm^2) and lower in resistant genotypes (74.10 mm^2) total phenols were found higher in resistant genotypes (0.99 mg/100mg) and lower in susceptible genotypes (0.54 mg/100mg) total proteins were found higher in resistant genotypes (1.99 mg/100mg) and lower in susceptible genotypes (1.54 mg/100mg). But, total sugars were found to be higher in susceptible genotypes (7.72 mg/100mg) and lower in resistant genotypes (5.49 mg/100mg).

P (S 04) 11: Multiple disease resistance and race pattern of leaf and stem rust of wheat in Northern Karnataka

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Although there is huge variation in climatic conditions wheat is grown in all parts of India. Rust diseases represent the most economically significant fungal diseases in wheat and they are widely distributed across wheat growing regions. With the capacity to form new strains of fungus, rusts can attack even previously resistant varieties. Leaf rust and stem rust are most commonly observed rusts in wheat growing areas of Northern Karnataka. The screening for multiple disease resistance was carried out in Main Agricultural Research Station of UAS, Dharwad during rabi 2018-19. The results of terminal disease severity revealed that, twelve genotypes were categorized under TMS, 5MS and 10MS for stem rust and the same lines were categorized as zero for leaf rust and resistant for spot blotch pathogens. Thus, these results need further confirmation for exploring them in breeding for multiple disease resistance and to protect the crop from diseases and subsequently increase the production. Among the race/pathotype pattern of leaf rust of wheat 77-5 and 77-9 races has covered 20.69% and 62.07% respectively and stem rust races 11 and 15-1 has covered 42.86 % and 34.92% respectively in wheat growing areas of Northern Karnataka.

P (S 04) 12: Genetic diversity and physiological race characterization of *Fusarium oxysporum* isolates infecting tomato in India

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Vascular wilt of tomato caused by species of *Fusarium* is a serious disease worldwide. In India, though both *F. oxysporum* and *F. solani* are associated with the disease, *F. oxysporum* appears to be widely reported. In *F. oxysporum*, though three different races i.e. race 1, race 2 and race 3 have been reported worldwide, no reports on physiological races of the fungus in India. Also, though three resistant genes, *I, I-2* and *I-3* are known in tomato cultivars worldwide, no reports on resistant cultivars in the country. Development of resistant varieties could have been hampered by lack of knowledge on the physiological races of the fungus. Hence, to characterize the pathogenic fungus, fungal isolates representing 18 locations and preserved as laboratory collections were characterised. These were characterized based on their cultural, and morphological characteristics and their identities were confirmed by sequencing of ITS region and translation elongation factor 1-alpha (EF-1á) gene. Pathogenicity was established in a susceptible cultivar, Pusa Rohini under artificial inoculation conditions in a polyhouse. In assessing their genetic variability using Inter Simple Sequence Repeat, the fingerprints showed genetic variability among the isolates and were grouped into two major clusters. Effector (Secreted In Xylem, *SIX*) gene screening of the pathogenic ones discriminated 8 as race 2 isolates. Since the race 2 isolates were grouped as one cluster in variability studies, they may belong to a single virulent group. In bioassays employing *I-2* cultivars (EC-12 and EC-814916), these race 2 isolates incited no or low vascular wilt incidence confirming their physiological race. This knowledge on physiological race may enable development and deployment of resistant cultivars for commercial cultivation.

P (S 04) 13: Relative expression analysis of putative genes related to pathogenesis in *Tilletia indica* infecting Wheat

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Karnal bunt (*Tilletia indica*) is an internationally quarantined disease of wheat prevalent in several countries. In modern resistance breeding, effectors are emerging as tools to accelerate the identification, functional characterization and deployment of resistance genes. Total seven pathogenicity related genes were selected on basis of transcriptome data and PHI database. Expression studies conducted under *in vitro* in the presence of resistant (HD29) / susceptible (WH542) host factor amendment does not showed significant increase in expression for all the genes. Under *in planta*, *Ti 2035, Ti 2347,* and *Ti 3774* showed maximum expression at 3 dpi in both the genotypes. Two genes(*Ti 57* and *Ti 198*) showed maximum expression at 3 dpi followed by 10 dpi and 15 dpi. Relating to earlier histopathological studies, these genes have role in penetration, infection and in establishment of local systemic infection. Further two genes(*Ti 10340* and *Ti 12741*) showed highest expression at later stages at 10 dpi and 15 dpi only in susceptible genotype may have role in pathogen establishment and sporulation. Gene expression data shall be utilized to understand the mechanism(s) of pathogenesis which will help in developing strategies for management of Karnal bunt disease.

P (S 04) 14: Plant growth promoting fungus- *Penicillium oxalicum* instigates defense mechanism in pearl millet upon infection with downy mildew disease

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Rhizosphere-resident antagonistic microorganisms (plant growth promoting fungi/ bacteria) are ideal biocontrol agents, as the rhizosphere provides the frontline defense for roots against infection by the pathogens. Pearl millet susceptible seeds (cv. 7042S) were treated with PGPF- *Peniciilium oxalicum* at l × l0^{8} CFU ml^{-1} to test its ability to enhance crop growth, induce resistance to downy mildew disease caused by *Sclerospora graminicola*. *P. oxalicum* treatment to seeds for 6 h, significantly enhanced the seed germination, seedling vigor and also offered 62% downy mildew disease protection. The spatio-temporal studies revealed that inducers *P. oxalicum* required a minimum of 72 h for developing maximum disease resistance which was maintained thereafter. Seed treatment with *P. oxalicum* offered defense at morphological (HR), histological (deposition of lignin and callose) and bio-chemical (peroxidase and chitinase) levels. The study highlights the efficiency of *P. oxalicum* in inducing resistance against upon infection with downy mildew upon seed treatment. The results of the study confirm that PGPF- *P. oxalicum* can be used as a source of inducer in pearl millet against downy mildew disease and the findings have also evidenced the inter-connection of induced systemic resistance and defense responses.

P (S 04) 15: Bioreporter strain mediated screening and isolation of novel and more virulent plant pathogen (*Pectobacterium carotovorum* subsp. *carotovorum*)

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Pectobacterium carotovorum subsp. carotovorum (*Pcc*), asoft rot causing phytopathogen, for which an arsenal of plant cell wall-degrading enzyme is produced in a cell density dependent manner called Quorum Sensing (QS), the ability of bacteria to sense their population density and respond by modulating a set of gene expression. *Pectobacterium* synthesizes different N-acylhomoserine lactone (AHL) which plays a key role in regulating gene expression in plant cell wall macerating extracellular enzymes (PCWME) production. The aim of the current study was to screen and isolate virulent soft rot causing bacterial strain from tomato plant. We have isolated soft rot causing bacterial strains from soft rot infested tomato plant, IARI vegetable Research Farm. Out of six different isolated strains one strain IS1 was characterized as one more virulent soft rot causing strain which showed 46% more disease severity in comparison to reference *Pectobacterium* strain MS1 and later on was confirmed as *Pectobacteriu mcarotovoum* subsp*. carotovorum* (Accession no.GU590785) by sequencing. The strain IS1 showed more carbon substrate utilization than the reference strain MS1. The transmission electronic microscopic (TEM) view of IS1 unveiled the rod shape with size of about 2-2.2µ x 1µ with 50-55 peritrichous prominent flagella where as MS1 has a size of 5µ x 1µ with around 30 peritrichous flagella. In bioreporter strain mediated C_{18} RP-TLC study we could detect another new HSL (Homoserine lactone) spot with $R_f$value 0.19 along with C6-OHHL, C6-HHL with an R_f value 0.68 & 0.47 respectively. The new spot HSL compound was confirmed by Mass spectrometer study as C10-Undecanoyl HSL. We are reporting the IS1 strain as more virulent and novel *Pectobacterium* isolate with massive soft rot capacity in tomato plant.

P (S 04) 16: Genotype x environment interaction among the wheat cultivars for resistance to spot blotch disease: A case study

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Spot blotch (SB) caused by *Bipolaris sorokiniana* Sacc. In Sorok. Shoem is a serious biotic stress to wheat in warm and humid areas, particularly South Asia. The yield loss due to this disease is very significant. The present investigation was carried out through screening of eight wheat genotypes under field conditions in post-rainy (*Rabi*) season of 2018-19 in five different locations West Bengal having different agro-climatic situations of to identify sources of resistance and level of aggressiveness of *B. sorokiniana* in wheat. Pathogenic variability was investigated on a susceptible wheat cultivar (Sonalika) in the aforementioned five sites. A clear evidence of relationship was observed between the spot blotch severity in wheat and weather parameters. The genotypes showed different levels of resistance to spot blotch across the different locations. The genotype plus genotype x environment (GGE) biplot grouped the five locations or environments (E) into different mega-environments (ME) with respect to spot blotch severity. Positive relationship was found between pathogenic variability and aggressiveness with agro-climatic condition.

P (S 04) 17: Understanding sheath blight disease: *Rhizoctonia solani* anastomosis group (AG) specific interactions in rice

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Sheath blight of rice is one of the important disease caused by a necrotrophic pathogen *Rhizoctonia solani* Kuhn. Economic losses up to a 50% decrease in rice yield has been observed around the world. Anastomosis is one of the important variability mechanism for gene exchange in fungi. AG is a collection of closely related isolates grouped together based on their capability to anastomose with each other. *Rhizoctonia solani* is classified into 14 genetically isolated anastomosis groups based on their hyphal interactions. Supporting to the classical anastomosis grouping, AG specific genes have been described by researchers. Initially, *Rhizoctonia solani* isolates were screened by dual culture technique and subsequently through sequencing of ITS region we identified AG1-IA as most occurring isolate and AG2-2 as least one among the forty isolates. In histopathological studies, we observed that AG1 and AG2 produced infection cushions as well as appressoria but other AG groups produced only infection cushions. Comparative genomic analysis results shown that AG1_IPT, AG1_BrD and AG1_HmPr were specific to *Rhizoctonia solani AG1-IA*. Further, qRT-PCR based analysis of these genes indicated an upregulation in Pusa Basmati 1 (susceptible variery) as compared to ILS (resistant genotype). Therefore this information on specific pathogenicity genes could be utilized in development of AG1-IA specific diagnostic tools and to understand the AG group specific interactions.

P (S 04) 18: Evaluating the potential of host delivered RNA interference approach for controlling Sclerotinia stem rot disease

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Sclerotinia Stem Rot (SSR) is rapidly emerging as devastating fungal disease of *B. juncea* especially in the northern plains. Integrated disease management practices have been largely unsuccessful in controlling the damage caused mainly due to its broad host range, prolonged persistence in the soil and complex resistance. Host delivered RNA interference (HD-RNAi), has been reported to be effective in controlling several fungal phytopathogens such as *Botrytis*, *Puccinia*, *Fusarium* etc. It involves the production of dsRNA against fungal pathogenicity genes within the host plant. These are uptaken during infection and target the candidate genes via degradation and modifications leading to a silencing in the pathogen genes. We aim to extend the strategy to control a notorious fungus-*Sclerotinia sclerotiorum*. We have tested the ability of *S. sclerotiorum*, a necrotrophic fungus, to assimilate dsRNA from external source. A fungal gene SS1G_08218 regulates the synthesis of Oxalic Acid (OA), an important pathogenicity factor. dsRNA targeting this gene when supplemented in the growth media, should downregulate the fungal endogenous gene there by reducing OA production. This can be visually estimated using Bromo Phenol Blue (BPB). Preliminary results distinctly show the ability of S sclerotiorum to uptake dsRNA. A transient system for the quick screening of candidate genes based on a HD-RNAi in the *Nicotiana benthamiana- S. sclerotiorum* patho-system is being developed. Initial set of experiments with two known pathogenicity genes –SS1G_00699 and SS1G_04805 , has been carried out. This can be a high throughput pipeline to evaluate different pathogenesis/ virulence/ essential genes.

P (S 04) 19: Modified *in vitro* infection models for charcoal rot pathogen and identification of potential fluorescent *Pseudomonas* against *Rhizoctonia bataticola* following tripartite interaction

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Macrophomina phaseolina (Mp) the causal agent of charcoal rot disease in soybean, attacks many economically important hosts, including cereals, legumes, vegetables, fruits and ber crops. High temperature conditions and low soil moisture favors appearance of charcoal rot symptoms. Initial infection occurs at the seedling stage, and remains latent until the soybean plant approaches maturity. Method to infect plants with soil borne pathogens described by Bressano et al 2010 allows to examine the pre-penetration and the penetration phases of other soil borne fungi as well as the early responses of the host plant. We propose a modification over method described by Bressano et al 2010 and report the identification of potential fluorescent *Pseudomonas* effective against charcoal root rot pathogen. Modified *in vitro* infection models for charcoal rot pathogen will not only help to evaluate the infection behaviour on susceptible host but can also be utilized in several ways in bi-partite or tri-partite interactions for evaluation of fungicide molecules / bio agents / botanicals.

P (S 04) 20: Pathogenicity and post harvest management of stem end rot caused by *Botriodiplodia theobrome* in mango

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Mango (*Mangifera indica*) popularly known as king of fruits is one of the delicious fruit grown in tropical and subtropical regions of the world. India has a rich wealth of mango and shares about 56% of the world mango production. Temperature, humidity and rainfall are the primary environmental factors that affect the outbreak of various mango diseases. A number of pre and post harvest diseases are reported to cause perceptible loss in quality and yield of mango. Stem end rot caused by *Botriodiplodia theobrome* (syn. *Lasiodiplodia theobrome*) is an important post harvest disease which caused quantitative and qualitative losses in mango fruits. In the present study, pathogenicity was assessed in five popular mango varieties namely Fazali, Langra, Chausa, Neelam and Dashehari by plug inoculation technique. The appearance of lesions was brownish black and started from stem end region and spread linearly along the fruit resulting softening of the skin. Colonies of the fungus on potato dextrose agar was moderately dense with raised mycelium mat and whitish to smoke grey in colour. Mean lesion length ranging from 2.9 to 15.9 cm and mean lesion size ranging from 8.4 to 254.4 cm^2 were recorded in mango varieties. Minimum lesion length and lesion size was recorded in Dashehari followed by Fazali. Whereas, maximum lesion length and lesion size were recorded in Neelam and Chausa. Percent reduction in TSS ranged from 9.8 to 42.9% and was maximum in Neelam followed by Chausa. These two varieties were found susceptible to stem end rot. Foliar spray of Difenoconazole 25 EC @0.5 ml per litre of water 30 days before harvest and hot water treatment at 52^{0}C for 10 minutes alone and in combination were studied for the management of post harvest stem end rot in mango variety Chausa and Neelam. Lesion length, lesion area and physiological loss in weight (PLW %) of mango fruit were recorded in both the varieties. Mean lesion length, mean lesion area and PLW (%) ranging from 0.0 to 17.6 cm, 0.0 to 133.9 cm2 and 1.7 to 13.8%, respectively were recorded in different treatments. Pre-harvest spray of Difenoconazole 25 EC @0.5 ml per litre of water 30 days before harvest and hot water treatment at 52⁰C for 10 minutes was found best in controlling stem end rot in Neelam and Chausa followed by only hot water treatment.

P (S 04) 21: Next-generation genomics in *Cicer-Ascochyta* pathosystem to elucidate the quantitative disease resistance genes

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Chickpea (*Cicer arietinum* L.) is an important cool season pulse crop of India and play important roles in human diet as a cheap protein source. The fungal diseases Ascochyta blight (AB) and Fusarium wilt (FW) are major impediments in its production. The best way to warfare these diseases is the development of resistant cultivars. In chickpea, molecular breeding for improved fungal resistance requires identification of robust narrowed QTLs/candidate genes. To decipher AB resistance, previously our lab has physically mapped two major QTLs (*qABR4.1* and *qABR4.2*) and a novel minor QTL (*qABR4.3*) on assembled Ca4 pseudomolecule of chickpea var. CDC Frontier. Under the major *qABR4.1*, a transcriptional regulator *CaAHL18* was identified as a candidate gene and CaNIP8 marker was developed from its polymorphic *cis*-regulatory region for molecular breeding. We have further fine-mapped major *qABR4.2* (27.55-33.49 Mb) and novel minor *qABR4.3* (38.78-39.48 Mb) to identify the candidate genes and their molecular mechanism of resistance. The genomic region under *qABR4.2* is rich in transposable elements and previously associated with segregation-distortion. We have narrowed *qABR4.2* to ~1.41 Mb by genotyping in a bi-parental CRIL-7 population and its association in various chickpea accessions. To translate the obtained genetic information and polymorphic markers from our AB resistance study, we intend to introgress multiple fungal resistance loci (for AB and FW resistant *desi* accessions) in few selected higher yielding cultivated varieties of chickpea. Our combinatorial approaches have helped in overcoming the *Cicer*-AB genetic mapping associated problems of AB resistance loci fine-mapping and their utilization in molecular breeding. Thus, our work will provide landmark information on chickpea AB resistance for the convenience of biotechnologists and breeders.

P (S 04) 22: Fine mapping of a major QTL RtAb3 for resistance against *Alternaria brassicae* in *Arabidopsis thaliana*

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Alternaria brassicae, a necrotrophic fungus, causes Leaf blight, an economically important disease in *Brassica* sp. It has been reported to cause yield losses of upto 70% in Indian subcontinent. The typical symptoms of *Alternaria* leaf blight include formation of necrotic lesions and chlorosis in surrounding tissues. Due to lack of resistant sources in *Brassica* sp, we have used *Arabidopsis thaliana,* a closely related member of Brassicaceae, as a model system to study the genetics of resistance against *A. brassicae*. Earlier work in lab identified natural accessions showing a spectrum of resistance against *A. brassicae*. Two accessions CIBC-5 and Zdr-1 showing highly contrasting response to A. brassicae challenge, were used to dissect the genetic factors underlying resistance to the pathogen. Screening a biparental F_2 population, identified a one major QTL RtAb3 (LOD 8.0) on Chromosome 5 covering 2.4Mb region. The aim of this study is to fine map the 2.4Mb region.

Based on the NGS resources available for various accessions of *Arabidopsis* ten polymorphic markers (Indels, CAPS and dCAPS) were developed and confirmed by PCR. 1500 F_2 plants were first genotyped with flanking markers on both sides. Lines homozygous for one flanking marker and heterozygous for the other flanking markers were selected and further screened with internal markers. Out of 1500 lines, 93 lines showed recombination breakpoint at various markers. These lines are now being tested for their phenotype in F_3 generation. The genotype-phenotype correlation in these lines will be used to narrow down the region for identification of candidate genes involved in resistance against *A. brassicae*.

P (S 04) 23: Correlation study for sheath blight of rice with different disease variables

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Rhizoctonia solani [Teleomorph: *Thanatephorus cucumeris* (Frank) Donk.] is a major disease of rice. The disease is increasing over the year in India and cause up to 69% yield loss under favourable conditions. The disease is highly influenced through different disease variables and environmental factors. A correlation study was done to know effect of different disease variables on disease pattern during screening of the wild germplasm and F_2 population. Based on screening during *kharif* 2015, 16 best accessions of *Oryza nivara*, 22 accessions from *Oryza rufipogon* were screened during *kharif* 2016 and 2017. Total of 480 plants in F_2 populations were also included for correlation study. The study revealed that in whole screening experiments, different disease variables were significantly ($P<0.05$) correlated. Relative lesion height had a positive correlation with lesion height and disease score. The lesion height showed positive correlation with disease score. There was a negative correlation between plant height and disease score.

P (S 04) 24: Influence of Silicon on leaf blast of rice and their relationship on morphophysiological and yield attributing traits under drought stress

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Rice (*Oryza sativa* L.) is the most important cereal crop grown in India, contributes 40% of total food grain production and cover 42% of the total cropped area. Productivity of the crop can be increased by adopting the hybrid rice and management of biotic stresses. Among the diseases, rice blast caused by *Pyricularia grisea* is causing heavy losses to the crop and become a major threat for cultivation of rice in irrigated ecosystem. The disease infection may kill seedlings or plant up to the tillering stage. At later growth stages, a severe leaf blast infection may cause devastation and reducing grain yield. Initial symptoms appear as white to gray-green lesions or spots, with dark green borders. Older lesions on the leaves are elliptical or spindle-shaped and whitish to gray centers with red to brownish or necrotic border. The spots are diamond shape, wide in the centre and pointed toward either ends. Silicon (Si) is the second most abundant element in soil and it is considered as an absolutely useful element for a large variety of plant. It is concentrated in plant tissues inquantities similar to that of macronutrients. Considerable damages to plants caused by abiotic stresses such as drought stress, salinity stress, heavy metal stress and nutrient imbalance, as well as biotic stresses like insect pests and disease have been reported to be reduced significantly by Silicon application. Silicon fertilization has been reported to be efficacious in controlling and mitigating rice blast severity.Two different hypotheses are proposed for the ability of Silicon to lessen disease severity. The first hypothesis is a mechanical barrier against appressorial penetration, & second hypothesis physiological roles in disease resistance. The study was carried out *in vitro* and *in vivo* condition by using the different concentration of Silixol and carbedazim fungicide for evaluation of fungitoxic potential against *Pyricularia grisea,* it was observed that Silixol@0.3% concentration gave outstanding result for reducing the mycelia growth of *Pyricularia grisea* (73.96 mm) followed by Silixol@0.6% concentration (72.33 mm) over untreated check. It was also recorded that carbedazim gave better performance for decreasing the mycelia growth of *Pyricularia grisea* (15.66 mm) and proved significantly superior over untreated check.

P (S 04) 25: An insight into *Arabidopsis thaliana-Alternaria brassicae* interactions: The story of *Arabidopsis* defense mediated through ROS, cell death and molecular interactions

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Alternaria brassicae is ascomycetes plant pathogen causing blight disease on many oleiferous Brassica crops. The pathogen falls into the category of narrow host-range necrotroph (NHN); therefore, the diseases are mainly confined to the plants belonging to the *Brassicaceae* family. Diseases in *Brassicaceae* caused by *Alternaria brassicae* can cause significant yield loss and are considered as one of the most critical global disease complexes. However, despite the importance of the pathogenic *Alternaria* spp. on *Brassicaceae*, there is no effective host resistance that is transferable within rapeseed-mustard breeding programs against the pathogen, nor is there sufficient resistance to *A. brassicae* in any of the cultivated varieties. Instead, *Arabidopsis thaliana* (family of Brassicaceae) population shows a continuum of resistance levels controlled by multiple genes, phenotype, ROS and cell death. Little is known about the molecular mechanism controlling the interaction between *Arabidopsis* and *Alternaria brassicae*. In the present study, we exploited the natural variation in *Arabidopsis* to understand the molecular and cellular mechanisms underlying resistance to *A. brassicae*. Using a subset of resistant (Ei-2, Ull2-3, Lz-0, and Cvi-0) and susceptible (Gre-0, Est-1, and Zdr1) accessions, we show that the susceptibility to *A. brassicae* is associated with higher ROS accumulation and cell death. Susceptibility to *A. brassicae* was reduced in the *rboh* (D, E and F) mutants that are incapable of producing ROS, suggesting that RBOH D, E and F may act as negative regulators of defence against this pathogen. Additionally, our data also supports the hypothesis that the Jasmonic acid (JA), Ethylene (ET) and Abscisic acid (ABA) signalling pathways positively contribute to resistance against necrotrophic pathogens. In summary, these results reveal the central role of ROS and cell death in the pathogenesis of *A. brassicae* and expand our understanding of plant-necrotroph interactions.

P (S 04) 26: Identification and expression analysis of a virulence gene *ToxA* in *Bipolaris sorokiniana* causing spot blotch of wheat

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Bipolaris sorokiniana causing spot blotch of wheat is an ascomycetes fungus with a wide host range in poaceae family, which is causing this disease in wide variety of cereal crops. It is considered as primary constraint to wheat production throughout North and South Asia. Metabolites produced by *B. sorokiniana* are considered to be toxins which are playing an important role in disease development. In present study, *ToxA* gene has been identified and characterized in Indian isolates of *B. sorokiniana,* which was earlier reported to be present in *Pyrenophora tritici repentis* causing yellow spot in wheat. *ToxA* gene was amplified in thirty nine *B. sorokiniana* isolates collected from different regions of India, which confirmed that *ToxA* was present in all the isolates of *B. sorokiniana.* Further, an amplicon of 600bp (approx.) was sequenced and analyzed against NCBI database. The analysis revealed 100% homology with *ToxA* gene in *Pyrenophora tritici repentis.* The coding length of *BsToxA* gene is 535bp (excluding intron) which was exactly same in all *B. sorokiniana* isolates. All these *BsToxA* sequences have been submitted in NCBI database (MN601358-MN601396). *In vitro* expression analysis of *ToxA* gene in *B. sorokiniana* isolate (BS112) using qPCR revealed maximum upregulation (14.67) at 1st day after inoculation (DAI), followed by 2nd DAI (11.83 fold), then gradually expression decreased at 3, 5 and 7 DAI in minimal basal medium. *In planta* expression analysis was also performed using qPCR. The maximum expression (2.13 fold) was observed at 3rd DAI in susceptible cultivar (Agra local), while minimum expression (0.23 fold) was observed in resistant genotype (Chiriya 7) at 3rd DAI. This study demonstrates that *ToxA* is present in *B. sorokiniana* which might have got transferred from *Pyrenophora tritici repentis* during evolution and its expression is high in susceptible genotype.

P (S 04) 27: Characterization of TALEs of Indian *Xanthomonas oryzae* pv. *oryzae* race 4 causing bacterial blight of rice

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Bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) is a significant constraint to rice production globally. Indian Xoo race 4 is the most virulent among the Xoo population from Northern India. Race 4 could effectively invade the host immunity resulting in breakdown of resistance by major *Xa* genes in rice. Type 3 secretion system effectors (T3SS effectors) of Xoo, both TALEs and non-TALEs are known to be involved to subvert rice immune response. Unlike TALEs, Xoo race4 is extensively characterized for its non-TALEs. The present study thus aimed to characterize the TALEs of Xoo race4. We employed a computer based AnnoTALE suite to predict 16 TALEs along with their RVDs sequences in race4. Xoo race 4 is having variable repeats for TALEs. We identified 16, 18, 22, 20 and 24 repeats in TALE1, TALE2, TALE3 TALE7 and TALE12, respectively. The RVDs of TALE1 is identical to that of TALE4, TALE2 to TALE 8a/7a, TALE3 to PthXo7 and TALE12 to tal9e of the Philippines strain PXO99A. RVD of TALE7 is identical to that of TalAH2 of the Japanese strain MAFF311018. In spite of identical RVDs, TALE 3 and TALE12 showed lesser number of amino acids than PthXo7 and tal9e of PXO99A, respectively. We also deduced the effector binding elements (EBE) corresponding to RVDs with Nipponbare cultivar as the background using daTALbase tools. Structural prediction of the major TALE proteins of Indian Xoo race4 was carried out using the software I-TASSER. This detailed insight would certainly help in predicting the rice targets and subsequent validating their role in disease development.

P (S 04) 28: Plant and soil microbes interaction under changing climate conditions in india

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Global environmental changes caused by natural and human activities have accelerated in the years. The increase in greenhouse gases is predicted to continue to raise global temperature and change water availability in the 21st century. Plant diseases are deeply influenced by the environment; a susceptible host will not be infected by a virulent pathogen if the environmental conditions are not conducive for disease. The change in CO2 concentrations, temperature, and water availability can have positive, neutral, or negative effects on disease development, as each disease may respond differently to these variations. Interactions between plants and soil microbes play an important role in structuring terrestrial ecosystems by influencing plant growth and competitive ability. Studies have shown that abiotic conditions such as varying nutrient levels or environmental stress can alter the direction and magnitude of plant–microbe interactions. To test for an interaction between water availability and soil microbes, plants were grown in either live or sterile soil treatments and with high, medium and low water availability. We found that the presence of soil microbes generally increased the strength of intraspecific competition relative to interspecific competition, but this effect depended on water availability. In the presence of microbes, as water availability decreased the strength of intraspecific competition generally increased. Our results suggest that soil microbes may play a role in stabilizing coexistence by increasing conspecific negative density dependence, especially in drier environments.

P (S 04) 29: Phytotoxin as a key component in pathogenicity and virulence of *Rhizoctonia solani* inciting sheath blight of rice

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Sheath blight (ShB), caused by the necrotrophic fungal pathogen *Rhizoctonia solani* AG1-IA is one of the most important rice diseases worldwide. Due to lack of tractable genetic resistance in rice plant, it is imperative to understand its pathogenesis to contain the disease, which are less understood at present. Like biotrophs, proteinaceous toxins or effectors also play a role in *R. solani* to condition the plant for susceptibility. Though several putative pathogenicity factors have been predicted, additional evidence is required to establish their roles in pathogenicity. However, the complex biology of the pathogen necessitates identification of interacting partners in rice for potential pathogenicity factors of the fungal pathogen. In the process of identifying the host interacting partners, the role of host-selective toxins elaborated by the fungal pathogen in ShB development has been elucidated. The fungal isolates were collected from six locations and preserved as laboratory collections. These were characterized using their cultural, and morphological characteristics and their identities were confirmed by PCR amplification of ITS region and sequencing. Pathogenicity assay was established in the polyhouse under artificial inoculation conditions. The phytotoxin was then extracted from the highly virulent isolate using ethyl acetate and tested for lesion development by both detached leaf and *in-planta* assays. The phytotoxin of the *R. solani* isolates was observed to reproduce symptoms of the disease independent of the pathogen itself, and induced maximum lesion development for a highly pathogenic isolate RIRS-K confirming its role as a key component in pathogenicity and virulence of the necrotrophic fungus.

P (S 04) 30: Biochemical defense reactions of black pepper varieties against *Colletotrichum gloeosporioides* incitant of anthracnose disease

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Anthracnose caused by *Colletotrichum gloeosporioides* in Black pepper is a serious disease which causes even upto 100 percent crop losses under epidemic conditions. Most of the cultivated varieties of black pepper are highly susceptible to the disease, especially Panniyur 1 which is the most predominant variety grown in coutnry. In our study we tested 11 genotypes for their biochemical defense reaction to anthracnose disease. The disease incidence under glasshouse conditions was minimum for the variety IISR Girimunda, defense enzymes such as peroxidase, polyphenol oxidase, catalase, phenylalanine ammonia-lyase, superoxide dismutase activities were very high in resistant cultivars upon challenge inoculation with *C. gloeosporioides*, when compared to local check and uninoculated control plants. The disease severity under field evaluation was also low for natural incidence of the anthracnose in resistant varieties. Thus, suggesting that the presence of strong biochemical defense molecules in the variety IISR Girimunda is attributed to its resistance to anthracnose disease in black pepper.

P (S 04) 31: Effect of Trichoderma formulation on the rhizosphere competence and biocontrol ability of *T.harzianum 5593* and ThL-4

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Fusarium oxysporum f. sp. *lentis* causing Fusarium wilt is a destructive seed borne disease of lentil which effect yield loss upto 10% every year. To control soil-born fungi the application of large amount of chemical fungicide may lead to environmental pollution. Applying chemical fungicides to control soil-born fungi may lead to environmental pollution. Using biocontrol agents, holds a great potential to enhance yield and quality of crop. The rhizosphere competence of the biological control agents*Trichoderma harzianum* isolates 5593 and ThL-4 were studied separately on lentil roots both in the glasshouse and in the field when introduced into soil in a range of formulations. To facilitate rhizosphere competence studies, in starting the soil was examined for their microbial load on potato dextrose agar (PDA) *and Trichoderma harzianum* specific medium (ThSM) and we found bacterial as well as fungal microfora. Bacteria includes isolates of *Bacillus*, *Pseudomonas* and *Actinomycetes* and fungal mycoflora included isolates of *Aspergillus niger, Aspergillus flavus*, *Penicillium* and *Fusariumoxysporum*. Proliferation of *T. harzianum* isolates in the rhizosphere was formulation dependent. A solid substrate and seed coating formulations gave concentrations of 10^4 and 10^3cfu per g soil, respectively. *Trichoderma harzianum* (5593 and ThL-4) were re-isolated when recovered from soil separately. When isolates 5593 and Thl-4 were introduced into *Fusarium oxysporum* infested soil there was a significant difference in the disease control by both isolates as compared to control but isolate 5593 was found more efficient todouble the percentage of healthy plants compared with the control treatment.Here, it might be stated that isolate

5593 is most effective biocontrol agent against Fusarium wilt. It leads to plant growth promotion activity of lentil crop and can be used as bio-fungicide in reducing wilt disease of lentil.

P (S 04) 32: Assesmemnt of fusarium wilt tolerance of pigeonpea genotypes by molecular markers and biochemicalparameters

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Thirty pigeonpea genotypes collected fromwilt sick plot and grown under water culture technique in green housewere screened for Fusarium wilt tolerance.The susceptible genotype ICP-2376 showed100 % wilt incidence which was 30.99 per cent in field. Thegenotype PT-03-142 from inoculatedpot and genotypes Vipulla, ICP-8863, BDN-711, PT-012-6, PT-012-1, PT-012-3 did not show any wilt symptoms in pot andrecorded wilt incidence less than 10 per cent. Three Fusarium wilt resistant and three susceptiblegenotypes of pigeonpea which were tested under field conditionand water culture technique were evaluatedforbiochemical constituents.Significant increase in the activity of â -1,3-glucanase under wilt sick condition withthe mean 90.11 in resistancegenotypes as against 57.03 nmoles of glucose releasedmg^{-1}proteinmin^{-1} in susceptible genotypes.The mean chitinase activity was 12.27 in resistantgenotypes as against 7.00 nmoles of NAG releasedmg^{-1}proteinmin^{-1}in susceptible genotypes. The activity of PAL was recorded3.46 in resistant genotypes as against 1.32Fmoles of transcinnamic acid formedmg^{-1}proteinmin^{-1} in wiltsusceptible genotypes.The activity profile of polyphenol oxidase increased in wiltresistant genotypes The APX activity was induced more in susceptible genotypes under wilt sick condition. An RAPD marker OPG-08 was tested for differentiating Fusarium wilt resistant and susceptible genotypes using one resistant (PT-03-142) and one wilt susceptible (ICP-2376) genotypes. A specific amplicon of 920 bp size wasprominently observed in Fusarium wilt resistant genotype PT-03-142. The SCAR-1 primer when used for amplification ofgenomic DNA exhibited the amplicon of 937 bp as reported in five Fusarium wilt resistant genotypes. The SCAR-2 did not show amplicon of 504 bp as reported.ASSR-229 was also tested and observed amplicon of size 160 bpin resistant and moderate resistant pigeonpea genotypes.

Session 5
Climate change influencing plant diseases

Keynote Papers

KN (S 5) 01: Crop disease management needs in rainfed cropping systems under changing climate scenarios

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Indian agriculture is impacted by climatic variability and climate change thereby exerting pressure on food- and nutritional-security. Despite India being food self-sufficient, frequent occurrence of extreme weather events could lead to regional imbalances. Research on establishing the impacts of climate change on pathogens and their natural enemies is at its infancy. However, independent studies show that in some crops, elevated CO_2 levels increased foliar density with changed microclimate could possibly influence host-pathogen interactions. In vector-transmitted pathogens, the impact on the vector is an additional dimension adding to the complexity. Extreme weather events due to climatic variability like high and low temperature stresses; soil-moisture deficit stress; flooding, and hailstorms, etc., could lead to i) less-known diseases becoming major problems; ii) spread of the pathogens to new areas/crops; iii) emergence of new pathotypes; iv) disappearance of current pathogens; v) new/modified host-pathogen-biocontrol tritrophic interactions; vi) modified vector development patterns; and vii) variable overwintering or over-summering of the pathogens/vectors. At ICAR-CRIDA, efforts are made to exploit microbial biodiversity for crop health management, understand impacts of elevated CO_2 (550 ppm) on plant pathogens and biocontrol agents over generations. In plant pathogens, impacts of elevated CO_2 (550 ppm) on the pathogencity related aspects were studied whereas in *Trichoderma*, *Pseudomonas*, the biocontrol ability, hydrolytic enzyme production systems were studied in detail. Also, as part of adaptation strategy, ability of these biocontrol agents to withstand abiotic stresses such as high temperature, osmoricum and salinity were characterized. The complex host-pathogen-biocontrol interactions need to be studied for impacts of climate change and climatic variability; identify eco-friendly novel disease management strategies; screen the microbial diversity for their ability to withstand the extreme weather events and perform; to integrate various methods of disease management strategies taking into consideration the agro-ecosystem basis; and enhancing awareness about the climate change impacts and adaptation strategies to minimize crop losses due to diseases. Also, there is a need for constant survey and surveillance for emergence of new pathotypes and spread of existing pathogens to new domain areas. Robust modeling systems will help to understand changing plant-pathogen interactions and thus identify the probable risk-prone areas and thus target the management strategies.

KN (S 5) 02: Arbuscular mycorrhizal technology for improved phosphorus nutrition in rainfed, direct sown rice: A climate smart technology

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Poor phosphorus (P) nutrition is one major constrain to sustainable productivity of rainfed rice which accounts for about 43% of national (India) rice growing area. Arbuscular-mycorrhiza fungi (AMF), which form symbiotic association with most terrestrial plant species, including rice, promote enhanced P acquisition by associated plant. AM-fungi produces extra-radical mycelia network which extends beyond rhizosphere and promote greater soil exploration. Thus, the association helps plant to acquire adsorbed (on soil particles) P which is, otherwise, inaccessible to plant. Native AMF based technology package involving AMF-supportive crop culture components have been established and recommended for rainfed upland rice ecology by this research station (CRURRS). The components include (i) optimum, off-season tillage scheduling, (ii) suitable rice based cropping system options, (iii) optimum P fertilizers dose and (iv) application of on-farm produced native AMF based mass inoculums for which production protocol has been developed by this research station. Long term (1999-2010), fixed plot experiment data on the integrated native AMF based technology components revealed that AMF aided P acquisition is more during moisture stress (low seasonal rainfall during wet season when rainfed rice is grown) years. This makes the AMF technology, climate smart integral part of rainfed rice production package for maintaining plant health and sustainable productivity, particularly under the growing concern of global climate change scenario.

Invited Papers

I (S 5) 03: Integrated management of important diseases in mango in view of climate change

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Mango (*Mangifera indica* L.) – the king of all indigenous fruits in India is ranked as one of the better fruits in the international market because of its delicious taste and high caloric value. Mango is now grown in over 87 countries. More than 1000 varieties are grown in India. Among them Alphonso, Banganapalli, Langra, Mallika, Totapuri, Dasheri, Raspuri, Amrapalli are commercially exploited. Impact of climate change on the altered scenario of diseases on the crops has been emphasised worldwide. There has been a shift in the flowering pattern and fruit production in mango and disease scenario in mango been changed. Though mango crop is known to suffer from several fungal diseases, some diseases that were considered as miner are becoming severe in mango. Mango leaf blight (*Pestaliopsis mangiferae*), Stem end rot (*Phomopsis mangiferae*) and black banded disease have become prominent. Post harvest rots are equally important because these not only deteriorate the nutritive value and quality in mango fruits but also render them unfit for consumption and trade resulting into great economic losses. *C. gloeosporioides* (anthracnose), *Lasiodiplodia theobromae* (stem-end rot) and *Aspergillus niger* (fruit rot) are the most important pathogens causing fruit rots in mango during ripening and storage. The infection of the pathogens occurs in the in quiescent form during the premature stage as well as during harvesting, transportation and storage (especially *A. niger*). *C. gloeosporioides* had recorded maximum associated frequency in increasing order with all the developmental stages of fruit (20 %

with unopened flowers to 80% with the mature fruits) compared with *L. theobromae, Phomopsis mangiferae, Pestalotiopsis mangiferae, A. niger, Rhizopus arrhizus* and *Alternaria alternata* that were the other important associated fungi and are known to cause diseases in mango. Management of such diseases is mostly achieved through the pre harvest application of agrochemicals (fungicides) whereas post harvest treatments with such chemicals are discouraged because of health hazards due to residues. Hence safer and non-injurious methods devoid of such chemicals are favoured and accepted. Field trials revealed that as pre harvest treatment, application of Azoxystrobin was most effective in controlling rots that resulted in 10.00 & 8.00% fruits infected with anthracnose and stem end rot, respectively. Usage of the extracts obtained from Turmeric and Neem leaves recorded 16.00 % diseased fruits in each with anthracnose and 12.00 and 14.00 % fruits had stem end rot, respectively. None of the treatments recorded Aspergillus rot except control had the disease. In untreated control 36.00; 26.00 and 6.00% fruits were rotten due to anthracnose, stem end rot and Aspergillus rot, respectively. Post harvest treatment with Azoxystrobin preceded by the pre harvest application of Turmeric extract / *Vitex negundo* leaf extract were next in the order where 3.33% fruits had both anthracnose and stem end rot. In all the integrated treatments involving pre and post harvest application fruits were free from *Aspergillus* rot. Hot water treatment for 10 min at 52°C preceded by pre harvest application of Azoxystrobin resulted in complete control of storage rots. Mango fruits those did not receive any pre harvest treatment but were subjected to hot water treatment (Control) recorded 32.00%, 24.00% and 6.00% fruits infected with anthracnose, stem end and Aspergillus rot, respectively. Influence of climatic facotors in view of disease progression and importance of integrated approach in managing diseases in mango has been discussed in the paper.

I (S 5) 04: Effect of climate change on maize diseases and their status in Rajasthan

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Rajasthan is the state where, maximum maize is being grown and having largest area under cultivation. There has been a taboo that maize is considered as prime staple food. There is another bottleneck that maize is being cultivated under rain fed conditions which has more than 68 % area. Assured irrigation is limited. The average productivity is less than the national average. The crop has been challenged by several pathogens and dominant are fungal ones. Post Flowering stalk rot is major disease caused by *Fusarium verticillioides* and bacterial association also. This is called as rot complex. This causes more than 38 % losses in yield followed by Banded leaf and sheath blight which causes more than 70% losses. Banded leaf and sheath blight is more prominent where rice- maize pattern is seen. The sheath blight pathogen *Rhizoctonia solanii* is same. Foliar pathogens like Curvularia leaf spot (Curvularia lunata), Maydis leaf blight (*Bipolaris maydis*) and one systemic pathogen Rajasthan Downey mildew (*Peronosclerospora heteropogonii*) are also causing severe damage. The climate change is causing many diseases to be severe and some are moderate. The change is rainfall pattern and rise in temperature greatly affecting the severity of disease. If there is 20 days gap or dry period at flowering, this will cause high severity of PFSR and more foliar pathogens, many a times if the rainfall distribution is not proper it will cause earlier onset of diseases. The pattern of symptoms also changed. Earlier the MLB and CLS used to appear at 50-55 DAS, but now these are occurring at seedling stage. The Rajasthan Downey Mildew is coming on both sides of leaves; otherwise principally it used to be on downy side only. Even there are observations that it also infects the plants at 30 DAS, which are new reports. Overall, the disease scenario is changing due to climate change and five years data has been used to depict the effect which proves the change is relation to aberration in climate.

I (S 5) 05: Dry Root Rot: Increased severity, molecular diagnostics, pathogen diversity and management of newly emerging chickpea disease under changing climatic scenario

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Climate change is predicted to have a direct impact on the occurrence and severity of diseases in crops, which will have a serious impact on our food security. Climate change will result in rise in temperature and carbon dioxide levels and will also have a varied effect on moisture. In many cases, temperature increases are predicted to lead to the geographic expansion of pathogen bringing pathogens into contact with more potential hosts and providing new opportunities for pathogen hybridization. A recent study dealing with all production constraints on chickpea in 13 Asian and African farming systems showed that losses caused by diseases ranged from 3-14%. Keeping this in view, the studies on impact of climate change on severity, molecular diagnostics, pathogen diversity and management of newly emerging chickpea dry root rot caused by *Rhizoctonia bataticola* were conducted. Disease incidence varied from region to region and highest incidence of 45.55 per cent was recorded in Kalaburagi district and the least of 0.50% in Yadagiri. Cultural and morphological characters showed variation among *R. bataticola* isolates. Detection of twenty isolates through PCR indicated amplified product size of 550-600 bp. In molecular diversity, amplified products with all the primers showed polymorphic and distinguishable banding pattern indicating the genetic diversity among the isolates of *R. bataticola*. Further, maximum colony growth of *R. bataticola* and disease severity was observed at 30-35ºC which is considered as optimum temperature. Maximum dry root rot and lesser root length, shoot length and total biomass were recorded at 40%, 50% and 60% moisture. Elevated CO_2 @ 550 ± 25 ppm with 2ºC rise in temperature showed higher disease severity and reduced growth parameters. Hence, increasing incidence of dry root rot indicate strong influence of climate change variables such as temperature and moisture on the development of disease. The role of temperature and soil moisture associated with infection, colonization and development of dry root rot under controlled environment was quantified. The dry root rot incidence was significantly affected by high temperature and soil moisture deficit. Combination of high temperature (35°C) and soil moisture content (60%) predisposes chickpea to dry root rot. Advanced screening of genotypes under phenotyping technique yielded only four resistant and five moderately resistant genotypes. Seed treatment followed by soil drenching to infected and surrounding plants with Mancozeb 50% + Carbendazim @ 3.5 g/kg was highly effective for reduced dry root rot (7.79%), highest seed yield (12.26 q/ha), test weight (38.90 g) and higher BC ratio (3.40).

I (S 5) 06: Exploiting AM fungi in sequestering soil carbon and enhancing the crop productivity assessed under soybean-based cropping system

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Global change, partly mediated by the agricultural magnification, is the foremost challenge of this age and endangers the sustainability of agricultural production in the long run. The atmospheric CO_2 concentration has reached 400 ppm which is much above the upper safety limit of 350 ppm. The world is not on track to regulate the atmospheric carbon emissions with agricultural soils being one of the largest emitters. In this context, microbial interventions provide a sustainable alternative to conventional approaches. Arbuscular mycorrhizal fungi are obligate symbionts of the majority of terrestrial plants that nurture plants by enhancing nutrient acquisition and providing increased resistance against a wide array of abiotic and biotic stresses. An important contribution provided by AMF includes the production of a thermostable glycoprotein glomalin, which substantially aids in soil carbon sequestration. Moreover, soil management practices and crops play a central role in determining the functioning of AMF. In our study, we examined the soil carbon sequestration potential of AMF in a field experiment consisting of organic and inorganic soil management practices in soybean-maize intercropping system. It was observed that AMF inoculation in maize grown in intercropping with soybean particularly under organic practice enhances AMF biomass assessed microscopically and via the signature fatty acid biomarker for AMF i.e., phospholipid and neutral lipid fatty acid 16:1ù5cis. Apart, from this the stocks of soil organic carbon and glomalin were also found to be the highest in the same system. Microbial biomass carbon and the activity of soil enzyme â-glucosidase were also found to be higher under AMF inoculated plots managed with organic practice. The system was also accompanied by lower CO_2 emissions. In anotherstudy, dealing with a long term field experiment managed with organic, inorganic and integrated nutrient management practice having soybean-wheat (S-W) and soybean-chickpea (SC) rotation, we explored the role of native AMF species in SOC sequestration. It was observed thatboth integrated and organic practice of the SW system and the organic practice of the SC system, harboured the highest SOC and glomalin stocks. A similar trend was observed with microbial biomass carbon, the activity of enzyme â-glucosidase and AMF biomass assessed microscopically and through phospholipid and neutral lipid fatty acids (PLFA and NLFA)16:1ù5cis where higher values were observed in the case of organic practice followed by the integrated practices in both the cropping systems. Furthermore, the plots of organic practicewere recorded with the lowest CO_2 emissions.These findings justify the functioning of glomalin which together with AMF hyphae works as a soil particle binding machinery and sequesters carbon therein without compromising soil quality. Thus, it is concluded that AMF by producing glomalin sequesters excess soil carbon in a form that stable enough to prevent its release into the atmosphere. This ability is particularly enhanced under organic practice, intercropping and crop rotation systems comprising mycorrhizal crops such as maize and soybean and sustained the productivity of soybean-based cropping system.

Oral Papers

O (S 5) 07: Reduced expression of *Brn1* and *AbCbh7* and its association with blight incidence in Indian mustard caused by *Alternaria brassicicola* under warmer conditions.

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Globally places worldwide are witnessing an increase in temperatures and tropical warming is becoming more prominent and is expected to have far reaching consequences in near future. By the end of 22nd century increase in average global temperatures are expected to be within the range of 0.9 °C - 3.6 °C, with a likely increase of at least 2.7 °C with respect to the present greenhouse emissions. According to the Intergovermental Panel on Climate Change reports; global rise in temperature is likely to influence the distribution pattern of pathogens and might alter the challenges of pathogen threats in near future. Among the various oilseed crops Indian mustards occupies a major share in production as well as consumption in Indian subcontinent. This crop suffers from major abiotic stress in form of blight incidence caused by *Alternaria spp.* Among the various species associated with Alternaria blight; *Alternaria brassicicola* represents one of the most successful necrotrophic interactions causing black spot disease on crucifers under relatively warmer conditions. Changing climatic conditions are likely to affect fungal growth patterns and as a result a pathogen might migrate to newer locations or evolve itself to adapt. The present study was undertaken to find out the likely affect of warmer condition on the expression of *AbCbh7,* responsible for cellulase production and its interaction with *Brn1. Brn1* encodes first catalytic step in DHN pathway of melanin biosynthesis. Results indicated that restricted radial growth and diminished expression of *Brn1* and *AbCbh7* upon exposure to warmer conditions of 35 °C when compared to those at 25 °C *In vitro* studies also revealed a shift from dark coloured mycelia growth to white coloured mycelia growth at 35°C. Although, extracellular production of cellulase enhanced at 35°C when compared to 25°C. Artificial Inoculations of leaves of *Brassisca juncea var varuna* with *A brassicicola* at 35°C. resulted in larger chlorotic zones. Indicating increased virulence of the pathogen at higher temperature 35°C most likely due to reduction in melanin productions in the cell walls of melanised fungi *A brassicicola*. Melanins in cell walls acted as barrier for the release of cellulase extracellularly. Reduction in barriers possesed by melanins under warmers conditions resulted in enhanced release of extracellular cellulase as evident under in vitro conditions as well as larger chlorotic zones at warmer temperature of 35°C.

O (S 5) 08: Prospect and retrospect of Karnal bunt in Central zone

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Karnal Bunt disease of wheat caused by *Tillitia indica* is one of the important post-harvest diseases of wheat. Often it occurs in bread wheat. Although irregular and sporadic occurrence of Karnal bunt was reported from Madhya Pradesh as well, but by and large the entire Central Zone comes under low risk zone. The major reasons behind seldom occurrence of Karnal bunt is the fact that during anthesis the temperature and humidity regime normally in the month of February in C.Z. is quite unfavorable for sporidia production and subsequent florets infection. Most of the time in the month of February, the temperature remain above 24 – 26 ^{0}C and humidity remains below 70%. Since, the Madhya Pradesh comes under wheat export zone, we always remain vigilant to Karnal bunt. We used to collect and examination wheat grain samples from major irrigated wheat growing areas in Central Narmada Valley. The trend of result since last 8 – 10 years clearly indicates that Central Zone in general and M.P. in particular, the burden of Karnal bunt is negligible. Sometimes migratory farmers of Madhya Pradesh borrow the seed from North Western Plane Zone which is prone for Karnal bunt and they sow it in Central Zone particularly in some areas of Harda and Hoshangabad districts of Madhya Pradesh. Here sprinkler irrigation is common among the farmers and owing to which they likely to unknowingly introduce Karnal bunt in those areas. But in due course of time, because of unfavorable environmental conditions and suggestive interventions, the diseases get subsided and it never gets established.

O (S 5) 09: Current scenario of Pokkah boeng disease of sugarcane in sub- tropical India

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Sugarcane an important field crop cultivated around the globe. The crop is affected by several diseases, among these *Pokkah boeng* (PB) a foliar disease of sugarcane caused by *Fusarium sacchari* infects the crop throughout the world is found to cause major yield losses in most sugarcane producing regions, including

South Africa, Malaysia, Iran, China, and India. This disease was reported for the first time in sugarcane by Wakker and Went (1896) in Java Island of Indonesia and they coined the term "Pokkah boeng" in the Javanese language, which means malformed and twisted top. In early 1930's PB was reported as minor disease. In India, this disease was reported first time in 1983 from Maharashtra, but in subsequent years it was noticed in most of the sugarcane growing states. A widespread incidence of the disease has been noticed during recent past under tropical and subtropical regions of the country therefore, to know current scenario of the disease in the sub-tropics, surveyed the reserved areas of sugar mills of Haryana, Punjab, Uttar Pradesh, Bihar and Uttrakhand states regularly since 2010. The overall information generated over the years revealed that incidence of pokkah boeng has increased many folds in most of the cultivated commercial varieties in the region and it is attaining the status of major disease. In Haryana, pokkah boeng was noticed as a major disease in most of the sugar mills with moderate to severe incidence. During 2019-20 crop season, maximum disease incidence (up to 38.0%) was recorded in ratoons and traces to 15.0% in plant crops of the cv CoH 160 in Kaithal and up to 10.0% incidence on the cv Co 0238 and Co 89003 in Karnal. Similarly, in other varieties viz. Co 0118, Co 05011, CoH 116, CoH 119, CoH 156, CoS 8436, CoJ 85 and CoPb 09181 the disease incidence ranged between traces and 5.0%. The acute phase of the disease i.e. top rot was also recorded in the cv CoJ 85 (20.0%), CoS 8436 (trace -14 %), CoH 119 (6.0%) and Co 89003 (3.0%) under different areas of the state. The combined infection of PB along with top borer (*Scirpophaga excerptalis*) was also noticed in the cv Co 0238 and Co 89003 in some fields, but there was no association between PB and top borer. In Punjab, 0.1 -10% incidence of PB and trace to 5.0% top rot were noted in the varieties under cultivation viz. Co 0118, Co 0238, Co 89003, CoH 119, CoJ 85, CoJ 88 and CoS 8436. In reserved area of 14 sugar mills of Uttar Pradesh, the disease was noticed by traces to 20.0% on the leading variety Co 0238 and trace to 5.0% on other cultivated varieties. Further, in Laksar Sugar Mill (Uttrakhand), trace incidence of PB and top rot was observed on the cvs Co 0238 and CoH 160. By and large, chlorotic phase of infection was found in most of the cultivated varieties, which recovered itself after rain or due to change in weather without fungicide spray. However, under severe disease incidence or top rot phase, farmers resorted to spray the crop with Carbendazim (400g) + Streptocycline (6.0 g) or Copper oxychloride (800g) per acre and successfully manage PB in sugarcane.

O (S 5) 10: Crop disease scenario and organic disease management in the land use systems of North East India

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Agriculture is the mainstay of the 84.34% rural population in North East India. The agrarian economy provides livelihood support to 70% of the region's population. Despite the region being resourceful, it produces only 1.5% of country's food grain production and continues to be a net importer of food grains even for its own consumption. *Jhum* cultivation is an intrinsic culture of the people and the major agricultural land use systems in Mizoram, Nagaland, Arunachal Pradesh and Meghalaya. In these hilly tracts terrace cultivation is also prevalent with only small portion of settled cultivation in the valley lands. Settled cultivation in the plane lands are comparatively more productive. The ever increasing population pressure resulted reduced *jhum* cycle and in turn *jhum* lands have become less productive. Disease incidence is recorded less (20-40%) in the jhum lands as compared to conventional agriculture. In Nagaland, survey of the land use system in *jhum* and conventional agriculture showed that *jhum* paddy was infected by blast disease (2-6%), colocasia by leaf spot or blight (>10%) and beans by anthracnose (0-1%)were the major diseases in *jhum* lands which were significantly lower than in conventional land use system. Variations in weather parameters might have led to changes in disease dynamics especially in the north eastern hill region. Incidence of the soil borne fungal pathogen *R. solani*and *S. sclerotiorum* was found to cause 20-30% of vegetable crops at Umiam. Organic disease management treatment combination of seed and soil application of the bioagents, gave control of *jhum* crop diseases over untreated control. Organic disease management of *jhum* crops can provide scope for improving the *jhum* cultivation production and productivity thereby improving the plant health. Soil pH, EC, OC and the status of the nutrients N, P, and K changed at different stages. Increase in the innate fungal population and decrease in bacterial population was recorded during the different stages of experiment period.

Poster Papers

P (S 5) 01: Onion leaf rot - A novel disease in major onion growing districts of Karnataka

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The Onion (*Allium cepa* L.,) is a vegetable and the most widely cultivated species of the genus *Allium*.A new symptoms of leaf rot observed in Onion. To know the incidence, the roving survey was conducted in major onion growing districts of Karnataka *viz.,*Chitradurga, Bagalkot, Dharwad, Vijayapura and Gadag in *kharif* season of 2017-18**.** The roving survey revealed that, the leaf rot disease of onion was noticed in all the surveyed locations with varied incidence levels. The average disease incidence (16.50%)was found to be highest in Gadag districtfollowed by Bagalkot (14.78%), Dharwad (10.93%), Vijayapura (8.73%) and the least average disease incidence (7.35%)was noticed in Chitradurga district.

P (S 5) 02: Potential impact of climate change on plant pathogens and management strategies in India

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Climate change has become a topic on which everyone has to talk about. There has been remarkable scientific contribution related to the topic of how climate change is likely to affect plant diseases. There is burgeoning need for reviewing the recent studies on the impacts of climate change on plant health. The effect of climate change on plant pathogens is multi dimensional. The adaptive population of plant and the pathogen is the determining factor for the magnitude of the effect of the climate change. The number of diseases in tropics is much higher than that in temperate climate. This indicates that the rise in global temperature will gradually lead to increase in number of diseases and pests per crop. In this situation the facultative pathogen with wide host range may survive better. Increased level of CO_2 on the other hand is responsible for pathogen aggressiveness thereby helping in initial establishment of the pathogen in the plant canopy. The unpredictable changes that are occurring in the climate will make the disease forecasting a difficult task. On vector transmitted pathogens the change in climatic factors may lead to even more diversion in risk analysis due to involvement of vectors as an important additional link. There are many more factors that affect the occurrence of plant diseases and therefore the management strategies need a gradual shift from the existing one to more prudent approach. This review focuses mainly upon the various effect of climate change on plant diseases in Indian context and evaluating whether the management strategies are being focused accordingly.

P (S 5) 03: Role of macro and micro-nutrients on development of the wilt disease in chickpea

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Chickpea (*Cicer arirtinum*) is the third most important grain legume after common bean and pea (Anwar *et. al*., 2009). Asia covers 89.7 per cent of the area in chickpea cultivation followed by 4.3 per cent in Africa, 2.6 per cent in Oceania, 2.9 per cent in America and 0.4 per cent in Europe. India ranks first in terms of chickpea production and consumption in the world. About 65 per cent of the global area with 68per cent of global production is contributed by India.The major chickpea producing countries are India, Pakistan, Ethiopia, Burma, Turkey, Mexico and Australia. It accounts for 70 per cent to the cultivated *Rabi* pulses in India. Among the fungal diseases, chickpea wilt caused by *Fusarium oxysporum* f. sp. *ciceri* is widespread in several countries of the world like India, Iran, Pakistan, Nepal, Burma, Spain, Mexico, Peru, Syria and USA. It is one of the important limiting factors of chickpea production in India. The disease causes substantial yield losses which may reach even 100 per cent under favorable weather conditions. Wilt disease of chickpea induced by *Fusarium oxysporum* f. sp. *ciceri* (Padwick) was found increasing levels of nitrogen application had increased wilt incidence successively in both the years. Whereas, a reverse trend was observed with the application of phosphorus, incidence of wilt was decreased with increasing levels of phosphorus. Minimum disease incidence of 39.19 percent was recorded when no (zero) nitrogen was applied to the plants in the years 2014-15. Next year the minimum disease incidence of 44.01 percent was noted with the highest dose of phosphorus were not found to be significant. Application of zinc and calcium reduced the wilt incidence significantly over check. Zinc was found to be most effective in minimizing the disease with incidence of 41.68 and 41.10 per cent in the year 2014-15 and 2015-16.

P (S 5) 04: The impact of different sowing methods on Sclerotinia stem rot and white rust of rapeseed-mustard

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India is the third largest Rapeseed-Mustard producing country in the world. In India, rapeseed-mustard (22.40%) group of crop rank second among the oil seed crop after soyabean (38.52%). Together they occupy an area of about 7.0 million hectare with about 7.8 million tones production. Madhya Pradesh contributed about 12% of National Production and Morena district is the major rapeseed-mustard growing area which contributed about 33% of the state contribution and very high productivity about 1900kg per hectare. The experiment was conducted at RVSKVV- Zonal Agriculture Research Station A.B road Morena. The experiment design in RBD in three replication with four treatments (Broad bed, Permanent bed, Zero tillage and Conventional tillage) with JM-3 varietyThe whole experiment was based on four planting methods for find out minimum disease pressure and no fungicide was used in this experiment. The weather is generally dry except during monsoon the annual rainfall about 750mm. The soil in the project area fall under alluvial group in general the texture of the soil is sandy-loam to clay with pale dark brown in colour. Five disease (Sclerotinia stem rot, Downy mildew, Powdery mildew, Alternaria blight and white rust disease) are appear in all the crop season in every year and have economical importance but Sclerotinia stem rot and white rust disease are major constrains in the rigion. The maximum disease severity [Sclerotinia stem rot (*Sclerotinia sclerotiorum*) and White rust (*Albugo candida*)] was observed in Zero tillage followed by permanent bed and conventional tillage. Minimum disease severity of Sclerotinia stem rot and White rust of rapeseed-mustard was found Broad bed.

P (S 5) 05: Optimization of medium for *Ophiocordyceps neovolkiana* (Kobayasi) from Kasargod district of Kerala, India

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The genus of fungi *Ophiocordyceps* includes more than 500 unique species of entomopathogens parasitizing different insect hosts. These mysterious fungi have a long reputation of being the most expensive raw material used in traditional Chinese medicine due to its dearth in availability. As a result of its high efficacy and potency in curing various diseases, this fungus has been called as 'panacea of all ills'. *Ophiocordyceps* attacks coconut root grub (*Leucopholis coneophora* Burm.), an endemic pest in coastal sandy areas of Kasargod district of Kerala. Isolation of the fungus was done in potato dextrose agar medium during June-September months of 2017-2018. The molecular characterization showed homology with *Ophiocordyceps neovolkiana* (Kobayasi). To find out the optimum medium for the growth of fungal mucelia, five different media were selected. Among these, yeast extract potato dextrose agar (YPDA) was found to be the best. Evaluation of physiological parameters of *O. neovolkiana* showed 30ºC as optimum temperature, 7.0 as optimum pH, fructose as the best source of carbon, yeast extract as the best source of nitrogen, KH_2PO_4 and $ZnCl_2$ as the best source of macro and micro minerals, folic acid as the best source of vitamin, when grown under 24 h darkness in incubator. By combining all the optimum parameters, a new medium was standardized and named as yeast extract potato fructose agar (YEPFA). The ITS sequence of the fungus was deposited at the Gen Bank of NCBI with accession number MH 668282 and the culture was deposited at National Fungal Culture Collection of India by MACS Agharkar Research Institute, Pune with accession number NFCCI 4331.

P (S 5) 06: Impact of abiotic factors on symptomatology and secondary metabolites production of *Fusarium fujikuroi* causing bakanae disease

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The bakanae disease of rice incited by *Fusarium fujikuroi* Nirenberg has recently become a serious threat to rice cultivation in India and other countries. It produces a vast variety of symptoms like foot rotting, lanky, tall slender culms with pale yellow flag leaves and sterile grains. The pathogen is known to produce different secondary metabolites and mycotoxins like Gibberellic acid (GA), Fusaric acid (FA), Fumonisins, Bikaverin etc. which affects the pathogen virulence and type of symptoms produced. The abiotic factors might play an important role in the development of various symptoms and secondary metabolites production. In present study, we evaluated the effect of different abiotic factors (soil moisture, soil pH, temperatures and soil type) on disease severity, symptomatology and secondary metabolites production. For this, F250, an isolate of *F. fujikuroi* and a susceptible rice genotype, Pusa Basmati 1121 were used for evaluation of disease. The highest disease severity was observed at 30% soil moisture, 7.0 soil pH, 35°C temperature and silty clay loam soil collected from Hapur. Plant samples from the different moisture experiment were selected for

quantification of secondary metabolites by HPLC and GC-MS. Total detected 139 metabolites were grouped into two clades on the basis of their expression in different samples. A remarkable increase in GA (486.13 µg/gm) and FA (48.04 µg/gm) was recorded in disease inoculated plants showing elongation and rotting symptoms respectively. The Fumonisin B1 (FB1) production was found to have no correlation with symptom development. The FA inoculation reduced the seed germination and caused rotting of seedlings. The GA inoculation increased the seed germination and root length and stem elongation symptoms. The disease severity was found to be negatively correlated with soil moisture level. The diseased plants were observed with stem elongation and rotting symptoms which might be attributed to an increased gibberellic acid or Fusaric acid respectively.

P (S 5) 07: *Cylindrocladium* die back - an emerging threat to cashew cultivation in Konkan region of Maharashtra

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Cashew is a million dollar crop and it is the second important cash crop of the Konkan region of Maharashtra after mango. After implementation of EGS in Maharashtra in 1990, many small and marginal farmers in the hilly terrain of this region, switched over to this hardy and highly remunerative crop owing to its minimal crop management requirements. As a result, the barren and fallow land has been brought under extensive cashew cultivation. Till recently, the cashew plantations in Konkan region were free from destructive diseases leading to economic losses. But in the July and August 2019, the total monthly rainfall was 1711 and 1312 mm respectively, supported by cloudy weather and high humidity above 93 % which lead to the sudden outbreak of defoliation followed by dieback of new vegetative flush of the plants, throughout the region. In order to combat against this unexpected natural calamity thorough investigations were carried out. Extensive surveys conducted during the season revealed that in the primary phase of the disease, new and old cashew plants as well suffered from severe defoliation. On establishment of the pathogen the infection progressed to the newly emerged main and lateral branches which consequently lost vigor, turned brown and then black. The colonization of pathogen within the tissues of the host leads to formation of small white encrustations on the upper surface of the dead twigs. The pathogen was isolated and identified as *Cylindrocladium* spp. The *in vitro* experiments on chemical management clearly indicated that contact fungicide- mancozeb as well as combination fungicide with mancozeb is very effective against the pathogen. The Ad –hoc recommendation of immediate sprays of one of these fungicides followed by 2 more sprays at an interval of 15 also worked very effectively under field conditions in different pockets of the region.

P (S 5) 08: Influence of climate change on plant diseases and their management in Betul district of Madhya Pradesh

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Change in environmental conditions is strongly associated with the crop losses caused by insect-pest and diseases because the environments directly or indirectly influence the growth, survival and dissemination of the causal organism.Soybean and Chickpea are the major crops of Betul district. Continuous cultivation of Soybean followed by chickpea and non adoption of suitable integrated disease management modules cause heavy loss due to various diseases. Apart from this, climatic variability plays an important role in heavy infestation of white fly in Soybean resulting yellow mosaic disease, incidence of root rot and collar rot in Chickpea were noticed in the present scenario. Keeping the infestation of above insect-pest and diseases, On farm trials were conducted by Krishi Vigyan Kendra, Betul at 60 farmer's fields during the year 2015 to 2018 with farmers participatory approach. Heavy infestation of white fly was noticed, which resulted severe incidence of yellow mosaic disease in the fields of Soybean. Due to yellow mosaic disease, the area of Soybean gradually decreased year after year. Results of trails showed the adoption of seed treatment with Imidacloprid 48 % and foliar spray of systemic insecticide Imidacloprid 17.8 SL minimized the disease incidence up to 55 per cent and increased yield of Soybean by 25 per cent. High incidence of dry root rot and collar rot in chickpea were noticed due to increased temperature and more frequent moisture stress. The results of on farm trails showed that the seed treatment with *Trichoderma viride* @ 10 gm/kg seed, soil application of *Trichoderma viride* @ 2.5 kg/ha with FYM reduced the incidence of both the diseases by 82 per cent and given 32 per cent more yield in comparison to farmers practice.

P (S 5) 09: Development of chickpea wilt incidence in relation to adaphic and epidemic factors

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The present investigation on wilt of chickpea caused by *Fusarium oxysporum* f. sp. *ciceri* was carried out to study the adaphic and endemic factors responsible for development of wilt. In the present study, correlation between chickpea wilt disease incidence and adaphic factors on resistant to highly susceptible four lines revealed that there was a significant strong correlation between disease incidence and soil temperature and soil moisture (%). All the four entries were showed positive correlation with soil temperature, while negative correlation with soil moisture. Coefficient of determination (R^2) showed that both the factor contributes 54.70 % (JG-315), 56.32 %, (IGP-187), 54.88 % and 39.42 % in development of wilt. Pot experiment was carried out in environmental growth chamber with combination of three different level of temperatures viz., 20, 27 and 34, two different level of relative humidity viz., 60, 80 % and two inoculums load (5 and 10%) were evaluated to find out the effect of temperatures, relative humidity and inoculums load on disease incidence of chickpea wilt. All the three factor viz., air temperature, relative humidity and inoculum load were found positive correlation with wilt incidence. Statistically aerial temperature (0.7226**) and inoculums load (0.6435**) were found significant positive correlation with wilt incidence, while relative humidity (0.1315) was found non-significant.

P (S 5) 10: Effect of date of sowing on yield and disease intensity of Alternaria blight in safflower

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The field experiment were carried out, during *Rabi*, 2013-14 and *Rabi*, 2014-15 at Research Farm, AICRP (Safflower) and Department of Agronomy, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra. Alternaria blight caused by *A. carthami* (Chowdhury) is one of the most widely spread and destructive disease of safflower (*Carthamus tinctorius* L.). The pathogen induces damping-off, leaf blight and stem canker, which accounts for about 25 - 60 per cent seed yield losses. Though Alternaria blight disease in safflower and other crops can be managed by spraying chemicals / biological fungicides, but by adjusting sowing time one can avoid susceptible stage of the crop to Alternaria blight disease. The adjustment of sowing dates / seasons is an obviously best strategy, escaping the crops susceptible stage and also constitutes one of the components of integrated disease management. Investigations were made on the effect of sowing dates on disease intensity and yield of safflower crop. Highest disease intensity was recorded when crop was sown early during first fortnight of September was found to suffer severely with Alternaria blight disease with significant reduction in seed yield; however delayed sown crop from second fortnight of September onward the blight disease intensity was found to decrease drastically.

P (S 5) 11: Scenario of white mold disease with special reference to its emerging severity in the North East India

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Sclerotinia sclerotiorum (Lib.) de Bary, non-host specific, homothallic, ascomycetous fungus reproduces asexually through sclerotia and sexually through ascospores, infects about 500 plants species. It is more common in the cool moist parts of the globe, but is now also known to occur in hot as well as dry areas because of its genetic diversity and greater adaptability. The pathogen has been recorded since long in the North East region. Attempts were made to understand the white mold disease dynamics on various crops. *Sclerotinia* rot was recorded on maximum number of crops during the winter months of 2015-16, 2016-17, 2017-18 and 2018-19 in the states of Assam, Mizoram, Nagaland, Sikkim and Meghalaya. A total of nine host plants were found infected in the two districts – Darrang and Kamrup of Assam during the winter months of 2015-16 with maximum disease incidence of 18% on mustard and pea. Minimum incidence (3.33%) of the disease was recorded on periwinkle (*Catharnthus roseus*) and gerbera. *Sclerotinia* disease on chilli and urdbean with incidence of 10% and 6.66% respectively was recorded from Kolasib, Mizoram during 2016, January. During the winter of 2015-16, the pathogen was observed on nine different hosts in different locations of Dimapur district of Nagaland causing incidence in the range of 3.33-20%. Only one host crop, chayote (*Sechium edule*) and cabbage of the pathogen was recorded from Sikkim and Meghalaya during December, 2016 and 2018 respectively. Analysis of long term weather variables indicates that the climate of North East region is also undergoing unparallel changes during the last three decades. At Umiam, the annual maximum (Tmax) and minimum temperature (Tmin) exhibited reverse trend, the former increased significantly from 24.3°C to 26.4°C while the later decreased significantly from 14.8°C to 13.8°C. The change in weather parameters may result in the increasing host range of *S. sclerotiorum*.

P (S 5) 12: Relationalship of Karnal bunt occurrence with weather parameters

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Karnal bunt caused by *Tilletia indica* Mitra [syn.*Neovossia indica* (Mitra) Mundkur] is one of the major disease of wheat causing quality losses and monetary losses due to international quarantine regulations. In the present investigation from wheat grain samples (80-120) were collected during 2017 and 2018 to see the incidence of Karnal bunt of wheat. Wheat grain samples were collected from different wheat grain markets and farmer's fields of Hisar, Karnal, Rewari and Sirsa district. Karnal bunt incidence of each district was correlated and regressed with fifth to ninth standard meteorological weeks of weather parameter. Karnal bunt incidence was significantly correlated with maximum temperature and rainy days. The regression equations were also developed for each district. Through knowing these significance weather variables responsible for induction of KB and vulnerable stage of wheat. This susceptible window remain open 21 days after booting stage, disease can be managed through natural means of irrigation by adopting prophylactic measures.

P (S 5) 13: Prevalence of maize diseases in India

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Owing global climate change, surveillance is essential tool to detect changes in pattern of diseases in the crops. To fulfill this purpose surveys were conducted from 2013-18 in five maize growing zones of India *viz.*, Northern hill Zone (NHZ), Northern West Plain Zone (NWPZ), Northern East Plain Zone (NEPZ), Peninsular Zone (PZ) and Central Western Zone (CWZ). The percent disease index (PDI) of maydis leaf blight (MLB) was moderate (45) to high (65) in 4 zones (NHZ, NWPZ, NEPZ and PZ) while low in CWZ (25). Though the lowest incidence of turcicum leaf blight (TLB) was reported from CWZ in 2013 but it has increased consistently. PDI of TLB was highest (46) in 2016 in NHZ whereas banded leaf and sheath blight (BLSB) appeared at higher intensity in NHZ and NWPZ. Moderate (42) infection of curvularia leaf spot (CLS) was observed in all the five zones whereas bacterial stalk rot (BSR) was restricted to NHZ and NWPZ with moderate infection (33-47). Post flowering stalk rots (Charcoal and Fusarium stalk rot) appeared at higher intensity in all the 4 zones except NEPZ. PDI of brown spot (BS) ranged from 15-47 in NHZ and CWZ. Sorghum downy mildew (SDM), polysora rust (PR) and wilt were observed with very low infection from PZ while bacterial leaf streak (BLS) and brown stripe downy mildew (BSDM) were observed in NWPZ. This study revealed that there is need to develop effective management toolsfor MLB, TLB, PFSR and BLSB as these are the most prevalent maize diseases in present scenario.

P (S 5) 14: Impact of climatic factors on fungal and bacterial infections affecting tomato crops in Mauritius

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Tomatoes represent one of the most widely consumed vegetables in Mauritius with an average per capita consumption of ca. 12 kg/year. Unfortunately, locally-produced tomatoes are highly susceptible to various pathologies in Mauritius with an incidence rate ranging from 10-100%. This project was aimed at conducting a surveillance of diseases affecting tomato crops grown in different regions of Mauritius. Tomato plantations in different agroclimatic zones were surveyed for key diseases during the period of March – October 2019 and disease incidence was computed. A digital hygrometer was used to measure the temperature and relative humidity of the visited areas *in situ*. Tomato samples (leaves, stems, fruits, roots) displaying specific signs such as spots, lesions and wilting were recorded and further examined. Isolation and identification of the etiological agents were performed. Pathogenicity trials were done to confirm the ability of the isolated agents to cause diseases on healthy hosts. The main microbial diseases encountered in fields were Early blight, Fusarium wilt, Gray leaf spot, Alternaria stem canker (ASC), Late blight, Anthracnose, Gray mold, Bacterial spot, Bacterial speck and Bacterial wilt. In greenhouses, the diseases detected included Early blight, Gray Mold, Leaf mold, Bacterial wilt, Bacterial speck and Pith necrosis. The disease incidence for each fungal and bacterial disease ranged from 1.4 to 100% and 3 to 58% respectively. The overall temperature varied between 23.5 and 30 °C. The minimum humidity recorded was 50% while the maximum was 80%. Infections mostly caused by fungi were more prominent in super-humid areas. So far, fungus *Alternaria alternata* responsible for ASC was molecularly confirmed. Future work will involve aligning climatic variables with disease incidence, the molecular identification of other isolates, and the detection of mycotoxins on tomatoes. This research highlights the possible impacts of climatological factors on the susceptibility of tomato crops to microbial diseases which could adversely affect food security in Mauritius.

P (S 5) 15: Study of seasonal incidence of prevailing diseases of okra

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The intensive survey was conducted at different location of Raipur and Durg district of Chhattisgarh viz. Parsada, Godhi, Bhatagaon, Ganiyari, and Baktara to record the seasonal incidence and severity of prevailing foliar diseases of okra (*Cercospora* leaf spot, Alternaria leaf spot, powdery mildew disease, okra leaf curl disease and Yellow vein mosaic) during Kharif and Rabi season of 2016-17. Observations were recorded from farmer's fields under natural condition. Per cent Disease Incidence (PDI) of *Cercospora* leaf spot of okra was highest (55.60%) in Kharif season then Rabi season (33.80%), on context of location specific highest PDI was recorded in Kharif sesson was from Baktara (63%) followed by Ganiyari (61 %), Bhatagaon (55 %), Godhi (52%) and lowest was from Parsada (47%), and in Rabi season highest PDI was also recorded from Baktara (41%), followed by Bhatgaon (37%), Godhi (34%), Ganiyari (32%) and lowest was recorded from Parsada (25%). In order to Per cent Disease Severity (PDS) of Cercospora, leaf spot of okra was also higher in Kharif season (56.18%) than Rabi season (36.92%). On perticular location highest PDS in Kharif season was recorded from Baktara (61.10 %) followed by Bhatagaon (56.90 %), Parsada (55.10 %), Godhi (54.90 %), and lowest was from Ganiyari (52.90%), and in Rabi season highest PDS was from Ganiyari (39.50 %) followed by Bhatagaon (39.00 %), Baktara (37.00 %),Godhi (35.80%), and lowest was recorded in Parsada (33.30 %). In case of all the diseases which was observed in survey the average PDI was highest in Kharif (39.72 %) than in Rabi season (37.56). In context of disease severity average PDS was observed highest in Kharif (37.46 %) than Rabi (35.90 %). In case of both the season (Kharif and Rabi) highest prevailing foliar disease of okra was powdery mildew (60.42%) followed by *Alternaria* leaf spot (52.67 %), *Cercospora* leaf spot (45.63 %) okra leaf curl virus (16.17 %) and lowest was okra mosaic disease (13.42 %).

P (S 5) 16: Conservation agriculture *vis-à-vis* disease scenario in field crops

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The UN sustainable development goals have been framed to achieve a better and sustainable future for all. They are aimed to address the global challenges of climate change, food security, equality etc. A change in any of the goal brings change in all other targets as they seems to be interconnected with each other. As a result now climate resilient agriculture is gaining importance every day. Recent advances in that direction indicates that conservation agriculture (CA) is probably the future in most of the developing countries as an strategy to combat climate vagaries. FAO have defined “CA as an approach to managing agro ecosystems for improved and sustained productivity, increased profits and food security while preserving and enhancing the resource base and the environment”. CA is characterized by three linked principles, namely, Continuous minimum mechanical soil disturbance; Permanent organic soil cover; Diversification of crop species grown in sequence and/or association. As all adopted technologies, CA also has its own advantages and limitations. From pathological point of view, no or minimum tillage of soil and retaining residues in the field principally increases the residue and soil borne pathogens, and poses challenges to pathologists to grow a crop in healthy state. The literature in this regard is meagre and scattered and gives conflicting information on the effect of conservation agriculture on disease development. Few attempts were taken in Eastern India to evaluate the disease dynamics under CA in different principal crops. For the purpose a permanent conservation agriculture plot is being maintained in the University since 2006. Regular monitoring of the crop is done by a group of scientists and regular data recording is continuing. The results indicate that the different diseases behave differentially to the changed agronomy. Initial results indicate that spot blotch of wheat increases in no-tilled condition, but over the years gradually the disease decreases in the crop, whereas, sheath blight in rice was always found higher under zero tilled condition than under conventional tillage. Relationship of different physiological and morphological parameters of the crop was correlated with severity of spot blotch and NDVI was found to be negatively correlated with disease. Thus, it gives an opportunity to manage the crop architecture and nutrient under conservation agriculture to reduce the disease severity. Also the scope of residue management with biological agents may be a useful tool in managing diseases under CA.

P (S 5) 17: A study on the prevalence of pre- and post-harvest fungal diseases affecting the onion crop in Mauritius

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Onion (*Allium cepa* L.) is a crop of high economic importance for Mauritius with an annual value of Rs 126 M. With climate change, the occurrence of pathogenic and mycotoxigenic fungi on onions at the pre- and post-harvest stages will likely increase. The aim of the study was thus to undertake a surveillance of fungal diseases affecting the onion crop and correlate them with climatic factors. A disease incidence survey was carried out in onion plantations from sub-humid, humid and super-humid agroclimatic zones of Mauritius while recording temperature and relative humidity on-site. Diseased leaves and bulbs were sampled and examined microbiologically. Bulb samples were also collected post-harvest from storage areas during the months February-April (Summer) and September (Winter) and inspected for diseases. To determine their ability to cause disease, the isolates were subjected to pathogenicity trials in healthy bulbs. The main fungal diseases encountered on field in all climatic zones were *Stemphylium* leaf blight and pink root with a mean incidence of 64.8% and 34.9% respectively. Additionally, purple blotch caused by *Alternaria* spp. and damping-off caused by *Fusarium* spp. were detected in sub-humid and super-humid regions respectively. Prevalent post-harvest diseases included brown stain typically caused by *Botrytis cinerea*, basal rot caused by *Fusarium* spp., pink root caused by *Phoma terrestris* and neck rot caused by *Fusarium* spp. Commensals such as *Aspergillus niger* and *Penicillium* were also potentially noted. Pathogenicity tests proved the pathogenicity of *Stemphylium* spp., *Alternaria* spp., and *Fusarium* spp. So far, PCR and DNA sequencing revealed *Fusarium oxysporum* as the etiological agent of basal rot and identified *Aspergillus fumigatus* as a post-harvest commensal. Future work will involve the definitive identification of the remaining isolates using DNA sequencing, and analysis of bulbs for mycotoxins such as aflatoxins, ochratoxins and fumonisins produced by *Aspergillus*, *Penicillium* and *Fusarium* spp. (Taniwaki et al. 2018) occasionally present on onions.

P (S 5) 18: A surveillance of pathogenic fungi on potatoes from different agroclimatic zones of Mauritius

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Potatoes are considered as one of the strategic food crops of Mauritius, however their production may be at risk with the effects of climate change. Climate change has an influence on the prevalence of fungal diseases affecting potatoes due to weather factors such as temperature (T) and relative humidity (RH) which affect fungal growth. The objective of this research was to investigate the prevalence of fungal diseases affecting potatoes grown in different agroclimatic zones. Disease surveys were carried out in open fields in sub-humid, humid and super-humid regions of Mauritius from November 2018 to October 2019. Moreover, Disease Incidence (DI) was determined on field and T and RH were recorded using a digital hygrometer *in situ*. In the laboratory, suspected fungal agents were identified using microscopy, culturing and molecular methods. Pathogenicity trials were also conducted to confirm the virulence of the fungi on healthy leaves and tubers. Leaf Blight (LeB) and Late Blight (LaB) were the most encountered fungal diseases on leaves. The DI of LeB varied from 0.5% to 33.3% during summer while that of LaB ranged from 0.94% to 100% during winter with T and RH fluctuating from 21oC to 28oC and from 50% to 88% respectively. Major fungi identified on leaf and tuber samples from open fields were presumed to be *Alternaria alternata*, *Phytophthora infestans* and *Fusarium* spp. Post-harvest pathogens isolated from tubers were suspected to be *A. alternata* and *Fusarium* spp. So far, *F. oxysporum* and *A. alternata* on tubers from storage areas have been confirmed at the molecular level. Moreover, pathogenicity tests done for *Fusarium* spp. confirmed the identity of the etiological agents. Future work will involve detection of mycotoxins on infected potatoes and assessment of the mycotoxin-producing ability of *Fusarium* and *Alternaria* using mycotoxin testing kits. Overall, we can infer that potato cultivation in Mauritius is susceptible to climate-dependent fungal diseases that can compromise the yield and safety of this important commodity.

P (S 5) 19: Effect of abiotic factors on disease incidence of pea and correlation coefficient between major diseases of peas

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Pea is most extensively grown in Madhya Pradesh, India. It is infested by many seed, soil and air borne diseases. Among soil borne, collar rot (*Sclerotium rolfsii*), Vascular wilt (*Fusarium oxysporum* f. sp. *ciceri*) and dry root rot (*Rhizoctonia bataticola*) are the most important diseases causing heavy losses from seedling to pod filling stage and disease severity depends upon the temperature and moisture condition (Munjal *et al.*,1963). Considering the importance of diseases of pea present investigation is proposed with the effect of biotic factors and correlation between abiotic factors. Results revealed that mean incidence of powdery mildew was significantly negatively correlated with maximum and minimum temperature (-0.874 and -0.669, respectively). It means powdery mildew incidence increased as the temperature decreased. Similarly, mean incidence of downy mildew was also significantly negatively correlated with maximum temperature (-0.868). Seedling disease is positively correlated with minimum temperature. It increases as the minimum temperature increase.The incidence of diseases symptoms on pea plant started in the fourth week of October (43th *SMW) and wilt incidence increased up to the third week of December (50th SMW), powdery mildew incidence increased up to the first week of January (1st SMW) and downy mildew incidence increased up to the first week of December (49th SMW). Crop was harvested in the first week of February. The seedling disease incidence ranged from 5.12 to 13.25 to and high disease incidence was recorded in (43th SMW) or fourth week of October. The wilt disease incidence ranged from 2.66 to 9.66 and highly disease incidence was recorded in (50th SMW) or third week of December. The powdery mildew disease incidence ranged from 3.86 to 21.43 and highly disease incidence was recorded in (1st SMW) or first week of January. The downy mildew disease incidence ranged from 2.76 to 16.21 and highly disease incidence was recorded in (49th SMW) or first week of December

P (S 5) 20: Land use, change detection and plant disease analysis of Central India using satellite data

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Study was carried out to LULC analysis of AABR, India using geospatial techniques and ground measurements. LULC detection analysis was identified using digitally classifying Landsat 5 (2008) and Resourcesat 2A (2018) satellite data using MLA. The results revealed that the AABR is unique plant species, rich in biodiversity, however many plant species are lost due to human pressure, and many species are replaced by exotic species which is affecting the ecology of this region. We conclude that the Landsat 5 and Resourcesat 2A satellite images are most suitable for the identification of LULC change and plant disease analysis. The study indicates adopting the rigorous conservation measures, especially in Open, Dense and young Teak forests. Moreover, Sal regeneration would be essential because Sal plant are lost due to Sal borer disease, human pressure and many species are replaced by exotic species which is affecting the ecology of this region and also in restoring the moist tropical forest is many ways which can be linked to global climate change. Tropical forests including trees outside forest are the treasure of biodiversity and a vehicle for sequestering atmospheric carbon needs conservation. The continuous emission of GHGs in the atmosphere is due to conversion of natural forest for cultivation and other land use changes. The removal of biomass and destruction of forest have contributed to depletion of natural biodiversity and added to climate change. One of the vital solutions of mitigating climate change & reducing the CO_2 concentration is the atmosphere is carbon sequestration in which forests can play a vital role.

P (S 5) 21: Survey of pearl millet blast in Gird zone of Madhya Pradesh during 2017-18 and 2018-19

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Pearl millet is an important for grain and forage cereal of India which is traditionally accepted as bajra. Blast, downy mildew, smut, ergot and rust are the major diseases occurring across the country. Among these, blast incited by *Pyricularia grisea* is a serious disease in many parts of the India causes severe losses in terms of grain and fodder yield of pearl millet. In Madhya Pradesh, Most of the area of this crop is confined in its northern region comprising Morena, Bhind, Gwalior, Shivpuri and Sheopur districts were the pathogen has established a key position among all the diseases. The disease showed wide variation in terms of disease intensity. None of the surveyed fields were free from the blast disease in localities of blast PDI. The maximum PDI was recorded in Morena (40.59%) followed by Bhind (37.96%), Gwalior (32.24%) and Sheopur (31.51%), while the minimum blast PDI was calculated in Shivpuri district (26.22%). The blast severity across the state during 2017-18 and 2018-19 was 45.83 and 21.59 per cent respectively with the two years mean severity of 33.71 per cent. The disease pressure was higher in 2017 as compared to 2018.

P (S 5) 22: Long term effects of climate change on soil properties in rice-wheat cropping system in Chhattisgarh

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Soils form through the multifarious interaction of a number of forces, including climate, relief, parent material, organisms, all acting over time. It takes thousands of years for a soil to form and most soils are still developing following changes in some of these soil forming factors, particularly climate and vegetation, over the past few decades. Climate is one of the most important factors affecting the formation of soil with important implications for their development, use and management perspective with reference to soil structure, stability, topsoil water holding capacity, nutrient availability and erosion. Further Indirect effects corresponds to changes in growth rates or water-use efficiencies, through sea-level rise, through climate-induced decrease or increase in vegetative cover or anthropogenic intervention. Assuming constant inputs of carbon to soils from vegetation, different estimate predict that expected changes in temperature, precipitation and evaporation will cause significant change in organic matter turnover and CO_2 dynamics. In conclusion, increased productivity would generally lead to greater inputs of carbon to soil, thus increasing organics.

P (S 5) 23: Isolation and characterization of *Ustilaginoidea virens* incitant of an emerging disease of rice

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False smut caused by *Ustilaginoidea virens* is an emerging disease of rice. The occurrence of the disease was initially considered as an indicator of good harvest. However, the frequency of disease is now increasing rapidly with a 0-70% disease occurrence. The rise in chemical exposure, planting of high yielding varieties and change in weather conditions at booting stage is aggravating the problem. The disease is responsible for high yield losses and reduced quality of rice grains. In spite of its increasing importance, the studies related to the disease incidence, distribution and its control are very rare. Hence, we elucidate a comparatively fast and novel method for isolation of the fungi followed by morphological and molecular characterization. For this, the infected smut balls were taken and sterilized using sodium hypochloride (1% v/v). After washing with sterile water the smut balls were halved and spores were dusted from inner surface on the petri plate containing streptomycin added potato sucrose agar. The method is recorded with a marked success rate of 80-85%. The identity of the pathogen was further confirmed through internal transcribed spacer (ITS) region with 98-100% identity. Isolates were variable morphologically i.e. colour, size and shape of conidia and cultural characteristics. Information generated could be utilized for the *U. virens*-rice interaction and management of false smut disease of rice. Isolates were further characterized of different molecular markers like TEF, IGS, â-tubulin etc. In conclusion, the developed methodology could be useful in *U. virens* epidemiological studies.

P (S 5) 24: Survey for prevalence and severity of yellow mosaic disease and its vector (*Bemisia tabaci*) in Uttarakhand

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Yellow mosaic is a destructive disease of soybean and is caused by four distinct species of *Begomovirus*. It has been reported to cause widespread yield loss in all the major soybean growing areas of the country. A roving survey was carried out to know the per cent disease incidence and severity of yellow mosaic disease and occurrence of its vector in the major soybean areas of Uttarakhand during two consecutive crop seasons *i.e.* 2018 and 2019 from July to October. In each district minimum five villages and from each village minimum three soybean fields were selected for recording the observations. In each field, the observations (Disease incidence and severity) were recorded on 25 plants in all four corners as well as center of the field. Number of whitefly population was assessed by counting the number of whiteflies in three trifoliate leaves one each at top, middle and bottom. The results revealed that the yellow mosaic disease incidence varied from 0-35 percent in the fields surveyed. The disease was found maximum in the tarai region of Udham Singh Nagar and Nainital districts followed by the lower hills. The disease was absent in the upper hills *viz.,* Tehri Garhwal, Rudraprayag, Chamoli, Pithoragarh, Almora, Champawat and Bageswar districts. Similar trend was obtained in the case of its vector as well. Whitefly population varied from less than from 3 in the high hills to 17 per plant in the tarai region. A positive correlation was obtained for the whitefly population and disease severity.

P (S 5) 25: Screening of different brassica genotypes against white rust under artificial condition

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Rapeseed-mustard group of crops are the major rabi oilseed crops of India. The group is mainly constituted by *Brassica rape* (Syn. *B. compestries L*),*B. napus L*., *B. juncia (L).* Czern and Coss and *B. carinata* Braun). The oil content in the species of the group varies from 28.6 to 45.7 per cent.Among the four species *B. juncea* which is commonly known as Indian mustard is the most important oilseed crop of the country. *B. juncea*is the most important oilseed crop of Northern Madhya Pradesh comprising Morena, Bhind, Gwalior, Sheopur and Datia districts contributing more than 75% share in the production of this crop in the state. White rust incited by *Albugo candida* (Pers. ex. Lev.) Kuntze has been reported to be wide spread and destructive fungal disease of mustard throughout the world (Kolte, 1985).The pathogen is an economically important obligate parasite of cruciferous species and it is soil and seed borne. The experiment was conducted at RVSKVV - Department of Plant Pathology, College of Agriculture, Gwalior (M.P) during *Rabi* season 2016-17 and 2017-18.The experiment designin RBD in sthree replication with eighty four genotypes.Out of 84, *Brassica* genotypes SBG-15-6, SBG-15-36 and SBG-15-54 were found immune to white rust under artificial inoculation. Six genotypes *viz.,* JM-1, JTC-1, JM-4, SBG- 15-24, Swarmin and Pitambra were found highly resistant. Eight, thirty and thirty five were found resistant, moderately resistant and susceptible to the disease, respectively. While the remaining two entries Varuna and Rohini, were found highly susceptible to the disease.

Session 6
Epidemiology and forecasting of plant diseases

Keynote Papers

KN (S 06) 01: Modelling of plant disease emergence over multiple successive seasons

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Plant disease emergences have dramatically increased recently as a result of global change, which includes trade expansion, loss of host genetic diversity, and climate change. Recent examples of emergence of pathogens or pathogen strains include *Puccinia graminis* f. sp. *tritici* lineages Ug99 (stem rust of wheat) first in sub-Saharan Africa and now in other continents, *Puccinia striiformis* f. sp. *tritici* strains (yellow of wheat) in Europe, *Pyricularia graminis-tritici* (wheat blast) in south Asia, and *Xyllela fastidiosa* on olive in Southern Europe. A better understanding of the processes and conditions which determine disease emergence and new epidemic outbreaks is required to develop strategies and to inform management decisions. Here, we consider the emergence of new pathogens, as well as of new pathogen strains using a process-based simulation model. The model includes polyetic processes, that is, successive cropping cycles where polycyclic epidemics during the growing season are followed by pathogen survival between growing seasons. The model also represents yield losses caused by epidemics. This framework is used to explore the dynamics of a pathosystem consisting of an immigrant strain incoming into a system where a resident strain is already established. Outcomes are presented in terms of probability of emergence, time to emergence, and yield loss. The model is considered with two regimes: deterministic and stochastic. An analytical solution to determine a threshold for emergence is also developed. Analyses focus on the effects of two key fitness parameters on emergence: the relative rate of pathogen reproduction during epidemics, and the pathogen relative rate of (inoculum) decay in the absence of host. We report three key findings: (1) the developed framework is suitable to analyse disease emergence; (2) stochasticity of reproduction and survival over seasons constitutes a critical feature of disease emergence; and (3) pathogen survival plays an essential role in disease emergence.

KN (S 06) 02: Epidemiology and prediction models for the management of rapeseed–mustard diseases- current status and future needs

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Brassica oilseed crops have a significant role in Indian agriculture since almost each part of the plant is consumed either by human beings or animal depending upon the crop stage. The production and productivity of these crops is limited by a number of biotic and abiotic stresses. More than twenty five diseases are known to affect these crops all over the world**.** However, diseases like Alternaria blight [*Alternaria brassicae* (Berk.) Sacc.], White rust [*Albugo candida* (Pers. ex. Lev.) Kuntze], Downy mildew [*Peronospora parasitica* (Pers. ex Fr.) Fr.], Powdery mildew (*Erysiphe cruciferarum* Opiz. ex. Junell) and *Sclerotinia* stem rot [*Sclerotinia* *sclerotiorum* (Lib.) de Bary] are of major consequences because of their widespread distribution, severity and resulting considerable yield losses. The control of these diseases through chemicals is readily available but the efficiency of these chemicals depends upon the interaction between pathogen and host which is influenced by environmental factors. The epidemiology provides the framework for efficient control of these diseases. The various weather parameters such as temperature, relative humidity, and rainfall, wind velocity with direction, leaf wetness, its duration and solar radiation influence the various stages of infection process and disease development. The studies on interaction between these weather parameters (independent variables) and disease development (dependent variables) may pave the way for the development of the prediction models which can determine the disease situation in advance. However, sometimes, the prediction models developed at one location do not fit for other areas. It indicates that data needs to be generated for quite a long period and needs to be tested at multiplications. Further, for greater efficiency, forecasting models must be developed by taking into account the variety being grown, prevalence of a particular pathotype along with microclimatic factors. To achieve tangible results, inter/intra institutional network research projects for validation of results especially epidemiological models to manage *Brassica* oilseed crop diseases more effectively are required. The areas which need in-depth study are epidemiology and forecasting, host resistance including nature and mechanism, physiologic specialization using conventional and molecular tools, rapid diagnostic biotechnological techniques and integrated disease management including biological control measures. It has been experienced that disease management technology has very slow percolation to the end users. Hence, concerted efforts are required in this direction. Some future priority research areas of *Brassica Pathology* include: standardization and validation of prediction models, standardization of host differentials and nomenclature of pathogenic races; Identification of broad-spectrum sources of resistance, resistant loci and resistant genes in each locus; Identification of slow blighting, slow mildewing, slow rusting genes, tolerant, partial resistant, strong and weak genes with suitable combinations; Genetics of virulence and virulence spectrum; Mapping, cloning, characterization and identification of genes; Development of varieties through tissue culture or micro spore culture techniques; Biochemical basis and genetics of *Albugo-Peronospora* association. Besides this, integration of bioagents application; use of organic amendments and systemic acquired resistance (SAR) chemicals would go a long way in devising suitable IPM and IDM modules for economical management of *Brassica* diseases.

Invited Papers

I (S 06) 03: Powdery mildew of wheat: Present status and future perspective in India

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Powdery mildew (PM) caused by *Blumeria graminis* f. sp. *tritici* (*Bgt*) is one of the most damaging diseases of wheat causing 13- 34% and 50-100% yield losses, under moderate and severe infection, respectively. The disease can be effectively managed by cultivation of resistant varieties. However, fast emergence of new virulent races in *Bgt* makes the resistant varieties susceptible in short time. Studies on pathogenic variation in Bgt, based on reaction of more than 300 isolates on International Differential Set during 1994-1998 and 2015-2019 inferred that genes *Pm2*, *Pm4a*, Maris Dove (*Pm2, mld*) and Normandie (*Pm1,Pm2,Pm9, Pm12*) were highly effective. Virulence on gene *Pm1* and *Pm8* increased tremendously during 2015-2019 compared to 1995-98. Hence, it is essential to identify new sources of resistant sources to maintain diversity of resistance and till date about 85 PM resistance genes located at 58 loci (*Pm1 to Pm64*) have been designated and the same number of genes have been located but are designated temporarily. In India, numerous sources of resistance have been identified among the national and international (CIMMYT and ICARDA) wheat material. Race specific resistance genes *Pm 3c, Pm 5* and *Pm 8* were identified in Advanced Breeding Material and promising wheats following infection-type matching technique. Slow mildewing resistant sources were identified among Indian and CIMMYT material based on AUDPC, 'rAUDPC' and infection rate 'r'. It was attributed to longer incubation and latent period, number of colonies/area and colony size and sporulation in varieties viz. HS 240, HS 295, Amigo, Transec etc.. In incompatible host parasite interactions, resistance was attributed to less conidial germination and appressoriurn formation eg. in Norka x Cc^8 (*Pm l*); weak, shrivelled and distorted germtubes in Sappo (*Pm 2+4b)* and Kronjuwel (*Pm4b+8*) and development of haustoriurn and ESH was completely absent in these genotypes. Haustorial abortion, less secondary haustorium production and restricted growth of mycelial wefts was recorded in TP 114 (*Pm 2+6*). Triazole fungicides and fungicidal mixtures eg Nativo, Takkar and cow urine based plant extracts of neem, *Acorus calamus*, *Lantana* sp.*, Calotropis gigantia, Justicia adhatoda* etc. were highly effective in reducing the disease severity and increasing the yield. Wheat PM has become a challenging disease and its incidence and severity is increasing in NWPZ, but no consistent efforts are being made to breed for PM resistance in the National Breeding Program. All the commonly grown varieties of *T. aestivum* and *T. durum* are susceptible. Hence, work on virulence analysis of Bgt population in epidemiologically important areas should be undertaken. Designated genes *Pm*1 to *Pm64* with 85 alleles and the non-designated genes, land races, allied species and allied genera, etc. may be evaluated under Indian conditions to identify PM resistant sources to identify suitable donors to develop resistant wheat varieties. Use of molecular markers has led to Successful gene identification and mapping could be undertaken using molecular markers. These markers may be utilized in marker-assisted selection (MAS) for precise and accelerated PM resistant varieties. The management of disease using fungicides has proved useful in susceptible varieties and in event of sudden break down of resistance. However, fungicides with multiple disease control and different mode of action should be preferred.

I (S 06) 04: Epidemiology and management of aerial blight (Rhizoctonia Solani Kuhn) in soybean

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Soybean is an important pulse cum oilseed crop and is a major source of income for farmers both in the Tarai and hilly tracts of Uttarakhand. Aerial blight caused by *Rhizoctonia solani* is one of the most threatening diseases of soybean. Extensive survey is being carried out every year (2013-2019) in major soybean growing areas of Uttarakhand for estimating the disease severity and dynamics of the disease spread. The epidemiological factors that lead to development of the disease have been elucidated and models for disease and crop loss assessment have been developed. Weather conditions during September and October were most favourable for the disease development. Maximum progression was observed from pod initiation to full pod stage. PDI in all varieties exhibited negative correlation with temperature and humidity and a positive correlation with rainfall and sunshine during all the years of study. The varietal response of soybean genotypes to RAB has been documented and SSR markers for marker assisted selection of resistant genotypes have been identified. Eighteen genotypes of soybean showed resistance response against RAB both in the markers analysis. Eleven out of the twelve markers showed clear polymorphism for the genotypes under study. The SSR markers Satt 119, Sat_076, Satt 433, Satt 281, Satt277, Satt245 and Satt 520 were able to differentiate clearly between the resistant and susceptible genotypes and will be useful in the screening of resistant genotypes against RAB. For the effective management of RAB under field conditions, effective new generation fungicides having low residue level on the produce have been identified. In the field experiments, two sprays of pyraclostrobin, fluopyram and pencycuron significantly reduced the disease with 53.35, 48.72 and 49.47 per cent reduction in disease and 43.56, 43.12 and 42.87 per cent increase in soybean seed yield. These fungicides were also found to have positive effect on the nutritional parameters of soybean. Moreover, molecules capable of inducing resistance in the host have also been investigated. Elicitor compounds including chemicals, hormones and bioagents increased the content of defence compounds such as H2O2, APX, POD, PPO, SOD and PAL while the endogenous enzyme concentration decreased post pathogen inoculation. The future thrusts and follow up research efforts may aim to study the effect of weather changes and need based chemicals on plant disease control under field conditions. This will provide an opportunity for eco-friendly disease management in soybean.

I (S 06) 05: Development of decision support system (DSS) for forecasting of gray mold disease of castor using Internet of Things (IOTs)

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Castor (*Ricinus communis* L.) is an important non-edible oilseed crop with immense industrial and medicinal value. India is the world's largest producer of castor meeting most of the global demand for castor oil. Gray mold caused by *Botryotinia ricini* is one of the most destructive diseases of castor in Telangana state of India. The occurrence of gray mold is strongly governed by weather conditions. Intensive research efforts lead to establishment of biophysical relationship between the weather parameters and disease incidence so that they could be used for developing weather based disease prediction models and decision support system. Unless we closely monitor the climate and progress of gray mold which can cause devastation in short time under favorable weather it is tough to provide precise advisories to farmers for its management. Fortunately, Internet of things (IOTs) made it possible to observe the changes happening in the castor crop in time and space. IoTs is the network of devices that contain electronic, software, sensors and the internet connectivity etc. The devises are embedded with technology so that they can communicate and interact over the internet, and they can be remotely monitored and controlled. Thus, to collect weather data remotely, Wireless Sensor Networks (WSN) were deployed in farmer's field in Mahabubnagar dt., Telangana State. Data on temperature, relative humidity (RH) and capsule wetness hours in half an hourly intervals were recorded by WSNs and the data received at central server at IIOR through GPRS system enabled Gateways. The disease severity was recorded at 24-hour interval manually. Minimum temperature of 21°C, maximum temperature of 28°C, a mean RH of 94 per cent and 14 h of continuous wetness for a period of 4-5 days favoured disease development. Based on the data acquired from WSN a weather indices based model was developed using temperature, relative humidity, wetness hours and their interactions on disease severity ($Y=-1034.63+ 37.97Z_{\text{temperature}} +3.58 Z_{\text{RH}} +224.03 Z_{\text{wetness hours}} -8.392Z_{\text{temperature*wetness hours}}$). The model is tested and further improved during 2018-19 incorporating the date of sowing, spike initiation, number of rainy days and continuous wetness as decision rules. Further, model validation in farmer's fields has been taken up during *kharif* 2019-20 and advisories were sent to 4000 castor growers through SMS and voice alerts in advance to take up disease management interventions. It is observed that timely advisories helped the farmers to protect the crop and minimise the losses. On farm demonstrations were also conducted to showcase effectiveness of prophylactic spray of fungicide propiconazole in management of gray mold.

Oral Papers

O (S 06) 06: Understanding the virus-vector epidemiology using rapid diagnostic assays for thrips vectors

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Thrips transmit tospoviruses in a persistent propagative manner. To date, sixteen thrips species have been reported to transmit twenty-nine tospoviruses infecting over eight hundred plant species. Their identification at an early stage is crucial to understand the disease epidemiology and formulating appropriate pest management strategies. Since morphometric key-based thrips identification of adult thrips vectors is time-consuming, there is a need to develop diagnostic tools that are rapid, accurate, and independent of developmental stages. Here, we report a multiplex PCR assay to identify four major thrips vectors *viz*. *Thrips palmi, T. tabaci, Scirtothrips dorsalis,* and *Frankliniella schultzei present* in India. Further, a rapid identification assay for *T. palmi* has been standardized based on recombinase polymerase amplification. These assays were used to understand the occurrence of thrips and tospoviruses in different crops. *T. palmi* was predominated thrips vector infesting groundnut, soybean, and mungbean and could transmit groundnut bud necrosis virus (GBNV) in these crops. In addition, the occurrence of *S. dorsalis* was also recorded that might spread both GBNV and peanut yellow spot virus (PYSV) in groundnut, soybean, and mungbean. *S. dorsalis* was predominant on chilli throughout the season transmitting both GBNV and capsicum chlorosis virus (CaCV). Only *T. tabaci* was identified on onion plants transmitting Irish yellow spot virus. We did not observe any incidence of *T. palmi* on tomato. However, the incidence of *F. schultzei* was recorded only during the flowering season that might transmit GBNV and CaCV in tomato.

O (S 06) 07: Effect of different dates of sowing, weather factors on Alternaria blight of mustard under rainfed condition of Jharkhand

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Mustard (*Brassica juncea* (Linn.) Czern. and Coss.) is an important oilseed crop, grown both in tropical and sub tropical regions of the world. Mustard is grown an area of about 5.97 m. ha, production of 8.43 m. tons and productivity of 1410 Kg/ha in India during 2017-18. Whereas, in Jharkhand, The area is 3.05 L.ha, production and productivity are, 2.18 L.ton and 715kg/ha, respectively. The Production and productivity of Eastern India particularly Jharkhand state is very low as compare to India (WWW.drmrrs.in). Diseases are important limiting factors, which restrict the fast expansion of cultivation and abade the productivity of the mustard. More than 30 diseases like *Alternaria* blight, downy mildew, powdery mildew, *Sclerotinia* stem rot and white rust etc. which causes heavy yield loss in Brassica crops in India (Kolte *et al.,* 1987; Saharan, 1992). Among them *Alternaria* blight caused by *Alternaria brassicae* (Berk) Sacc. is most destructive disease in India, particularly in Jharkhand State. Hence an attempt was made to study the effect of different dates of sowing, role of various weather factors on infection and development of the disease at Darisai Research Farm of Birsa Agricultural University, Ranchi during *Rabi* season, 2015-16, 2016-17 and 2017-18. Early sowing of mustard suffers less infection of Alternaria blight disease in comparison to late sown crop. Crop sown on 16 October recorded lowest disease intensity of 15.6% and highest grain yield of 7.48 q/ha. This treatment was followed by crop sown on 30 October which recorded disease intensity of 17.4% and grain yield of 7.32 q/ha. Maximum temperature, Minimum temperature, Average temperature showed significantly negative correlation with disease intensity during 2015-16, 2016-17 and 2017-18. Whereas, relative humidity showed negative correlation with disease intensity during above three years total evaporation showed negative correlation with disease intensity during 2015-16, 2016-17 and positive correlation with disease intensity during 2017-2018.

O (S 06) 08: Epidemiology and integrated disease management module for post flowering stalk rot of maize

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Post flowering stalk rot (PFSR) of maize caused by *Fusarium verticillioides* is rapidly gaining economic importance in India and has potential to inflict economic loss up to 100 %. The disease, poses challenge to maize growers due to its soil borne nature and lack of resistant cultivars. Therefore, attempts were made to identify epidemiological factors and promising management components to develop effective IDM strategy. Eight different stages of maize plants of 25, 35, 45, 55, 65, 75, 85 and 95 days were evaluated under artificial inoculations. Results showed that PFSR incidence was maximum when plant was 55-65 days old, which coincides with tasselling and silking stage. Significantly maximum disease severity at 10 days interval from 5th May to 25th August was noticed in crop wsown on 5th July and crop sown on 25th August showed less severity. The observations on meteorological factors in relation to PFSR development revealed that minimum temperature (24.4-25.8 C), maximum temperature (33.3-35.8 C), RH (44.5-54.5%) and rainfall (4.0-6.0 mm) were most favorable for the development of PFSR. Application of an additional irrigation (level- II), at tasselling and silking stages reduced the disease from 60.37 to 15.03 per cent. Maximum lodging (47.68%) was noticed at irrigation level- I while, minimum at level- II with 11.14%. All the three irrigation levels differed significantly with each other and least disease rating (3.2) was observed at irrigation level- II, whereas, maximum disease rating (7.3) was recorded with irrigation level III. Low inoculum density of pathogen i.e. 7.1 $\times 10^4$/g soil at irrigation level II was observed whereas, irrigation level-III showed 15.9 $\times 10^4$/g soil which was significantly superior to irrigation level-I i.e.11.4 $\times 10^4$/g soil. Grain yield recorded in irrigation level-I was 1.12 kg/10 plants, whereas, irrigation level-II and level-III at 1.45 and 0.93 kg/10 plants, respectively were recorded. Biochemical parameters viz. total phenol content, total soluble sugar, polyphenol oxidase and Peroxidases were assayed between infected and uninfected samples in different maturity groups. A negative correlation could be deduced for these parameters in the highly resistant and resistant germplasm lines. Systemic fungicides bavistin (100%), *Trichoderma viride* (46.77%) and 0.2% neem seed extract (76.4%). were found most effective in inhibiting the mycelial growth of *F. verticillioides* in vitro whereas under field conditions, combination of bavistin+ *T. viride* as seed treatment with susceptible cultivar Surya revealed maximum increase in seed germination (89.4%), population density of *T. viride* (23.5 x 10^4/g soil), reduction in disease severity (83.8% efficacy of disease control) and mortality at 70 DAS (3.9), average disease rating (1.0) and population density of *F. verticillioides* (3.3 x 10^4/g soil). The seed treatment with moderately resistant variety (Pratap Makka 3) + bavistin +*T. viride* showed superior results on plant vigour and yield component of maize. Thus with the help of these strategies we can reduce the losses caused due to PFSR and can grow maize successfully.

O (S 06) 09: Predisposing factors for charcoal rot disease caused by *Macrophomina phaseolina* in spring sown maize

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Five different stages (55, 65, 75, 85 and 95 days old plants) of three maize hybrids *viz.* PMH 10, DKC 9108 and PMH 2 were evaluated for determination of most susceptible growth stage against charcoal rot during spring season. The data revealed that 75 days old plant was the most susceptible growth stage for charcoal rot. At this particular stage, mean disease severity (60.83 %) was maximum, resulting in minimum mean grain yield (55.27 q/ha).This stage also coincides with tasseling and silking stage of the plant. The effect of five different sowing dates on disease severity of charcoal rot of five maize hybrids during spring 2018 and 2019 revealed that crop sown on 20th January suffered minimum disease severity (40.91 and 36.3 %) resulting in maximum grain yield (74.27 and 77.89 q/ha) during spring 2018 and 2019 respectively. The plant height and cob height was found maximum on this date. As sowing date was delayed, severity of charcoal rot increased, thus decreasing grain yield, plant height and cob height. Among meteorological factors, disease severity was found positively correlated with mean temperature (+0.98) and negatively correlated with mean relative humidity (-0.92) and total rainfall (-0.90).The effect of three irrigation schedules (additional irrigation at tasseling and silking stage, local practice and stress at tasseling and silking stage) on the development of charcoal rot showed that application of an additional irrigation at tasseling and silking stage had least mean disease severity (36.28%) compared to other irrigation schedules and resulted in highest mean grain yield (72.61 q/ha). Water stress at tasseling and silking stage of the crop aggravated the disease development. Thus it can be concluded that inoculating the plant at most susceptible stage, delayed sowing and water stress at flowering and tasseling stage predisposes the plant to charcoal rot during spring season in Punjab.

Poster Papers

P (S 06) 01: Quantitative analysis of wheat germplasms in relation to spot blotch resistance

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Wheat (*Triticum aestivum L.*), 215 mha coverage and around 780 million metric tons of production supporting 2.5 billion people in 89 countries. Due to the change of cropping system, cropping intensity, crop management, and climatic change, the spot blotch caused by *Bipolaris sorokiniana* is resulting in great quality losses to wheat in all major wheat growing Eastern parts of India. A set of 52 genotypes received by the University as International Septoria Observation Nursery was evaluated for disease variation and a few parameters were tried to relate with disease intensity as well as productivity in micro plots. Quantitative analysis calls for precise phenotyping of different morphological, physiological and genetic traits along with accurate disease quantification is extremely important for durability of the resistance in a population. Here an attempt was made to correlate the quantitative disease data with non-destructive reflectance based estimate of the crop health, such as use of infra-red thermometer for canopy temperature, SPAD for chlorophyll fluorescence and green seeker for vegetative index. A significant variation was observed in the germplasm for spot blotch disease. The genotypes was divided into 3 major cluster resistant, moderately resistant, susceptible genotypes. Physiological fitness of the crop was measured by NDVI at different stages were used separately. Correlation

studies with the data indicated that plant height, NDVI value at heading, flowering and milking growth stages of wheat are negatively and significantly associated with disease. The, NDVI value at an early stage may be indicative of the disease reaction at a later stage and thus may be utilized to screen large number of genotypes at an early stage. As NDVI showed negative association with disease development, NDVI values and their respective disease severity values were plotted in a scatter plot to find out the best fit line which may be further used estimation of disease by using reflectance data. The best fitting line had correlation coefficient of -0.78 indicating that NDVI can be of use to estimate disease up to a significant extent. Multiple correlation studies indicated that variation in plot yield is associated with variation in NDVI values at milking and dough stage of growth.

P (S 06) 02: Roving survey for the incidence *Cucumber mosaic virus* in cucumber (*Cucumis sativus* L.) in Bagalkot district

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Cucumber mosaic virus (CMV) is most destructive disease in cucumber. To know the incidence in Bagalkot district. Roving survey was conducted during 2018-19 revealed that, disease incidence ranged from 13.33 to 66.66 per cent in six taluks of Bagalkot district. The highest incidence observed in Badami taluk (49.58%) and lowest in Jamkhandi taluk (29.50%). Different symptoms of CMV *viz*., small greenish mosaic patches on young leaves shown, dark green mottling, leaf crinkling, down ward curling of leaves and stunting of plants was observed in field condition.

P (S 06) 03: Occurrence of *Cucumber mosaic virus* in *cucurbita pepo* and *Rumex hastatus* from Himachal Pradesh, India

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Cucumber mosaic virus (CMV) is currently ascribed to the family *Bromoviridae* and genus *Cucumovirus*. Since its first report in 1916 from USA, its occurrence has been recorded from different ecological locations throughout the world, infecting more than 1200 plant species including 18 weed species. In this study, the CMV isolates originating from squash (*Cucurbita pepo*) and weed (*Rumex hastatus*) hosts from Himachal Pradesh were characterized based on the coat protein (CP) gene. Symptomatic samples of squash and *R. hastatus* exhibiting mottling, chlorotic rings, necrotic rings and mosaic on leaves revealed the association of isometric virions of ~29 nm in leaf-dip electron-microscopy, which were decorated with polyclonal antibodies to CMV. EM positive samples were subjected to PCR amplification of the CP gene (657bp), followed by cloning and sequencing. The CMV-CP gene sequences from squash and *R. hastatus* hosts shared 91-100 and 95-100% nucleotide and amino acid sequence identities respectively with CMV Subgroup-I isolates, whereas 76-78% nucleotide and 81-85% amino acid identities with Subgroup-II isolates. These results confirmed the association of CMV (Subgroup-I isolates) with the symptomatic samples of squash and *R. hastatus* and suggested that the virus is still expanding its host range as well as ecological niche. To the best of our knowledge, this forms the first report of the occurrence of CMV on squash in India and *R. hastatus* (weed host) in the world.

P (S 06) 04: An efficient technique for isolation and inoculation of *Ustilaginoidea virens* causing false smut of rice

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False smut disease of rice was regarded as a minor disease, occurring sporadically in certain regions, but now epidemics of the disease are also being reported. In fact, there is no efficient and reliable technique for isolation of *Ustilaginoidea virens* as well as identification of resistance under artificial inoculation conditions sofar. Isolations were made from smut balls collected from previous seasons (dark black balls) and the current season (yellow, green, black and dark black balls) on Potato Dextrose Agar (PDA), Rice Yeast Dextrose Agar (RYDA), Yeast Peptone Potato Dextrose Agar (YPPDA), XBZ Agar and PS liquid. Fungal growth developed from all the balls, except the dark black, irrespective of season. However, pure culture of the pathogen only on slants was obtained only from yellow smut balls collected from the current season. Maximum vegetative growth and sporulation of pathogen was recorded on RYDA followed by YPPDA, XBZ, and PS liquid media. The growth on PDA was very poor or negligible. The pure culture was slow growing and was yellow to greenish in color. Pathogenicity test (Koch's postulate) was done successfully and the symptoms appeared after 15 days of inoculation. Artificial inoculation technique for false smut of rice was studied under poly-house conditions. Highly susceptible genotype RH-10 grown in poly-house was inoculated at boot leaf and 50% flowering stages by smut spore suspension prepared from previous and current season's rice smut balls. At booting stage, the spore suspension was injected into boot leaf enclosing the young panicle during the evening hours, while at 50% flowering stage, the spore suspension was sprayed when the spikelets were open (9.30 AM-11.30AM). Panicles inoculated at flowering stage were either covered with moist polyethylene for 48 hours or left open. Appropriate checks were maintained. Inoculation with chlamydospores collected from the smut ball developed in the current season produced one smut sorus on a panicle inoculated in boot leaf and also a sorus on an uncovered panicle inoculated at 50% flowering stage. When the plants were inoculated by pure culture suspension, the smut incidence was increased significantly. Maximum smut incidence (9 smut balls/panicle and 24 balls/hill) was obtained by injecting pure culture suspension in boot leaf followed by incubation at low temperature and then maintaining it under high (>90% during night hrs) humid condition in poly-house at 24-28°C up to 20-25 days.

P (S 06) 05: Epidemiology, variability and management of purple blotch of onion caused by *Alternaria porri*

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Onion (*Allium cepa* L.) literally called to be queen of kitchen is an important commercial vegetable crop grown throughout the world for domestic as well as export purpose. The crop suffers from various biotic and abiotic stresses. Among the biotic factors hindering the production purple blotch caused by *Alternaria porri* (Ellis) Cifferi is a major threat causing huge crop loss under field conditions. Intensive roving survey conducted in ten major onion growing districts of Karnataka revealed that, the mean maximum severity in Gadag (55.91 %)

followed by Chitradurga district (52.29 %) during *kharif* 2017-18 and 2018-19. Thirty different *Alternaria* isolates showed variability with respect to cultural, morphological and pathogenic traits. For the molecular confirmation full length ITS rDNA region was amplified using ITS1 and ITS 4 primers for the isolates of *Alternaria* spp. The DNA amplicon was observed at the region 580 bp. Based on rDNA sequence comparison, the isolates were confirmed as *A. porri* and *A. alternata* respectively. Out of 30 isolates only fast growing ten isolates were sequenced and were deposited in the Genbank for which the accession numbers were obtained. Variability of twenty four *A. porri* and six *A. alternata* isolates were studied by using ten Inter Specific Sequence repeats (ISSR) primers *viz*., ISSR-1 to 10. All the thirty isolates showed polymorphic and distinguishable banding pattern. Epidemiological studies revealed positive correlation of purple blotch with maximum temperature and rainfall. Real time and lead time equations computed at weekly intervals, showed the increase in the severity of the disease at third date of sowing in *kharif* during both the seasons. Study on estimation of rhizosphere colonization using organics as food base revealed that the treatment amended with farm yard manure had the highest number of colony forming units (cfu's) with a comparatively high vigour index of seedlings. The antagonist isolated during rhizosphere population estimation at 40 and 80 days after sowing were identified as *T. harzianum*, *B. subtilis* and *P. fluorescens* by various morphological and biochemical tests. In the study on *in vitro* efficacy showed bio agents, *T. viride* and *P. fluorescens* commercial botanicals perfekt, plant extracts *E. globules* and *A. sativum* and fungicides *viz*., mancozeb, difenconazole, hexaconazole and propiconazole (tebuconazole 50 % + trifloxystrobin 25 %), (hexaconazole 4 % + zineb 68 %), (fluopyram 17.7 % + tebuconazole 17.7 %) and (carboxin 37.5 % + thiram 37.5 %) to be significantly superior in inhibiting the mycelial growth of *A. porri.* Management trials during both the years revealed seed treatment with *T. harzianum* @ 10 g/kg, furrow application of enriched *T. harzianum* (*T. harzianum* 1 kg + vermicompost 100 kg) @ 250 kg/ha followed by spray of (tebuconazole 50 % + trifloxystrobin 25 %) @ 0.5 g/l was proved to be significantly superior in terms of reduction in the disease and increasing in the bulb yield.

P (S 06) 06: Epidemiological studies and molecular characterization of Phytoplasma associated with sugarcane

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A survey conducted during 2017-2019 in Meerut, Muzaffarnagar, Saharanpur and Shahjahanpur districts of Uttar Pradesh, India revealed the presence of Sugarcane grassy shoot (SCGS). Symptomatic as well as asymptomatic sugarcane plants were examined for phytoplasmal infections by polymerase chain reaction (PCR), using primers directed to phytoplasma ribosomal DNA (rDNA) sequences. The phytoplasma presence was confirmed in 61 out of 107 sugarcane plants by highly sensitive nested-PCR assays using universal phytoplasma primers. The phylogenetic relationship of SCGS phytoplasma strains was determined with other closely related phytoplasmas, at both 16S rRNA gene and 16S/23S rDNA spacer region sequence. The SCGS phytoplasmas is in the study was found to be associated with phytoplasma 16SrXI group and closely related to the sugarcane with leaf (SCWL) agent. Subgroup based classification demonstrated that sequences with accession numbers: Meerut- MN124377, MN124378, MN124368; Muzaffarnagar- MN136044, MN136051, MN124371 and Shahjahanpur-MN124369 belongs to 16Sr XI B subgroup. SCGS sequences with accession no. MN136048, MN124369 from Shahjahanpur and MN124372 from Muzaffarnagar represent to be a member of 16Sr X-C sub group. Whereas, SCGS sequences with accession numbers MN136049 from Meerut was found to be associated with 16Sr XI-F subgroup. This is the first report of 16Sr XI-F subgroup phytoplasma on sugarcane from Meerut district of western Uttar Pradesh, India. It was demonstrated that distantly related phytoplasmas to the SCGS agent, are sorghum grassy shoot (SGS), Bermuda grass white leaf (BGWL) ('*Candidatus* Phytoplasma cynodontis') and RYD ('*Candidatus* Phytoplasma oryzae') phytoplasmas. The results of the study indicate the importance and wide spread of this disease in the state and its impact with severe losses on yield and quality parameters of the sugarcane.

P (S 06) 07: Studies on influence of weather parameters on progression of soybean aerial blight

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Rhizoctonia aerial blight is one of the most destructive diseases of soybean contributing to huge yield losses every year. Weather factors viz., temperature, relative humidity, rainfall, wind velocity and sunshine hours play an important role in determining the severity of the disease. To study the effect of weather parameters on the progression of aerial blight, an experiment was conducted at Soybean Pathology block, Norman E. Borlaug Crop Research Center, Pantnagar with twenty cultivars of Soybean during two consecutive *Kharif* seasons of the year 2016 and 2017 following randomized block design with three replications. The observations on severity of disease on the foliage were recorded using 0-9 scale. The data of disease severity was correlated with the weather data for maximum and minimum daily temperature, rainfall, relative humidity, daily sunshine hours and wind velocity recorded from meteorological observatory, Crop Research Center, Pantnagar. The observations recorded from the two crop seasons revealed that the period from the month of September to October is the most favorable time for the development of RAB of Soybean. Disease incidence started in second week of September with maximum temperature of 35°C and highest incidence was recorded in third week of October with temperature 33.5°C. The maximum and minimum temperature, rainfall and relative humidity were found to be negatively correlated with the disease development. However, the correlation of wind speed and daily evapo-transpiration with severity index of the disease was found to be significant and negative while the correlation of the disease severity with sunshine hours was found to be positive.

P (S 06) 08: Effect of different date of planting seasons and cultivars of tomato on leaf curl virus disease

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An experiment was conducted at Horticulture Research Scheme (Vegetable) VNMKV, Parbhani during *Rabi,* 2017-18 and Summer 2018-19 to detect the effect of different dates of planting and cultivars of tomato on leaf curl virus disease. The effect of planting dates / seasons and tomato varieties on tomato leaf curl virus disease indicated that the crop grown during summer season suffered most severely which consequently caused drastic reduction in whitefly population, disease incidence and fruit yield than that of crop grown during *Rabi*. During summer season, of the three planting dates, the crop planted on 17/01/2018 (D1) was found to escape with comparatively least average whitefly population and leaf curl disease incidence as well as significantly highest fruit yield of 152.0 q/ha was noted in Arka Rakshak and 91.8 q/ha in Pusa Ruby. During *Rabi* season, of the three plating dates, the crop planted on 17/10/2017 (D1) was found to escape significantly least average whitefly population and leaf curl disease incidence as well as significantly highest fruit yield of 182.0 q/ha was observed in Arka Rakashak and 163.0 q/ha in Pusa Ruby. A strong positive correlation was obtained between vector population dynamics and disease incidence in tomato plants.

P (S 06) 09: Management of *Tomato leaf curl virus* by insect vector (whitefly) control with various pest management components

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The field experiment was conducted at Horticulture Research Scheme (Vegetable) VNMKV, Parbhani during *Rabi,* 2017-18 and Summer 2018-19 to find out the effect of different insecticides *viz.,*imidacloprid, thiomethoxam, azadirachtin, chlorantraniliprole and pyriproxyfen for management of whitefly (vector of tomato leaf curl virus). The results showed that treatment T1 (Imidacloprid seed treatment + spraying of Imidacloprid at 15 days interval from 30 days after emergence of crop) recorded lowest whitefly population i.e 3.23 whitefly / leaf in *Rabi* season, whereas it was 5.15 whitefly/leaf in Summer season. The disease incidence was also found less in this treatment i.e. 14.28 per cent and 23.81 per cent in Rabi and Summer season, respectively. The highest fruit yield during *Rabi* season (347.83 q/ha) with best ICBR (1:15.48) was observed in treatment T1, while during Summer season the fruit yield in this treatment was 306.13 q/ha with best ICBR of 1:22.80.

P (S 06) 10: Survey on prevalence and severity of anthracnose of soybean (*Colletotrichum truncatum*) in Uttarakhand

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Soybean (*Glycine max* (L.) Merill) is one of the most important oilseed crop. Due to its short duration, drought resistance, high yielding ability and nutritive value, this crop gaining importance in last few years. It is the world's foremost provider of protein and oil. Anthracnose/pod blight caused by *Colletotrichum truncatum* is one of the most important and destructive fungal disease of soybean. The crop soybean is susceptible to *C. truncatum* at all stages of development particularly from bloom to pod fill. To assess the prevalence and severity of anthracnose diseases of soybean in Uttarakhand, a 2-year survey was conducted (September 2018 to 2019). Districts of Garhwal region: Chamoli, Rudraprayag, Dehradun, Haridwar, Pauri garhwal, tehri garhwal and districts of Kumaun region: Udham Singh Nagar, Nanital, Almora, Bageshwar, Champawat and Pithoragarh were surveyed for incidence and intensity of Anthracnose of Soybean. The survey was carried out at Pod formation and Pod filling stages. Soybean crop was distributed in almost all districts but majorly in Kumaun region and the disease was prevelent predominantly in kumaun hills. The anthracnose severity was recorded in 0 to 9 scale. The maximum and minimum per cent disease incidence and severity was recorded in the Pithoragarh district (Hilly region) and Dehradun district (Foot hill region), respectively. During Kharif 2018, average disease incidence and per cent disease index in the twelve districts surveyed were ranged from 13.02 (Dehradun) to 63.14 (Pithoragarh) per cent and 8.44 (Dehradun) to 44.42 (Pithoragarh) per cent respectively and during Kharif 2019, average disease incidence and per cent disease index were ranged from 10.6 (Dehradun) to 59.53 (Pithoragarh) per cent and 9.1 (Dehradun) to 44.15 (Pithoragarh) per cent respectively. The huge difference in the range of altitude and climatic conditions of different districts, even in different areas of a same district, changes the disease occurrence and disease pressure.

P (S 06) 11: Tristeza and Huanglongbing: The major biological agents causing citrus decline in Northeast India

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Tristeza and Citrus greening (Huanglongbing/HLB) are the most economically important diseases associated with citrus decline in India. The tristeza is caused by *Citrus tristeza virus* (CTV), a *Toxoptera citricidus* transmitted, +ve sense ssRNA virus, whereas the citrus greening is induced by *Candidatus* Liberibacter (*Ca.* L), a *Diaphorina citri* transmitted, non-culturable alpha-proteobacteria. A survey was conducted in three citrus farms of Assam; Horticulture Research Station (HRS), Assam Agricultural University (AAU), Kahi Kuchi, Guwahati; Center of Excellence for Citrus (CEC) farm, Kamrup Rural district, and Research farm, AAU, Jorhat. Seventy citrus samples were collected from seven different citrus cultivars belonging to four species; *Citrus reticulata* cultivars Khasi, Kinnow and Nagpur mandarin; *C. sinensis* cultivars Sweet and Valencia orange; *C. limon* cultivar Assam lemon; *C. jambhiri* cultivar Rough lemon. The samples were brought to laboratory to detect CTV and *Ca.* L asiaticus (*Ca*. Las). The diagnosis results of DAC-ELISA of CTV, and PCR targeting the 5'ORF1a gene fragments (404nt) of CTV and short sequence region (452nt) of 16srRNA of *Ca.* Las showed that 46 samples are infected by CTV and 32 samples by *Ca*. Las. All the cultivars tested found to be infected by CTV and *Ca*. Las. Mixed infection of CTV and *Ca*. Las was observed in all the citrus cultivars. The PCR amplicons obtained from different cultivars in this study were sequenced, nucleotide sequences were analysed and phylogenetic relationships were made. The present CTV isolates shared 91-100% nt identities among them, and majorities of the sequences fell into the decline inducing/severe CTV isolate group Kpg3/VT. The HLB isolates showed 99-100% nt identities among them and they fell into the same clade with the other *Ca*. Las isolates of India. The present study showed that CTV and *Ca*. Las are prevalent in Assam and they are major causes for citrus decline in Assam leading a threat to the citrus industry in Northeast India.

P (S 06) 12: Effect of environmental factors on Alternaria leaf blight and leaf spot disease severity of makhana (*Euryale ferox*) in Koshi region of Bihar

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Makhana *(Euryale ferox* Salisb) is an imperative shallow annual aquatic crop, belonging to family Nympheaceae. It is commonly known as 'fox nut' or 'gorgon nut' that grow in stagnant perennial water bodies generally around 1.5 m deep, occurring within a wetland ecosystem. Its cultivation is limited to tropical and sub-tropical regions of South East and East Asia. Bihar, Assam, West Bengal and Odisha are some of the states in India where it is grown commercially as a high value commodity. It is cultivated in an area of about 20,000 ha and Bihar contributes 80 % acreage and more than 90 % production. Congenial environmental factor plays an important role on the growth, multiplication, dissemination and infection of pathogen. It also influences the expression of susceptibility/resistance of the host plant after infection. Therefore, an experiment was conducted during two consecutive cropping seasons i.e. 2018 and 2019 to study the influence of weather parameters such as temperature, humidity, rainfall and wind direction on the development of the major diseases of makhana in *Koshi region* of Bihar. Percent disease severity of alternaria leaf blight and leaf spot were observed during the month of April, which was continued up to the harvesting stage. Highest per cent severity of both diseases was observed during the month of June-July. High temperature (31°C) and relative humidity (>85%) was found correlated with higher severity of alternaria leaf blight and leaf spot disease. Effect of rainfall on the incidence of disease was also studied and congenial conditions were manifested. On the basis of congenial mean temperature, mean relative humidity and average rainfall a geopahytopathological model for the prediction of alternaria leaf blight and spot disease has been developed.

P (S 06) 13: Alternate host of Phytoplasma diseases

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Weeds which may act as natural alternative hosts facilitating the spread of phytoplasmas to other economically important plants and thereby increasing economic losses at alarming rate. Symptoms observed on weeds include yellowing ,extensive chlorosis, proliferation of axillary shoots, witches'-broom and little leaves. Till now more than 70 weed species were reported having phytoplasma infections from all over the world important associated families are Amaranthaceae, Asclepiadaceae, Asteraceae, Verbenaceae , Poaceae, Cannabinaceae , Fabaceae , Labiatae and Euphorbiaceae. Nucleotide sequence studies have shown that weed-infecting phytoplasmas mainly belongs to 16SrI, 16SrIV, 16SrVIII, 16SrXI and 16SrXIV groups. Among them, 16SrI and 16SrXIV phytoplasmas have a more wide occurrence in nature all over the world. The weeds identified as phytoplasma hosts often grow abundantly around field crops, the possibilities of transmission of phytoplasmas related to important agricultural, economical and horticultural crops from weed to the mentioned crops and vice-versa can not be ignored. This could be because phytoplasmas are able to survive in many potential economical crops or because an insect vector is capable of transmitting phytoplasmas from other weeds to crops which are already known as phytoplasma hosts. In either case, the chance of transmission in the future seems high, given the large phytoplasma reservoir already revealed, the propensity of new phytoplasma strains to evolve. Knowledge of the diversity of phytoplasmas will be expanded by recent studies and the availability of molecular tools for pathogen identification. On that basis we are able to study the epidemiology of phytoplasma diseases as now a days phytoplasma diseases are increasing at alarming rate in nature.

P (S 06) 14: Impact of climate change on plant diseases

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Climate change is one of the many ways in which the environment can move in the long term from disease-suppressive to disease-conducive or vice versa. So, plant diseases can be even used as indicators of climate change. Climate affects all life stages of the pathogen and host and clearly poses a challenge to many pathosystems which affects the survival, vigor, rate of multiplication, sporulation, direction and distance of dispersal of inoculum, rate of spore germination and penetration of pathogens. Major climatic changes over the past 50 years are primarily caused by various human activities. Climate change has become a burning issue in the present century by changing the properties of atmosphere like rainfall, humidity, temperature etc.

Also greenhouse gases have a major share in the climate change. Climate change has also led to some of the severe epidemics in all over the world. Climate changes are in response to changes in the hydrosphere, biosphere and other atmospheric and interacting factors. It has not only increased the biotic stresses of plants, but also increased the cost of their management. Climate change has both positive and negative effect on crop diseases. So, there is an urgent need of an hour to integrate all the mitigating strategies to tackle this global problem by new innovation in pest management and commitment in anticipatory research against emerging pathogens through multidisciplinary techniques may be better strategies under climate change.

P (S 06) 15: Leaf blast of rice caused by *Pyricularia grisea*-an appraisal

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Rice leaf blast, caused by the fungus *Pyricularia grisea* is one of the most important rice diseases found throughout the globe. The disease started appearing after seedling transplanting and epidemiological studies were performed till harvesting. It usually damages leaves and panicles and reduces the photosynthetic area of the plant and may even lead to the death of the plant. It was observed that temperature, relative humidity and rainfall were responsible factors for the appearance and progress of this disease. The leaf blast intensity initiated during the month of September and gradually increased and progressed up to harvesting stage during the month of October continuously. The leaf blast was more prominent and progressive during first fortnight of October when maximum temperature, range temperature and relative humidity were increased. Rice is subjected to many fungal diseases but leaf blast is one most destructive one.

P (S 06) 16: Occurrence and distribution of chickpea diseases in Bundelkhand region of Uttar Pradesh

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Periodically survey was conducted was conducted during *Rabi* 2017-2018 to obtain information on the distribution and incidence of chickpea diseases in respect to cultivar used, seed treatment in Bundelkhand region (comprises 7 districts namely Banda, Chitrakoot, Hamirpur, Jalaun, Jhansi, Lalitpur and Mahoba) of Uttar Pradesh (India). Old varieties are predominated in most farmers' fields (35% - 55%) and 25% of the farmers were practices seed treatment with fungicide. Collar rot and dry root rot diseases were found at all of the sites and incidence ranged from 6.8% - 15.50% and 8.2% - 12.50% respectively irrespective of cultivar type and locations. Incidence of wilt and Sclerotinia stem rot disease ranged from 8.2% - 12.5% and 3.5% - 6.5% respectively. Among the chickpea diseases collar rot and dry root rot is highly distributed in all seven districts of the region. Therefore, possible management strategies are needed to devise to alleviate the problem.

P (S 06) 17: Forewarning of cotton disease complex in North Karnataka

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Cotton is one of the important cash crops in India. However, the crop is affected by multitude of diseases, like grey mildew, alternaria blight, bacterial blight, rust etc. In view of this the farmers face great loss in cotton yield as well as its quality. In order that this loss is reduced, it is necessary to forewarn the incidence of diseases in advance, so that the farmers can take precautionary measures to prevent disease enhancement rather than wait for curing the diseases. As most crop diseases are weather induced, it is possible to forecast the diseases in advance and thereby forewarn the farmers not only on disease incidence but also on necessary advice in a timely manner so that the farmers get ready to face the adverse eventualities. Field experiments were conducted over 5 years on different cotton varieties, namely, Dr.Brent, DCH32, Jayadhar and Abhadita. Observations on incidence of diseases, namely, grey mildew, alternaria blight and bacterial blight were collected on weekly basis. Disease progress curves were constructed, and correlation analysis was performed to identify meteorological variables that affect the diseases in initial, progress and peak periods of respective diseases. Specific weather situations were identified for individual diseases. Limits of temperature and humidity conditions, namely, maximum temperature, minimum temperature, morning relative humidity and afternoon relative humidity for disease levels of 20% and 30% in August, 30% and 40% in September and 40% and 50 % in October were identified. The sensitivity of individual varieties to different weather variables was also evaluated. Results showed that morning relative humidity at all lead weeks (0 to 3) is important in influencing the Alternaria blight, Bacterial blight and Grey mildew disease incidence on varieties. Afternoon relative humidity at all lead weeks is important in influencing Grey mildew disease. Lead weeks 1 and 2 it influences Bacterial blight disease and Lead weeks 0, 1, and 2 influences grey mildew disease on variety Jayadhar. Afternoon relative humidity at lead week 0, 2 and 3 influences Bacterial Blight disease and at all lead weeks it influences grey mildew disease on variety DCH-32. At LW0 it influences Alternaria blight disease and at lead week 1, 2, and 3 it influences grey mildew disease on variety Jayadhar. The differences in response of individual cotton genotypes to the three diseases in different periods of crop disease growth are discussed in detail. Multiple regression analysis was performed and disease forewarning models were developed. An excel template is also made to progressively monitor the estimation of diseases on daily basis, which will help in timely management advice to the farmers.

Session 7
Plant health management vis-à-vis human health

Keynote Papers

KN (S 07) 01: Tackling maize lethal necrosis (MLN), a complex disease in Eastern Africa

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Maize (*Zea mays* L.) is the most important cereal crop in sub-Saharan Africa (SSA), covering over 35 million ha, largely in smallholder farming systems that produce over 70 million metric tons (MMT) of grain. Maize Lethal Necrosis (MLN) disease first appeared in Kenya in 2011, and became a major threat to maize production in eastern Africa in subsequent years. In eastern Africa, MLN is caused mainly by synergistic interaction between two viruses, Maize Chlorotic Mottle Virus (MCMV) and Sugarcane Mosaic Virus (SCMV). MLN can cause up to 100% yield loss in susceptible maize varieties. The disease poses a complex challenge as the MLN-causing viruses are transmitted by insect vectors, and also through contamination of the seed, especially by MCMV. CIMMYT implemented a multipronged strategy in partnership with several international and national partners to tackle the MLN challenge. These efforts included: a) b) establishing a state-of-the-art MLN Screening Facility in partnership with Kenya Agriculture and Livestock Research Organization (KALRO) in Naivasha for identifying sources of resistance to MLN, MCMV and SCMV under artificial inoculation; b) accelerated breeding and deployment of MLN-tolerant/resistant maize varieties with other relevant traits preferred by African smallholders; c) optimizing MLN diagnostic protocols; c) strengthening capacities of national plant protection organizations (NPPOs) across sub-Saharan Africa on MLN diagnostics, monitoring and surveillance system; d) creating awareness among the maize seed sector institutions on SOPs for producing and exchanging MLN-free commercial seed; e) disseminating information on farming practices for minimizing MLN incidence; e) establishing an MLN Phystosanitary Community of Practice involving various stakeholders, including national plant protection organizations (NPPOs), seed companies, regional/sub-regional organizations, etc.; and f) probing the epidemiology of the disease, especially the factors underlying seed contamination by MCMV. These comprehensive efforts have led not only in preventing the further spread of MLN into other major maize-growing countries in sub-Saharan Africa, especially southern and West Africa, but also minimized the incidence of the disease in the MLN-endemic countries in eastern Africa.

KN (S 07) 02: Sustainable disease control technologies to help feed the world

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Feeding the world as the human population reaches an unprecedented level will present the agricultural community with major challenges. Current estimates indicate that crop production must as much as double. We will need to increase production of nutritionally dense plant crops and decrease the negative impacts of agriculture on land, water, and climate. We must develop new approaches and technologies to employ sustainable production systems and, importantly, to control plant diseases. Thus, there is need to modify current disease control technologies and to develop new environmentally benign technologies. By leveraging advanced bioinformatics techniques, advances in computing infrastructures (e.g., cloud-based, big data-driven application) will aid in the monitoring and management of pesticides and biologicals such as cover crops and beneficial microbes in order to reduce the impact of plant disease control on the environment. Further, improving crop genetics for advanced germplasm with enhanced tolerance to biotic and abiotic stress is the need of the times. Such crop germplasm must be robust in appropriate levels of nutrients for human health and be in tune with different cropping systems and environmental conditions. Finally, the impact of technologies used to control plant disease on crop nutritional quality must be evaluated.

KN (S 07) 03: Integrated disease management in vegetable and fruit crops in Illinois

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More than 60 vegetable and 12 fruit crops are commercially grown in Illinois. Sustainable production of vegetable and fruit crops in Illinois is not possible without using integrated disease management strategies. This presentation will discuss how to successfully use integrated strategies to manage Phytophthora blight of cucurbits, internal root discoloration of horseradish, and summer diseases of apples in Illinois. Phytophthora blight, caused by *Phytophthora capsici*, is one of the most important diseases of cucurbits worldwide. There is no cucurbit cultivar resistant to *P. capsici* and no single method provides adequate control of Phytophthora blight in cucurbits. An integrated strategy was developed that reduces crop losses of cucurbits to *P. capsici* to negligible levels. The strategy includes a four-year crop rotation with nonhost plants, seed treatment with mefenoxam, scouting field and removing early-season infected plants in low areas of the field, and spray-applications of effective fungicides (e.g., oxathiapiprolin, mandipropamid, cyazofamid, ethaboxam, triflumizole) at the first sign of the disease at 7-day intervals. Illinois is the leading state in horseradish production in the United States. Internal discoloration of horseradish roots is a disease complex caused by the soil- and set-borne fungi *Verticillium dahliae*, *V. longisporum*, *Fusarium commune*, *F. oxysporum*, and *F. solani*. The disease occurs worldwide and can cause up to 100% root rot or root discoloration, reducing marketability. An integrated method was developed to manage internal root discoloration of horseradish. The procedure includes hot-water treatment of sets at 47ºC for 20 minutes to eradicate set-borne inoculum and then application of fludioxonil fungicide or *Trichoderma virens* GL-12 (biocontrol SoilGard 12G) onto sets. Set treatments are carried out a few days prior to planting. This integrated management controlled root rot and significantly improved marketing yields of all horseradish cultivars. Commonly occurring summer diseases of apples in Illinois are bitter rot (*Glomerella cingulata*), black rot (*Botryosphaeria obtusa*), white rot (*Botryosphaeria dothidea*), sooty blotch (*Peltaster fructicola*, *Leptodontium eliatus*, and *Geastrumia polystigmatis*), and fly speck (*Zygophiala jamaicensis*). A wetness-based disease-warning-system was developed to manage summer diseases of apples in Illinois. Traditionally, eight sprays (cover sprays), at 14-day intervals, are applied following petal fall to control summer diseases of apples in Illinois. According to our warning-system, the second-cover spray is applied after accumulation of 175 h of wetness of 4 h duration or greater, measured by a sensor placed under the canopy of a tree in the low area of the orchard. The disease-prediction system was tested in 18 orchards throughout Illinois. The system saved from 2 to 7 sprays (average 3.2) – 29 to 100% (average 46%) – on a biweekly spray schedule, saving more than $80 per ha on fungicide costs.

KN (S 07) 04: ACC Deaminase producing plant growth-promoting rhizobacteria for the suppression of abiotic stress in sunflower

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Rhizobacteria inhabiting the soil adhering to the root of the host plants are generally recognized to possess plant growth-promoting properties. In the present study, a total of 120 rhizobacterial isolates from native soil samples of sunflower plants were isolated and screened for their ACC deaminase (ACCd) activity and plant growth-promoting properties against drought and salt stress in Sunflower. The significant ACCd producing rhizobacteria were selected to evaluate their efficacy to promote the plant growth under laboratory and greenhouse conditions. All the significant ACCd positive isolates were found to exhibit at least four different PGP traits and three were found antagonistic to *Fusarium oxysporum* and significantly enhanced both seed and vegetative growth parameters compared to control with a maximum enhancement showed by *Bacillus subtilis*. Based on the findings of the efficacy of ACCd producing PGPR in promoting growth parameters upon seed treatment, further studies are promising to test their ability on the suppression of biotic and abiotic stress. The enzyme 1-aminocyclopropane-1-carboxylate deaminase (ACCd) isolated from bacteria has been spotted in a limited number of bacteria and plays an essential role in supporting plant growth and development under abiotic stress conditions by limiting the production of ethylene in plants. In the present study, ACCd producing PGPR were screened for their plant growth-promoting properties in sunflower upon induction of drought and salt stress. Among the ten isolates, *Bacillus thuringiensis* Rhizo SF 23 and *Bacillus subtilis* Rhizo SF 48 were able to tolerate a maximum PEG 6000 concentration with an IC_{50} value > 10 and *Pseudomonas otitidis* Rhizo SF 7 and *Acinetobacter calcoaceticus* Rhizo SF 9 upon salt stress. The ACCd producing PGPR apart from increasing plant growth-promoting properties in sunflower also enhanced the enzymatic (APX and SOD) and non-enzymatic (proline) antioxidants in sunflower upon drought and salt stress induction compared to respective control. The MDA content decreased in ACCd producing PGPR treated sunflower plants, while proline increased, thereby indicating that ACCd producing PGPR (Rhizo SF 23 and Rhizo SF 48) were effective in protecting the plants against drought stress induction. The study confirms that the ACCd producing PGPR possessed the ability to improve plant growth parameters by inducing antioxidant capacity through detoxification of important ROS molecules upon drought stress induction and support in agricultural production as effective bio-inoculants. The seed treatment with ACCd producing PGPR isolates enhanced the enzymatic (APX and SOD) and non-enzymatic (proline) antioxidants in sunflower upon stress induction compared to respective control. The MDA content decreased in ACCd producing PGPR treated sunflower plants. The antioxidant activities evaluated in the study indicated that the ACCD producing PGPR were able to mitigate the adverse effects of enhanced ethylene level, by utilizing the precursor of ethylene (ACC) produced by the plants and convert them to á-ketobutyrate and ammonia. The results confirmed that the ACCd producing PGPR possesses a dual role in plant growth promotion and withstand drought and high salt stress as observed by the decrease/increase in the levels of proline, APX, and SOD and decrease in the levels of MDA content.

Invited Papers

I (S 07) 05: Bioinoculants: My experience with large scale field demonstration trials

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Trichoderma spp. And rhizosphere inhabiting fluorescent Pseudomands are among the most widely used bioagents in today's agriculture owing to their bio-control and plant growth promoting activity and their ability to produce several hundred secondary metabolites (some are antimicrobial). They maintain soil health by deploying a wide variety of mechanisms, improve nutrient (especially nitrogen) use efficiency that positively impact plant growth, and impart tolerance to abiotic stresses. There is always a scope for isolating better, locally adapted strains for large scale fielddeployment. Major constraints in wider adaptability of these bio-agents by the farmers are un-availability of right kind of formulation, field application technology and inconsistent performance. We report here the isolation two locally adapted strains of *Trichoderma* spp. (94a and T14) with high lingo-cellulosic activity and phytohormone biosynthesis. I share my experience in the deployment of these two strains of *Trichoderma* spp. and a mutant strain of *Trichoderma virens* (developed using gamma-ray-induced mutagenesis, named TrichoBARC) kindly provided by Dr. P K Mukharjee for the large scale field demonstration trials. We also report here the isolation locally adapted strains of fluorescent *Pseudomonas* useful for abiotic stress (drought) management in rice and observed growth promotion, early flowering (7–10 days) and yield improvement in legumes, cereals and vegetables in replicated field trials and demonstration trials on farmer's field.

I (S 07) 06: Management of emerging nematode problems in protected cultivation of vegetables

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The drastic off-season demand of vegetables such as tomato, cucumber, capsicum broccoli, lettuce etc. has greatly increased the need for protected cultivation in recent years. The protective cultivation also offers an effective solution to weed infestation, water conservation and lower crop productivity. However, the nematode infestation in all type of crops under protected conditions has emerged as an alarming disease problem leading to extensive crop losses that may reach up to 80% in certain crops. Besides causing direct damage, nematode infestations may exacerbate the severity of fungal diseases leading to complete crop failures. Root-knot nematodes, *Meloidogyne* spp. are most important nematode pests of horticultural crops and cause 5-43% yield loss throughout the world. The two predominant species, *M. incognita* and *M. javanica*, which attack more than 2000 plant species, including crops grown under protected cultivation and inflict exceedingly high yield loss especially under poly house farming. Other important nematodes that may inflict serious loss in vegetable crops under protected cultivation are reniform nematode (*Rotylenchulus reniformis*), lesion nematode (*Pratylenchus* spp.), foliar nematode (*Aphelenchoides fragariae*), burrowing nematode (*Radopholus similis*) and stem-bulb nematode *Ditylenchus dipsaci*). In India avoidable losses in individual fields in various high value horticultural crops range 10-69% in fruits, 13-99% in vegetables, and 14-70% in ornamentals. In polyhouse, the root-knot nematodes alone, may cause 20-40% average yield losses in tomato and cucumber but in disease complex situation, the losses may increase to 50-70%. Various methods of management of root-knot and other nematodes under protected cultivation such as chemical and biological control techniques are available. In greenhouses or poly houses, chemical treatment with methyl bromide against root-knot nematodes has been found quite effective. Fumigation of polyhouse with methyl bromide treatment once in every two years, besides the use of Metham sodium, Dazomet etc. may effectively control root-knot problem. Other popular and effective nematicides are Oxamyl, Fenamiphos, Cadusafos and Ethoprop which may offer satisfactory nematode control under covered structures. Biological control strategy may work nicely in the protected farming because of easy and effective control over temperature, organic matter and soil moisture which are critical for establishment and multiplication of biocontrol agents. In view of increasing preference for organic foods, the biocontrol strategy may act as a value addition to the produce. The application of biocontrol agents such as *Trichoderma harzianum*, *Aspergillus niger*, *Purpureocillium lilacinum, Pochonia chlamydosporia, Pseudomonas fluorescens* and *Bacillus subtilis* can effectively control root-knot and other nematodes under protected cultivation. To achieve, effective control the biocontrol agents may be used in integration with pesticides.

I (S 07) 07: Hyperparasites in managing plant pathogens: Status and future prospects

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Plant pathogens cause heavy losses especially rust and powdery mildew diseases in North East India are very prominent pathogens inflicting serious losses. We have been trying to explore the diversity of hyperparasites on important plant pathogens in this region. We have already published the reports on the presence of hyperparasites like *Ramularia coleosporii* on *Coleosporium plumeriae*, *Verticillium epiphytum* on *Uromyces mucunae* and *Simplicillium lanosoniveumim* on *Aecidium elaeagni-latifoliae*. *Ramularia coleosporii* on *Coleosporium plumeriae* was identified with the help of scanning electron microscopy and molecular characterization since conidial scar type is a very prominent character used to delimit the genus and it can only be clearly observed using scanning electron microscopy, molecular characterization using ITS was done for species delimitation. Similarly for identification of other hyperparasites scanning electron microscopy and molecular characterization was used. We have also published a report of hyperparasite *Tuberculina* sp. on rust pathogen *Nyssopsora thwaitesii* from northeast India. We have also observed *Sphaerellopsis filum* (telomorph *Eudarluca carices*) on groundnut, pea and pear rust, and *Ampelomyces quisqualis* on many powdery mildew pathogens of economic importance like vegetable and ornamental crops. Scanning electron microscopy as well as molecular tools (ITS based) are being used for further exploration. In literature several fungal hyperparasites have been reported, *Sphaerellopsis filum*, *Fusarium chlamydosporum*, *Tuberculina* sp., *Scytalidium uredinicola*, *Cladosporium* spp. and *V. epiphytum*. Latest evidences in available literature shows that host specificity is present in mycoparasites although earlier they were thought to be non-specific. Latest molecular evidence also indicates presence of several cryptic species within accepted species, which cannot be identified morphologically. So in this regard, it is necessary to characterize the strains/isolates of these mycoparasites with the help of molecular tools. These hyperparasites can be successfully exploited in future for ecofriendly management of plant pathogens.

I (S 07) 08: Paradigm shift in identification and management of red rot of sugarcane

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Sugarcane (*Saccharum officinarum*) is an important cash crop cultivated in tropical and sub- tropical regions of the world. Globally, sugarcane is an important source of commercial sugar accounting for almost two thirds of world sugar production. Sugarcane is cultivated in most of the states of India and is the second most important agro industrial crop in India. It is exposed to various biotic and abiotic factors. Over 100 fungi, 10 bacteria, and 10 viruses and about 50 species of nematodes are pests of sugarcane. Among them, red rot caused by *Colletotrichum falcatum* is the most common disease of sugarcane. It causes severe loss in yield and quality of juice of the susceptible cultivars in the Indian subcontinent. It can reduce cane weight by up to 29% and loss in sugar recovery by 31%. Red rot pathogen hydrolyse the stored sucrose by producing the enzyme invertase which breaks the sucrose molecule into its components namely glucose and fructose which result in increased quantity of molasses. The disease was first reported from Java, Indonesia, where it was known as “Sereh”. The breakdown of resistance of commercial sugarcane varieties is due to the development of new races of *C. falcatum*. The pathogen mainly infects canes through nodes and main portal of entry are leaf scar, growth ring, root primordia and buds. Till now, 11 races have been identified and prevalent in sugarcane growing area. Various serological and molecular techniques have recently employed for different races of *C. falcatum* including ELISA, DIBA, western blotting and polymerase chain reaction using ITS region amplification. These techniques have not only been proved simple, rapid and specific for the laboratory analysis of sugarcane red rot in the early growth stage of the plant but also enabled detection of the pathogen colonization before symptom expression. Hence for the management, IDM strategy is the best possible option in controlling this disease, rather than relying upon a single method. In addition to the existing control measures, novel strategies should be thought of to explore the possibility of inducing systemic resistance. Though limited information is available regarding the true basis of disease resistance, molecular tools are now available to identify suitable markers that can be relied upon for supporting the conventional breeding approaches. The identification of candidate genes for red rot resistance through association mapping (Marker trait analysis) in sugarcane using Simple sequence repeats (SSRs) markers have opened a new avenue for management of this disease. Knowledge about the functions controlled by resistance loci to red rot will allow breeders to construct novel resistant genotypes by association of complementary mechanisms with durable resistance to red rot. In view of the above, these biotechnological approaches should be supplemented with different other control measures like quarantine regulations, clean cultural practices, use of chemicals, biocontol agents and heat therapy.

I (S 07) 09: The American Cranberry: History, current horticultural trends and sustainable disease management strategies

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The American or large-fruited cranberry (*Vaccinium macrocarpon* Ait.) is indigenous to the North American continent. Cranberry is found in the northern portion of the United States from Maine to Wisconsin, and along the Appalachians to North Carolina. Cranberry is introduced to Oregon, Washington, British Columbia, Chile and some countries in Europe. Native Americans did not cultivate cranberries but gathered wild berries and used them as food, poultice for food poisoning and as a dye for clothes. Narragansett tribe called it "sasemineash". The early European settlers called it "craneberry" (as initial flowering stages resembled the neck, head, and bill of a crane) which eventually reduced to cranberry. Domestication is believed to have started in 1816 in southeastern Massachusetts and spread to New Jersey, Wisconsin, Oregon, Washington, Michigan, Maine as well as to several Canadian provinces. Research has linked nutrients and antioxidants in cranberries to a lower risk of urinary track infections, the prevention of certain types of cancers, improved immune function, and decreased blood pressure. In 2018, a total of 16,511 hectares (40,800 acres) of cranberries are cultivated in the US with a production of 391 metric tons. Major importers of American cranberry products are European Union, Great Britain, Australia and Mexico. Unlike many other crops, cranberries thrive in acidic soil conditions with low nitrogen requirements. The major challenges in cranberry production include fungal diseases such as fruit rot, Phytophthora root rot, upright dieback, cottonball; insects such as cranberry fruit worm, cranberry weevil, black headed fire worm, cutworms and scale insects, and weeds such as dodder, sphagnum moss, poverty grass, and poison ivy. Among these, fruit rot is the major limiting factor in cranberry production. In this presentation, the spectrum of unique cultural practices followed for cranberry cultivation, sustainable disease management and harvest in the US will be discussed.

I (S 07) 10: One health one omics: Molecular insights into multi-host resistance in fungal disease

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Impending changes in the global climate coupled with rapidly growing population have resulted in challenges related to food and nutrition. On the other hand, recent years have shown increased frequency of high complexity diseases worldwide. Pathogenic microbes, antimicrobial resistance and diet play pivotal roles in infectious and life style diseases. A number of human health maladies have been associated with diet due to the presence of intrinsically low level of the essential phytonutrients or the presence of anti-nutrients, which are not always at par with the recommended dietary allowance (RDA). Moreover, morbidity and mortality associated with fungal infections and emergence of resistant fungal strains necessitate study of fungal pathogenesis and host innate immunity. *Fusarium oxysporum*, a medically and agronomically important multi-host fungal pathogen is known to be associated with neuronal stress in humans and vascular wilt in plants, while Fusarium-mediated killing of worm has recently been described. Despite significant advances in our understanding of the molecular basis of diseases, gaps remain in terms of disease pathogenesis as well as diagnosis and treatment. One Health One Omics is a holistic approach that integrates multiple biological disciplines, biogeography and organismal diversity linking human and animal health care to plant and environment. I shall review the progress made, identify challenges, opportunities and strategy towards multi-host resistance and discuss our effort towards longitudinal integrative omics profiling that reveal extensive dynamic biomolecular changes and biological pathways that occur during such perturbations. Our study for the first time provides novel insights on host-specific immune signaling that impinge upon the surveillance mechanism of innate immunity in multi-host pathogen response and facilitated discovery of cellular therapeutic targets for Fusarium-associated disease.

I (S 07) 11: Strategic management of Maydis leaf blight and banded leaf and sheath blight of maize

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Maize is the most versatile crop among cereals grown in many countries of the world. It occupies a position of industrial crop globally owing to its utilization in feed, starch and bio-fuel industries. Out of several diseases affecting maize yields, maydis leaf blight (MLB) and banded leaf and sheath blight of maize (BLSB) are the emerging constraints in attaining its potential yield in north western India. Paucity of resistance sources against these diseases led us to identify potential components for the management of these diseases and further development of management strategy for them. Three modules (Organic, Chemical and IDM) consisting of effective components identified over the years were evaluated for their efficacy in the management of MLB and BLSB at Delhi, Karnal, Ludhiana and Pantnagar (BLSB only) centres. In case of MLB, disease control by chemical module ranged from 52.17 to 55.6% followed by IDM (30.43 to 48.9%) and organic modules (13.04 to 35.3%) with significantly higher yield over check. In case of BLSB, disease control by chemical module ranged from 54.55 to 62.37% followed by IDM (51.85 to 68.18%) and organic modules (I and II) (5.56 to 50.01%) with significantly higher yield over check. A cultural practice *viz.;* stripping of 2-3 basal leaves evaluated at 4 locations on different cultivars, recorded BLSB control upto 12.9-55.0% with 8.1-45.3% increase of yield compared to respective checks. Out of 10 bio-extracts/natural products evaluated for management of MLB at Delhi over three years revealed that *Azadiracta indica* (neem extracts) @ 10%, *Allium sativum* (garlic cloves) @10%, *Polyalthia longifolia* (False Ashoka) @10% and *Parthenium hysterophorus* (congress grass) @10% recorded 20.75%, 20.75%, 15.09% and 15.09% of disease control with higher yield over check. Both findings would be useful in organic disease management in maize. Further to boost up disease management in maize, weather based forewarning models for BLSB and MLB have been developed so that stakeholders can take judicious and timely decision for management of these diseases.

I (S 07) 12: Sclerotinia rot: A major constraint of mustard cultivation in India and its management

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Sclerotinia rot caused by *Sclerotinia sclerotiorum* (Lib.) de Bary is a significant agricultural problem of worldwide occurrence. Indian mustard (*Brassica juncea* L. Czern & Coss.) is one of the major oilseed crops cultivated in India. Among the diseases of Indian mustard, *Sclerotinia* rot has become a major yield-reducing factor and results in 40-80 per cent losses in the seed yield. Being a seed and soil borne pathogen with widest host range, it is difficult to manage this disease. The resting stage sclerotia survive in seed as seed contaminant as well as in soil as soil-borne pathogen, which provide primary source of inoculum. *Sclerotinia* infection on above ground parts of the plant is due to the ascosporic inoculum resulting from carpogenic germination of sclerotia. Therefore, preventing apothecia formation and subsequent release of ascospores is the key to the

successful management of this disease. Surveys revealed that heavy textured soil, mono-cropping, high seed rate, high nitrogenous fertilizers, excess irrigation and unhygienic field conditions are prime factors responsible for heavy severity of the disease. Fungicides are frequently recommended for disease management that may negatively affect the environment and non-target organisms. Identification of improved source of resistance is an important prerequisite for disease management. Field experiments were conducted during 2007-2014 at IARI Farm, New Delhi for development of Sclerotinia rot management technology and virulence assessment of notified varieties under artificial disease inoculated soil as well as in stem-inoculated conditions. Out of four different combination of *T. harzianum* treatments, least (4.2%) Sclerotinia rot incidence was found in combination of seed treatment @10g/kg, soil application @ 2.5 kg/ha and two foliar sprays @ 0.2% of *T. harzianum* at 50 and 70 days after sowing which gave maximum seed yield (2080 kg/ha). In virulence assessment studies (2007-11), eight genotypes *viz*., Pusa Aditya, NPC 16, DMH 1, HYT 8, Pusa Swarnim, RGN 73, Bio-YSR and EJ 15 having < 5% incidence and low severity (0-1 grade) were rated as tolerant. Simultaneously, multilocational validation of integrated disease management (IDM) technology was conducted against Sclerotinia rot at 24 places in Haryana and Rajasthan on 117 ha under assured incidence of Sclerotinia not on farmers' field in the district Alwar, Sriganganagar, Hanumangarh in Rajasthan and Mewat, Mahindergarh and Gurgaon in Haryana. The IDM technology includes improved cultural practices *viz*., deep summer ploughing, preparation of levelled and well drained field, balanced use of nitrogenous fertilizers, sowing between 16-31 October, use of clean, certified healthy, disease tolerant seeds along with soil application of Potash (K_2O) @ 40.0 kg, Sulphur @ 40.0 kg and *T. harzianum* @ 2.5kg/ha pre-incubated in 50 kg of well decomposed FYM followed by seed treatment with *T. harzianum* @ 10g/kg along with foliar sprays at different crop stages. The IDM was found better over Farmers' practices (FP) in reducing the disease incidence and increasing the seed yield at all places. This strategy were found effective in reducing the indiscriminate use of chemical pesticide and safe guarding the other beneficial microbes.

I (S 07) 13: Perspective on the role of microbe-plant interaction in improvement of plant health through alleviation of stresses

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Plant health is a serious concern to humankind as plants provide all the necessary requirements for life. Besides being the source of food, fodder and accommodation recent studies emphasize on the connection between plants and human health. A new generation of botanical therapeutics, which include dietary supplements, functional foods, pharmaceuticals and multi-component drug mixtures have been launched. Thus, healthy plants are essential for humans, but plants, on the other hand are being exposed to increasing stresses and the various stressors include pathogen and insect attacks, low and high temperatures, drought and flooding, salinity, heavy metals, UV-rays etc., to name a few. It is well known that the rhizosphere is the store house of large number of microorganisms and these microorganisms interact among themselves and with the plant and much of this interaction turns out to be beneficial for the plants. Many of the beneficial microbes improve the growth of plants, as well as protect the plants against abiotic and biotic stresses. Research has been directed towards isolation and identification of beneficial microbes from the rhizosphere, with special emphasis on those microbes which have multiple beneficial traits such as plant growth promotion, alleviation of abiotic stresses and protection against disease. Use of such microbes is an environment friendly, cost effective method. Some of the groups of microorganisms used in stress alleviation are the plant growth promoting microorganisms (PGPM) including bacteria (PGPR) as well as fungi (PGPF), arbuscular rmycorrhizal fungi and endophytes. The mechanisms by which these microbes act against biotic stresses maybe due to direct antagonism in the soil, or indirect through production of volatiles, siderophores etc. They also induce systemic resistance in the host through activation of defense mechanisms in the crop such as enhancing activities of defense enzymes- phenyl alanine ammonia lyase, chitinase, glucanase, peroxidase etc. and increase accumulation of phenols and other such metabolites. In general alleviation of abiotic stresses occur through mechanisms such as enhancing antioxidant activities, reducing membrane damage, accumulation of osmolytes such as proline, glycine betaine, mannitoletc Besides, certain signal molecules such as hydrogen peroxide and calcium are involved in both abiotic and biotic stress alleviation and cross talk between the two. Thus it is clear that judicious use of such microbes can go a long way in achieving a resilient agriculture where crops can be made tolerant to the different stresses as well as more healthy and productive. Such eco friendly microbes can be used for improvement of plant health, which in turn can improve human health and life style.

Oral Papers

O (S 07) 14: Eco-friendly management of sheath rot in paddy caused by *Sarocladium oryzae* disease complex in India

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Rice (*Oryza sativa* L.) is the second largest crop grown in the world in terms of both area and production. Sheath rot caused by *Sarocladium oryzae* (Sawada) W. Gams & D. Hawksw is an important seed borne fungal disease of paddy which is becoming a major concern to the rice growing farmers in our country. Due to the introduction of high-yielding and semi-dwarf rice cultivars the sheath rot pathogen of rice has become a major production constraint in all rice-growing countries of the world. The availability of the sheath rot pathogen both in seed and soil makes the conditions much complex. Both invivo and invitro experiments were carried out at IARI New Delhi in three consecutive years during Kharif 2017, 2018 and 2019 to find out suitable ecofriendly management strategy against this disease. Seed treatment with *Pseudomonas flourescens* @10.0 gm kg^{-1} seed in combination with seedling dip in suspension of streptocycline@200ppm followed by one spray of *Ps. flourescens* @ 10 gm/liter water at 50 days after transplanting was found most effective as it gave maximum yield and minimum disease incidence. Minimum disease incidence of 5.2% and maximum yield (58.7 Q/ha) was seen in this treatment while in control the disease incidence was 10.7%. with reduction in yield upto (46.3Q/ha). As far as chemical maangement is concerned, seed treatment with Carbendazim (12%) + Mancozeb (63%) WP @3.0 gm kg^{-1} seed in combination with seedling dip in suspension of streptocycline@200ppm followed by one spray Tebuconazole 50% + Trifloxystrobin 25% @ 1 gm/liter water at 50 days after transplanting was found most effective for management of sheath rot in paddy. The efficacy of these bioagents as well as fungicides were observed by carrying out dual culture and poisoned food technique and field trials gave similar findings as observed under laboratory conditions.

O (S 07) 15: Integrated disease management of Alternaria leaf blight disease on sesame

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Alternaria blight caused by *A. sesami* (Kawamura) is one of the most widely spread and destructive disease of sesame (*Sesamum indicum* L.). The pathogen induces damping-off, leaf blight and stem canker, which accounts for about 80 per cent losses in seed yield. High fungicide input is required to control it. Therefore, to reduce the yield losses caused due to disease, to minimize cost of chemicals and the hazardous effects due to excessive use of the chemicals, present investigations were carried out against Alternaria leaf blight of sesame with the objective to develop the integrated disease management strategies for ecologically sound management of disease at VNMKV, Parbhani farm (M.S.), India. During experiment, total 14 treatments of solo fungicide, fungicides in combination with biocontrol agents and plant extracts were evaluated under field conditions for integrated management of Alternaria blight of sesame. Untreated control was kept as check. All the treatments imposed were found efficient in control of the disease with increase in seed yield. However, on the basis of pooled integrated cost benefit ratio (ICBR), the treatments found most effective and most economical in their order of merit were: T_9 (*T. viride* ST @ 10 g/kg + Garlic clove extract ST @ 10 ml/kg + Hexaconazole FS @ 0.1 %) followed by T_{10} (*T. viride* ST @ 1 ml/kg + Garlic clove extract ST @ 10 ml/kg + Mancozeb FS @ 0.25 %), T_4 (Hexaconazole ST @ 1 ml/kg + It's FS @ 0.1 %) and T_5 (Mancozeb ST @ 2.5 g/kg + It's FS @ 0.25 %), with ICBR of 3.19, 3.18, 2.83 and 2.59, respectively.

O (S 07) 16: Integrating seed biopriming and soil solarization for management of seedling damping-off in tomato and chilli nurseries

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Agriculturally sustainable plant protection technologies need to be adopted in integrated manner for effective plant health management. The effect of integration of seed biopriming with soil solarization for management of seedling damping-off was evaluated in tomato and chilli nurseries during *Kharif* 2017 and 2018 under coastal zone climatic conditions of Odisha. Seed biopriming with biocontrol agents *Pseudomonas* and *Trichoderma*, and seed treatment with Carboxin+Thiram in solarized and non-solarized nursery-beds were assessed. The average weekly maximum soil temperature during the course of soil solarization for four weeks ranged between 38.6 to 42.3^{o}C, 37.6 to 40^{o}C and 36.6 to 40.6^{o}C at 5.0cm, 7.5cm and 10.0cm soil depth respectively compared to 33.8^{o}C, 33.9^{o}C and 33.7^{o}C respectively in non-solarized soil at three different soil depths. The soil temperature increased to the range of 6.9-8.9 ^{o}C at 5cm, 5.0-8.3^{o}C at 7.5cm and 4.4-7.9^{o}C at 10cm respectively in solarized beds. The pooled incidence of seedling damping-off in tomato reduced to 22.2% with seed biopriming with *Pseudomonas*+*Trichoderma* compared to 51.7% in non-solarized control. In chilli too, it reduced to 22.2% with same treatment compared to 53.5% in non-solarized control. Seed biopriming in integration with soil solarization also resulted in increase in seedling growth response. The maximum shoot length and root length of tomato seedlings was recorded 16.3cm and 12.2cm respectively compared to10.6 and 7.8cm in control. In chilli, shoot length and root length increased to 14.8cm and 7.0cm respectively compared to 12.4cm and 5.9cm in control. The significant improvement in seedling growth was also recorded as increased fresh weight and dry weight of seedling shoots and roots with seed biopriming and soil solarization. The study revealed desirable impact of eco-friendly technologies like seed biopriming and soil solarization for managing the seedling damping-off and improving the seedling growth response in tomato and chilli.

O (S 07) 17: Analysis of rhizospheric soil supporting Bharat Moni cultivar (Plantain type) of banana in Lakhimpur district of Assam, North East India

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Bharat Moni, an indigenous cultivar o *Musa*, is one of the important banana varieties of Assam, Northeast India. It is popular for its sweet tasted fruits and pleasant aroma. Soil properties play a vital role in the growth and development of plants. Therefore, the objective of the present study was to analyse and compare the physico-chemical and biological properties of rhizospheric soil supporting the Bharat Moni cultivar of banana growing at six sites of Lakhimpur district of Assam, India. The soil samples were collected and analysed qualitatively and quantitatively following the standard methodologies. The soil physical properties such as soil moisture and soil pH were recorded. The soil chemical analysis included total nitrogen, available phosphorus, available potassium, available sodium and available organic carbon while biological properties, such as mycorrhizal spore count, total fungal and bacterial counts for Colony Forming Units (CFUs) per 100 gm of soil were carried out. The root colonization percentage (%) was also calculated. All soil samples were recorded acidic in nature with pH ranges from 5.53-6.42 while moisture contents ranged between 21.81%-31.9 %. The total nitrogen, available phosphorus, potassium, sodium and organic carbon values were in the range of 0.944-1.222 gm/kg, 1.567-9.272 gm/kg, 0.098-0.228 gm/kg, 0.004-0.033 gm/kg and 7.018-15.533 gm/kg respectively. The root mycorrhizal colonization percentage was found to be between 40-90 %. Mean root colonization, spore abundance, species richness and diversity in rhizospheric soil supporting Bharat Moni cultivar of banana were not significant ($p<0.05$). The selected sites were recorded with low mycorrhizal species richness and low spore abundance.

O (S 07) 18: Anti-oxidative machinery plays a vital role in the induction of drought tolerance in pearl millet upon the application of ACC deaminase producing PGPR–*Bacillus amyloliquefaciens* MMR04

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A total of 96 bacteria were isolated from rhizosphere soil samples of pearl millet grown in and around Mysore, Karnataka (India) and evaluated for their ability to produce ACC deaminase. Among the isolates evaluated, 28 rhizobacteria were found positive for ACC deaminase activity. Among the ACC deaminase producing bacteria, nine isolates were found positive for root colonization and they showed varied results among plant growth-promoting traits evaluated, but only four were non-pathogenic in nature. ACC deaminase positive and non-pathogenic PGPR were primed to pearl millet seeds and evaluated for their seed and plant growth-promoting properties. Among the four ACC deaminase producing PGPR, *Bacillus amyloliquefaciens* MMR04 enhanced significant seed and plant growth parameters compared to other isolates. The genomic study confirmed the presence of ACC deaminase gene in the isolate MMR04 and the obtained gene sequences were deposited to the NCBI database with the Accession No. MN038394. Further, pearl millet seeds primed with MMR04 also enhanced plant growth even after exposing to four different levels of drought stress as compared to stress-

induced control plants. An increase of 0.37, 0.34 and 0.29 fold in proline, SOD and APX activity, respectively and a decrease of 0.19 fold in MDA content were observed in MMR04 primed plants compared to control plants grown under S4 conditions. The qRT-PCR studies on the SOD and APX genes showed that the expression levels of genes were in line with the quantification results of SOD and APX. From the results, it can be attributed that ACC deaminase producing isolate MMR04 can be used as an alternative to enhance pearl millet plant growth under drought stress conditions in arid and semi-arid regions with water deficit.

O (S 07) 19: Mango wilt disease management

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India, with cultivated area of 2.26 million hectares, ranks top in the fruit production (19.69 million metric tonnes) of mango (*Mangifera indica* L.). Mango wilt disease caused by *Ceratocystis fimbriata* has recently been identified as major constraint throughout mainland with varying incidence among the major mango growing states. Although annual wilting of trees has been recorded <0.5 per cent, but wilting of a full grown tree was considered a huge loss and management efforts have been made to provide instant solution to farmers. The expression of symptoms was observed either in the form of sudden wilt or decline of trees. Factors aggravating disease development were identified and farmers were educated to take care. Efficacy of botanicals, *Trichoderma asperellum* and fungicides was evaluated against the pathogen under laboratory conditions and most effective ones were applied in hot spot orchards. Out of 18 fungicides available in market, 13 fungicides (captan + hexconazole, carbendazim, copper hydroxide, hexaconazole, difenoconazole, hexaconazole + zineb, metalaxyl + mancozeb, myclobutanil, propiconazole, propineb, iprovalicarb + propineb, tetraconazole and thiophanate methyl) were found effective at standard rates of their application and; thiophanate methyl and carbendazim were found effective at minimum (10 ppm) dose. Neem, tobacco and mango leaf, and neem cake extracts were not found effective but culture filtrate of *T. asperellum* was found effective. *T. asperellum* based bio-pesticide formulation was developed and evaluated in potted seedlings of mango along with fungicide, *T. asperellum* culture and neem cake, and it was found at par with thiophanate methyl. Multi-location trials had 86.6 per cent success rate with the application of best treatments. Integrated disease management package of practices was developed and extended to farmers. Since, mango is a perennial crop and disease incubation period is too long, multi-location management efforts are being continued to further refine the management strategies.

O (S 07) 20: Adoption of multiple approaches for management of banded leaf & sheath blight of maize

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Banded leaf and sheath blight (BLSB) of maize (*Zea mays* L.) is caused by most widespread and versatile pathogen *Rhizoctonia solani* f. sp. *sasakii*. The disease is difficult to manage through fungicides or crop rotation alone due to its soil borne nature and unavailability of resistance sources. Present investigation was carried out to manage BLSB adopting four strategies during *kharif* 2018 and 2019. In chemical approach, seed treatment with Salicyclic acid [100 ppm] was done followed by foliar spray with Azoxystrobin (Azoxytrobin 18.2%w/w + Difenoconazole 11.4% w/w SC@0.1%) twice at 3 and 15 DAI. In the first organic approach, soil amendment was done with *Trichoderma* formulation @6t/acre FYM, seed treatment with *Trichoderma* @20g/kg seed followed by foliar spray with neem leaf extract @ 1% twice at 3 and 15 DAI. The second organic approach was slightly different from the first one where *Trichoderma* @1% was sprayed on foliage twice at 3 and 15 DAI instead of the neem leaf extract. In IDM approach, soil was amended with *Trichoderma* [@6t/acre FYM], seed treatment with Salicylic acid [100 ppm] followed by foliar spray with Azoxystrobin at 3 DAI and neem leaf extract @1% at 15 DAI. The treatments were compared with the foliar spray of Carbendazim @ 0.1% twice at 3 and 15 DAI. All the treatments significantly reduced BLSB disease. Of which, disease reduction was highest in the IDM approach (59%) followed by chemical approach (50%), carbendazim (47%), first organic approach (43%) and second organic approach (40%). Keeping same trend of disease suppression by the treatments, IDM approach contributed higher yield (35 q/ha) followed by carbendazim (34 q/ha), chemical approach (33 q/ha) and second organic approach (31 q/ha). The IDM approach formulated for this study has established a promise and potential of effective management of BLSB disease of maize.

O (S 07) 21: Management of major soilborne diseases of pigeonpea: An integrated approach

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Pigeonpea (*Cajanus cajan* L. Millisp) is a most important legume crop worldwide. India is the largest producer and consumer of pigeonpea in the world. It is a protein rich staple food, contains about 22 percent protein, which is almost three times that of cereals. Pigeonpea supplies a major share of protein requirement of vegetarian population of the country. Its split grain is mainly consumed in the form of Dal, which is an essential supplement of cereal based diet. The crop is affected by many biotic and abiotic stresses at various stages of its growth. Among the biotic stresses, Wilt and Phytophthora stem blight (PSB) are the two most important yield limiting factors. Every year, these soilborne diseases cause enormous economic loss and exports are restricted owing to poor quality produce. For the management of these diseases, chemical pesticides are generally used. It is well established that agricultural chemicals cause not only environmental pollution but also pose serious health hazards as their injudicious use often results in toxicity to man, plants, domestic animals and wild life and therefore are regarded as ecologically unacceptable. The management of wilt and PSB by chemicals has not yielded the anticipated results. Therefore, a renewed knowledge is needed to assess the current severity of these problems and to develop or refine integrated disease management (IDM) modules to protect crops in a cost-effective and eco-friendly manner. IDM is a multidisciplinary approach that manages diseases effectively by integration of host plant resistance, cultural, physical, biological control, safer chemical and molecular approaches. We have identified several resistant donors/lines for wilt and PSB to utilize resistance breeding program. Several indigenous potential *Trichoderma* spp. characterized and identified for management of both the diseases. These approaches can play a major role in reducing the losses due to the soilborne diseases under subsistence farming conditions. Since IDM comprises of many approaches, it will definitely prove to be an effective strategy for enhancing pigeonpea production under the changing climate scenario.

O (S 07) 22: Effective modules for management of soil borne diseases of groundnut

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Groundnut is one of the important oilseed crops of India and annually it is cultivated on an area of 5.12 M ha with production of 7.10 M tonnes and productivity of 1384 Kg/ha (Average of last five year, 2012-17). It plays an important role in the dietary requirement of resource poor families. Its haulm provides an excellent fodder for milch animals. The productivity of groundnut in India is quite low as compared to USA (»3500 kg/ha) and China (»3000 kg/ha). Such a low productivity is attributed to several production constraints including soil borne diseases. The soil borne diseases cause substantial losses. Collar rot (*Aspergillus niger*) causes 25-50% losses and stem rot & pod rot (*Sclerotium rolfsii*) up to 27% losses. Dry root rot (*Macrophomina phaseolina*) and Sclerotinia stem rot (*S. sclerotiorum*), however causes comparatively less losses to the crop. An attempt was made to manage the soil borne diseases as well as support the yield of the groundnut. The different components available for management of soil borne diseases were integrated and evaluated with farmers' practice as checks at ICAR-DGR, Junagadh, Gujarat (India) during both the summer and *Kharif* seasons of 2014-2016. The results revealed that during summer seasons of 2015 & 2016, the maximum inhibition of stem rot was achieved by Module M11 followed by M17. The maximum pod yield and haulm yield increase was supported by M17 over farmers' practice. During *Kharif* season of 2014 & 2015, the maximum stem rot inhibition was achieved by M17. The maximum pod yield of and haulm yield increase was supported by M5 and M11 respectively, over farmers' practice. The modules have components of "deep summer ploughing with moldboard plough, seeds of popular variety (GG20/TG37A), seed treatment with tebuconazole @ 1.5g/kg of seeds (M17) or with PGPR @625g/ for per ha of seed (M15), soil application of *Trichoderma* @ 4 kg/ ha enriched in FYM first at the time of sowing, second at 35 DAS (days after sowing) and third at 80 DAS". The module with slight modification in refinements were validated at different AICRP-G locations and found suitable for managing soil borne diseases. The best modules would be recommended for use by the farmers after final validation at farmers' field.

O (S 07) 23: Management of bakanae disease of paddy integrating cultural, chemical and biological control options under field conditions

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Rice (*Oryza sativa* L.) is one of the most important food crops cultivated globally. Many important diseases like blast, BLB, brown spot, etc attack on rice. Recently, Bakanae disease has emerged as potential threat to rice cultivation especially to the cultivars of Basmati rice. Bakanae disease of rice caused by *Fusarium fujikuroi* is widespread in all rice growing countries of the world. A field study was conducted during *Kharif* 2016-19, different management practices *viz.,* cultural, chemical and biological control options were integrated for effective management of the disease. Among cultural practices effect of transplanting time and uprooting of infected plants on the disease incidence was evaluated in paddy cv. Pusa Basmati-1121. The maximum incidence of Bakanae disease (13.92%) was recorded in paddy cv. PB–1121 transplanted in second transplanting i.e., 15th July. The uprooting of infected plants had non-significant effect on the field incidence of Bakanae disease. In second part of the study, conducted simultaneously, chemical and biological control options were evaluated. Seed treatments (untreated; Carbendazim 50% WP; *Pseudomonas fluorescens, Trichoderma viride*), soil amendments (un-amended soil; Carbendazim 50% WP; *P. fluorescens*; *T. viride*) and foliar sprays [(control; Carbendazim 50% WP @ 0.25%; Nativo (Tebuconazole 50% + Trifloxystrobin 25%)] @ 0.1%) were integrated for the management of Bakanae disease in paddy cv. PB-1121 under field conditions. Out of the treatments evaluated, a combination of treatment using nursery raised from Carbendazim 50% WP treated seed @ 2.0 g/Kg seed, plots amended with Carbendazim 50% WP 8 DAT @ 1.0 Kg/acre and foliar spray with Carbendazim 50% WP @ 2.5 g/L water, was most effective with 0.30% disease incidence in managing the disease, as against 12.73% in control (natural incidence) and 27.58% in pathogen culture (*Fusarium fujikuroi*) inoculated seed raised without any treatment.

O (S 07) 24: Application of ACC deaminase producing plant growth promoting rhizobacterium *Bacillus subtilis* Rhizo SF 48 on tomato plants for the induction of drought tolerance

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A total of ten 1-aminocyclopropane-1-carboxylate (ACC) deaminase producing PGPR isolates were selected and evaluated for the induction of drought stress tolerance in tomato. Among the selected PGPR, maximum seed (laboratory) and plant growth promotion (greenhouse) was observed in tomato seeds bacterized with *Bacillus subtilis* Rhizo SF 48. The genomic study confirmed the presence of ACC deaminase gene in Rhizo SF 48 and the obtained sequence was deposited to the NCBI database with the Accession No. MK652706. The tomato plants grown upon treatment with Rhizo SF 48 significantly enhanced plant growth even after exposing to different levels of drought stress as compared to stress induced control plants. About 7.5% and 38% increase in RWC were observed in Rhizo SF 48 treated tomato plants grown under well-watered and stress conditions (S4) compared to their control plants, respectively. An increase of 0.76, 0.23 and 0.78 fold in proline, SOD and APX activity and a decrease of 0.3 fold in MDA and H_2O_2 contents were observed in Rhizo SF 48 treated plants compared to control plants grown under S4 conditions. The histo-chemical studies showed lower accumulations of H_2O_2 and superoxide anion in the leaves of Rhizo SF 48 treated plants under drought stress, which was in confirmation with the quantification results of H_2O_2 and SOD. The qRT-PCR studies on drought (*Le25*) and ethylene responsive factor (*SlERF84*) marker genes showed that a significant decrease of 0.75 and 0.81 folds, respectively in *Le25* and *SlERF84* accumulation was observed in Rhizo SF 48 treated plants compared to untreated plants grown under S4 conditions. From the results, it can be attributed that ACC deaminase producing Rhizo SF 48 was able to protect tomato plants against oxidative damage caused due to drought stress and enhanced plant growth promotion. It can be concluded that ACC deaminase producing Rhizo SF 48 can serve as a useful bio-inoculant for sustainable tomato production in arid and semi-arid regions with water deficit.

O (S 07) 25: Evaluation of antagonistic potential of different bio-control agents against *Rhizoctonia solani* causing sheath blight of rice

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Sheath blight caused by a fungal pathogen *Rhizoctonia solani* is one of the major constraints in the cultivation of rice in the country resulting in 5.2 to 50.0% losses in the yield. The management of this disease is mainly dependent upon the use of chemicals but their application alone is not advisable keeping in view the effect on the environment, human health and expensiveness. On the other hand, bio-control agents are found to be eco-friendly, less expensive and compatible with other agricultural practices. In the present investigation the antagonistic potential of sixteen bio-agents including eight isolates of *Trichoderma* species (I_1 – I_8) isolated from rhizospheric soils of different rice growing areas of Himachal Pradesh and eight standard bio-control agents viz., *Trichoderma koningii* (DMA-8), *T. koningii* (JMA-11), *T. harzianum* (JMA-4), *T. harzianum* (SMA-5), *T. harzianum* (TH-4), *T. asperellum*, *T. viride* and *Pseudomonas fluorescens* was evaluated *in vitro* against sheath blight pathogen. All the bioagents were found to be antagonistic against *R. solani* however, *T. harzianum* (TH-4) gave maximum inhibition of mycelial growth (83.81%) and sclerotial formation (90.63%) in dual culture plate method. It was followed by *Trichoderma* sp. (I_8), *Trichoderma* sp. (I_3), *Trichoderma* sp. (I_7) and *T. asperellum* which were statistically at par for mycelial inhibition and *Trichoderma* sp. (I_3), *Trichoderma koningii* (DMA-8), *T. asperellum*, *Trichoderma* sp. (I_7), *Trichoderma* sp. (I_8) and *T. koningii* (JMA-11) which were statistically at par for sclerotial inhibition. The assay of non volatile compounds in culture filtrates of bio-agents at highest 1:3 ratio revealed the maximum inhibition of mycelial growth (72.59 and 86.30%) and sclerotia formation (69.82 and 91.42%) of *R. solani* in sterilized and unsterilized culture filtrates, respectively followed by *Trichoderma* sp. (I_8) for mycelial and *Trichoderma* sp. (I_3) for sclerotia inhibition. Similarly, the volatile compounds produced by *T. harzianum* (TH-4) gave maximum inhibition of mycelial growth (80.74%) and sclerotia formation (93.39%) of the pathogen followed by *T. asperellum* and *P. fluorescens,* respectively. The sclerotial dipping of *R. solani* in culture filtrates of *T. harzianum* (TH-4) for 36 hours gave maximum inhibition of sclerotial germination (76.00 and 81.32%) and mycelial growth of sclerotia (91.48 and 96.67%) in sterilized and unsterilized filtrates, respectively. Treatment of sclerotia with spore suspension (10^9/ ml) of *T. harzianum* (TH-4) resulted in maximum inhibition of sclerotial germination (26.68 and 72.00%) and mycelial growth of sclerotia (85.56 and 70.74%) after 15 and 30 days of incubation in soil, respectively.

O (S 07) 26: Virus free potato mini tubers production through combined intervention of tissue culture and aeroponics

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Biotechnological interventions in the line of tissue culture and suitably fabricated growing structure called aeroponics can provide a future solution to the rapid production of virus free quality as well as breeder seed of potato. With this aim, CPRI has developed and standardized aeroponics system in India. Our Team in CRPI Regional station, Shillong, Meghalaya has initiated a modified prototype of net house cum aeroponics structure suitable for the NEH region at Central Potato Research Station, Shillong (1800 m AMSL, 25.54°N, 91.85°E). Under this system, virus free microplants of potato are mass multiplied through nodal cutting on Modified MS media for three weeks after proper diagnostic test of mother plants by ELISA, Nucleic acid spot hybridization test or PCR etc. Then the full grown harden microplants are planted on aeroponics panel for soilless production of mini tubers. Root zones of the micro plants are regularly feed with standard nutritional mixture through automatic injectors. The study was conducted during Summer & Autumn season (March to August, 2013-14, 2014-15, 2015-16) and six notified varieties *viz*. Kufri Girdhari, Kufri Megha, Kufri Jyoti, Kufri Kanchan, Kufri Himalini and Kufri Himsona were evaluated under this system. First harvest was taken after 30-45 DAP depending on varieties by picking the mini-tubers with diameters larger than 20-25 mm (^{3}3g). Subsequent harvesting was taken at an interval of 10 days. Maximum number of mini-tubers/plant was recorded in Kufri Kanchan (40.78) followed by Kufri Megha (29.36) and Kufri Himalini (22.78). Kufri Girdhari and Kufri Himsona both produced more or less equal number of tuber per plant (~16 minitubers/plant) and Kufri Jyoti produced least number of tuber of approx. 9 mini tubers. Kufri Kanchan (123.97g) produced maximum yield of mini-tubers/plant followed by Kufri Himsona (96.77g) and Kufri Himalini (93.17g). The average minitubers weight was highest in Kufri Jyoti (8.96 g) followed by Kufri Himsona (6.16 g) and Kufri Girdhari (5.00 g). In general, Kufri Kanchan (40.78) produced more number of small sized minitubers (3.04g) while Kufri Jyoti produced less number of large sized minitubers. Kufri Kanchan exhibited an optimum combination in terms of number of mini-tubers produced and its size. Tissue culture along with aeroponics system thus can be a potent tool to increase the production of virus free mini-tubers which, in turn, can be used for production of quality seed tubers of potato.

O (S 07) 27: Diversity, pathogenic effect, biology and management of root-knot nematode, *Meloidogyne incognita* infecting black gram (*Vigna mungo*)

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Survey of black gram fields were conducted for the occurrence of economically important plant parasitic nematodes of some localities of Jammu and Samba districts of J&K. Among the different plant parasitic nematodes *Meloidogyne* spp. was more frequently encountered in maximum localities of Jammu and Samba districts. Significant reduction occurred in plant growth parameters of inoculated with 500, 1000 and 2000 J_2/ pot. The highest gall index was recorded at inoculums levels of 1000 and 2000 respectively. Total nematode population /pot significantly increased progressively with an increase in nematode population from 20-2000J_2/ pot. Reduction in multiplication of the nematode was observed with increase inoculum levels. Effect of different organic amendments such as neem cake and leaves of neem *Azadirachata indica*, madar *Calotropis procera* and behaya *Ipomea fistulosa* @2.0 and 4.0% on the biology, multiplication of nematode and plant growth character. Observations on penetration and development of various stages of nematode were recorded on every alternate day and continued until completion of the life cycle. Application of organic amendments significantly increased plant growth and decreased the host infestation by root knot nematode, *Meloidogyne incognita* over control. Maximum plant height was recorded in poultry manure @4q/ha treated soil followed by vermicompost@10q/ha, neem cake @5q/ha and mahua cake @5q/ha respectively. The minimum population was recorded in neem cake @5q/ha. treated soil and maximum population in mahua cake @5q/ha treated soil.

O (S 07) 28: Evaluation of new fungicide combinations against sheath blight of rice in irrigated ecosystem

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Rice (*Oryza sativa L.*.) is a most important food crop serving as a primary source for more than 60% of the world population. Production and productivity of rice is affected by many biotic and abiotic factors. Biotic factor includes many diseases caused by fungi, bacteria, viruses, nematodes and several physiological disorders which cause annual loss to the tune of 12 to 25 % of the total production. Among the fungal diseases, Sheath blight of rice caused by *Rhizoctonia solani* Kuhn is one of them. The symptoms appears on aerial part of the rice plant. The lesions first appear on the leaf sheath at /or above water level as water soaked circular to oblong ellipsoid to ovoid, somewhat irregular greenish gray patches. Sclerotia are formed on or near these spots depending on the weather conditions All the rice cultivars are susceptible to the pathogen and no any resistant variety has been reported for this disease. The present study was undertaken to evaluate some fungicide in combination to manage the disease. The Fungicides Flusilazole 12.5%+Carbendazim 25% SC (luster37.5SE)@ 1.0ml/l, Azoxystrobin 18.2% w/w+Difenoconazole 11.4% w/w SC (Amistar Top 32.5SC)@ 1.0ml/l, Azoxystrobin 11.0% w/w+Tebuconazole 18.3% w/w SC (Custodia)@ 1.5ml/l, Tricyclazole 18%+Mancozeb62% WP(Merger)@ 2.5g/l, Zineb 68%+Hexaconazole 4% WP(Avatar)@ 2.5g/l, Trifloxystrobin25%+Tebuconazole 50%WG (Nativo 75WG)@ 0.4g/l, Mancozeb 50%+ Carbendazim 25%WS (Sprint)@2.5g/l, Fluxapyroxad 62.5g/l+Epoxyconazole 62.5g/l EC (Adexar)@ 1.5ml/l and untreated check (total treatment combinations-9) were evaluated against sheath blight of rice on the susceptible variety Pusa basmati-1 under field condition. The experiment was laid out in RBD with four replication in 5X2 m plot size with 15X15 cm spacing. Among the new fungicides Fluxapyroxad 62.5g/l+Epoxyconazole 62.5g/l EC (Adexar) was found best in checking the Sheath blight severity (21.8 %), Incidence (20.6 %) and increase the grain yield of rice (37.5 q/ha) followed by Azoxystrobin 11.0% w/w+difenoconazole 18.3% w/w SC (Custodia)@ 1.5ml/l.

O (S 07) 29: Association of causal agents inciting boll rot complex of cotton and its management in northern Karnataka

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Cotton is the most important cash crop of India contributing 7.00 per cent to our GDP, fetching an export earning besides providing employment in the production, promotion, processing and trade of cotton. The present investigations were under taken at Agril.Research Station,Dharwad during 2017-18.The study clearly identified the association of *Alternaria macrospora, Fusarium oxysporum* f. sp. *vasinfectum, Exserohilum rostratum, Colletotrichum gossypii, Phoma* sp., *Trichothecium roseum, Aspergillus niger, Nigrospora oryzae* and *Rhizopus stolonifer* were found to be associated in causing boll rot complex disease of Bt. cotton and were identified on the basis of pathogenicity, morphological and molecular characteristics. The various symptoms were characterized as small brown or black dots, infected inner tissue and rotted seeds and lint. Among the areas surveyed, more than two pathogens associated two places while more than three and four pathogens were associated in four and three areas. Based on results pathogens associated in boll rot complex have been divided into three groups *viz*., those capable of penetrating intact bolls, those which are introduced by insects and those are introduced after the boll are damaged by insects or after the suture of the boll lobes are broken. Among eleven different new molecules tested, spraying with trifloxystrobin 25%+tebuconazole 50%WG @ 1.0/lit at 75 and 90 days after sowing was found effective followed by tebuconazole 25.9 %EC at the rate of 1.0 ml/lit was found economical with the highest B:C ratio (1.52:1) followed by trifloxystrobin 25%+ tebuconazole 50%WG @ 1.0/lit with B:C ratio fo 1.43:1. The present study clearly demonstrated the association of more than four pathogens in causing boll rot complex and can be managed by triazole fungicides in northern Karnataka.

O (S 07) 30: Effect of date of sowing and IDM components on the management of root rot and foliar diseases of forage cowpea

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Cowpea (*Vigna unguiculata* (Linn) Waip.*)* is the most important leguminous forage crop and *mainly cultivated in tropical and sub-tropical regions of India for its food and fodder value*. Cowpea is susceptible to many diseases which causes significant losses in Himachal Pradesh. Monitoring of cowpea diseases for three years showed that average incidence/severity of root rot, leaf blight and anthracnose was 47.3, 35.0 and 26.0 per cent, respectively. To assess the effect of date of sowing on the intensity and management of cowpea diseases, the crop was sown on three dates at 15 days interval. The average data of three years indicated that minimum incidence of root rot was observed 10.8 per cent in early sown crop (4th June) and maximum incidence of 37.8 per cent in late sown (4th July) crop. However, the disease severity of anthracnose was increased with the delay in the sowing of crop and was maximum of 25.9 per cent on 19th June sown crop & minimum of 13.1 per cent in crop sown on 4th July. In case of leaf blight, the severity was maximum i.e. 25.7 per cent in the normal sowing date (19th June) and minimum i.e.13.8 per cent in late sown crop. For the management of diseases, seed treatment with tebuconazole 2DS @ 1g/kg seed + NSKP (Neem seed Karnel powder) @ 50 g/kg seed (T3) or metalaxyl 8% + Mancozeb 64% @ 2.5g/kg seed + NSKP @50 g/kg seed (T4) followed by two foliar spray with propiconazole @ 1ml/l at 15 days interval were found effective with normal date of sowing which controlled 55.3 & 55.1 per cent of root rot, 74.1 & 71.8 per cent of anthracnose and 76.8 & 77.7 per cent of leaf blight, respectively. These treatments also recorded highest green fodder yield (60.3 & 61.9 q/ha) and dry fodder yield (16.8 & 16.8 q/ha) at normal date of sowing, with 21.4 & 23.4 per cent and 10.7 & 10.8 per cent increase in yield over control, respectively.

Poster Papers

P (S 07) 01: Positive and negative effects of the thermotherapies employed in Brazil to control ratoon stunt of sugarcane

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Ratoon stunt (RSD), caused by the fastidious bacterium *Leifsonia xyli* subsp. *xyli* (Lxx), is one the major disease of sugarcane due to the high yield losses and difficulty of control. The use of clean seedcane is an important measure successfully control RSD because infected seedcane is the main source of primary inoculum in newly established fields. Thermotherapy is the most employed control method used in Brazil to eradicate Lxx in seedcane. Two treatment protocols are employed: 52°C/30min and 50ºC/2h. The former treatment is preferred by the industry because larger amount of seedcanes can be treated per unit of time. However, previous works showed that this treatment did not completely eliminate Lxx while the latter treatment resulted in a better Lxx control but negatively affected bud germination. Therefore, this work examined the effect of these two thermotherapy protocols on Lxx survival, bud germination and stalk weight in the three most important current cultivars. Sap of RB867515, BR92579, and RB966928 was extracted and Lxx quantified by dot blot immunoassay, and then the two thermotherapies were applied to single bud setts and compared to Lxx-positive and -negative controls. Bud germination, Lxx eradication efficiency, and stalk weight were evaluated 30 days after treatment and nine months after transplanting to the field (one year after thermotherapy). When applicable, differences among treatments were tested by Tukey at 5% probability. Our data showed that the 50ºC/2h treatment had more deleterious effect on bud germination than the 52°C/30min one, but the damage level varied among cultivars: RB7515 had 14%, RB92579, 37.6%, and RB966928, 73.2%. The latter cultivar was the only one that showed damage to bud germination at 52°C/30min (68.6%), demonstrating that cultivars reacted differently to the hot water treament. Moreover, 50ºC/2h was efficient in eliminating Lxx when pathogen titer was equal or below 107 CFU/mL, whereas at 52°C/30min treatment failed to eradicate Lxx in all pathogen concentration. No statistic difference on stalk weight among treatments within cultivars was observed in plant cane of nine months of age.

P (S 07) 02: Bio-activity of graphene oxide nanosheets on *Sclerotinia sclerotiorum*, a causal agent of stem rot disease

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Sclerotinia sclerotrium de Bary, is a causal agent of stem rot disease of 450 host plants including Brassica and have a serious threat to crop production worldwide. This disease is very difficult to manage using different fungicides and no disease resistant varieties are available till date to the farmers. This disease caused huge losses under the climatic conditions that favor the growth of fungus and spread of the disease. Chemical control using the various fungicides are almost in-effective to control this disease. However, significant development in nanotechnology, where various nanostructures such as polymeric nanoparticles, carbon nanotubes, metal and metal oxide have been projected to be used in managing plant diseases. Toxicity considerations, including negative environmental effects, have also led to the redesign of nanomaterials by tuning the size and shape and by surface modification, leading to increased antimicrobial activity and decreased ecological toxicity. Literature revealed that silver nanoparticles are most potential candidate and have high antimicrobial activity though its high toxicity is a bottleneck. To overcome such issues, graphene oxide (GO), composed of a single layer of sp^2 bonded carbon atoms with active surface hydroxyl, epoxy and carboxyl groups is a more suitable candidate material.

P (S 07) 03: Heavy metal uptake, accumulation and translocation characteristics of *Typha latifolia*

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Heavy metals in soils originate from both natural and anthropogenic sources, and intense anthropogenic activities can lead to excessive heavy metal levels, which are harmful to the environment. Contaminants accumulate in sedimentary environments where they may affect resident macro- and microorganisms responsible for driving major biogeochemical cycles and providing a range of ecosystem services. The presence of heavy metals in the aquatic environment is a threat to the ecosystem and human health. Lead is one of the most toxic metals and it comes from industrial waste into water resources. Several processes such as ion exchange, solvent extraction, chemical precipitation, etc. have been used to remove heavy metal ions from water. This study aimed at analysing the bioremediation of varying concentrations of lead by *Typha latifolia* grown in constructed wetland. Lead tolerance in *Typha latifolia* checked from plants collected from metal-contaminated and uncontaminated tanks were investigated. Metal concentrations in uncontaminated plant populations showed that Pb in the shoot were maintained at low levels (Pb: 3·2–30 mg/L) and in the roots (Pb: 25–57.2mg/L). Although concentrations in contaminated plant populations showed that Pb in the shoot were maintained at (Pb: 30 mg/L) and in the roots (Pb: 57.2mg/L). Plants from metal-contaminated populations accumulated considerably more metals (up to nearly twice as much Pb) in roots than the uncontaminated population in trial experiment.

P (S 07) 04: Management of cucumber powdery mildew caused by *Erysiphe cichoracearum* (DC)

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Cucumber (*Cucumis sativus* L.) is one of the oldest cultivated vegetable crop belongs to family cucurbitaceae. Powdery mildew is a serious disease of cucumber, caused by *Erysiphe cichoracearum* (DC). Symptoms first appears as white nearly or fluffy somewhat circular patches or spots which appear on the upper surface of the leaves and spreads to petiole, stem and fruits. Severely infected leaves become brown , shrivelled and defoliation may occur. Yield loss due to powdery mildew disease was estimated to be 50-70 per cent. Field experiment was conductedat at MARS, Raichur to evaluate various fungicides, botanicals and bio agents which are found to be efficient under laboratory studies. Fungicides, botanicals and bio agents spray was taken after disease appearance three sprays given at an interval of 15 days. The results revealed that minimum disease severity of 6.67 per cent was recorded in trifloxystrobin 25 % + tebuconazole 50 % after the third spray and recorded highest yield of 11.20 t/ha followed by azoxystrobin 23 % SC which showed the disease severity of 9.53 per cent with yield of 10.42 t/ha . While, *Pseudomonas flourescens* has shown least disease control with disease severity of 28.26 per cent compared to control plot which recorded highest disease severity of 75.67 per cent. Result indicated that combi fungicide trifloxystrobin 25% + tebuconazole 50% (0.30%) has proven to be most effective followed by azoxystrobine 23 % SC (0.15%) in management of disease.

P (S 07) 05: First report of *Pseudomonas aeruginosa* causing mummy disease of button mushroom (*Agaricus bisporus*) in India

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Mushroom fungi are very sensitive to different biotic stresses under uncontrolled weather conditions. Mushrooms are attacked by number of pathogens and insects/pests during the course of their growth and development. Till the end of 19th century mushroom cultivation was in patches in India. Thereafter, increase in demand and production is recorded and currently it has become an industry in the country. However, increase in area and production has also built up the population of crop enemies. Sometime complete crop failure and severe economic losses to the growers have been recorded. Most of the major mushroom pathogens are re-occurring in mushroom house and causing economic losses if not managed well in time. A new threat of bacterial pathogen was recorded on white button mushroom in India and identified as *Pseudomonas aeruginosa*. Till date in India, this pathogen was reported from human, animals and plants. On isolation on selective media of *P. aeruginosa* (Hi media, MP406-50PT), it produced red – brown, yellowish and watery pigments in the media after 6-7 days of inoculation. It is an indication that more than one strain of *P. aeruginosa* are present in the mycosphere and phyllosphere of button mushroom. In the sick beds/bags, pinhead formation was delayed after case run for at least one weak and fruit bodies remained under sized. Sunken water soaked/brown spots, red/brown tissue layer at the base of the stipe and cracks on the infected surface were identified as the characteristic symptoms of the *P. aeruginosa* in button mushroom. These blemishes rendered the fruit bodies unmarketable completely. About 70-80 per cent incidence of bacterial infection was recorded during first flush and onwards. Crop losses are more severe under low temperature conditions (>15^{0}C) and winter season of mushroom cultivation under low cost huts.

P (S 07) 06: Integrated disease management of banded leaf and sheath blight (*Rhizoctonia solani* f. sp. *sasakii)* of fodder maize

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Maize (*Zea mays* L) is one of the most versatile crops having wider adaptability under varied agro-climatic conditions. Globally, maize is known as queen of cereals because it has the highest genetic yield potential among the cereals. *Rhizoctonia solani* f. sp. *sasakii* causing banded leaf and sheath blight disease is one of the most important diseases of maize. It has rapidly gained economic importance in several parts of world. It has potential to inflict economic losses up to 100 per cent and also causes severe losses in Himachal Pradesh. The disease was monitored at Palampur for three consecutive years and average 7 per cent disease incidence was observed. A field experiment with 13 treatments was conducted during *Kharif* 2017 and 2018 for integrated management of the disease by using chemicals, bioagents, cultural practices individually and in combinations. Among these 13 treatments, seed treatment with carbendazim followed by the two foliar sprays with tryfloxystrobin + tebuconazole @ 1g/l was found highly effective with 79.6 per cent average disease control and 11.8 average increase in yield over check. This treatment was followed by seed treatment with carbendazim @ 1g/l and foliar sprays with two sprays of carbendazim @ 1g/l provided average control of 74.1 per cent with 11.2 per cent average increase in yield over check with non-significant differences. As a non-chemical method seed treatment with *T. viride* followed by two foliar sprays with *P. fluorescens* @ 5g (CFU 10^7)/l provided average control of 38.5 per cent with 4.4 per cent average increase in the yield. Seed treatment with *T. viride* @ 5g/kg alone and stripping of the lower leaves of the plant resulted least with no economic control of the disease.

P (S 07) 07: Study on antifungal activity of plant extracts, organic inputs and elicitors on berseem stem rot

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Stem rot, incited by *Sclerotinia trifoliorum* Eriksson is one of the most devastating soil borne fungal pathogens of berseem inflicting significant fodder and seed yield losses. Eleven plant extracts, six organic inputs, one elicitor and five organic and inorganic salts were assayed for their effectiveness against *S. trifoliorum* under *in vitro* conditions. Extracts of *Aegle marmelos* and *Cymbopogan citrates* showed complete mycelial inhibition of *S. trifoliorum* at 5% concentration. Among organic inputs, panchgavya and fermented cow urine recorded100% inhibition to mycelial growth of stem rot pathogen at 10% concentration. Elicitor (chitosan) and salts namely copper sulphate and potassium carbonate provided complete mycelial inhibition of test pathogen under *in vitro* conditions at 0.1, 2.0 and 5.0% concentrations respectively. The plant extracts, organic inputs and salts that exhibited highest mycelial inhibition to *S. trifoliorum* under *in vitro* conditions were evaluated for their antifungal efficacy under greenhouse and field experiments during *rabi* 2017-18 and 2018-19. The extracts of chitosan (7.73; 9.53; 11.17%), panchgavya (8.67; 13.30; 16.47%), *A. marmelos* (10.20; 20.11; 19.53%) and copper sulphate 10.33; 17.50; 17.67%) have recorded lowest percent disease severity as compared to untreated control in greenhouse and field trials in *rabi* 2017-18 and 2018-19 respectively. Significant increase in green fodder yield of berseem from 9.87 to 33.38% was also recorded after treatment with plant extracts, organic inputs and some salts. The current study showed that plant extracts, organic inputs and salts have potential for the management of stem rot of berseem.

P (S 07) 08: Integrated management of chickpea (*Cicer arietinum)* collar rot

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Collar rot (*Sclerotium rolfsii*) of chickpea is one of the most serious soil-borne fungal diseases. Due to which 10 –30% yield loss is recorded annually according to severity of the disease. Management of this disease is not feasible in the absence of IDM. However, considering the importance of disease an experiment was carried out with IDM method by use of *Trichoderma viride* through On farm trials in Kabirdham district of Chhattisgarh during 2016-17,2017-18 and 2018-19 at different locations of farmer's field on variety JAKI-9218 and JG-14 by supervision of Krishi Vigyan Kendra Kabirdham (Chhattisgarh). The *T. viride* was applied with seed treatment and followed by soil application with FYM. The population of *T. viride* was maintained up to 10^6spore/ml. The *T. viride* was used as talk base powder formulated product with dose 4gm/kg for seed treatment and 400gm/quintal FYM, applied one day before sowing. The experimental data was recorded by calculation of No. of infested plants/m^2, no. of Pod/plant and yield data with cost: benefit ratio. The disease-controlling efficacy of *T. Viride* was associated with the increase in yield 11.88 % and also reduced the disease incidence by 50.17% compared to farmer management practices. The control of chickpea collar rot by biocontrol agents is safe and ecologically sound and appears to be a healthy approach to the disease control.

P (S 07) 09: Effect of Integrated pest management on yield and economics of chilli *Capsicum annuum* L. in Andhra Pradesh

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A field experiment was conducted to study on integrated pest management (IPM) in chilli crop with comparison to Non- IPM at Regadaguduru village, Velugodu mandal, Kurnool district, Andhra Pradesh. Repeated usage of the pesticides causes severe ecological consequences. Alternate approach consisting of ecofriendly components are safe and is most preferable in plant health management. In this view, an investigation was carried out on evaluation of different IPM modules against pest complex of chilli. In the year 2013-14, the numbers of IPM interventions were 16 as against 21 numbers of interventions in Non-IPM plot for cultivar Devanur Deluxe, whereas in case of Super-10 cultivar, it was 16 in IPM plots as against 21 in Non-IPM plots. The IPM plot planted with Devanur Deluxe recorded an average yield of 43.55 q/ha with a net profit of Rs. 1,63,598/- as against 42.25 q/ha of dry chilli with a net profit of Rs1,54,088/- in Non-IPM plot which is a net gain of Rs. 9,510/- in IPM plot. The production cost was Rs. 550/- less in IPM plots and the protection cost was Rs. 17,103/- less compared to Non-IPM plot. The IPM plot Planted with Super-10 recorded an average yield of 51.25 q/ha with a net profit of Rs. 1,68,868/- as against 47.35 q/ha of dry chilli with a net profit of Rs.1,48,882/- in Non-IPM plot which is a net gain of Rs. 19,986/- in IPM plot. The production cost for Super-10 was Rs.3,150/- less and protection cost was less Rs.13,723/-. In Devanur Deluxe, the cost benefit ratio was recorded as 1:2.39 in IPM field and 1:2.06 in Non- IPM field where as in Super-10, it was 1:2.29 in IPM field and 1:1.97 in Non- IPM field respectively.

P (S 07) 10: Management of bacterial wilt of tomato through induced resistance

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Bacterial wilt, caused by *Ralstonia solanacearum*, is one of the vexatious diseases of all the solanaceous vegetables. The disease can cause upto 90 per cent yield loss in tomato. In the absence of resistance in commercial cultivars limited available options in chemical control, it is very difficult to manage the disease. In the present investigations, different abiotic resistance-inducers evaluated. Potassium chloride and oxalic acid at 300 and 200 mM concentration were most effective in managing the disease and increasing plant weight and plant height with minimum disease incidence of 24.44 and 35.55 per cent and maximum disease control of 70.27 and 56.76 per cent, respectively. Sodium salicylate was least effective in managing the disease. Study of mechanism of induced resistance revealed that total phenol content progressively increased in all the treatments upto 7th day after the spray of abiotic inducers of resistance and thereafter it declined. Maximum increase was observed in potassium chloride sprayed leaves (94 ìg/g tissue) followed by oxalic acid (92 ìg/g tissue). It was recorded the lowest in sodium salicylate sprayed leaves (72 ìg/g tissue). While, polyphenol oxidase, peroxidase and phenyl alanine lyase activity was found to be at the peak immediately after 24 h of elicitation and was found maximum in potassium chloride treated leaves and minimum in sodium salicylate treated leaves. These abiotic inducers have the potential to be used for the development of environment-friendly disease management strategy for bacterial wilt of tomato.

P (S 07) 11: Management of black rot of crucifers through abiotic inducers of resistance

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Black rot, caused by *Xanthomonas campestris* pv. *campestris*, is one of the most devastating disease of crucifers. Limited chemicals are available for the management of black rot disease. In the present studies, evaluation of abiotic inducers of resistance under pot conditions against black rot disease of cabbage revealed that all treatments of abiotic inducer of resistance resulted in disease reduction as compared to control. Foliar spray of salicylic acid (20 mM) was most effective with 14.5 per cent disease incidence reducing the disease incidence up to 85.24 per cent followed by sodium salicylate (10 mM) and potassium dihydrogen phosphate (200 mM) with 33.00 and 34.75 per cent disease incidence respectively, while reduction in disease incidence was 66.41 per cent and 64.63 per cent, respectively. All the treatments resulted in significantly increase plant height as compared to control treatment. However plant height was found maximum (9.7 cm) in salicylic acid (20mM) followed by sodium salicylate (10 mM) and potassium chloride (100mM) with 8.6 cm and 8.2 cm respectively. The activity level of key enzymes of plant defence namely polyphenol oxidase, peroxidase and phenyl alanine lyase was maximum at 3 days after he challenged inoculation with bacterium and thereafter declined. Further evaluation of abiotic resistance inducers against black rot disease under field conditions revealed that minimum disease incidence of 10.10 per cent was observed with foliar spray of Salicylic acid (20 mM) which gave 77.23 per cent disease reduction and also increased yield followed by sodium salicylate (10 mM) with disease incidence of 26.03 per cent giving 41.32 per cent disease reduction. These abiotic inducers could be used effectively for the management of black rot of crucifers.

P (S 07) 12: Utilisation of rhizospheric proteobacteria from red and lateritic regions of West Bengal for plant growth promotion and pathogen suppression

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The survey was conducted for collection of rhizospheric soil samples of various cultivated and wild plants from different locations of Birbhum district under lateritic regions of West Bengal. Plant growth promoting Proteobacteria are attractive alternatives as bio-inoculants and bio-control agents. They have received much attention because of their involvement in biotic and abiotic stress tolerance; representing a healthy alternative to the application of chemical fungicides. In the present investigation attempts were made for the enumeration, characterization and application of the most efficient native proteobacteria inoculants for accruing benefit to agricultural crop production in the problematic acid soil. Among 46 native rhizobacterial isolates, 41 % isolates were found as highly acid tolerant and seven isolates (VE1, VE5, VE3, VE2, VE7 VE23 and VE39) were found to be antagonistic against both the *Rhizoctonia solani* and *Sclerotinia sclerotiorum*. VE7 was found to be potent antagonistic bacteria against two soil borne pathogens. Highest mycelial inhibition of *R. solani* was recorded 58.89 % and 52.78 % respectively, when challenged with VE19 and VE7 isolates. The rhizobacterial isolates VE32 and VE7 exhibited maximum mycelial inhibition (62.22 % and 60.56 %, respectively) against *S. sclerotiorum*. VE7, VE9 and VE10 rhizobacterial isolates were found to be the most effective isolates for rhizosphere competence and plant growth promotion of cowpea seedlings. Highest root length were recorded in VE10 and shoot length were recorded in VE7 treated plants, while highest fresh root weight and shoot weight were observed in VE7 and VE10 treated cowpea seedlings respectively. Rhizobacterial isolates VE9 and VE10 were found to be more effective in suppressing the pre & post emergence incidence of damping off as compared to other isolates. Seed and soil treatment with VE9 and VE10 shown significantly least post-emergence damping off (9.7 %) in comparison to control pot (51.4%). The rhizobacterial isolates VE9 and VE10 may be in future be used as microbial consortia for sustainable plant health management under acidic problems of lateritic soils.

P (S 07) 13: Evaluation of different agri-substrates for mass multiplication of potential fungal bio-agents for the control of sheath blight of rice

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Rice crop is severely affected by a large number of fungal, bacterial and viral diseases of which “Sheath Blight” disease caused by *Rhioctonia solani* is one of the most significant disease causing about 50 per cent of yield losses. It is mainly managed through the application of fungicides however, keeping in view their hazardous impact on environment and beneficial microflora, the use of biological control agents has emerged as an important alternative in the modern agriculture. The major constraint in the extensive use of biological control under field conditions is with respect to mass production and delivery systems of bio-agents. In the present investigation seven different agri-substrates *viz*., wheat bran, wheat straw, paddy straw, shelled maize, FYM, vermicompost and cow dung were evaluated for the growth of potential fungal bio-agents including three standard fungal bio-agents *Trichoderma koengii* (DMA-8), *T. harzianum* (TH-4), *T. asperellum* and two *Trichoderma* isolates *Trichoderma* sp. (I-7) and *Trichoderma* sp. (I-8) isolated from the rhizospheric soils of different rice growing areas of Himachal Pradesh under *in-vitro*. Wheat bran, wheat straw and vermicompost agar media provided the maximum growth (90.00 mm) of all the isolates whereas, paddy straw agar medium also gave highest (90.00 mm) growth of bioagents except *Trichoderma* sp. (I-8) which gave 81.00 mm growth. The most effective bioagent *viz*., *T. harzianum* (TH-4) was formulated with three different agri-substrates *viz*., wheat bran, wheat straw and vermicompost and evaluated as soil treatment for the management of sheath blight. *T. harzianum* (TH-4) formulation in wheat bran showed maximum reduction of 56.67 and 34.27 per cent in disease incidence and severity followed by wheat straw based formulation with 50.00 and 28.54 per cent reduction in disease incidence and severity, respectively.

P (S 07) 14: Evaluation of Tebuconazole 50% + Trifloxystrobin 25% WG for bio efficacy against Alternaria blight & powdery mildew disease in cumin

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Cumin is an important seed spice crop of India. *Alternaria blight* and powdery mildew diseases are important limiting factors for production of cumin. In the present study, the experiments were conducted during Rabi 2016-17 and 2017-18 at Agricultural Research Station, Mandor, Jodhpur for the management of *Alternaria* blight and powdery mildew disease of cumin in Western Rajasthan. During the study, cumin blight showing the symptoms of dark brown spots on leaves and stems and later complete drying of the plants was observed with severity ranging from 7 to 36 percent. Powdery mildew was observed with incidence in the range of 3 to 17 percent. On the basis of field experiments, the dose of Tebuconazole 50% + Trifloxystrobin 25% WG @350g/ha was found effective to manage *Alternaria* blight and powdery mildew disease and gave maximum seed yield (508 kg/ha. And 597 kg/ha) followed by Tebuconazole 700 ml (404 kg/ha and 525 kg/ha) and Tebuconazole 50 % + Trifloxystrobin 25% WG@ 300g (395 kg/ha and 503 kg/ha) during 2016-17 and 2017-18 respectively. The application of fungicides in combination resulted in significantly greater disease control, over their individual applications as well as over untreated control.

P (S 07) 15: Integrated disease management technology for sesame

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Sesame (*Sesamum indicum* L.) is one of the world's oldest oilseed crops and has been cultivated in Asia since ancient times and largely produced for its oil and is also used as a flavoring agent. The seeds of sesame contains 40 to 63 percent oil, which contains significant amount of oleic and linoleic acids. In the country, it is grown in 15.62 lakh hectares area with production of 7.84 lakh tones and productivity of 502 kg/ha during 2018. Sesame phyllody is the most destructive disease in India. Among the fungal diseases, *Macrophomina* root & stem rot, *Alternaria* leaf blights, *Phytophthora* leaf spot, *Cercospora* leaf spot, Powdery Mildew are important diseases of sesame. The incidence of important diseases varies from state to state based on agro climatic situations. Seed treatment with Thiram (0.2%) + Carbendazim 50WP (0.1%) and two foliar spray should be done with wettable sulphur (0.25%) was most effective to minimize the incidence of powdery mildew. Seed treatment with Thiram (0.2%) + Carbendazim 50WP (0.1%) or *T. viride* @ 10 g/kg and two foliar sprays of (Mancozeb 2%+ Carbindazim1%) was effective for management of the *Alternaria* and *Cercospora leaf spot* disease. Seed treatment with Imidacloprid (17.8 SL @ 5 ml/kg) followed by foliar spray of Acetamiprid 20% SP @ 0.3 g/l was found effective in reducing the vector population and phyllody incidence. Seed treatment with *T. viride* @ 10 g/kg, furrow application of enriched *T. viride* (2.5 kg in 100 kg of FYM) @ 250 kg/ha followed by two foliar spray of combo-product (Tebuconazole 50% + Trifloxystrobin 25%) @ 0.5 g/l was found and economical for the management of *Macrophomina* root and stem rot of sesame.

P (S 07) 16: Efficacy of various compatible insecticides for management of sesame phyllody

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Sesame (*Sesamum indicum* L.) is one of the world"s oldest oil crops and has been cultivated in Asia since ancient times and largely produced for its oil and is also used as a flavoring agent. In the country it is grown in 15.62 lakh hectares area with production of 7.84 lakh tones and productivity of 502 kg/ha during 2018. Sesame phyllody is an important disease caused by a phytoplasma and is transmitted by a leaf hopper called *Orosius albinctus*. The affected plants become stunted and floral parts are modified in to leafy structures bearing no fruits and seeds causing yield loss up to 33.9 per cent. Keeping this in view, a field experiment was conducted during 2018 at research area of AICRP on Sesame and Niger for the effective management of

phyllody in sesame. The experiment comprising eight treatments (T_1- Seed treatment with Imidacloprid 17.8 SL@ 5ml/kg seed;T_2- T1+ Spray of Imidacloprid 17.8% SL @ 0.25ml/l;T_3- T_1 + Spray of Acetamaiprid @ 0.3g/l;T_4- T_1 + Spray of Thiocloprid @ 1ml/l;T_5- T_1 + Spray of Thiomethaxam @ 0.25 g/l;T_6- T_1 + Spray of Lambda cyhalothrin@ 1ml/l;T_7- T_1 + Spray of Azadirachtin @ 0.03%;T_8- Control was laid out in Randomized Block Design with three replications. Among the eight treatments tested a positive and significant response was found with the seed treatment of imidacloprid 17.8 SL @ 5 ml/kg + spray of Acetamaiprid 20 % SP @ 0.3 g/L recorded the least disease incidence (7.05 per cent) and maximum seed yield (5.21 q/ha).The results on benefit cost ratio revealed that highest benefit cost ratio was recorded in treatment T_3(4.39). All the treatments are superior over the control.

P (S 07) 17: Efficacy of various fungicides against *Sclerotium rolfsii,* causing stem rot of groundnut (*Arachis hypogaea* L.)

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Groundnut (*Arachis hypogaea* L.) crop is prone to many fungal diseases, of which stem rot caused by *Sclerotium rolfsii* Sacc. has been emerging as major threat, under changing climate. Various fungicides have been reported as effective to manage the disease. Therefore, the present study was attempted to assess *in vitro* the efficacy of 20 fungicides (seven systemic, seven contact, six combi / co-formulation fungicides), applying CRD and all the treatments replicated thrice, during *Kharif*, 2018, at the Department of Plant Pathology, Dr.BSKKV, Dapoli. Results revealed that among seven systemic fungicides evaluated (each @ 500, 750 and 1000 ppm), except Carbendazim 50% WP and Fosetyl-Al 80% WP rest five *viz.,* Propiconazole 25% EC, Tebuconazole 25.9% EC, Difenconazole 25% EC and Triadimefon 25% WP, resulted with 100 per cent mycelial growth inhibition, at all of the test concentrations, followed by Thiophanate methyl 75% WP with 100% mycelial growth inhibition @ 750 and 1000 ppm. Among seven contact fungicides evaluated (each @ 2000, 2500 and 3000 ppm), except Copperoxy chloride 50% WP, rest six *viz.,* Captan 50% WP, Copper hydroxide 77% WP, Zineb 75% WP, Mancozeb 75% WP, Chlorothalonil 75% WP and Propineb 70% WP resulted with 100 per cent mycelial growth inhibition. All of the six combi- / co-formulation fungicides evaluated (each @ 1500, 2000 and 2500 ppm) resulted with 100 per cent mycelial growth inhibition of the test pathogen, over untreated control.

P (S 07) 18: *Fusarium fujikuroi* sensitivity against carbendazim: An increasing concern for bakanae disease management

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Bakanae caused by *Fusarium fujikuroi* is one of the emerging diseases of rice in India. High bakanae disease incidence (upto 40%) was observed in Punjab, Haryana, western Uttar Pradesh and Uttarakhand states of India. Most of the basmati rice varieties are susceptible to the disease. Carbendazim (MBC) is the only fungicide recommended for the seed treatment for the bakanae disease management. To maintain sound rice cultivation, it is important to locate the MBC resistant populations and prevent their development. The present study was conducted in a means to identify the resistant isolates of *F. fujikuroi* and to discover the mutation at the significant codon at different concentrations of carbendazim. A total of 86 isolates of *F. fujikuroi* collected

during the years 2011 to 2017 were screened for the fungicidal tolerance against carbendazim, using different concentrations of the fungicide in potato dextrose agar (PDA) media until a concentration was identified where most of the isolates were sensitive while only few were resistant. Most of the isolates could not grow above the concentration of 100ppm. However, some newly collected isolates could tolerate it upto 500ppm.7 isolates of the total were found resistant, 5 upto a concentration of 400 and 2 at a further concentration of 500ppm of carbendazim. PCR-based detection for the â2-tubulin gene was done for the resistant and sensitive isolates. The gene was purified, cloned and sequenced. The sequences of isolates from different concentrations were analysed using bioedit software and checked for point mutations in the carbendazim resistant isolates at the specified codons. Results indicated the presence of point mutations in the resistant isolate (500ppm). The current study provides strong evidence that MBC resistance in *F. fujikuroi* results from changes in *â2 tub* and that highly resistant MBC strains had mutations at codon 198 and 235, and moderately resistant MBC strains had mutations at codon 200 and 235.

P (S 07) 19: Rhamnolipid biosurfactants: Novel elicitors against banded leaf and sheath blight (BLSB) of maize

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Rhizoctonia solani f. sp. *saskii* is an important pathogen causing banded leaf and sheath blight (BLSB) disease of maize. The disease is mainly prevalent in South and South-east Asian countries. It is a major disease and can cause complete wipeout of the crop. The disease symptoms appear as irregularly globular to elongated lesions which are soon bleached and enlarge rapidly resulting in discoloured areas alternating with dark bands, apparent on lower leaves after 7-8 days. Management practices for the disease by chemical and biological procedure is extremely important to minimize the destruction of crop and to prevent yield losses. Rhamnolipids (RLs) are glycolipids produced by bacteria and are involved in surface motility and biofilm development and have recently been shown to elicit plant defense responses. The present study was carried out keeping with the biological approach of BLSB management during *kharif* 2017, 2018 and 2019 by five simultaneous treatments of RL biosurfactant using maize variety Vivek QPM9. Four main treatments were designed, *viz*., Biosurfactant seed treatment 100mg/lt (T1), Biosurfactant seed treatment 100mg/lt + foliar spray (100mg/lt) (T2), Biosurfactant foliar spray (100mg/lt) (T3), Hexaconazole foliar spray (1ml/lt) (T4) and inoculated control (untreated) (T5). Maximum disease inhibition was found in the biosurfactant seed treatment (76.76%) along with maximum yield (50.47 q/ha) followed by Biosurfactant seed treatment + foliar spray which provided 49.30% disease inhibition and 45.31 q/ha yield. The results stated in line that RL biosurfactants act as a systemic substance in management of BLSB disease of maize and that a combination of RL biosurfactants in various seed treatments and foliar sprays as booster dose can participate in the protection of maize crops from the foliar disease.

P (S 07) 20: Field evaluation of various chemicals and bioagent against bacterial blight of Bt cotton.

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In India, the states of Maharashtra (26.63%), Gujarat (17.96%) and Andhra Pradesh (13.75%) and also Madhya Pradesh are the leading cotton producing states, these states have a predominantly tropical wet and dry climate. Bacterial blight cause yield loss of 38.78 per cent (Bhattiporlu, 2013). Losses are less when only leaves are infected but when stem lesions are formed, the losses may be high as upto 90%. The experiment was planned to evaluate the twelve spray treatments *viz.* 10 chemicals, one bioagent and one untreated control in natural field cnditions against *Xanthomonas axonopodis* pv*. malvacearum* causing bacterial blight of cotton. First Spray was given at first apperance of disease and subsequent two sprays at 15 days interval were given. observations on disease incidence (PI) and disease severity (PDI) were recorded before one day of each spray. Amongs the chemicals and bioagent tested the results obtained after third spray indicated that significantly lowest disease incidence of 20.84 % was recorded by the treatment streptocycline + copper oxychloride followed by the treatment streptocycline + carbendazim (20.92 %), streptocycline + copper hydroxide (20.96 %), bordeaux mixture (21.35 %), but all four treatments found at par in succession as against the unsprayed control 51.18 per cent (PI) and lowest disease severity of 10.22 % was recorded by the treatment streptocycline + Copper oxychloride followed by the treatment streptocycline + carbendazim (11.33 %), streptocycline + copper hydroxide (13.00 %), streptocycline (13.45 %).

P (S 07) 21: Efficacy of extracts of aromatic plants against early blight disease of tomato

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Early blight disease in tomato (*Solanum lycopersicum*) caused by *Alternaria solani* (Ellis and Martin) which causes great reduction in the quantity and quality of fruit yield. The objective of this work to study the effect of six plant extracts *i.e. Ocimum basilicum* (Basil), *Azadirachta indica* (Neem), *Datura stramonium* (Jimsonweed) *Eucalyptus chamadulonsis* (Eucalyptus), *Murraya koenigii* (Curry tree) and *Allium sativum* (Garlic) against *Alternaria solani in vitro* and *in vivo*. In *in vitro* study the leaf extracts of *O. basilicum, A. indica* and *A. sativum* at 10% concentration caused highest reduction of mycelial growth of *A. solani* (68.4, 64.3 and 60.2%, respectively), while *D. stramonium* and *M. koenigii* at 10% caused the lowest inhibition of mycelia growth of the pathogen. In greenhouse experiments the highest reduction of disease severity was achieved by fungicide (Ridomil Gold 50% WP, 15% metalaxy+35% at 2 g L^{-1}) 82.8% followed by the extracts of *O. basilicum* and *A. sativum* at 10% concentration. The greatest reduction of disease severity was achieved by Ridomil Gold 84.2% followed by *O. basilicum* at 10% and the smallest reduction was obtained when tomato plant was treated with *D. stramonium* and *M. koenigii* 10% (46.1 and 45.2%, respectively). Fungicide, *O. basilicum* and *A. sativum* at 10% increased the fruit yield 85.7, 76.2 and 66.7% compared to infected control. All treatments, plant extracts and fungicide (Ridomil Gold) significantly reduced the early blight disease as well as increased the yield of tomato compared to infected control under field condition.

P (S 07) 22: Natural products an important alternative to pesticides for the management of viral diseases and enhance the growth of musk melon

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Different natural products *viz.* Buttermilk, Kaolin and natural oils were used in this study for the management of viral disease on musk melon. Among these spray of buttermilk at 20 per cent concentration was found to be highly effective with minimum mean per cent disease incidence (50.8%) and mean per cent disease severity (21.3%) followed by Kaolin 2% having mean per cent disease incidence 60 per cent and diseases severity of 24.3 per cent. Other treatments were also found to be significantly effective in the management of viral disease as compared to control having 100 per cent mean per cent disease incidence and 73 per cent mean per cent disease severity. In addition to disease control buttermilk 20 per cent was also found to increase mean vine length (200.3 cm), mean primary branches (4.7), number of fruits per plant (2.2), number of marketable fruits per plant (2.2), fruit weight (983.3 g), total soluble salts (11.5 brix), ascorbic acid (33.1 mg 100^{-1} ml), beta carotene (4.5 mg 100^{-1} g), Chlorophyll content (26.91 mg m^{-2}) and Photosynthetic activity (43.80 mg m^{-2}). Along with buttermilk 20%, kaolin spray at 2 per cent was also observed to have significant effect on all above mentioned traits. As buttermilk 20 per cent spray was found to increase growth and yield of sprayed plant along with controlling viral disease. Therefore, use of buttermilk could be an alternative to avoid residue, pest resistance and pest resurgence problem

P (S 07) 23: Potential of leaf blotch disease of turmeric (*Taphrina maculans*) on crop phenology and its yield attributing character

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Turmeric is very important spice in India, which produces nearly entire whole world's crop and consumes 80% of it. India is by far the largest producer and exporter of turmeric in the world. Turmeric occupies about 6% of the total area under spices and condiments in India. The spice turmeric, derived from the rhizome of *Curcuma longa* L, has been used for centuries in food preparation and in traditional medicines to treat numerous diseases. Rhizomes of turmeric are used in several culinary preparations. They have been used as household remedies since time immemorial. The turmeric crop suffers severely due to leaf blotch disease which is caused by *Taphrina maculans* (Syd.) Buttler and Bisby. The losses by leaf blotch are always considered to be a limiting factor for yield and quality of rhizomes. Losses occurred in green rhizome due to the leaf blotch were estimated at Tirhut College of Agriculture Dholi, Muzaffarpur during 2018-19. Losses were found in all the growth parameters viz., Number of leaves per plant, Number of tillers per plant, Leaf area, Number of fingers, Weight of fresh rhizomes Due to leaf blotch of turmeric, maximum losses were noticed in leaf area (26.27%) and in weight of fresh rhizomes (25.18%).

P (S 07) 24: *In vitro* effect of various seed dresser on seed mycoflora, seedling vigour and seedling mortality

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Among the diseases leaf spot / blight caused by *Alternaria carthami* (Chowdhury) is wide spread and have continued to be the major constraints in the production and productivity of safflower all over the country in general as well as particularly in the state of Maharashtra. The disease (*A. carthami*) has been reported to cause yield losses to the tone of 25 to 60 per cent all over India (Singh and Prasad, 2005) and 20 to 80 per cent in Maharashtra state. A *In vitro* experiment was conducted with 9 seed dressing fungicides *viz*., Thiram, Carbendazim, Carboxin, Mancozeb, Thiram + Carbendazim, Thiram+ Carboxin, Thiram+ Mancozeb, Carbendazim+ Carboxin and Carbendazim+ Mancozeb against safflower seed mycoflora by rolled towel paper method.Observations on effect of these fungicides in percent seed mycoflora were recorded upto 7 days of incubation. Results revealed that among these seed dresser fungicides, the lowest seed infection with *Macrophomina phaseolina* was observed in seed treatment Thiram + Carboxin, Thiram+ Mancozeb and Carbendazim+Mancozeb (0.00%) whereas, the maximum percent seed infection with *Alternaria carthami* and *Fusarium oxysporum* f. sp. *carthami* was observed in seed treatment Thiram+Carbendazim (10.50 % and 8.00 % respectively) whereas, the lowest percent seed infection was observed in seed treatment Thiram + Mancozeb (6.66% and 3.33 % respectively). At 48 hrs, 72 hrs, 96 hrs, 120 hrs, 144 hrs and 168 hrs incubation the lowest percent seedling vigour was observed in seed treatment Thiram + Carbendazim (13%) whereas, the maximum percent seedling vigour observed in treatment Thiram+ Mancozeb (16%), which was significantly superior over all the treatments.At 48hrs.and 72 hrs. maximum percent of seedling mortality was observed in treatment Thiram+Carbendazim (5.3 % and 10.9% respectively) and lowest percent seedling mortality was observed in seed treatment Thiram+ Mancozeb (0.00% and 5.5% respectively), which was significantly superior over all the treatments.

P (S 07) 25: Management of leaf, node and neck blast disease cented rice KN -3 caused by *Pyricularia oryzae* Sacc. (sexual stage *Magnaorthe oryzae*) in Siddharthnagar of Uttar Pradesh, India.

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Kalanamak is one of the finest quality scented rice of India. Its name derives from black husk (kala = black; the suffix ‘namak’ means salt. Kala namak is cultivated in Trai Belts, Sidhharthnagar. Rice blast is one of the most destructive diseases of rice. Because neck and node blast affect the panicle directly, yield losses in affected plants are very high. Blast is caused by the fungus *Pyricularia oryzae* Sacc. It can affect all above ground parts of a rice plant: leaf, collar, node, neck, parts of panicle, and sometimes leaf sheath. Leaf, node and neck blast commonly occur together and have similar symptoms. When a node or neck blast infection is present, it is the main cause in plants to develop few or no grains at all. Blast can occur wherever blast spores are present. It occurs in areas with low soil moisture, frequent and prolonged periods of rain shower, and cool temperature in the day time. In upland rice, large day-night temperature differences that cause dew formation on leaves and overall cooler temperatures favor the development of the disease. Rice can have blast in all growth stages. However, leaf blast incidence tends to lessen as plants mature and develop adult plant resistance to the disease. Adjust planting time. Sow seeds early, when possible, after the onset of the rainy season. Split nitrogen fertilizer application in two or more treatments. Excessive use of fertilizer can increase blast intensity. Flood the field as often as possible. The harvest time of this rice is 6-7 months. It can be used judiciously for control to control blast was sprayed thrice at weekly interval starting from the booting stage. All these fungicides were found to be effective in controlling node and neck blast disease as compare to control one. Among them, Krishi vigyan Kendra, Experimental Farm was conducted during kharif season of 2017-18 to 2018-19 at Siddharthnagar to know the efficacy of different commercially available Systemic fungicides like Propiconazole 25% EC (0.1%) + Potassium chloride, Tricyclazole 22% + Hexaconazole 5% SC (0.2%), Streptomycin 5% + Thiophanate Methyl 50% WP (0.15%), , Kasugamycin 2% WP (0.2%), Hexaconazole 5% + Zineb 68 % WP (0.2%) and bio-agent against the disease under field condition. Results exhibited that Propiconazole 25% EC (0.1%) + Potassium chloride was found to be the most effective leaf blast severity (6.23%), neck blast incidence (8.97%), and highest percentage disease control (87.08% and 79.62% in leaf blast and neck blast respectively) and rice yield (28.23qt/ha) was recorded under control treatment. The least rice yield was obtained in *Trichoderma viride* (24.22 qt/ha.).

P (S 07) 26: Integrated disease management of spot blotch of wheat

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Spot blotch caused by *Bipolaris sorokiniana* is prevalent in warmer and humid wheat growing regions of the world. Climate change has aggravated the disease scenario in India, which has led to increase in the incidence of spot blotch of wheat caused by the *Bipolaris sorokiniana.* The area under North-eastern plains of India is extremely affected by spot blotch disease. An experiment was conducted during *Rabi* 2017-18 to explore the possibility of Integrated Disease Management (IDM) on spot blotch disease of wheat. Two most effective fungicides (Propiconazole and Hexaconazole), two plant extracts (garlic clove and eucalyptus leaf extracts) in combination with two date of sowing (25th November and 26th December 2017) were applied under field conditions for the management of spot blotch of wheat. Two sprays of Propiconazole gave lowest PDI, highest disease control, yield and 1000-grain weight in both timely and late sowing (25th November and 26th December). Two spray of Propiconazole (0.1 %) at 15 days interval under timely sown condition was best in controlling spot blotch of wheat with significant increase in yield over unsprayed crop. With the delayed sowing (26th December) there was significant decrease in disease control with significantly less yield. Hexaconazole was equally effective and on the basis of cost- benefit ratio, has an edge over Propiconazole.

P (S 07) 27: Eco-friendly management of charcoal rot of sesame

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Sesame (*Sesamum indicum)* commonly known as til is one of the important edible oilseed crops that is having good nutritional value. The crop has remarkable antioxidant properties and used in various skin care cosmetics. Its seeds are rich source of oil (around 50%), proteins (18-20%) and contains about 85% of unsaturated fatty acids. The crop is infected by many diseases as sesamum phyllody,charcoal rot,fusarium wilt,phytophthora blight. Charcoal rot caused by *Macrophomina phaseolina* has been a major threat to successful cultivation of sesame. The disease is reported to cause about 5-100% losses.The pathogen being facultative in nature survives as microsclerotia in soil and infested plant debris that serve as the primary source of inoculum and have been found to persist in the soil up to three years. The control of plant disease using pesticides raises serious concerns about food and environment. Due to build up of high inoculum in soil and to avoid soil pollution through chemicals it has become necessary to test phyto-extracts and bioagents against the pathogen. As the eco-friendly management of charcoal rot of sesame can be done with the help of botanicals and bioagents. The phytoextracts of different plants have been tested against the pathogen by using poison food technique. In the present study the extract of neem,garlic,bougainvillea,lantana and parthenium were used under *in-vitro* conditions and the percent growth inhibition of mycelium was observed. The biological control agents were also tested for their efficacy under *in-vitro* conditions. Among Phyto-extracts tested, maximum growth inhibition was recorded with *Lantana camara* and *Allium sativum* respectively. While among the bio-agents tested, *Trichoderma* sp. Was found most effective in inhibiting the growth of the pathogen. So the management of disease can be done with the help of botanicals and bio-agents.

P (S 07) 28: Biofumigation: Management of soil borne disease

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Soil borne diseases are very challenging to control, traditionally chemical soil fumigants were used to manage them but they are harmful to the environment and human health. Biofumigation is based on the incorporation of fresh plant mass into the soil, which will release several substances that would suppress soil-borne diseases. When managed properly mustard offers another tool to help growers control soil born pests and diseases. The use of mustard as a biofumigant is particularly interesting for organic producers. It is important to strictly follow the outlined cultural practices if you want to have any chance of success using mustard as a biofumigant. Proper chopping of plant material and soil incorporation is of utmost importance. Although mustard is a remarkable biofumigant, it has similar benefits that is expected from any other cover crop such as; prevention of soil erosion, recycling of soil nutrients, improved soil structure and maintaining soil organic matter. Mustard can also acts as a deterrent to many insects (wireworm) and pests therefore it may prevent many problems from occurring in your field. Interestingly, there are other crops that show possible biofumigation effect.

P (S 07) 29: Eco-friendly management of web blight disease of cowpea through bioagents

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Cow pea (*Vigna unguiculata* (L.) is attacked by many fungal, bacterial and viral diseases. Among the diseases, web blight caused by *Rhizoctonia solani* Kuhn is the most serious soil borne disease in cow pea growing areas due to environmental conditions like high temperature and humidity causing severe yield loss. A field trial was conducted during 2016 *kharif* season to manage web blight disease of cow pea. Combination of *T. harzianum* (Th-BKN) plus *B. subtilis* (Bs-BKN) used as seed treatment (5 + 5 g kg^{-1}) and soil application (5+5 kg ha^{-1}) proved to be most effective against web blight incited by *R. solani* in field conditions and provided maximum disease control (79.5%). Seed emergence, plant survival, , fresh and dry weight, root and shoot lengths and grain yield was higher and per cent cowpea plant mortality was lower in treatment *T. harzianum*

(Th-BKN) plus *B. subtilis* (Bs-BKN) used in combination as seed treatment (5 + 5 g kg^{-1}) and soil application (5+5 kg ha^{-1}). The bioagents studied in the present investigation could be therefore, used as part of Integrated Disease Management (IDM) strategy for web blight of cowpea in areas where the disease is reported to cause yield loss.

P (S 07) 30: Antifungal potency of plant extracts against *Alternaria solani* and *Colletotrichum capsici*

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Crop protection prefers the use of fungicides as the most important method of shielding the crop plants against the fungal attack. But the development of resistance in pathogenic fungi to the fungicides and increasing residual hazardous effects has given a thrust to search for phytoextracts derivatives that can obstruct the fungal pathogenicity. Against these backdrops, this study was aimed to evaluate the efficacy of different medicinal and weed plants in managing the early blight of tomato caused by *Alternaria solani* and anthracnose of chilli caused by *Colletotrichum capsici*. The methanol extract of ten plants species *viz., Lantana camara, Argemone maxicana, Urtica dioeca, Cannabis sativa* (weed species), *Azadirechta indica*, *Terminalia arjuna*, *Eucalyptus globus, Cymbopogon citratus*, *Cassia fistula* and *Legistromia indica* (medicinal plant species) at different concentration (1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%) in Potato Dextrose Agar by poison food technique. Out of these screened plant, three extracts (2% concentration) showed significant growth inhibition namely, *C. fistula*, *E. globus* and *A. indica* against both the test pathogen. The plant extracts shortlisted for pathogen inhibition have potential to be developed as potent fungicides in organic farming.

P (S 07) 31: Gamma radiation effects on seed germination, root and shoot attributes in lentil

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Lentil (*Lens culinaris*) is one of the important and nutritious cool season pulse crop. Lentil contains about 25% protein, 2.1% mineral, 59% carbohydrate 0.7% fat and 0.7% fiber, it's also rich source of phosphorus and carotene. Lentil is generally grown in dry (rainfed) areas. India ranks 1st in area 39.79% and 2nd in lentil production 22.79%.The seed germination test was designed after irradiating the lentil seeds of popular local variety Maitree using Gamma Chamber 5000 with gamma irradiation ranging between (50,100,150,200,250,300,400 Gy). The LD_{50} was calculated to be 400Gy. These studies revealed that the maximum germination percentage was observed in control seedlings plate 81.33% germination. The germination percentage decreases with the increases gamma ray doses. The lowest percentage observed in 400gy and 500gy gamma radiation respectively 40% and 38.17%. The root emergence measurement showed a significant decrease after 12 days after irradiation. The maximum root length was recorded in the control samples 6.95cm and the minimum length was observed at 500gy treated plate 0.74cm and it was found that root lengths at doses of 50, 100, 150, 200, 250, 300, 400gy were 6.83, 6.67, 6.09, 5.35, 2.80, 1.30, 1.23 cm respectively. Whereas, shoot length was found be the maximum in control plate with 18.25 cm, and the minimum length 0.74cmin 500gy irradiated seeds. The root weight followed the same pattern with the increase in irradiation doses, showed a reduction in the root weight, the minimum root weight was observed to be 0.005g in 500gy dose and maximum weight was recorded 0.022g in control plot. The shoot weight also decreased with the increase in irradiation doses. The maximum weight of 0.077gm was recorded in control plate and minimum was 0.007gm in 500gy treated seeds. Root and stem attributes are vital in exploiting the disease resistance genes for mutation breeding instead of using the fungicides.

P (S 07) 32: Efficacy of bio-agent and fungicides for the management of charcoal rot of soybean

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Soybean (*Glycine max* (L.) is an important oilseed crop grown in 108.83 lakh hectare areas in the country and have fifth position in production in the world. Soybean contained 40% protein, 20%oil, 20% carbohydrates and 5% mineral. This is the main crop of Madhya Pradesh sown in 22 hectare and covered 55% share of the total production. Gradually soybean production and quality goes down due to occurrence of biotic and abiotic factors. An extensive surveyed have been done during the crop period from seedling stage to pod formation stage in the kharif season of year 2017 and found that nearly 63 percent crop was damaged due to occurrence of charcoal rot. A field experiment was conducted to study the efficacy of fungicides for the management of charcoal rot in two successive soybean season such as in kharif 2018 and 2019. Experimental results indicated that bio-agent and fungicides alone and in combinations significantly reduced the incidence of disease in comparison to control check. Seed treated with Carbendazim before sowing and plant sprayed by Tebuconazole+Sulphur before flowering gave maximum disease control(78.93%) followed by seed treatment with *Trichoderma viride* and spraying of Azoxystrobin (71.37%) in comparison to *Pseudomonas fluorescens* used for seed treatment and Tebuconozole as spray (61.95%). However seed treatment with Thiram and plant sprayed with Carbendazim noted 35.63% disease control. Application of farm yard manure applied before sowing and soil treated with *Trichoderma viride* had to reduce 58.37% disease incidence. Application of Carbendazim and Tebuconazole+sulphur was found better (16.39q/ha yield and net return Rs. 36365/ha) than *Trichoderma viridae* and spraying of Azoxystrobin in term of seed yield of soybean and net return due to better control of disease. Minimum yield (6.35q/ha) was recorded in control check.

P (S 07) 33: Evaluation of fungicides and botanicals as seed treatments on seedling vigour & seed germination and viability of sclerotia admixtured with moongbean seeds

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Different fungicides and botanicals were evaluated for their effect on seed germination, seed vigour and viability of sclerotia admixtured with moongbean seeds. Among various fungicides tested *in vitro* condition, vitavax power (carboxin 37.5 % + thiram 37.5 % WS) 3gm/Kg seed azoxystrobin 23% SC 2ml/Kg seed and adexar (fluxapyroxad 62.5 g/l + epoxiconazole 62.5 g/l) 2ml/Kg seed gave 100 per cent suppression of mycelial growth from sclerotia of *R. solani* even after 72 hours of incubation. Like wise different botanical extracts of same concentration (10% each) were tested. Thuja gave best results as compared to others. In case of *in* *vitro* and *in vivo* evaluation of fungicidal and botanical seed treatment on seedling germination and plant vigour of moongbean, it was observed that in both the conditions, vitavax power (carboxin 37.5 % + thiram 37.5 % WS) and carbendazim respectively were found highest germination per cent and vigour index among all the fungicides while in case of botanicals neem was found most effective under *in vitro* condition with 100 per cent germination and heighest vigour index (1643.3) and thuja was found significantly superior in order to germination per cent (93.33%) and vigour index (1353.29) under *in vivo* condition.

P (S 07) 34: Impact of seed priming with fungicides and biocides on germination of wheat caused by *Bipolaris sorokiniana*

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B. Sorokiniana is a most destructive fungus causing foliar disease of wheat and spreading all the wheat growing area' s of country. The present investigation were taken to evaluate the potentiality of different seven fungicides (Raxil 060 FS, Trifloxystrobin 500SC, Trifloxistrobin + Tebuconazole 080FS, Vitavax, Flint (Trifloxystrobin 50WG), Nativo 75WG (Trifloxystrobin 25% + Tebuconazole 50%) and Tebuconazole 2% D S), bioagent (*Trichoderma viride*) and botanical (Neemexcel) were tested against *B. Sorokiniana* on wheat seed in blotter paper method. It was revealed that seed treatment with fungicides and biocides significantly increased the germination percentage of wheat seed over the control except Nativo 75WG and Trifloxystrobin + Tebuconazole080FS. The maximum germination with 100 per cent was recorded in the treatment of *Trichoderma viride* followed by Raxil 98.64%, Tebuconazole 2%DS 98.24 per cent and vitavax 96.00.Seed treatment with neem product (neemexel) gave(93.88per cent) the superior result over the control(92.00 per cent) but inferior to other treatment *viz*. Trifloxistrobin +Tebuconazole 080FS (82.00 per cent), Nativo 75WG (Trifloxystrobin 25% + Tebuconazole 50%) 84.40 per cent, Flint (Trifloxystrobin 50WG), 90.40 per cent and Trifloxystrobin 500SC (91.20 per cent) .

P (S 07) 35: Efficacy of plant extracts, bio-agents and fungicides to control Alternaria blight of tomato in Western parts of Rajasthan

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Tomato (*Lycopersicon esculantum* L.*)* is the third most important crop in India. The crop suffers from various fungal, bacterial, viral, and nematode diseases. Among the various diseases, early blight or fruit rot disease that is caused by *Alternaria solani* [(Ell. and Mart.) Jones and Grout] is one of the most destructive diseases of tomato resulting losses as high as 78 per cent. In the present study efficacy of plant extract, bioagents, cow by product and fungicides was evaluated against *A. solani.* The efficacy of different plant extracts and bio-agents were evaluated against *A. solani in vitro.* At 15% concentration, Datura extract was most effective among tested plant extracts. Efficacy of different bio-agents *i.e. Trichoderma viride, T. harzianum, Pseudomonas fluourescens and Bacillus subtilis* were evaluated, among them *T. harzianum* was most effective *in vitro*. Efficacy of novel fungicides and cow by products were evaluated against *A. solani in vitro* at different concentrations. At 250 ppm, Propiconazole 25%EC was found most effective followed by Mancozeb 50%WP, among the tested fungicides. Among the cow by products*,* 20% concentration of cow urine was found most effective followed by cow dung and butter milk *in vitro*. Under *in vivo* condition, the efficacy of eight fungicides and cow by products was tested against *A. solani*. Foliar application of Propiconazole @ 0.2% was found highly effective as it gave minimum disease intensity and maximum fruit yield followed by Mancozeb 64% + Thiophenate methyl 12%. 10% concentration of combined effect of seed treatment and foliar application of cow urine was most effective followed by cow dung and butter milk.

P (S 07) 36: Management of shoulder browning disease of mango at different geographical locations

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Diseases have great significance in productivity, quality and production of mango (*Mangifera indica* L.). Shoulder browning has emerged as a great threat to aesthetic value of mango wherever fruits stay on trees after the onset of monsoon. The disease mostly appears in the form of browning of epicarp in the shoulder region of fruits in slightly tear stain pattern. During rainfall, water draining through canopy usually contain canopy wash along with pollutants, sooty mould and spores of pathogens, and when it drop and stay on shoulder region of fruits, after drying it stain the fruit epicarp. With the intermittent rains, the process is repeated and heavy inocula load is deposited on fruits. The infection process begins in fully mature fruits and colonization by pathogens becomes rapid during ripening of fruits. Survey studies indicated variation in disease incidence in central and western Uttar Pradesh due climatic variation. Therefore, the effective treatments identified at Rehmankhera, Lucknow during 2018 were tested at two locations (Khakhara and Rehmankhera) in Lucknow district and two locations (Behat and Ighari) in Saharanpur district during 2019 fruiting season. Bagging of fruits was done during June, first spray was done during second fortnight of June and II spray during first fortnight of July at 15 days interval and fruits were harvested about 30 days after II spray. Maximum incidence and severity of disease in untreated fruits was recorded 100 per cent and 90 PDI at Rehmankhera, Lucknow and minimum, 90 per cent and 32.5 PDI at Ighari, Saharanpur respectively. All the treatments significantly suppressed the incidence and severity of disease in comparison to control. However, difenoconazole (0.05%) and agrospray oil (2.0%) were most effective followed by agrospray oil (1.0%), agrospray oil (0.5%) and Tebuconazole+Trifloxystrobin (0.025%) respectively. Results provided conclusive evidence of success in management and residues under permissible limits.

P (S 07) 37: Soil fertility and plant nutrient management under different rice genotype

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The soil is the primary resource for life on this planet, but it is a very vulnerable resource. Increased food security and the alleviation of poverty require improvements in the productivity of food crops. The Ethiopian population has been consistently increasing, and to fulfill their demand for food and raw materials, improved plant nutrition has remained as one of the major factors to increase crop yields. As a result, use of our knowledge of plant nutrition to maximize agricultural yields grows in importance. Smallholder farmers require simple and sustainable techniques to improve the productivity of crops. Fertilizer-use recommendations need to change with new developments, such as new varieties or better methods for assessing crop requirements. This information needs to reach the farmers and be implemented. Fertilizers have played an important role in increasing crop production, especially cereal yields, which is responsible for 40–60% of food production. In Ethiopia, the gap between potential and actual yield is very wide. Thus, developing effective and efficient soil fertility and plant nutrient management practices is indispensable for enhancing agricultural productivity and safeguarding the environment. The Natural Resource Management Research Directorate of the Ethiopian Institute of Agricultural Research has been conducting research on soil and water resources to enhance and maintain the overall resource base and to improve and sustain agricultural productivity in the country. The first volume of this publication, which is the first in its kind, is based on reports on soil fertility and health, and fertilizer management research, which may have an important role in management of inorganic and organic fertilizers, enhance the stability of agricultural systems, help users to maximize nutrient use efficiency and improve crop yields. This publication also provides recommendations on inorganic and inorganic fertilizers and their combinations to correct nutritional deficiencies and improve the entire fertility of soils, and other amendments such as lime that can be applied to remedy soil acidity to the desired pH level. Of great value to users, researchers, postgraduate students, and agronomists are that it also provides an easy-to-use reference for improving the nutritional needs of crops and information for further research.

P (S 07) 38: Antibacterial and antioxidant attributes of potential *Ganoderma* species

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For thousands of years, mushrooms have been prized as highly nutritious foods by many civilizations in the world. More than twenty species of the medicinal mushrooms are currently being produced, of which *Ganoderma* is the “king of medicinal mushrooms”. In the modern world, Lingzhi has a long list of beneficial properties viz. anti-viral, anti-bacterial, antioxidant, anti-tumor. In the present investigation, four different species of *Ganoderma* have been taken i.e. *Ganoderma lucidum* (DMRO-44), *Ganoderma lingzhi* (DMRO-45), *Ganoderma resinaceum* (DMRO-90), *Ganoderma lucidum* (DMRO-207) and two solvents for extraction viz. acetone and methanol were taken. The acetone extracts showed higher antimicrobial activity against all the pathogenic strains in comparison to the methanol extracts. The acetone extracts exhibited a higher range (43.37mm) in case of *Ganoderma resinaceum* (DMRO-90) against *Bacillus subtilis.* On the other hand, methanol extract also showed higher activity in *Ganoderma lucidum* (DMRO-207) against *Bacillus subtilis* (31.00 mm). Preliminary biochemical analysis revealed the presence of alkaloid, carbohydrates, flavonoids, phenolics, terpenoids and tannins. Subsequently, estimation of phenolic compounds namely phenol, ˜-carotene and lycopene were done. *Ganoderma resinaceum* (DMRO-90) showed phenolic compounds in high amount in both methanolic and acetone extract. However, *Ganoderma resinaceum* (DMRO-90) showed a high amount of ˜-carotene in methanolic extraction and in acetone extraction *Ganoderma lingzhi* (DMRO-45) shown highest. *Ganoderma lucidum* (DMRO-207) showed a high amount of lycopene content in methanol extraction and in acetone extraction *Ganoderma lingzhi* (DMRO-45) was found to be highest. From this study, it was inferred that both methanolic and acetone extract of four *Ganoderma* species showed significant antioxidant activity but methanolic extract showed better results in comparison to acetone extract. In case of DPPH and ABTS radical scavenging activity of *Ganoderma resinaceum* (DMRO-90) exhibited the highest per cent of radical scavenging in methanol extracts. In case of reducing power highest absorbance was noticed in *Ganoderma resinaceum* (DMRO-90) in methanol extracts.

P (S 07) 39: *In vitro* evaluation of different phyto-extracts against *Fusarium oxysporum* f.sp. *chrysanthemi*

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The Investigations were carried out following the intensive and eco-friendly methods of controlling *F. oxysporum*, by using phyto-extracts in laboratory during the year 2018-19. The result obtained on mycelial growth and inhibition of *F. oxysporum* f. sp. *chrysanthemi* with six fungal antagonists and one bacterial antagonist. Results revealed that all the evaluated bio-agents were exhibited fungistatic cum antifungal activity against *F. oxysporum* f.sp.*chrysanthemi* and significantly inhibited its growth over untreated control. The antifungal activities of eight plant extracts were assessed at 10% concentration in the Laboratory for evaluation of their efficacy against *Fusarium oxysporum* f.sp. *chrysanthemi* by using Poisoned Food Technique. Plant-extract of eight botanicals were evaluated *in- vitro* (each @ 10% concentration) against test pathogen and the results obtained revealed that all the eight botanical extracts tested were as fungistatic cum anti fungal to *F. oxysporum* f.sp. *chrysanthemi* which were significantly reduced mycelial growth and increase d its inhibition over untreatedd control. At 10per cent concentration, radial mycelial growth of test pathogen was ranged from 31.40 mm (Garlic clove extract) to 61.56 mm (Parthenium leaf extract) as against 90 mm in untreated control. However, significantly least mycelial growth was recorded with garlic clove extract (31.40 mm) followed by neem leaf extract (34.82mm). The next best botanical found was tulsi leaf extract (37.87mm). It was followed by botanicals *viz*., onion bulb extract (43.91 mm), drumstick seed extract (47.21 mm), ghaneri leaf extract (52.04 mm) and glyceridia leaf extract (57.71 mm). Parthenium leaf extract was recorded comparatively less effective with maximum mycelial growth (61.56 mm) and still significantly superior over untreated control (90 mm).

P (S 07) 40: Glasshouse evaluation of chitosan and microbial based iron nanoparticles against bacterial wilt of tomato (*Ralstonia solanacearum*)

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Nanotechnology is innovative area in the agricultural research. Conversion of macromolecules into nano size gives birth to new characteristics to the molecules. If zinc is converted into nano size, it acquires antibacterial properties. Hence, in present investigations chitosan and microbial based zinc nanoparticles were synthesized and evaluated against bacterial wilt of tomato (*Ralstonia solanacearum*). The five kinds of ZnNPs were green synthesized using extracts of *Pseudomonas fluorescens* (Pf-ZnNPs), *Bacillus subtilis* (Bs-ZnNPs), *Trichoderma harzianum* (Th-ZnNPs), *Saccharomyces cerevisiae* (Sc-ZnNPs) and chitosan (Ch-ZnNPs) as natural reducing agents by following magnetic stirring (24-48 hr) and ultrasonication (30 min) methods. Particle size analyser was used to confirm the nano sizes of ZnNPs. The sizes of five kind of nanoparticles, Pf-ZnNPs , Bs-ZnNPs, Th-ZnNPs, Sc-ZnNPs and Ch-ZnNPs were 21.40 nm, 25.20 nm, 52.00 nm, 33.40 nm and 33.40 nm respectively. ZnNPs were evaluated against bacterial wilt of tomato through seedling dipping and soil drenching applications under glasshouse condition. The result revealed that, among different ZnNPs tested against bacterial wilt of tomato, lowest wilt incidence was recorded in Ch-ZnNPs (16.67 %) at 1250 ppm which was on par with other ZnNPs *viz.,* Pf-ZnNPs (20.00 %), Th-ZnNPs (23.33 %) and Bs-ZnNPs (23.33 %) at 1000, 1250 and 1250 ppm concentrations respectively over untreated control (83.33 %) and Bulk ZnO (76.67 %). Among checks, lowest wilt incidence (13.33 %) was recorded in streptcocycline-500 ppm + COC-3000 ppm. The reducing agents (checks) *viz.,* microbial extracts and water soluble chitosan were ineffective in managing the wilt disease under glasshouse condition.

P (S 07) 41: Establishment of a rapid screening method for drought tolerance of small cardamom genotypes at seedling stage

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Small cardamom is a premier spices crop of India. Drought is the chief abiotic stress causing up to 50-70% crop loss in small cardamom. Lack of accurate *screening techniques* is a limiting factor to *develop* small cardamom cultivars *tolerant* to *drought*, which is the most important constraint in small cardamom productivity. In order to optimize the osmotic stress induced by different concentrations of PEG-6000 for moisture stress tolerance screening in small cardamom, a laboratory experiment was conducted in a factorial randomized complete design with four replications. Four different concentrations of PEG-6000 (5, 10, 15 and 20 per cent) along with a control were used in small cardamom cv. Appangala-1. PEG-6000 concentration above 15% has reduced per cent seedling survival almost by 50%. However, at 15% PEG-6000, a significant increase in proline, phenolic content and scavenging enzyme activity and decreased chlorophyll fluorescence were recorded. Hence, 15% PEG-6000 appears to be an ideal concentration for moisture stress tolerance screening of small cardamom genotypes.

P (S 07) 42: *In vitro* evaluation of different phytoextracts against *Fusariumoxysporum F.spcarthami*

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Safflower (*Carthamustinctorius*L.), is one ofimportant *Rabi* oilseed crops cultivated from centuries in India for its valuable oil and also orange color dye. Wilt disease caused by *Fusariumoxysporum F.spcarthami (Klisiewicz and Houston)* is one of the most destructive and wide spread disease of Safflower causing accountable qualitative and quantitative losses of about 21-64 per cent. Eight plant extracts were used for testing against *Fusariumoxysporum* f. sp. *carthami in vitro* by Poison food technique. Result revealed that all the plant extracts tested (@ 10 per cent and 20 per cent), significantly inhibited mycelial growth of the test pathogen over untreated control and per cent mycelial inhibition was increased with increase in concentrations of the botanicals tested.At 10 % and 20% significantly highest mycelial inhibition was recorded with Neem (59.63% and 75.08%) followed by Garlic (56.41% and 69.63 %), Onion (52.85% and 65.19%), and least, mycelial inhibitionwas recoreded in Mehandi (37.30 % and 43.07%) and Shatwari (36.30 % and 40.45%).

Session 8

Post-harvest diseases and mycotoxins

Keynote Papers

KN (S 08) 01: Antifungal effects of leaf extracts of three plant species against *Colletotricum musae* the causal agent of anthracnose postharvest disease of banana fruit

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Anthracnose is a postharvest disease of banana caused by the fungus *Colletotrichum musae* that results in major economic losses during transportation and storage. For the management of banana anthracnose, antifungal effects of three medicinal plants *(Azadirachta indica, Calotropis procera* and *Anacardium occidentale)* were assessed in this study. The extracts of the plants were prepared using water, the phytochemical constituents were determined and agar well diffusion method was used to assess the toxicity of each extract at 50mg/mL100mg/mL and 150mg/mL. The pathogen was isolated from banana infected with anthracnose disease. The results revealed the presence of one or more phytochemicals in each of the plant extracts. Among these were alkaloids, saponnin, tannins, anthocyannin, phenol and flavonoids. All the extracts inhibited mycelia growth of *Colletotrichum musae*. The inhibition of mycelia growth of the pathogen increased with increase in concentration and days of incubation. At the end of day 5 of incubation, the inhibition at 150mg/mL of all the extracts was significantly different($P<0.05$) from other concentrations. However, in all, *C. procera* extracts gave the highest percentage growth inhibition of the pathogen at all levels of concentrations tested while *A. indica* extracts though effective was the least but not significantly different from *A. occidentale*. Therefore, since these plants are cheap, easy to obtain and extract with a simple process of maceration or infusion, more trials on the dosage and formulation on the control of banana anthracnose disease are recommended.

Invited Papers

I (S 08) 02: Impact of post harvest pathogens and their role in mycotoxin production in spices

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India despite being the largest producer of the spices also the great potential for increasing the export of Indian spices to realize the potential there must be improvement and enhancement of the quality spices as per international standard. India does not export more than 10% of it's production due to lack of improved seed varieties that should adopt difference agrocliamatic situation, proper adaptation of storage and package practices Lack of systemic control measure of post harvest pathogens .Pathogens play the vital role adversely affect on production and quality of spices. The associated post harvest pathogen are one of the main cause of poisonous of spices. To realize these aspects and work on the line for isolation of post harvest pathogen. Isolation, identification and the role of deterioration and toxification of post harvest pathogens on spices.

Analysis of total composition of post harvest pathogen from the different samples of the spices were made in order to understand varietal variation and bearing capacities of host harvest pathogens and their role in production of mycotoxins. The different fungal genera such as the species of *Alternaria, Aspergillus*, *Fusarium* and *Helminthosporium* with their maximum percentage incidence were found on Ammi, Caraway, Cardamon, Coriandor, Cumin, Pepper and Opium. The isolated fungal pathogens were employed for their ability to produce mycotoxins. Among the isolated fungi species of *Fusarium* and *Alternaria* were found to be highly toxigenic which were detected by standard methods. The detected toxins are highly toxified and elicite toxic response which may results in mycotoxicosis which may consumed by animals and human beings. Seven species of *Fusarium* and two species of *Alternaria* were served for toxin production among these different toxins from *F. avanaceum, F. chlamadosporum, F. graminerum and F. moniliformi* were detected which of them toxin Deoxynivalenol (DON) is one of the well known mycotoxin which causing mycotoxicosis as feed refusal and induced vomiting. Therefore, it is known as vomitoxin, detected from *F. chlamadosporum and F. graminanerum.* Similarly, Nivalenol(NIV) was found from *F. avnaceum, F. chlamadosporum* and *F. graminerum*. Whereas, Diacetoxyscripenol (DAS) was a detected from *F.moniliformi* the tested *F. culmurum, F. roseum* and *F. semitectum* were unable to produce the toxin.

I (S 08) 03: Potential for biological control of postharvest fungal rot of white yam (*Dioscorea rotundata* Poir*)* tubers in storage with *Trichoderma harzianum*

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Potential of *Trichoderma harzianum* for biological control of postharvest fungal rot of white yam (*Dioscorea rotundata* Poir*)* tubers in storage was studied. Pathogenicity test revealed the susceptibility of healthy looking yam tubers to *Aspergillus niger*, *Botryodiplodia theobromae* and *Fusarium oxysporum* f. sp. *melonganae* after fourteen days of inoculation. Treatments comprising *A. niger*, *B. theobromae* and *F. oxysporum* each paired with *T. harzianum* and were arranged in completely randomized design and stored for five months. Experiments were conducted between December, 2015 and April, 2016 and December, 2016 and April, 2017. Results showed that tubers treated with the pathogenic fungi alone caused mean percentage rot of between 6.67 % (*F. oxysporum*) and 22.22 % (*A. niger*) while the paired treatments produced only between 2.22 % (*T. harzianum* by *F. oxysporum*) and 6.67 % (*T. harzianum* by *A. niger*). In the second year of storage, mean percentage rot was found to be between 13.33 % (*F. oxysporum*) and 28.89 % (*A. niger*) while in the paired treatment rot was only between 6.67 % (*F. oxysporum*) and 8.89% (*A. niger*). Tubers treated with antagonist alone produced 0.00 % and 2.22 % in the first and second year respectively. There was a significant difference in mean percentage rot between the first year and the second year except where *B. theobromae* was inoculated alone, *A. niger* and *T. harzianum* paired and *B. theobromae* and *T. harzianum* paired. The most antagonised fungus in paired treatment for both years was *F. oxysporum* f. sp. *melonganae* while the least antagonised was *A. niger* and *B. theobromae*. It is therefore, concluded that *T. harzianum* has potentials to control rot causing pathogens of yam tubers. This can provide better alternative ways of reducing rot in yam tubers than by the use of chemical fungicides which are not environmentally friendly.

I (S 08) 04: Challenges for maize production in India: Biotic constraints for production and post harvest storage

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In the global climate change perspectives both pathogens and diseases may be affected by the climate change to shape the impacts of devastation due to impacts of warming and draught on the resistance of crops to specific diseases and through variations in pathogenicity of organism by mutation induced by environmental stress. This may significantly, affect the production due to disease outbreaks. The impacts of invasive alien species may be very devastating. Therefore, safeguarding the food supply chain from the bio security threats is the need of time to meet the food security goal. Maize or corn, (*Zea mays* L.) is important crops in the world. Maize is the third most important food grain in India next to wheat and rice with about 9.26 million hectares area under cultivation and an annual production of 2.4 million tons. Maize industry is growing every year in terms of trade and consumption. In the global climate change scenario vulnerability of maize to several pre and post harvest biotic stresses particularly root rots, soft rots, damping off, seedling blights, leaf and sheath blights, rusts, mildews and wilts caused by several genera of fungi, bacteria and viruses (maize streak virus, sugarcane mosaic virus, maize stripe virus, maize chlorotic virus) is a serious concern for maize program in India. . Incidence of virus diseases is posing a new threat to the maize improvement program. Several inbreds/hybrids have been developed and released for cultivation by extensive screening of germplasm against the major diseases in maize viz., maydis leaf blight (*Bipolaris maydis*), polysora rust (*Puccinia polysora,* common rust *P. sorghi*) under simulated disease conditions at the identified hotspots of the diseases. However, stable resistant sources for banded leaf and sheath blight (*Rhizoctonia solani*) could not be identified. Several potential botanicals have been tested and recommended to minimize the pre harvest losses due to *Rhizoctonia* sp., and *Bipolaris* sp. Apart from traditional management of stored grains *in vitro* studies using botanicals for minimizing post harvest losses due to aflatoxin and fumonisin contamination have produced resourceful information. To cut short the agrochemicals input, biointensive integrated disease management modules have been tested to minimize the disease incidence. Survey and surveillance is conducted to monitor the disease scenario and race profiling of major pathogens is done to examine the virulence pattern of the diseases. Conventional management strategies with advanced, cost effective and eco-friendly measures targeting pathogens/genera based on extent of yield losses can give promising results to meet out the challenges of emerging diseases in maize agro ecologies. Traditional knowledge combined with newer approaches involving nanobotanicals, nanofungicides, nanotechnology enabled fertilizers (NEFs) and other nanotechnology based deliverables may have promising results at minimum or no social and economic cost apart from maintaining soil biodiversity. Focus on climate resilience, smart farming, and conservation agriculture for enhancing crop productivity with organic farming can play a pivotal role. The identified resistant inbreds/hybrids can be further used in breeding program for disease management.

Oral Papers

O (S 08) 05: Influence of pre-harvest sprays of particle films on postharvest diseases, disorders and quality of pomegranate (*Punica granatum* L.)

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With the increasing awareness among consumers about harmful effects of residues of chemicals and pesticides, there has been a persistent search for developing alternative approaches to reduce use of toxic chemicals. Development of a processed particle film (PF) is one of such technologies. It requires development of aqueous formulations from chemically inert mineral particles specifically formulated for fruit coating as protective films. Many countries have commercialized PFs such as Surround, Raynoux, Eclipse, Cocoon, Parasol, Anti-stress-500, Purshade, Screen, but there was no attempt from India. Thus, two films (Surround and Raynoux) were imported, and a systematic study was done on their effects on 'Kandhari' and 'Bhagwa' pomegranates. For this, three sprays each of Surround (3%) and Raynoux (1%) were given to 'Kandhari' and 'Bhagwa' trees at fortnightly interval at Bajaura, (Himachal Pradesh) startingfrom15 June every year in the fruiting season of 2017-18. All routine cultural practices were followed except use of fungicides and insecticides. Pomegranates were harvested on 15th October, every year, and observations were regularly recorded. Resultsindicated that particle films (PFs) developed very good red colour (Hunter 'a' values) than untreated (Control) fruits in both the varieties. Similarly, accumulation of anthocyanin was higher in the particle film-treated fruits. Interestingly, the incidence of sun burn and fruit cracking was drastically reduced in PF- treated pomegranates. Sprays of particle films also influenced the incidence of bacterial blight and anar butter fly, which are major problems in pomegranate. The fruit size and quality of pomegranates was also better in PF-treated pomegranates, and PF-treated pomegranates have higher amount of TSS, phenolics and antioxidant activity. Hence, it can be concluded that this technology has great future and it can become an integral part of organic pomegranate production in India.

O (S 08) 06: Evaluation of *Streptomyces* strains against *Aspergillus flavus* infection and aflatoxin contamination in groundnut

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Groundnut is an important oilseed crop and a grain legume of India and is majorly grown in Andhra Pradesh, Gujarat, Tamil Nadu, Karnataka, Maharashtra and Telangana states. Besides several biotic stresses affecting groundnut production in India, aflatoxin contamination by *Aspergillus flavus* continues to be a serious food safety issue at pre-and post- harvest stages, affecting yields and trade. In our studies on evolving a sustainable IDM package against pre-harvest aflatoxin problem, 19 strains of *Streptomyces* were screened *in vitro* against *Aspergillus flavus* toxigenic strain AF 11-4 using standard dual culture and crude extract methods (using elite strains) and growth inhibition of *A. flavus* was determined over control Petri dishes after incubation at specified temperatures. Our results on dual culture assays indicated significant differences in *A. flavus* growth over control by the *Streptomyces* strains. The *Streptomyces* strain, KA 1-26 was found to be superior over others with highest inhibition of *A. flavus* (60%). Comparable to its efficacy, the strains, MMA-32 (56.7%), CA 1-13 (55.9%), CA 1-155 (55.6%), KA 1-27 (55.2%), CA 1-24 (53.7%) and CA 1-85 (50.74%) were also effective. The elite *Streptomyces* strains with more than 50 per cent inhibition capacity in poisoned food assay with their crude extracts showed significant inhibition of *A. flavus*. The strain CA 1-13 had highest mycelial inhibition (55.7%) and was on par with strain KA 1-26 (53.3%) followed by strain MMA-32 (47.0%) and CA 1-24 (46.4%). Overall, our studies inferred the potentiality of *Streptomyces* strains in managing pre-harvest aflatoxin contamination in groundnut. Greenhouse and field studies with these elite strains will be taken up to evolve a sustainable bio-based IDM package for tackling aflatoxin problemin groundnut.

O (S 08) 07: Management of Aflatoxin contamination in peanut through good production, processing and storage practices in India

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Peanut (*Arachis hypogaea* L.) is an important oilseed and food legume crop of tropical and subtropical world. It is annually grown on about 24 million hectare of land in about 120 countries under different agro-climatic zones between latitudes 40°S and 40°N. With an annual production of about 7 million tonnes, after China, India ranks second in the world in peanut production. Peanut can be consumed directly and also in various processed forms. India had the distinction of the largest exporter of peanut in the world, earning 4000-5000 Crore Indian Rupees and one of the top ten agricultural commodities exported. Aflatoxin contamination caused by *Aspergillus flavus* and group of fungi negatively affects its trade and profitability in addition to posing serious health hazards to humans and livestock. With the growing health concerns, several importing countries have set very stringent maximum permissible limits for aflatoxins in peanut. For example, in EU countries maximum permissible limit is 2 ppb for aflatoxin B-1, and 4 ppb for total aflatoxins (B1+B2+G1+G2). Due to this, India has been losing its export market and aflatoxin contamination is recognized as the chief non-tariff trade barrier for the Indian peanut export houses. In this context, there is an urgent need to adopt and follow certain management practices by farmers as well as other value chain actors. Avoiding water stress during pod maturation, drying of pods to moisture content below 7%, using hermetic storage bags, avoiding of re-wetting of pods during shelling, sorting of kernels either by laser colour sorter or manual sorting or its combinations, roasting and blanching of peanut kernels at 120°C for ~8 minutes were found to be few important critical control points and interventions along the peanut value chain to reduce aflatoxin contamination.

O (S 08) 08: Soil application of beneficial microbes enhance fruit quality and shelf life of litchi

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The negative effects on the environment and human health caused by the current farming systems based on the overuse of chemical fertilizers have been reported in many studies. As an alternative, application of microbes in crop plants have been reported to enhance production in addition to positively influencing food quality such as improved vitamin, flavonoid and antioxidant content. However, similar studies in horticultural crops are fewer. Therefore, aim of this research was to evaluate the effect of soil inoculation of beneficial microbes on fruit diseases, quality attributes and post harvest shelf life. Field experiments in randomized block design were conducted during 2017-2019 at ICAR-National Research Centre on Litchi, Muzaffarpur (India), and observations were recorded at harvest and post-harvest stages. The microbial inoculants consisted of arbuscular mycorrhizal fungi (AMF), *Trichoderma viride* (TR), *Azotobacter chroococcum* (AZ) and *Bacillus megatarium* (BM) along with their combinations that were compared with application of recommended dose of fertilizers (RDF) and control (no application). Harvested fruits were brought to laboratory and stored in perforated polybags at ambient conditions (30±2 °C). Three replications, 30 fruits per replication, in each treatment were maintained. Results showed that all the microbial inoculants had significant effect on reducing incidence of sunburn, cracking, and disease like anthracnose and fruit blight. This clearly reinforces the hypothesis that application of microbes protected trees from foliar pathogens by activating defense genes regulating physiology of trees. Fruit size and percentage of good quality fruits were enhanced by treatments compared to control, and RDF. Significant decline were observed in progressive pericarp browning, activity of enzymes *viz.*, polyphenol oxidase and peroxidase, and fruit decay after harvest at different intervals of storage. Titratable acidity, anthocyanin and total phenolics content were significantly higher at different interval of storage in fruits obtained from trees receiving microbial inoculation. The combination AMF+TR and AMF+AZ+TR had outperformed than others. Thus, results conclusively proved that application of microbial inoculants to litchi trees improved fruit quality parameters and positively influenced shelf life of fruits.

O (S 08) 9: Postharvest rot in elephant foot yam: etiology, epidemiology and management strategies

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Elephant foot yam (*Amorphophallus paeoniifolius* (Dennst.) Nicolson (EFY) is an important tropical tuber crop popular as a food security crop and as a remunerative cash crop. The tubers are prone to several post harvest diseases due to their high moisture content and starch. Apart from causing serious post-harvest losses it leads to reduction in the quality and quantity of stored planting material. The recommended management practices are unable to reduce the disease incidence satisfactorily and suggest the involvement of more pathogens to the loss and need for refining management strategies. In present study, elephant foot yam tubers were collected from different locations, detailed symptomatology was studied, organisms associated with the rot were isolated, pathogenicity of the organisms were proved as per Koch's postulates, the organisms were identified based on morphological and molecular characteristics. Organic as well as chemical management strategies were developed and validated in two crop seasons. Nine major types of symptoms were identified from the tubers collected from different locations and brown discoloration of the tuber along with slight rotting was the most predominant symptom. The pathogenicity was successfully proved with fifteen isolates. Major symptoms produced by these isolates were discolouration, rotting and softening of tubers. The isolates were identified up to genera by morphological characterization. The species level identification of the pathogens was done by amplifying the rDNA ITS region using ITS1 and ITS 4 primers. The pathogens were identified as *Athelia rolfsii*, *Lasiodiplodia theobromae*, *Rhizopus oryzae*, *Cunninghamella elegans*, *Rhizoctonia solani*, *Ceratobasidium* sp., *Fusarium brachygibbosum*, *F. solani*, *F. oxysporum*, *Colletotrichum gloeosporioides*, *Aspergillus tamarii*, *A. nomius*, *A. niger* and *Penicillium citrinum.* Among the organisms identified, four genera and three species were reported for the first time causing tuber rot in elephant foot yam. Based on the *in vitro* study, fungicides (mancozeb, carbendazim and combination fungicide (mancozeb+ carbendazim) were selected for the management. The pre- storage treatment with bio-agent, bio-pesticide or fungicides could effectively

mitigate the postharvest loss in elephant foot yam. Minimum pathogen infection (only one spot) and least mealy bug incidence was noted with the treatment, mancozeb+ carbendazim 0.2% against 37% of the tubers showing spots in control followed by *Trichoderma asperellum* in cow dung slurry and Nanma 0.7% (bio-pesticide). The proper identification of the pathogens and the management strategy by giving emphasis to involvement of multiple pathogens, helped in developing an effective management practice. These were validated twice with more number of tubers and found giving consistent and effective disease reduction.

Poster Papers

P (S 08) 01: Evaluation of fungicides, antagonists, phytoextracts and cow urine against *Fusarium pallidoroseum* causing fruit rot of tomato

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Tomato (*Lycopersicon esculentum* Mill.) is the most popular vegetable grown in both tropics and sub tropics of the world. It is native of tropical America, and cultivation has become increasingly popular since the mid-nineteenth century. Tomato fruits lose their market value due to damage caused by many fungi. Among all, the fruit rot caused by *Fusarium pallidoroseum* [(Cooke) Sacc.] adversely affects the fruit quality, quantity and ultimately reduces the market value. .Bio-efficacy of different fungicides, antagonists, phytoextracts and cow urine were studied *in vitro* against tomato fruit rot pathogen [*Fusarium pallidoroseum* (Cooke) Sacc.]. Among fungicides screened *in vitro*, complete mycelial growth inhibition of *F. pallidoroseum* was observed in Carbendazim (12 %) + Mancozeb (63%), Hexaconazole (5%) + Captan (70%), Carbendazim and Propiconazoleat both conc. (500 and 1000 ppm). Antagonistic effect of various bioagents i.e. *Trichoderma viride, T. harzianum, T. virens, Pseudomonas fluorescens* and *Bacillus subtilis* were tested by dual culture technique for their antagonism against *F. pallidoroseum,Trichoderma harzianum* found most efficient antagonist in inhibiting mycelial growth of *F. pallidoroseum* (60.98 %) *in vitro.* Complete mycelial growth inhibition (100%) of *Fusarium pallidoroseum* was recorded in garlic and cinnamon leaves extracts at 10 per cent concentration.

P (S 08) 02: Optimization of nano encapsulated plant based synergistic formulation in post-harvest disease management of aflatoxin

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The synergistic application of bioactive compounds in the post-harvest disease management of aflatoxin has getting interest in pathology research. Synergistic use of compounds makes potent antimicrobial efficacy in adequately low concentrations along with inevitable reduction in negative sensory impacts. In our research, we have developed a novel synergistic formulation that is amalgamation of thymol (T), methyl cinnamate (M), and linalool (L) (TML), using the simplex centroid method (SCM) of Mixture design assay. Afterwards, nanoencapsulation of the developed formulation was prepared (Ne-TML) and characterised to test its antifungal and aflatoxin B_1 inhibitory efficacy. The Ne-TML causes inhibition of growth and aflatoxin B_1 production by *Aspergillus flavus* PN-05 at the concentration of 0.35 μl/ml and 0.2 μl/ml respectively. The elucidated mode of action of Ne-TML represented decrease in ergosterol content, membrane ions leakage, impairment in carbon-source utilization and *in-silico* validation of *ver1* gene product inhibition in aflatoxin B_1 biosynthesis.

P (S 08) 03: Pathogenicity and post harvest management of stem end rot caused by *Botriodiplodia theobrome* in mango

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Mango (*Mangifera indica*) popularly known as king of fruits is one of the delicious fruit grown in tropical and subtropical regions of the world. India has a rich wealth of mango and shares about 56% of the world mango production. Temperature, humidity and rainfall are the primary environmental factors that affect the outbreak of various mango diseases. A number of pre and post harvest diseases are reported to cause perceptible loss in quality and yield of mango. Stem end rot caused by *Botriodiplodia theobrome* (syn. *Lasiodiplodia theobrome*) is an important post harvest disease which caused quantitative and qualitative losses in mango fruits. In the present study, pathogenicity was assessed in five popular mango varieties namely Fazali, Langra, Chausa, Neelam and Dashehari by plug inoculation technique. The appearance of lesions was brownish black and started from stem end region and spread linearly along the fruit resulting softening of the skin. Colonies of the fungus on potato dextrose agar was moderately dense with raised mycelium mat and whitish to smoke grey in colour. Mean lesion length ranging from 2.9 to 15.9 cm and mean lesion size ranging from 8.4 to 254.4 cm^2 were recorded in mango varieties. Minimum lesion length and lesion size was recorded in Dashehari followed by Fazali. Whereas, maximum lesion length and lesion size were recorded in Neelam and Chausa. Percent reduction in TSS ranged from 9.8 to 42.9% and was maximum in Neelam followed by Chausa. These two varieties were found susceptible to stem end rot. Foliar spray of Difenoconazole 25 EC @0.5 ml per litre of water 30 days before harvest and hot water treatment at 52^0C for 10 minutes alone and in combination were studied for the management of post harvest stem end rot in mango variety Chausa and Neelam. Lesion length, lesion area and physiological loss in weight (PLW %) of mango fruit were recorded in both the varieties. Mean lesion length, mean lesion area and PLW (%) ranging from 0.0 to 17.6 cm, 0.0 to 133.9 cm2 and 1.7 to 13.8%, respectively were recorded in different treatments. Pre-harvest spray of Difenoconazole 25 EC @0.5 ml per litre of water 30 days before harvest and hot water treatment at 52^0C for 10 minutes was found best in controlling stem end rot in Neelam and Chausa followed by only hot water treatment.

P (S 08) 04: Impact of botanicals for management of post harvest pathogens from pulses

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The tested botanicals from different families and different localities were collected for evaluation of antifungal potentialities against post harvest pathogens, which were associated on pulses. The composition of fungi such as species of *Aspergillus*, *Fusarium, Alternaria* and *Curvularia* were isolated variety of pulses. The isolated mycoflora were recorded their pathogenicity. Which were mainly responsible to cause harmful effect on health of pulses and the resulting into deterioration and poisoning of the pulses. Therefore, importance of their role in deterioration and toxification were found phragmentory. Considering these important facts, the topic has been undertaken for study and carried out the management of fungal pathogens by using different botanicals with their different concentrations were tested against isolated fungi. The results are remarkable to note that, the leaf extract of *Vitex nigundo* was highly beneficial for maximum growth inhibition of screened fungi followed by leaf extract of *Lantena camera*. It is interesting to note that leaf extract of *Argimon maxicana* responsible to prevent growth of *Alternaria alternate, Fusarium* moniliformi, *Fusarium culmorum, Fusarium gramineram* while, species of *Aspergillus* not responded to leaf extract of *Lantana camera*.

P (S 08) 05: *In vitro* efficacy of plant extracts against major postharvest pathogens of nectarine (*Prunus persica* var. *nucipersica*)

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Nectarine is an important stone fruit after peach and plum. It offers an impressive array of powerful antioxidants and phenolic compounds along with dietary fiber, vitamins and poses many health benefits. Nectarine fruits have a very short shelf life of 5-6 days at room temperature. Due to succulent nature and high juice content, it is highly prone to postharvest diseases. The major postharvest diseases of nectarines are brown rot caused by *Monilinia fructicola*, Rhizopus rot caused by *Rhizopus stolonifer* and gray mold caused by *Botrytis cinerea*. Several chemicals are used to control postharvest decay in stone fruits but pesticidal residue is major concern among consumers. To overcome this problem, alternative and eco-friendly approaches are gaining popularity. Hence, use of plant extracts is considered as a easy to apply and safe method to human beings. In this study, we attempted methanol and aqueous extracts of neem, marigold, ocimum, moringa and eucalyptus at different concentrations (50,100, 200 and 400µl and mixture of all extracts) against the postharvest pathogens of nectarine under *in vitro* conditions. The results showed that under *in vitro* conditions, methanolic extract performed better in inhibiting the growth of pathogens compared to aqueous extract. All the plants extracts showed inhibition of the studied pathogens but mixed plant methanolic extract at 200 µl concentration showed the maximum inhibition in *Rhizopus stolonifer* (96.2%) and *Penicillium expansum* (92.6%) and the least inhibitions were observed at 50 µl concentration. It can be concluded that use of plant extracts will be highly useful for controlling postharvest diseases and extending the shelf/storage life of nectarine which will in extending its availability in the market.

P (S 08) 06: Antifungal activity of six invasive plant extracts against *Fusarium* sp. isolated from *Dracaena sanderiana* leaf spots

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Leaf spots caused by phytopathogens reduce export quality in ornamental foliage plants. Although chemical fungicides are used to control phytopathogenic diseases, negative impacts on the environment and human health is a concern. Development of safe and eco-friendly fungicides is urgently needed. This study focused on antifungal properties of some invasive plant extracts against *Fusarium* sp. that causes leaf spot disease on

Dracaena sanderiana ornamental plants. Invasive plants are a significant threat to natural ecosystems, are readily available, and thus a low cost material for developing plant-based fungicides. *Fusarium* sp., isolated from diseased leaf samples of *D. sanderiana*, was identified employing Koch's postulates. Antifungal activity of leaf and root extracts of six invasive plants (*Mikania micrantha*, *Tithonia diversifolia, Lantana camara, Clusia rosea, Chromolaena odorata* and *Clidermia hirta*) collected from Central Province, Sri Lanka was determined against isolated *Fusarium* sp. Air-dried and powdered plant parts were sequentially extracted into *n*-hexane, dichloromethane (DCM) and methanol at room temperature using an ultrasonicator (40 kHz), and the solvent evaporated using a rotary evaporator. Each extract (2 mg/disc) was subjected to disc diffusion assay; mancozeb and propineb (50 µg/disc) served as positive controls. Experiments were conducted in completely randomized design and the area of inhibition corresponding to each disc was measured. Data were analyzed using one-way ANOVA*.* All assays were carried out in triplicate and the procedure was repeated twice. The extracts tested, showed varying degrees of antifungal activity while the extracts of *L. camera* were inactive*.* The DCM leaf extract of *C. odorata* (area of inhibition, 0.99 ± 0.09 cm^2) and DCM root extract of *T. diversifolia* (1.11 ± 0.07 cm^2) displayed the highest antifungal activity, while mancozeb and propineb displayed areas of inhibition, 0.95 ± 0.03 and 1.07 ± 0.04 cm^2, respectively. *Chromolaena odorata* leaves and *Tithonia diversifolia* roots could be potential sources for developing plant-based fungicides against phytopathogen *Fusarium* sp.

Session 9

Disease management in organic and protected cultivation

Keynote Papers

KN (S 09) 01: Organic/non-chemical disease management in crop production in the sub saharan Africa: Prospects and problems

David B. Olufolaji

Sub-Saharan Africa lies south of the Sahara Desert. It consists of 46, out of the 54, countries that makes up the African continent. Plant diseases, as one of the major limiting factor in farming systems, has been a major concern in this region. It militates against crop production and pose a serious threat to food security, especially with increasing human population. Organic plant disease management has been employed since time immemorial by rural African farmers. Shifting cultivation (which involves abandoning a field after few years of cultivation when the nutrient status declines), land fallowing (in which case the field is allowed to recover from lost nutrient by abandoning it for some years before it is re-cultivated), crop rotation, planting of resistant varieties (determined by size and aesthetic features) and application of botanicals, in form of dry powder, ash or liquid extracts are common. Unfortunately, however, the adoption of these organic disease management strategies is not without its challenges. Increasing population, urbanization and industrialization has reduced land availability, making bush fallowing and shifting cultivation almost impossible in most communities. The high rate of criminality and insecurity in most sub-Saharan African countries has also made wondering in search of new and fertile field to cultivate a risky and dangerous venture. In addition, emergence of exotic and new strains of pathogens has made it clear that resistance is not based of size and aesthetics. Crops that were once thought to be resistant to diseases have become susceptible to infection. Furthermore, environmental pollution and climate change has either altered the phytochemical constituent of some botanicals, thereby reducing their potency or caused such plants to disappear altogether. There is therefore a need for a modern approach to these practices with a view to making them more sustainable. In addition, modern organic disease management options like solarization (achieved by covering the soil surface with polythene for a given period of time), biological control with antagonistic microorganisms (especially with fungi in the genus Trichoderma), development of transgenic plants and genetically engineered crops (GM crops) should be adopted. While the adoption of these strategies may be faced with initial challenges, owing to the high technicality and facilities involved and especially considering the high level of illiteracy and poverty among peasant farmers, a lot can be achieved in the long run if it is done in collaboration with reputable agricultural institutes like International Institute of Tropical Agriculture (IITA) in Ibadan,Nigeria and other non-governmental agencies involved in agricultural development in sub-Saharan Africa. Training, awareness campaign and establishment of pilot farms are some of the approaches that can be adopted. Extension Departments in Agricultural institutions can also be of immense help. Furthermore, some of these organic disease control strategies can be combined in an integrated approach for better result. Organic plant disease management have numerous associated benefits. It improves soil health, prevents toxicity of plants and animals resulting from chemical use, prevents development of resistant strains of pathogens and protects the environment.

Invited Papers

I (S 09) 02: Emerging diseases of medicinal plants and their sustainable management

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The medicinal plants are cultivated or found in the wild round the year and are used for the treatment of various health problems and these plants have been an integral part of Indian health and livelihood systems. The medicinal plants are emerging in Indian agriculture due to heavy demand of raw materials in national and International market. It is estimated that the primary health care of over 80 per cent of the world's population still depends on plant based traditional medicines. The global market for herbal products is continuously expanding and it is expected to touch the mark of US$ 5 trillion by the year 2050. Since the demand for medicinal plants is increasing day by day in the national market., so farmers will get more profit than other traditional crops cultivation. Medicinal plants not only economical but is ecologically safer too. With increasing interest in natural products of plant origin for medicinal and health care benefits there is added emphasis on the quality of the source raw material. Healthy planting materials are essential for maintaining the product quality. Currently, the supply of raw planting material is inadequate and often is of inferior quality. The medicinal plants quantity and quality of biomass are adversely affected by various diseases caused by bacteria, fungi, nematodes, viruses and phytoplasmas. Changes in climate, adoption of intensive cultivation practices posing serious threat of pests, disease pathogens and nematodes. Their damage potential has increased in both intensity and frequency in various medicinal plants. Some diseases have become minor to major diseases and causing severe losses. Foliar diseases are most devastating, since in most cases, biomass of medicinal plants forms a major source of raw material for pharmaceutical industries. Currently, fungal diseases (root rot, wilt, leaf spots, blight/ anthracnose) and root-knot nematodes are important diseases during crop cultivation. Intensive agricultural practices relying heavily on chemical pesticides are a major cause of wide spread ecological imbalances resulting in serious problems of pesticide resistance and pesticide residues. Consequently, toxic residue of pesticides in raw material posed serious concerns of risk to human health. Thus, plant diseases create challenging problems in commercial agriculture and pose real economic threats. Therefore, the health of medicinal plants are of major concern, even there should be a common practice for no or minimal use of synthetic pesticides. There is a growing awareness world over on the need for promoting environmentally sustainable agriculture practices. Integrated Disease Management (IDM) is a globally accepted strategy for promoting sustainable agriculture. Plant-derived products, biopesticides containing bacteria and fungi, and bioagents have been exploited to check quality deterioration and improve crop productivity. Nevertheless, to reduce application of synthetic pesticides, other options including cultural practices, resistant/ tolerant crop cultivars, biocontrol agents are available which can be integrated and incorporated for medicinal plants health management.

I (S 09) 03: Influence of PGPR against fungal foliar disease of tomato under protected cultivation

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Bio efficacy of bio control agents (PGPRs) against fungal foliar disease of tomato in organic cultivation under protected condition was conducted during *kharif* 2017-18 and 2018-19 at bio-resource farm of Institute of Organic farming, UAS, Dharwad. The experimental results revealed that, Seed treatment with *Pseudomonas fluorescens*@5g/kg followed by seedling dip with *Ps. fluorescens* @10g/l and spray with *Ps.fluorescens* 10g/l 4times at 15 days interval was found promising in reducing the fungal foliar diseases, increasing the yields and obtaining the highest net returns and benefits. This was followed by ST with *Bacilluus subtilis*@5g/kg fb seedling dip with *B. subtilis* @10g/l and spray with *B. subtilis* 4 times at 10g/l at 15 days interval which was on par with *Pseudomonas* treated plots. ST with *T. harzianum*@5g/kg followed by spray with *Ps. fluorescens* @ 10g/l, 4 times at 15 days interval was the next effective treatment and found on par with ST with *T. harzianum*@5g/kg followed by spray with *B.subtilis* @ 10g/l, 4 times at 15 days interval. The net returns and benefits were also recorded highest in the plots treated sequential with *Pseudomonas fluorescens and Bacillus subtilis* respectively. However, spray with recommended check wettale sulphur 4 times at 15 days interval was also one of the effective treatment and found significantly superior to untreated control plots. Thus PGPR have a greater role in plant disease management, maximizing yields & returns and influence plant growth parameters under protected structures.

I (S 09) 04: Effect of botanicals on penetration and population of *Meloidogyne graminicola* J_2 in the roots of rice

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Meloidogyne graminicola is serious nematode pest of rice in eastern Uttar Pradesh; the pest is associated during the seedling stage of rice in nursery and cause severe damage and high yield losses in susceptible varieties like Pant12. This nematode completes one life cycle during seedlings stage of paddy within 20 days at 27-37 °C. It indicates that nematode completes many generations in one crop season. The characteristic infection symptoms produced by *M. graminicola* are in the form of terminal hook shaped or spiral galls. Second stage juveniles enter the roots through root tips and start feeding. Nineteen selected plant leaves *viz*. Madar (*Calotropis procera*), Barseem (*Trifolium alexandrinum*), Mustard (*Brassica juncea*), Neem (*Azadirachta indica*), Eucalyptus (*Eucalyptus globus*), Bael (*Aegle marmelos*), Ashwagandha (*Withania somnifera*), Kalmegh (*Andrographis paniculata*), Guldaudi (*Chrysanthemum*), Kaner (*Cascabela thevetia*), Lemon (*Citrus limon*), Giloy (*Tinospora cordifolia*), Castor (*Ricinus communis*), Ashoka (*Saraca asoca*), Night jasmine (*Nyctanthes arbor-tristis*), Papaya (*Carica papaya*), Plumeria (*Plumeria rubra*), Jasmine (*Jasminum*) and Peepal (*Ficus religiosa*) were collected from SHUATS campus. After fifteen days of amendment of botanicals, highly susceptible variety of rice, Pant-12 seeds were sown @10 seed/pot. After 60 days of germination plants were uprooted and examined for number of root galls/ plant root system under a stereoscopic binocular microscope. The results indicated that all the botanicals except Madar significantly suppressed the population of *M. graminicola* as compared to the untreated check. Results for the invasion of *M. graminicola* in botanicals at 1, 2, 3 and 4 days after germination, were recorded. It was observed that J_2 entered to the tip of the rice roots. However, till fourth day after germination no nematodes invaded the roots of rice. The penetration, post penetration development and reproduction of *M. graminicola* at 6, 10, 15, 20, 25 and 30 days after germination of rice seedlings were observed after staining the roots of rice. Results were classified in to four stages of development, J_2 vermiform (I stage), female sausage shaped juveniles (II stage), female without eggs (III stage) and female with eggs (IV stage). Female population, number of root knots and the rate of reproduction were high in control (without treatment) as compared to botanical treatments.

Oral Papers

O (S 09) 05: Antifungal activity of *Acacia tortilis* subsp. *raddiana* tar on *Fusarium oxysporum* f. sp. *albedinis*, the cause of Bayoud disease of the date palm in Southwest Algeria

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Bayoud caused by *Fusarium oxysporum* f.sp. *albedinis* (*Foa*), is the most destructive disease of the date palm (*Phoenix dactylifera* L.) in Morocco and Algeria, and there is no effective control strategy. The results of counting of the telluric flora obtained show the dominance of the bacteria with a percentage of 70% followed by fungi by 30% for the uninfected soil. Also in the infected soil, there is the dominance of fungi 55%, followed by bacteria 45%. The mycological analysis results show that the mycoflore of the infected soil is dominated by the genera of *Aspergillus*, followed by *Penicillium, Fusarium* and *Altern naria*. For the healthy soil, we note the dominance of *Penicillium*, followed by *Aspergillus.* We found that although *Foa* isolates vary morphologically, *Foa* strains can be identified by species-specific primers. PCR analysis revealed that the strains that we isolated from infected date palm rachis were the Bayoud pathogen *Foa*. We used these strains to evaluate the antifungal activity of tar extracted from *Acacia tortilis* subsp. *raddiana*. The *A. raddiana* tar had a density of 1.15, a refraction index of 1.3850, a pH of 5.2 and a dried matter ratio of 48.75%. The *A. raddiana* tar effectively inhibited the growth of *Foa in vitro* with a minimum inhibitory concentration of 3 µg/ml.

O (S 09) 06: Incidence of biotic stress, yield and economics of high value vegetable crops under greenhouse v/s open field condition in North Indian plains

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Insect pest are known to cause direct damage to horticultural crops as well as indirect damage by acting as vectors. Greenhouse structure acts a physical barrier for spread of the insect pest and consequently plant diseases also. Therefore, experiment comprised of three crops i.e. Tomato hybrid (GS-600), Capsicum hybrid (California Wonder) and Cucumber (Aviva) were conducted to assess the incidence of insect-pest stresses, yield and economics in open field and Greenhouse conditions at CPCT, ICARI, New Delhi, during 2014 – 2015. Data recorded on incidence of insect pest, plant mortality, non-marketable fruit yield and economic loss were statistically analyzed. Result revels that incidence of insect-pest, plant mortality, amount of insecticide (ml/plant) and 2-3 number of spraying were minimum under greenhouse condition as compared to open field condition. However, non-marketable (Insect-pest affected) fruits were almost nil in Greenhouse (polyhouse) but these were considerably higher in open field condition. The marketable fruits (free from insect-pest) yield of tomato, capsicum, Cucumber (7.75, 3.30, 3.3kg/plant) and net income (Rs 20.70, 25.50, 18.40./plant) were found maximum in Greenhouse as compared to open field condition (1.55, 1.12, 1.51 kg/plant and Rs. 4.75, 4.10, 5.40 /plant, respectively) in all crops. Percentage of yield, economic loss and use of insecticides were found comparatively higher in all season in open field vegetable crops. It was concluded that Greenhouse cultivation of high value crops was ideal technique to avoid and minimized insect and pest damage and can be used as component of integrated pest managements.

O (S 09) 07: Organic approaches for the management of plant diseases

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The continuous and indiscriminate use of chemical pesticides has posed several serious problems such as pesticide residue, development of resistant strains, environmental pollution and adverse effect on beneficial microorganisms and created a greater concern over global food safety and security. Organic farming relies on crop protection, crop residues, animal manures, legumes, green manures, off farm organic wastes, cultural practices, mineral bearing rocks and aspects of biological pest control to maintain soil productivity and to supply plant nutrients and to control Diseases. Management of diseases mainly involve Cultural Methods such as Selection of resistant varieties , adoption of suitable cropping system ,using clean seed and planting materials and maintaining optimum planting / sowing time and spacing. Moreover balanced Organic Nutrition and proper water management practice can reduce the chance of disease occurrence. Addition of Soil amendments followed by Biofumigation, Soil solarization and proper sanitation measures suppress the inoculum to greater extent. Botanicals synthesize a diverse array of chemicals to prevent the colonization by pathogens by producing secondary metabolites like terpenoids alkaloids, flavonoids, phenolic compounds and they are effective against nematodes, fungi, bacteria and viruses. Biocontrol agents multiply in soil and remain near root zone of the plants and offer protection even at later stages of crop growth. Using some of the chemical fungicides and antibiotics allowed in organic farming at right time render abundant control. For the effective management of diseases it is necessary to integrate many of these practices to synthesize a proper model to keep crops free from diseases.

O (S 09) 08: Role of casing soil health in mushroom production and management of biotic and abiotic stresses

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Casing is covering of top surface of the spawned compost of some humicolus fungi with a thin layer of nutritionally deficient medium. Casing provides physical and mechanical support of the mushroom fruits, preventing drying out of the compost lying under the casing surface, creating an environment to switch on reproductive phase of mushroom and regulate quality mushroom production. Several materials like peat moss, farm yard manure + loam soil etc. are used as casing for the production of button mushroom. Different biotic and abiotic stresses are occurred in cultivating mushroom due to the fault in preparing compost, casing soil, bad sanitary conditions and variations in humidity and temperature prevailing in mushroom houses. The biotic stresses are molds (green/olive/yellow/pink molds, brown/white plaster molds, ink cap and lipstick mold), fungal diseases (false truffle, dry bubble, cobweb and wet bubble), bacterial diseases (bacterial blotch, ginger blotch, mummy disease, pit disease and drippy gills), viral diseases (x-disease, la-France disease, brown disease, watery stipe disease, die-back Disease), nematodes (*Aphelenchoides composticola*, *A. avenae*, *Ditylenchus myceliophagus* and *Rhabditis lambdiensis),* mites (tarsonemid mites and red pepper mites) and insects (sciarid fly, phorid fly, cecid fly and springtail). The abiotic stresses occurred in cultivating mushroom are high pinning, stroma, sectoring, flock, hard cap, open veil, purple stem and scales. Physical and chemical properties as well as microbiological parameters of the casing play an important role for the proper fruiting of mushroom. Around 71.79 percent variation in the mushroom yield has been reported due to water holding capacity, porosity, particle density, bulk density, pH and electrical conductivity of casing soil. Several microbes like Actinomycetes, Fluorescent pseudomonads (*P. putida*), *Arthrobactor* sp. *Bacillus* species, *Ensifer* spp. *Sinorhizobium* spp. *Sporosarcina* spp. *Microbacterium* spp. *Sphingobacterium* spp. etc. may be present in casing soil. Some bio-chemicals like antibiotics, organic acids mostly ethylene and metabolism of 1-octen-3-01 and 2-ethyl-1-hexanol are also available in casing soil. No fructification can develop if sterile casing is used. Actinomycetes isolated from casing material had an inhibitory effect on the bacterial population. The microorganisms present in the farmyard manure and casing soils play an important role in the mushroom fruit body initiation and development. It has been proposed that fluorescent Pseudomonas isolated from the peat based casing material and found to adhere to hyphal wall of *Agaricus bisporus* could remove the fungal deposits of crystalline calcium oxalate from its hyphal walls which is a prerequisite for fructification.

O (S 09) 09: Bio-fumigation: an eco-friendly strategy for managing Fusarium wilt of tomato in Nigeria

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Field experiment was conducted during the rainy seasons of 2015 and 2016 in the Teaching and Research Farms of Federal college of Horticulture DadinKowa, Nigeria to evaluate the effect of soil amendment with animal manure and bio-fumigant crops on Fusarium wilt of tomato. The experiment was laid out in a split plot design with poultry manure (PM), cow dung (CD), CAMAZEB® (60% Mancozeb + 40% Carbendazim WP) and un-amended soil as main plots while bio-fumigant crop: - cabbage, garlic, onion and un-treated soils constituted the sub plots. Poultry manure and CD were applied at the rate of 22 tonnes ha^{-1} while cabbage residues and garlic/onion were used at 5.6 tonnes ha^{-1} and 2.8 tonnes ha^{-1}, respectively. Soil was inoculated with *Fusarium oxysporum* f. sp. *lycopersici* a day before amending soil with animal manure and bio-fumigant crops. Data on disease incidence, severity and growth/yield parameters were collected. Results showed that tomatoes grown on soil amended with poultry manure and cabbage residues significantly ($P<0.01$) led to lower Fusarium wilt incidence and severity throughout tomato growth period than the other treatments. Combined application of PM and cabbage residues among other organic amendments led to heavier shoot (351.8 g/plant) and root (110.4 g/plant) weights. Highest yield (7.5 tonnes ha^{-1}) was also recorded on same treatment, compared to tomatoes from the other treatments. Efficacy of PM manure and cabbage residues against Fusarium wilt of tomato is attributable to the volatiles biocides released by cabbage residues and poultry manure during decomposition and presence of bio-control agents on the organic amendments. Application of 22 tonnes ha^{-1} of PM and 5.6 tonnes ha^{-1} of cabbage residues as bio-pesticide to be applied during land preparation as eco-friendly approach in managing Fusarium wilt of tomato.

O (S 09) 10: Antifungal activity of biosynthesized silver nanoparticles (Ag NPs) against *Sclerotium rolfsii* causing collar rot of chilli

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Efficacy of biosynthesized silver nanoparticle at different concentration (250 ppm, 500 ppm and 750 ppm) was tested against *Sclerotium rolfsii* causing collar rot of chilli by poisoned food technique and the result showed that, *Trichoderma harzianum* silver nanoparticles @750 ppm was found most effective with least mycelial growth (24.56 mm) and numerically highest mycelial inhibition (72.71%), followed by *T. harzianum* silver nanoparticles @ 500 ppm (50.56 mm and 43.82 %) and *T. hamatum* silver nanoparticles @ 750 (73.50 mm and 18.33 %), respectively over control.

O (S 09) 11: The potential of antagonistic yeasts and bacteria isolated from tomato phyllosphere and fructoplane in the control of Alternaria fruit rot of tomato

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Tomato (*Solanum lycopersicum* Mill) is the most important vegetable crop in Oman, grown across the entire country. *Alternaria* fruit rot caused by the filamentous fungus *Alternaria alternata* is one of the major constraints in tomato production in Oman. This fungus invades the tomato fruits through injured or weakened tissues. The pathogenic infection of fruits occurs during crop growth in the field, harvesting, postharvest handling and storage. Ripe fruits are more susceptible to fungal infection because of high content of moisture and nutrients, and no longer protected by the intrinsic factors, which confer resistance during their development. Biological control by using naturally available antagonistic microorganisms has been preferred for the control of post-harvest diseases of fruits and vegetables because it is environmentally safer than other control methods. The objectives of this study were to isolate antagonistic yeasts and bacteria from tomato phyllosphere and fructoplane and to evaluate their ability to suppress Alternaria fruit rot of tomato. A total of 24 yeast and 48 bacterial isolates were isolated from tomato leaves/fruits collected from Barka, Muscat Governorate of Sultanate of Oman. These microorganisms were tested for their antagonistic activities against *A. alternata* by using an *in vitro* dual culture technique. Among the 72 bacterial and yeast isolates tested, one yeast (*Meyerozyma guilliermondii*) and two bacteria (*Cronobacter sakazakii* and *Pseudomonas aeruginosa*) showed inhibitory activity against *A. alternata*. Scanning electron microscopic observation of the hyphae of *A. alternata* at the periphery of the inhibition zone in dual culture assay plate showed morphological abnormalities such as shrinkage, distortion and loss of turgidity. *P. aeruginosa* and *C. sakazakii* were found to grow well at temperatures ranging from 25°C to 35°C and the optimum temperature for the growth of *M. guilliermondii* was between 25 and 30°C. Postharvest dip treatment of tomato fruits with *M. guilliermondii*, *P. aeruginosa* and *C. sakazakii* significantly reduced the incidence of Alternaria fruit rot.

O (S 09) 12: Search of resistance sources among cauliflower germplasm for Alternaria leaf spot caused by *Alternaria brassicicola*

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Cauliflower is an important vegetable crop world-over and grown on 1.39 million ha area with annual production of 25.98 million tonnes. In India, it is being almost year round with production of 8.48 million tonnes. However, production of quality curds with minimum fungicide residues is a challenge mainly due to diseases and pests. Among them, *Alternaria* leaf spot or curd blight caused by *Alternaria brassicicola* (Schw.) Wiltsh is a major disease of cauliflower particularly in hot-humid growing environment (temperature: 25 to 30 °C; relative humidity > 60%; frequent rains). Theseclimatic situations coincide with growing period of early (July- October) and mid-early (August – November) maturity groups as well as seed crop of all groups of cauliflower. Infected leaves show brown to black spots with concentric rings affects photosynthetic area and brown to black spots on curd losses their market value completely. It affects plants across the growing stages and causes huge economic loss to farmers. The study was aimed to assess the reaction of 131 and 356 genotypes of cauliflower against *A. brassicicola* at seedling and adult plant stages. The resistance screening was carried outat seedling stage (4-6 true leaf) through artificial inoculation in augmented net-house condition during September to November months of 2017-18 and 2018-19, respectively. In 2017-18, only four genotypes namely Kt-17, Kt-2, Sel-9 and Sel-23000 were found resistant and eight genotypes (AL-15, vv-17, Lawyana, DC-175-8, DC-SC-1, PNI, DC-300, DC-PCF and DC-306 exhibited moderate resistant reaction. In 2018-19, out of the screened 356 lines against *A. brassicicola* through artificial inoculation in pot culture under epiphytotic conditions and 07 lines namely-Lawyana, vv17, AL-15, DC KP-18, SM, EC 16258 and DC-53 were found resistant. The percent disease incidence in tested cauliflower germplasm was ranged from 0.0 to 83.3%. Further, these genotypes were subjected to disease reaction at adult plants (8-12 leaf stage) and curding stage and also variations in disease reaction in comparison to seedling and adult plant stages were also recorded. The mapping populations have been generated and detailed work on inheritance of Alternaria leaf spot resistance and identification of linked molecular markers is under progress.

O (S 09) 13: *In-vitro* efficacy of organically permitted bioagents, fungicides and botanicals against leaf blight (*Colletotrichum gloeosporioides*) of large cardamom (*Amomum subulatum roxb.*) in Sikkim Himalayas

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Large Cardamom (*Amomum subulatum* Roxb.), a member of Zingiberaceae family is perennial herbaceous spice crop cultivated in sub-Himalayan state of Sikkim and the Darjeeling district of West Bengal. India is the largest producer of large cardamom with 54% share in world production, and Sikkim contributes upto 88% of India's production. However, the area and production of large cardamom has declined due to several reasons, one among them being increase in disease-pest incidence. Recently, the widespread occurrence of leaf blight diesase has become the major concern to the large cardamom growers. The fungus known as

Colletotrichum gloeosporioides was responsible for leaf blight as reported in 2011. Under the changing climatic conditions and with shift in the habitat of large cardamom the disease incidence has increased over years making it the most important disease of concern. The present study was attempted with the objective of screening the efficacy of organically permitted fungicides, botanicals and bioagents against leaf blight (*Colletotrichum gloeosporioides*) of large cardamom. The bio-agents used were *Trichoderma viride*, *Pseudomonas fluorescens* which are commonly used in Sikkim and organically permitted fungicides like copper oxychloride, copper hydroxide, Bordeaux mixture, Sulphex, commercial neem-based formulation and botanicals like garlic (*Allium sativum*), mugwort (*Artemesia vulgaris*), needlewood tree (*Schima waliichii*) were tested against the fungus. The fermented leaf extracts of botanicals mugwort and needlewood tree is being used by the farmers of Sikkim as an ITK to manage diseases. The pure culture of the *Colletotrichum gloeospoirdes* was subjected to *in vitro* testing of these agents through poison food technique. Among the permitted fungicides tested, Sulfex @ 0.1% concentration was found to be significantly effective in inhibiting the growth of the pathogen (90.03%) followed by commercial neem based @ 0.3% (88.84% inhibition). Among the botanicals and bio-agents used, lowest pathogen growth *in vitro* was seen in *Trichoderma viride* with inhibition of 69.72% followed by *Schima wallichii* 2.5% (42.23%). The copper based fungicides did not show good *in vitro* efficacy against the pathogen with only 40.23% inhibition with copper oxychloride. The *in vitro* study is to be validated under the field conditions to fetch organic disease management implications.

O (S 09) 14: Increased plant growth, fruit production and health of cultivated tomato after treatment with *Trichoderma reesei* peptaibols

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Peptaibols are toxic secondary metabolites due to their ability of forming ion channels in bilayer membranes. They are short peptides usually consisting of 18-20 residues, which include unique amino acids like á-aminoisobutyric acid (Aib), isovaline (Iva), and the C-terminal 1,2-amino alcohol. Peptaibols are produced by most members of the genus *Trichoderma*. Studies on their bioactivities against various fungal plant pathogens revealed that peptaibols have the potential to be included in the arsenal to control plant pathogenic fungi affecting agricultural crops. Positive effects of *Trichoderma* strains on plants are commonly known from the literature like their role in plant growth promotion and induction of systemic resistance. In the present study, cultivated tomato plants were used to examine the direct effects of *Trichoderma* peptaibols on plant growth. *Trichoderma reesei* - a species commonly used in biotechnology due to its ability to produce hydrolytic enzymes degrading cellulose or hemicellulose - was selected for the experiments. A certain group of peptaibols, paracelsins are produced by *T. reesei*. The sequences produced by this strain are reported by Marik et al. 2019. After the HPLC-ESI-MS investigation of the crude extracts deriving from *T. reesei* SZMC 22616 (Rut-C30) cultures, 21 paracelsin-like peptaibol compounds could be identified along with 6 previously described (paracelsin B, D and H; saturnisporin SA IV and *Trichoderma citrinoviride* sequence 4 and 5) and 3 entirely new compounds. Many of the known peptides are positional isomers of each other therefore, the chances to identify new peptaibol compounds after the identification of the isomeric types of the amino-acid residues were high. The extracts were purified by preparative HPLC and plants were treated with a dilution series from 10 mg ml^{-1} to 0.005 mg ml^{-1} of the purified peptaibol extract. The treatment with high peptaibol concentrations proved to be deterrent for the germination and growth of tomato seedlings, though, after a certain level of dilution more intense growth could be observed. However, the quantification of photosynthetic pigments extracted from the second leaf of the treated tomato saplings resulted in no significant outcome. Consequently, the saplings were cultivated on field experiments which led to increased fruit production. Furthermore, less sensitivity to fungal diseases was observed in plants treated with *T. reesei* peptaibols. The same concentration of the peptaibol solution was also observed to directly inhibit the growth of many plant- and human pathogenic filamentous fungal species *in vitro*. Further studies will be carried out to evaluate the applicability of peptaibol compounds and their direct effect on the plants which eventually affects their healthy fruit production.

Poster Papers

P (S 09) 01: Use of soilless media and organic amendments for root knot nematode management in nursery

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The plant parasitic nematodes pre-disposessolanaceous plants in nursery to various soil borne diseases. The root knot nematode stimulatethe entry of soil borne pathogens leading to development of disease complex. In the geographies infested with root knot nematode raising of healty nursery for transplanted solanaceous crop has become a major impediment which results in poor plant stand and low productivity. Chemical use is a popular method for management of nematode induced plant disease complex, however relying completely on the use of chemicals is costly and may cause adverse impact on environment. Sustainable agriculture emphasises on using integrated disease and pest management strategies to provide effective, economically viable and environment friendly solutions. The study is based on the principle of exclusion of plant protection by using soilless media and organic amendments i.e. *Trichoderma*, crucifer residues and AM fungus individually as well as in combination with the objective to identifysustainable solution for raising healthy nursery. It is noteworthy to state that in the present study soilless media in combination with various organic amendments were found to be superior in all plant growth parameters in comparison to the use of conventional soil media. These findings can serve as a building block for creating awareness and acknowledging the benefits of use of various eco-friendly biological amendments and soilless growing media in geographies and fields infested with root knot nematode causing subsequently disease complex.

P (S 09) 02: *In vitro* evaluation of chemicals and antibiotics against bacterial leaf spot of mango caused by *Xanthomonas campestris* pv. *mangiferae indicae*

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Bacterial leaf spot of mango caused by *Xanthomonas campestris* pv. *mangiferae indicae* is an important disease of mango worldwide. The severity of the disease in all the mango growing areas of Maharashtra resulting deteriorating losses to the farmers both in terms of quality and quantity. Chemicals *viz.* copper sulphate, copper oxychloride, streptocycline, mancozeb, 2 bromo 2 nitro propane 1,3-diol, carbendazim and antibiotic streptocycline and their combinations were evaluated *in vitro* by applying inhibition zone assay method by using Nutrient Agar (NA) as basal medium. The results revealed that the highest mean bacterial inhibition zone was made by Streptocycline treatment 22.40 mm in diameter followed by Carbendazim +

Streptocycline (21.96 mm). The minimum mean inhibition zone was made by Copper sulphate treatment with 14.20 mm in diameter. Among individual concentrations the maximum inhibition zone was made by streptocycline (500 ppm) 27.6 mm in diameter followed by streptocycline + copper sulphate (250+2000 ppm) 25.3 mm in diameter. Streptocycline (500 ppm) and streptocycline + copper sulphate (250 + 2000 ppm) inhibited growth of the pathogen to the extent of 30.66 and 28.11 per cent over control followed by carbendazim + streptocycline (1000+500 ppm) with an inhibition growth of pathogen (24.60 mm) and per cent inhibition over control (27.33).

P (S 09) 03: Isolation, screening under *in vitro* and identification of phyllosphere microflora from maize

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Twenty-two bacterial cultures (P_1 to P_{22}) and six fungal cultures were isolated from the phyllosphere by leaf imprint method and dilution method. The colony characters of isolates of bacteria and fungi pertaining to their shape, size, elevation, margin, texture, appearance and pigmentation were recorded. Grams' staining and endospore staining revealed that P_1, P_4, P_6, P_7, P_{12}, P_{14} and P_{16} were Gram positive, endospores and rod shaped. Biochemical tests revealed that all the twenty-two isolates were positive for the catalase and oxidase test. Isolates $P_{1,}$ P_6, P_7, P_{14}, P_{16}, P_{17} and P_{22} showed positive results to Voges prausker's test. Isolates of phyllosphere bacteria $P_{2,}$ P_3, P_5, P_8, P_{10}, P_{11}, P_{13}, P_{15} and P_{21} revealed positive results to Indole test. Whereas, isolates P_1, P_4, P_6, P_7 and P_{22} showed negative reaction to methyl red test. The phyllosphere bacterial isolates P_8, P_{15}, $P_{17,}$ P_{18}, P_{19}, P_{21} and P_{22} recorded negative reaction to gelatin liquefaction. Screening of phyllosphere microflora against *E. turcicum* was conducted following dual culture technique for all the isolates. Phyllosphere bacterial isolate P_9 recorded maximum growth inhibition of 24.09 per cent radial growth of the test pathogen. Fungal isolate *Aspergillus niger* showed highest inhibition 60.6 per cent compared to other isolates. Compatibility of six fungicides with potential bacteria and fungi were tested by turbidometry and poisoned food technique. The growth of phyllosphere bacterial isolate of P_9 and isolate P_{16} was highest in carbendazim + mancozeb showing OD value of 3.14 and 2.54 respectively, indicating that carbendazim + mancozeb was compatible with the phyllosphere bacterial isolates. Propiconozole was compatible with *Aspergillus niger* fungal isolate. The potential phyllosphere isolate P_9 and isolate P_{16} along with compatible fungicide were tested for their growth promoting activities under laboratory conditions. Seed treatment with (carbendazim + mancozeb) + isolate P_9 + isolate P_{16} not only increased germination percentage by 95.22 per cent but also enhanced seedling vigour (2394.78). The potential isolate P_{16} of phyllosphere bacteria were sent to Eurofins for further characterization at molecular level by 16S rRNA gene sequencing for identification. Based on the sequencing, the phyllosphere isolate P16 identified as *Bacillus amyloliquefaciens*.

P (S 09) 04: Mechanism of antagonistic action of different endophytes of tomato against bacterial wilt disease

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The mode of antagonistic action of the endophytes isolated from tomato against bacterial wilt was studied estimating the production of volatile and non volatile metabolites, siderophore, indole acetic acid and salicylic acid. The endophytic isolates were tested for their ability to produce volatile metabolites to inhibit the growth of the bacterial wilt pathogen, *Ralstonia solanacearum* by sealed Petri plate technique. The qualitative estimation of ammonia production was done following the method of Dye (1962) with slight modification. All endophytic isolates showed positive reaction with peptone water on addition of Nessler's reagent indicating ammonia production in varying levels. None of the isolates showed HCN production as no colour change of filter paper was noticed. The volatile metabolites produced by the endophytic isolates showed 15.51 to cent per cent inhibition of the pathogen. The production of nonvolatile metabolites by endophytic isolates was studied by both culture filtrate and cellophane paper methods. All the selected endophytes produced nonvolatile metabolites as no growth of *R. solanacearum* was observed on culture filtrate amended media. The selected endophytes when tested for the production of siderophore, none of the isolates showed greenish yellow fluorescent pigments either on $FeCl_3$ amended King's B medium or in sodium succinate broth indicating the absence of siderophore. All the endophytic organisms produced varying levels of IAA quantitatively estimated by Salkowsky assay method ranging from 34 to 192.17 μgml^{-1}. With regard to salicylic acid production, all selected endophytes produced salicylic acid in varying quantities ranged from 3.42 to 23.48 μgml^{-1} with maximum production in *B. subtilis* and minimum production in *Streptomyces thermodiastaticus*. Summing up, volatile and nonvolatile metabolites and salicylic acid had role in the antagonistic activity of the endophytes on bacterial wilt pathogen in addition to the role of IAA in promoting plant growth.

P (S 09) 05: Survey of nematode-trapping fungi in Bundelkhand region of India and their nematophagous and mycophagous ability against plant pathogens

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The Bundelkhand region covers an area of 7.08 million hectares (mha) and is located between 23020' and 26020' N latitude and 78020' and 81040'E longitude. The Bundelkhand region is rocky and mainly constitutes non-arable land. The soil of in the region is a mixture of black and red-yellow soils which are poor in organic nutrients. Bundelkhand has a hot and semi-humid climate. Usually the hottest days are in May and coldest days in December or January. Nematode-trapping fungi are a group of soil living carnivorous fungi that capture and kill the nematodes by their trapping. These fungi are most important because of their potential use as bio control agenet of plant and animal parasitic nematodes and some other plant pathogenic fungi. Since no work has been done on the presence of nematode trapping in fungi in Bundelkhand region of India, the present investigation was carried out to know the presence and dominance of nematode- trapping fungi in some region of Bundelkhand area. The soil samples were collected from Bundelkhand area. Soil samples were collected from the agricultural crop soil, forest plant soil and fruit orchard soil and processed for isolation and characterization of nematode-trapping fungi by soil plate technique. Each species attacking on nematodes were isolates, purified and characterized. The most important nematode- trapping fungi recovered from the soil were *Drechslerella dactyloides, D. brochopaga, A. conoides, A. eudermata, Dactylellina gephyropaga, D. phymatopaga A. clododes and A. oligospora*. Orchard soil yielded maximum nematode-trapping fungi in comparison to other soils. The adhesive trap forming fungi was found more frequently in comparison to constricting forming fungi. These fungi were tested for their nematophagous ability against *Meloigodyne incognita* and mycophagous ability against *Rhizoctonia solani*. *Drechslerella dactyloides and Drechslerella brochopaga* were found more nematophagous against *M.incognita*. *R. solani* was found to susceptible against mycoparasitic nature of *Arthobotrys conoides, A. eudermata, A. cladodes and A. ologospora.*

P (S 09) 06: Studies on efficacy of aqueous seed extracts against *Pectobacterium carotovorum* causing black leg and soft rot of potato

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The use organic farming is now gaining popularity. Different parts of many plants have antimicrobial properties. In this context the seeds of some medicinal plants were tested agaist *Pectobacterium carotovorum* causing black leg and soft rot of potato. The seeds used in the studies were *Terminalia chhebula* (Chhebulic myrobalan),*T. belerica* (Beleric myrobalan), *Emblica officinalis* (Indian goose berry), (*Azadirachata indica*(Neem), (Greater cardamom), *Raoulvia sepentina* (Snake root), *Coriandrum sativum* (Dhania),*Cuminum cyminum* (Cumin), *Nigella sativa* (Black cumin),*Foeniculum vulgare* (Fennel), *Piper nigrum* (Black pepper,*Cassia fistula* (Indian laburn),*Cassia tora* (Senna tora). The healthy seeds were collected washed several times in sterilized water and air dried. Fifty grams from each selected plant part along with 50ml of double distilled water were taken band grinded with the help of pestal and mortar to a fine pulp.The pulp was filtered through two layers of muslin cloth and gently pressed to get maximum filterate.The filterate from each plant part was collected and kept separately in different sterile specimen tubes and centrifused at 1500rpm for 15 minutes. The supernatant liquid was drawn carefully into a 5ml syringe and then passed through membrane filter of 0.45nm size to sterilize the extract . The filter sterilized extract of each part collected in sterilized specimen tube with screw cap and stored in deep freeze maintain ed at -20^0 C. The extracts were evauated *in vitro* following the inhibition zone technique. In this technique, two drops of bacterial suspension of each test bacterium was transferred on to the petriplate containing NSA medium and spreaded over the surface of the medium with the help of a sterilized glass spreader. Three sets of Hi-media discs(5mm), soaked for one minute in each plant extracts were placed on the media surface of each petriplate at the equidistance from the centre. In each set four numbers of discs were used to hold sufficient quantity of the plant extract. Two sets of petridishes were used for testing each plant extract petriplates were incubated at 27 ± 1^0C for 24 hours in a BOD incubator. After the incubation period, the petriplates were examined for development of inhibition zone around the discs. The diameters of each zone of inhibition was measured and recorded to assess the antimicrobial properties of plant extracts against each test bacterium. In control the paper discs were soaked in sterilized water.The experimental results revealed all the seeds possess antibacterial peoperties.Significantly maximum zone of inhibition (11.33mm) was observed in *A. subulatum* followed by *T. chhebula* and *S. caryophyllus* (10mm). Minimum zone was recorded in *P. nigrum* and *C. fistula*. In control, no inhibition zone was recorded.

P (S 09) 07: Mechanism of activation and physiological role of a novel membrane bound NAC transcription factor of tomato

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Membrane-bound transcription factors can sense variations in the surrounding environment, detaches from the membrane, and migrates into the nucleus for gene regulation. Multiple members of plant-specific NAC family remain membrane-bound (NACMTF) under the normal physiological condition in all flowering plants. Tomato genome encodes 13NACMTFs, and some are highly responsive to biotic and abiotic stresses. Among these SlNACMTF3 is differentially expressed during early blight, tomato leaf curl New Delhi virus infections and thermal stress. The activated form regulates the expression of a set of stress-responsive genes. SELEX studies revealed the preferable DNA binding sites for SlNACMTF3, and bioinformatic analyses confirm the existence of these sites in the promoter region of different stress-related genes. In order to investigate the molecular mechanism of membrane release upon the perception of stresses, we have utilized N-terminal GFP tagged SlNACMTF3 (GFP-SlNACMTF3) construct, transient expression in onion epidermal cells, followed by confocal microscopic studies with or without stress-exposure. While GFP-SlNACMTF3 is found exclusively in the plasma membrane, nuclear localization is noticed in all stressed cells. Further, the transmembrane domain (TM) alone is able to sequester GFP to the membrane, validating its sole role in sub-cellular distribution. Application of inhibitors in the assays confirmed the involvement of protease, not proteasome, and specifically a rhomboid protease in membrane release upon application of different stresses. Accordingly, mutation of a putative rhomboid-protease cleavage site adjacent to the hydrophobic region of the transmembrane domain abolished membrane migration of SlNACMTF3. These studies establish essentiality of SlNACMTF3 in sensing stress on the membrane and rapid activation of signalling events. Supported by CSIR Ad hoc fellowship to HD, DBT RA fellowship to SC and a CSIR grant to PK.

P (S 09) 08: Morphological and physiological response of mung bean plants to combined inoculation of root-knot nematode and dry root-rot fungus

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The effect of single, sequential, and concomitant inoculation with root-knot nematode, *Meloidogyne incognita* (Mi) and dry root-rot fungus, *Macrophomina phaseolina* (Mp) were studied on mung bean, *Vigna radiata* cv. Samrat (PDM-139) under greenhouse condition. The sequential and concomitant inoculations with *M. incognita* synergised the infection by *M. phaseolina* leading to 20-40% increase in the disease severity. However, significant reduction in galling was recorded over single inoculation. Among all the combinations, *Mi*!*Mp* was recorded most destructive, followed by *Mp+Mi*, *Mp!Mi,* fungus/nematode alone. Maximum loss in plant growth (19-42%), nodulation (16-43%) and grain yield (40%) of mung bean was recorded in the treatment inoculated with the nematode 3 days before inoculation of *M. phaseolina.* In the treatment having nematode alone the Mi final soil population increased four times than the initial population, while population of Mp in alone treatment was also increased significantly in comparison to the initial population. In the dual inoculation treatment, the soil population of nematode significantly decreased (20-40%) and the population *M. phaseolina* increased by 80-110%. Physiological and biochemical parameters *viz*., photosynthesis rate, stomatal conductance, transpiration rate, total chlorophyll, total phenol, and salicylic acid contents were studied in response to the different combination of the pathogen. The physiological parameters viz., photosynthesis rate significantly decreased, whereas the transpiration rate and stomatal conductance increased with the progress of time in the disease complex. The total chlorophyll contents were reduced in the leaves of mung bean inoculated with the fungus or nematode over control. In the dual inoculation plants, total chlorophyll contents were reduced by 37-60% over control. Total phenol (TP) and salicylic acid (SA) contents of the mung bean leaves were highest in the inoculated plants (36-47%) than the un-inoculated plants. The concentration of TP and SA was much greater in the dual inoculation treatments than the fungus or nematode and highest content were recorded in the concomitantly inoculated treatment (*Mp+Mi*, 179-201%), followed by *Mi*!*Mp* (177-212%) and *Mp*!*Mi* (56-72%).

P (S 09) 09: Efficacy of organic manures and ginger garlic paste on blue mold disease of garlic (*Allium sativum* L.)

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Efficacy of organic manures namely Poultry manure, Goat manure, FYM and Neem cake as soil application and Ginger Garlic paste as foliar spray. Disease incidence of Blue mold/*Penicillium* decay on garlic blubs was recorded at 120 days after germination. Results showed that Poultry manure as soil application was most effective treatment followed by Neem cake, Goat manure, FYM and least effective results were observed in Ginger and Garlic extract treatment as foliar spray against Blue mold/*Penicillium* decay of garlic. The highest cost-benefit ratio was obtained with Poultry manure (1:3.71) while other treatments also showed significantly effective for the checking of disease incidence and yield over control in the field condition.

P (S 09) 10: Integrated management and host plant resistance against dry root rot of chickpea

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In the present experiment was planned integrated management of root rot pathogen in chickpea. Occurrence of root rot disease has become a major constraint in recent years for successful and profitable cultivation of chickpea. The efficacy of Bio-agent *viz. Trichoderma viride,* Organic amendment viz. neem cake, Plant extract, garlic, and Fungicide, Carbendanzim applied through seed treatment and soil application were evaluated against *Macrophomina phaseolina* causing root rot disease of Chickpea. Different alternative combination of most effective treatments that tested in pot conditions for controlling root rot of chickpea exhibited. Among the treatments soil application with neem cake @ 25g/ pot+ seed treatment with carbendazim @ 2g/kg seed (16.66 and 20.00%) followed by seed treatment with *T. viride @ 4* g/kg seed + carbendazim @ 2 g/kg seed (20.00 and 20.83%) found most effective to reducing root rot incidence over control at 40 and 60 days after sowing respectively. Twenty nine cultivars/ germplasms tested against dry root rot of chickpea in which none of cultivars found resistant. Entries H12-24, GNG 1958, IPC 2002-31, GNG 2299, IPC 10- 134, PG 0104, IPCK 2009 -165, GL 2003, H 12-26, IPC 2007-28, CSJ 515 and BG 0109 were found moderate resistance.

P (S 09) 11: Antagonism of *Bipolaris oryzae,* brown spot of rice by entomopathogenic fungus, *Beauveria bassiana* and its plant growth promoting activity in rice, *Oryzae sativa* Linn.

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Beauveria bassiana, a widely studied entomopathogenic fungus recently drawing attention worldwide as potential biocontrol agent not only against insect-pest but also against several plant pathogens. As potential alternative to injudicious chemicals use in crop protection, *B. bassiana* plays multifaceted roles as plant disease antagonist, endophytes, plant growth promoter as well as beneficial rhizosphere colonizers providing an excellent opportunity as biocontrol agent in plant disease management. The present investigation aim to evaluate antagonistic potential of entomopathogenic fungus *B. bassiana* against brown spot pathogen of rice and its role in plant growth promotion of rice. Eighty isolates of *B. bassiana* have been obtained from different districts of Meghalaya and evaluated for their antagonistic potential against rice brown spot pathogen, *B. oryzae* by employing dual culture technique. The potential isolates were further studied for antimicrobial traits *viz.* production of several hydrolytic enzymes, siderophore production and ammonia production as well as plant growth promoting attributes in rice crop *viz.* micronutrient solubilisation, ACC deaminase production and seed germination assay. About 39 isolates of *B. bassiana* have been found effective against *B. oryzae* and the highest inhibition percentage was observed by isolate B26 (83%) followed by B3 (77%) by lysis of fungal mycelia. In addition, potential *Beauveria* isolates also promotes per cent germination and seedling vigour of rice as compared to control. The multifaceted role played by entomopathogenic properties as plant disease antagonists and plant growth promoter provide opportunities for the dual purpose use of *B. bassiana* as biocontrol agent (BCA) in integrated pest management (IPM) as well as in integrated disease management (IDM) strategies.

P (S 09) 12: In vitro study on suitability of local microflora as ecofriendly biocontrol agents for location specific crops

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In order to understand the suitability of use of local microflora as biocontrol agents against the pathogens of location specific crops, twenty-one *Trichoderma* isolates viz., SMV, GMV, PSV, SDKd, CPV, RMy-B, RMy-P, RMy-SC, RMd-C, RMd-SC, RKp-CP, RSr-SC, RCh-S, RDA, RH-Co, RT-FM, RKd-Cu, RKd-HG, RMl-O, RMl-P, RMl-T were collected from different cropping locations of Karnataka. Species level identification of all isolates were done by BLAST analysis of 5.8S-ITS region amplified using ITS-4 and ITS-5 primers. The BLAST results assisted in species identification and classified into five clades (*T. harzianum*: eleven isolates (GMV, PSV, RMY-B, RMY-P, RMY-SC, RMd-SC, RH-Co, RTFM, RKd-Cu, RMl-O and RMl-T), *T. asperellum*; five isolates (CPV, RMd-C, RDA, RKd-HG and RMl-P), T. virde; two isolates (SMV and RSr-SC), *T. virens*; two isolates (RKp-CP and RCh-S) and *T. longibrachiatum* ; one isolate (SDKd)). To understand the variations among the isolates of each species, on the basis of 5.8SITS region, multiple sequence alignment was done using UPGMA approach. Multiple sequence alignment of ten *T. harzianum* isolates showed no major sequence variation except Rmy-B (*T. harzianum*, isolated from banana rhizosphere) but, all with similar *in vitro* antifungal activity on par with commercial biocontrol agent against eight major plant-fungal-pathogens. Similarly, all five *T. asperellum* isolates also showed comparable antifungal activity with no major sequence variation except in CPV (*T. asperellum*, isolated from coir pith). The above study shows that, there is no much sequence variation between the isolates belong to each species except Rmy-B and CPV. These isolates were probably got the drastic sequence variation due to change in the environment condition, natural selection, etc. and hence, such species will have a better survivability in their native location. Therefore, in order to control fungal diseases, location specific microflora with potential biocontrol agents can be explored for sustainable beneficial effect without disturbing local microflora.

P (S 09) 13: Management of wilt disease of lentil through bio control agents and organic amendments in Rajasthan, India

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Lentil (*Lens culinaris* M**)** has gained importance in various parts of Rajasthan as potential pulses crop. This crop suffers from many diseases among which Vascular wilt of lentil caused by *Fusarium oxysporum* f. sp. *lentis*, has become a thoughtful trouble in recent years in Rajasthan and in other lentil growing parts of India, resulting heavy yield losses. The present work aimed to evaluating the efficacy of bio agents and organic amendments against lentil wilt pathogen. Laboratory experiments were carried out in Completely Randomized design with four replications and field trials were carried out consecutively during 2016-17 and 2017-2018 crop season in Randomized block design (RBD) with four replications using L9-12 a susceptible cultivar. In *In Vitro*, bio efficacy of selected bio agents, maximum 81.33 per cent mycelial growth inhibition of pathogen was recorded in *Trichoderma harzianum* (local isolate) and minimum mycelial growth inhibition 55.00 per cent was recorded in *Bacillus subtillus*. In *In vivo* condition, effect of selected bio agents and organic amendments on disease incidence, percent disease control, pathogen spore in per gram soil and yield ha^{-1} of lentil was recorded. Application of *Trichoderma harzianum* (Local isolate) @ 6g/Kg seed was found most effective with maximum seed germination 91.95 and 90.62 per cent, lowest disease incidence of 24.22 and 25.39 per cent and higher pooled mean grain yield 774.31 kg/ha over check during 2016-17 and 2017-18, respectively. Among organic amendments maximum disease control 42.02% per cent, minimum average disease incidence 36.33 per cent and minimum pathogen spores (1.3×10^{4} per gram soil) were observed in neem cake amendment followed by poultry manure and Vermicompost amendments. This indicates that these treatments have significant role in biologically based management strategies for controlling Fusarium wilt disease under organic mode of lentil cultivation in Rajasthan.

P (S 09) 14: Disease management through soil amendments

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In present time disease is the main source in reduce yield. About 30 per cent losses occurs due to attack of disease on plants. To create unfavorable conditions for pathogens is the main aim of soil amendments. Any material such as gypsum, oil, cake, saw dust and farm yard manure etc. are added to soil to change its character as soil amendments. This is one of the cheapest, hazard free and ecofriendly method of modifying soil environment, it is amendment of soil with decomposable organic matter. This leads to changes in soil pH which is unfavorable to the pathogen. Other mechanism are increase host tolerance or resistance increased antagonism viz. wilt and root rot disease. Manures and by-products derived from processing of animals and plants used for centuries as sources of fertilizer,there beneficial or harmful effects never investigated. As we know that soil is the main source for plants nutrients viz. food. By natural amendments we can increase quality of products which we gain through plants. There are the many strategies by which disease management successfully controlled through using natural products which improve soil condition. Through these amendments beneficial microorganisms also increased which control disease attack and make the plant healthy. Soil amendment is one of the strategy of integrated disease control, which ecofriendly, harmless and beneficial by providing essential nutrients.

P (S 09) 15: Managing root knot nematode, *Meloidogyne incognita* in okra by using biopesticides

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Okra is the one of the most important vegetable crop worldwide being cultivated for human consumption and industrial purpose. The crop is having a huge socio-economic potential and a rich source of dietary fibres and distinct seed proteins. Root knot nematodes, *Meloidogyne* spp. are one of the major limiting factors in successful production of the crop. They attack the root system and form galls or knots on the roots which cause severe plant growth reduction. Yield losses upto 27% have been reported in okra due to root knot nematodes. As most of the chemical nematicides have been banned due to their hazardous effect on human health and environment, management of root knot nematode with eco-friendly methods is need of the hour. In the present study, formulations of *Bacillus pumilis* 1% aqueous suspension and *Pseudomonas putida* 1% aqueous suspension were evaluated for the management of root knot nematode for three continuous years (2015-2017). The trials were conducted in root knot nematode, *M. incognita* infested field. In all eight treatments including seed treatment and field application with *Bacillus pumilis* and *Pseudomonas putida* along with chemical control and untreated control were evaluated. Each treatment was replicated thrice in 3x3m plots. Observations were taken on soil nematode population, root gall index (0-10 scale) and marketable yield (q/ha). The results showed that seed treatment with *Pseudomonas putida* - 1% A.S. @ 10 ml/ kg seed + application of 20 tons of FYM enriched with 5 lit of *Pseudomonas putida*/ ha was found effective in reducing root galling index and soil nematode population and increasing marketable yield.

P (S 09) 16: Management of root rot (*Rhizoctonia bataticola*) of clusterbean through bio-agents

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Clusterbean [*Cyamopsis tetragonoloba* (L.)Taub.],is a major leguminous crop of kharif season in arid and semi-arid regions of India. India is the most important clusterbean producer in the world and contributes almost 75%-82% global clusterbean seed production followed by Pakistan. This crop has an important place in national economy because the gum extracted from seed has many industrial applications and great export value and is thus an important foreign exchange earner for the country. Hence, clusterbean is now considered as a source for providing livelihood security to arid zone farmers.Root rot caused by *Rhizoctonia bataticola* is an important disease of clusterbean, under severe infestation it cause 58-68 % losses in grain yield**.** Two-year field experiments were conducted in hot arid conditions at Bikaner, Rajasthan during *Kharif* seasons with the objective to find out suitable eco-friendly management strategies for root rot. The experiment was conducted on cv. RGC-1033 with seven different combination of *Trichoderma harzianum* + *Pseudomonas fluorescens* bio-agents *viz*, seed treatment, soil treatment and their combinations against the root rot disease and compared with an untreated control. Results of experiment showed that all the treatments brought significant decline in disease incidence and consequently enhancement of grain yield compared to control. The treatment having combination of *Trichoderma harzianum* + *Pseudomonas fluorescens* seed treatment (4+4 g/kg seed) + soil application of *T. harzianum* + *P. fluorescens* (1.25 +1.25 kg in 50 kg FYM for each/ha) had minimum (6.17%) root rot incidence, highest grain yield (16.52 q /ha) and net return (Rs. 19,016/ha). The *T. harzianum* seed

treatment 8 g/kg seed + soil application of *T. harzianum* 2.5kg in 100 kg FYM/ha was the next best treatment with 8.83 per cent disease incidence and 15.44 q/ha of grain yield. These treatments can provide an effective, economical and eco-friendly management of root rot of clusterbean for cultivators.

P (S 09) 17: *In vitro* evaluation of different phyto extracts against *Fusarium oxysporum* f. sp. *carthami*

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Safflower (*Carthamus tinctorius* L.), is one of important *Rabi* oilseed crops cultivated from centuries in India for its valuable oil and also orange color dye. Wilt disease caused by *Fusarium oxysporum* F. sp carthami (Klisiewicz and Houston) is one of the most destructive and wide spread disease of Safflower causing accountable qualitative and quantitative losses of about 21-64 per cent. Eight plant extracts were used for testing against *Fusarium oxysporum* f. sp. *carthami in vitro* by Poison food technique. Result revealed that all the plant extracts tested (@ 10 per cent and 20 per cent), significantly inhibited mycelial growth of the test pathogen over untreated control and per cent mycelial inhibition was increased with increase in concentrations of the botanicals tested. At 10 % and 20% significantly highest mycelial inhibition was recorded with Neem (59.63% and 75.08%) followed by Garlic (56.41% and 69.63 %), Onion (52.85% and 65.19%), and least, mycelial inhibition was recoreded in Mehandi (37.30 % and 43.07%) and Shatwari (36.30 % and 40.45%).

P (S 09) 18: *In vitro* antagonism of biocontrol agents against *Sclerotium rolfsii* causing collar rot of chilli

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Chilli collar rot caused by *Sclerotium rolfsii* is a serious soil borne disease. For devising an effective management strategy, the efficacy of different bioagents, *viz*., *Trichoderma viride*, *T. harzianum*, *T. hamatum*, *T. koningii*, *Pseudomonas fluorescens* and *Bacillus subtilis* were conducted under *in vitro* conditions. All the six antagonists have shown the potential of parasitizing the growth of *S. rolfsii in vitro*. The rate of inhibition was fastest in *T. harzianum* (81.33 %) followed by *T. viride* (78.31 %) and *T. hamatum* (75.40 %). Least inhibition was recorded in *B. subtilis* (62.59 %) after 72 hours of incubation. The antagonists such as *T. harzianum* and *T. viride* can be used as a bio-control agent against *S. rolfsii* of chilli.

P (S 09) 19: Occurrence and distribution of *Tobacco streak virus* (TSV) in the genotypes of cotton

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Various bacterial, fungal, and viral diseases hamper cotton productivity. Among the viral diseases infecting cotton, cotton leaf curl virus and tobacco streak virus are important. Cotton necrosis disease caused by *tobacco streak virus* (TSV) is an emerging threat in India. The germplasm of *Gossypium barbadense* (Suvin) were surveyed for the presence of TSV during the year 2018. The presence of disease affected plants in the varieties and hybrids of *Gossypium hirsutum* were observed at 60 to 70 DAS (Days after sowing). The present paper emphasised on the disease incidence of TSV and thrips population observed in 35 cotton genotypes in the fields of CICR. Typical symptoms observed were chlorotic with necrotic spots in young leaves and marginal necrotic streaks with leaf deformation. Whereas in matured plants venial necrosis, drying of squares and also in terminal shoots was observed. The symptoms were very distinct with necrotic spots dark purple in colour and also drying of squares. Other symptoms include necrotic streaks on petiole and necrosis on crown region in *Gossypium barbadense*. The highest per cent disease incidence of TSV was observed in PSCP 35 BG I (21.3%), PCH 2270 Bt (19.2%) and Vega (18.8%). The disease incidence was recorded low in P-15 (6.1 %) and Prathima (6.9%). The disease grade also observed in all the cotton genotypes and found to be in the grade of 2 and 3. Maximum thrips population was observed in the genotypes Vega (12.8) and Extreme okra (11.0). The disease incidence in Suvin was observed as 7.5% with thrips population of 5.8. The disease incidence in Surabhi was 10.5% and in Sumangala was 7.2%.

P (S 09) 20: *In vitro* and *in vivo* evaluation of botanicals and fungicide against leaf blast of pearl millet

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Pearl millet (*Pennisetum glaucum*) is an important nutri-cereal for human as well as a forage/fodder crop for livestock. It is the only cereal crop that is capable for adopting harsh climate condition and marginal soil. Blast incited by *Pyricularia grisea* (Cooke) Sacc. has occupied a key position among the pearl millet diseases resulting severe losses in high yield potential hybrids/ varieties particularly cultivated for fodder purpose. A total no. of eight botanicals (@ 20%) viz., *Azadirachta indica* (leaf); *Aegle marmelos* (leaf); *Catharanthus roseus* (leaf); *Nicotiana tobacum*(leaf); *Datura stramonium* (leaf); *Lantana camra* (leaf); *Allium sativum* (bulb); *Ocimum tenuiflorum* (Tulsi) and six fungicides (@ 0.1%), viz., Iprobenphos (Kitazin); Thiophenate methyl; Tricyclazole (Beam); Azoxystrobin; Trifloxystrobin+Tebuconazole; Propiconazole were evaluated under *in vitro* condition against *P. grisea*. Out of them three fungicides viz. Tricyclazole**,** Propiconazole and Trifloxystrobin+ Tebuconazole @ 0.1 percent absolute inhibited fungal growth and two botanicals *Lantana camra* leaf extract and *Allium sativum* bulb extract @ 20 percent concentration were found effective against the pathogen as in these two treatments 39 mm and 39.3 mm growth showed respectively. After *in vitro* evaluation five fungicides and two botanicals were further evaluated in the field condition. The findings reveals that all the tested fungicides and botanicals significantly check the blast but the combination of Trifloxystrobin+ Tebuconazole was found most effective as in this treatment the minimum disease was recorded followed by Propiconazole @ 0.05% (33.3%), Azoxistrobin 25EC@0.05% (35.5%) and Tricyclazole (Beam) @ 0.1% (39.4%). Among the botanicals *Lantana camra* @ 20% was also significant for check the blast.

P (S 09) 21: Integrated disease management through organic farming

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Integrated disease management (IDM) is a holistic approach which first assesses the disease situation, evaluates the merits of disease management options and then implements a system of complementary management actions within a defined area. Integrated disease management in organic farming combines the use of various measures. The usefulness of certain measures depends on the specific crop pathogen combination. In many crops, preventative measures can control diseases without the need of plant protection products. However, for certain disease problems, preventative measures are not sufficient. For example, blight in Potato, Chili leaf curl in chili, leaf curl virus in Tomato, viral disease in Cole crops and Cucurbits. Organic farming is a production system which accelerates and enhances agro-ecosystem health, including biodiversity, biological cycles and soil biological activity. Organic farming support stopping the use of chemical fertilizer, chemical pesticides and all other inorganic inputs in farming. Organic farming assist in creating an ecological balance and a micro-environment suitable for health and growth of soil micro-flora, plants, animals, farm workers and finally the vast population of consumers. Integrated Disease Management (IDM) as applied to diseases of vegetables means using all the strategy available to the grower (cultural, biological, host-plant resistance, and chemical) that provides acceptable yield and quality at the least cost and is compatible with the tenets of environmental stewardship. India has tremendous potential to grow crops organically and emerge as a major supplier of organic products in the world's organic market. According to the International Fund for Agriculture and Development (IFAD), about 2.5 million hectares of land was under organic farming in India in 2004. In India it is estimated that 18 million hectare land is available for organic cultivation in the NE, which can be exploited for organic production. In our country, the vegetable crops like tomato, brinjal, chilli, potato, capsicum, cole crops, onion, garlic, pea and pumpkin are growing through organically on commercial scale. Organic Farming seems to be more appropriate as it considered the important aspects of sustainable agriculture tool. It is a production system, which favors maximum use of organic materials like crop residues, FYM, compost, green manure, oil cakes, bio-fertilizers, bio-gas slurry etc. to improve soil health from the different experiment, microbial fertilizers like Rhizomic, Azotobacter, Blue green algae, Azolla etc. have increased the yield and also played important role for minimizing the harmful effect of pesticides and herbicides. Integrated disease management is the practice of using a range of measures to prevent and manage diseases in crops. Hazard analysis is used to identify the potential for infection so that preventative or curative measures can be put in place to minimize the risk of disease infection and spread. During the cropping cycle, regular crop monitoring is used to decide if and what action is needed. Integrated disease management is one of the best solutions for mitigate the disease in vegetable crops through cultural, biological, mechanical and chemical methods.

P (S 09) 22: Cultural and morphological characterization of rhizospheric *Trichoderma* isolates

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Trichoderma species are promising bioagents due to their ability to control a wide array of plant pathogens. The fifteen isolates of *Trichoderma* were obtained from the rhizospheric soil of rice, soybean and mungbean crops from different locations of Pantnagar and Dehradun. These isolates were characterized based on their cultural and morphological characteristics. The cultural characters like colony colour, presence or absence of concentric rings, surface topography, pigmentation on the lower side of the plate, time of first appearance of green conidia were determined on the basal media Potato Dextrose Agar. The growth of *Trichoderma* isolates were also recorded at varying temperatures like 5, 10, 15, 20, 25, 30, 35 and 40. The colonies were observed under the microscope for various morphological characters like conidiophores, their branching pattern, phialide number, their arrangement, conidial shape and formation of chlamydospores. The cultural study revealed that among fifteen isolates of *Trichoderma*, four were dark green, two light green, seven lightish to dark green and two whitish to light green in colour. Eleven isolates exhibited rough, spongy and raised colony, two showed smooth and flat colony, one isolate was having smooth and flat colony with dense sporulation at the border and one showed spongy and fluffy growth. One isolate produced light brown pigmentation, 5 showed whitish creamy, 3 yellowish, 5 yellowish green and 1 pinkish pigmentation on the reverse side of the plate. Seven isolates produced conidia at 48 hrs, three at 48-72 hrs and one at 72 hrs. The optimum temperature for the growth was 25-30°C. On the basis of morphological studies the isolates of *Trichoderma* were categorized into 4 groups. The Group I isolates was having ampulliform phialides and globose to subglobose conidia. Group II isolates consist of lageniform phialides and globose conidia while Group III showed lageniform phialides and globose to subglobose conidia. Group IV comprise of lageniform phialides and globose to ellipsoidal conidia. These cultural and morphological characteristics of *Trichoderma* play a key role in identification of species of *Trichoderma*.

P (S 09) 23: Efficacy of *Trichoderma viride* and different fungicides against spot blotch of wheat caused by *Bipolaris sorokiniana*

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The present experiment was conducted at Students Experimental farm and in the laboratory of Department of Plant Pathology, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, during Rabi season 2018-19. Wheat (*Triticum aestivum*) is one of the largest growing and consuming crop in the world including India as well. Disease is one of the major constraint in production of wheat. Wheat crop are suffering from diseases such as, Rust, Smut and Spot blotch *etc*. Among them Spot blotch caused by *Bipolaris sorokiniana* is an important disease of wheat gaining much importance in central region in Uttar Pradesh because of the occurrence of severe outbreak every year (25-40%). The fungus as a pathogen is most aggressive under the conditions of high relative humidity and temperature. All the above ground parts of the plant are affected. The first symptom of the disease appeared on the lower leaves during first week of December. The present finding is revealed that Seed treatment with vitavax power @ 3g/kg of seed + two spray of propiconazole @ 0.1% at the time of disease initiation on flag^{-1} leaf found best. Avoidable yield losses were also calculated and it was maximum (23.49%) with treatment T_5 followed by T_6 (22.55%), T_3 (21.25%), T_4 (17.91%), T_7 (12.15%) and T_2 (10.27 %). maximum benefit cost ratio (7.55) was found in treatment T_2 (seed treatment with *T. viride*), followed by treatments T_1 (5.11), T_3 (3.56) and T_4 (3.38).

P (S 09) 24: Bioefficacy of various antagonists against *Macrophomina phaseolina* causing charcoal rot of sesame

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Sesame (*Sesamumindicum*) an important oilseeds crop is vulnerable to number of diseases caused by fungi, bacteria, viruses and phytoplasmas. Among the fungal diseases, charcoal rot caused by *Macrophominaphaseolina* is one of the constraints in profitable protection of sesame.Though the disease can be controlled by chemicals, but the pathogen being mostly soilborne it is uneconomical to control soilborne diseases, alone with chemicals. Therefore, present *in vitro* evaluation of eight biocontrol agents/ antagonists was planned in CRD and all the treatments replicated thrice. The study was attempted at the Department of

Plant Pathology, College of Agriculture, Latur (MS) during *Kharif,* 2017-18. The result revealed that all of the eight biocontrol agents as efficient antagonists with significant mycelial growth inhibition of *M. phaseolina,* over untreated control. However, it was significantly highest with *T. viride* (69.26%), followed by *T. hamatum* (68.37%), *T. koningii* (62.18%), *T. harzianum* (60.18%), *Aspergillusniger* (59.82%) and *T. virens* (59.07 %), later two were on par. *Pseudomonas fluoroscens* (37.63%) and *Bacillus subtilis* (34.18%) were found comparatively less effective against *M .phaseolina*.

P (S 09) 25: Management of sesame charcoal rot (*Macrophomina phaseolina*) with organic amendments

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Charcoal rot (*Macrophomina phaseolina*) is one of the widespread and most destructive soil borne diseases of sesame (*Sesamum indicum*). Its control with fungicides alone seems to be impracticable as well as uneconomical. Among various alternative means to combat such soilborne diseases, use of organic amendments has been found to be most promising. Therefore,present study was conducted using polybags and the experiment was planned in CRD with 11 treatments replicated thrice, by applying sick soil technique and by sowing sesame cv. Sweta. The results revealed that all of the treatments imposed resulted with significant reductions in pre-emergence seed rot (PRESR), post-emergence seedling mortality (POESM) and average mortality, over untreated control. However, Neem seed cake resulted with significantly highest reduction in PRESR (76.00 %), POESM (71.60 %) and average mortality (73.80 %). It was followed by Cotton seed cake(67.49 %, 65.73 % and 66.61 %, respectively),Sunflower seed cake(52.49 %, 51.63 % and 52.06 %, respectively), Safflower seed cake(44.99 %, 45.63 % and 45.31 %, respectively), Soybean seed cake (40.00%, 41.32% and 40.66%, respectively) and Karanj cake(37.49%, 35.39 % and 36.44%, respectively). Rest of the test amendments were also found effective against the disease.

P (S 09) 26: Organic disease management for sustainable production of rapeseed (*Brassica campestris* L.)

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A field trial was conducted at RARS, Shillongani, Assam during *Rabi* 2016-17, 2017-18 and 2018-19 to develop organic package of practices for rapeseed (*Brassica campestris* var. *toria*). Two organic modules along with absolute control and control (all recommended practices) were tested in a randomized block design with six replications. Module I comprised soil application of enriched *Trichoderma viride* @ 2.5 kg/ha + soil application of FYM @ 2 t/ha + rock phosphate @ 30 kg/ha + biofertilizer (*Azotobacter* & PSB each @ 50 g/kg seed) + foliar spray with *Bacillus megaterium* @ 5 ml/l of water at 30 & 45 days after sowing (DAS) + 2 - 4 foliar sprays of NSKE 5% (need based) + Installation of bird perch @ 40 nos./ha + installation of yellow sticky trap (0.5 m x 0.5 m) @ 20 nos./ha. Module II consisted of seed inoculation with *Trichoderma viride* @ 10 g/kg seed + biofertilizer (*Azotobacter* & PSB each @ 50g/kg seed) + soil application with vermicompost @ 1 t/ha + rock phosphate @30 kg/ha + foliar spray with *Bacillus megaterium* @ 5ml/l of water (30 & 45 DAS) + 2 - 4 foliar sprays of NSKE 5% (need based) + installation of bird perch @ 40 nos./ha + installation of yellow sticky trap (0.5 m x 0.5 m) @ 20 nos./ha. The per cent severity of *Alternaria* leaf blight caused by *Alternaria brassicae* at 60 DAS was minimum under control (21.2, 20.8 and 18.95 in 2016-17, 2017-18 and 2018-19, respectively), closely followed by that under Module II (24.6, 25.8 and 22.6 in respective years). The magnitude of aphid (*Lipaphis erysimi*) infestation was the least under control, and there was no considerable variation under Module I and Module II. Soil microbial population (fungi and bacteria) build up was considerably higher under organic modules than that under control and absolute control. Module II recorded the highest values for soil fungi of 31, 39 and 26 (x 10^4 cfu g^{-1} of soil) and bacteria of 39, 52 and 43 (x 10^7 cfu g^{-1} of soil) in respective years of study. The yield loss varied from 2.4 - 5.6 % under Module II and from 10.7-13.0 % under Module I as compared to control.

P (S 09) 27: Development of turmeric based nano formulation and its characterization

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Pest management is one of the vital factors for stepping up agricultural production. The need for the safer means of pest management has become crucial in order to overcome the growing detrimental effects of using synthetic pesticides. Botanical pesticides are regarded as an eco-chemical and sustainable strategy in the effective management of disease and pest in agricultural crops. The fungicidal, bactericidal and antioxidant potential of plant extracts offers sustainable alternative to commercial synthetic pesticides because of its favourable safety profile without upsetting nature's balance. Turmeric (*Curcuma longa*) of Suranjana variety is one of the miraculous plants having multifaceted beneficial properties such as antioxidant, antifungal, antibacterial, anti-inflammatory, analgesic and digestive properties. The present study development of an eco-friendly and cost-effective turmeric based botanical pesticides nano formulations were attempted via Green synthesis approach. The oil emulsion nano particles were also generated from the essential oil of turmeric. The characterization of synthesized nano formulations was done by UV-VIS spectrophotometer and particle size analyzer (Dynamic Light Scattering Method). The antioxidant potential of NPs was determined by ABTS and DPPH radical scavenging assay. Further the antifungal activity of different nano formulations was evaluated in vitro against Sheath blight causing fungus *Rhizoctonia solani* following the Poison food technique. Water and ethanolic turmeric extract-based silver nano particles were found to perform better than crude rhizome extracts against *Rhizoctonia solani* in plate culture as well as in *vivo* experiments. The formulation did not show any phytotoxicity and the plant vigour was not affected by the treatment with the AgNPs.

P (S 09) 28: Integrated management of *Alternaria* blight of safflower caused by *Alternaria carthami* under field conditions

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Safflower (*Carthamus tinctorius* L.), is one of the most popular oilseeds crop grown throughout the world. The crop suffers many fungal diseases among that leaf spot / blight caused by *Alternaria carthami* has become one of the major constraints in the production and productivity of safflower all over the country as such and in the state of Maharashtra also. The disease has been reported to cause 25 to 60 per cent yield losses in safflower. Management of safflower Alternaria blight with chemicals alone needs to be discouraged due to their ill- effects. Therefore, present field experiments were conducted to manage the disease with integration of the effective fungicides, bioagents and phytoextracts under natural epiphytotic condition at VNMKV, Parbhani, Maharashtra, India. The experiment was designed with RBD and all the treatments replicated thrice using Cv. Manjira, during *Rabi*, 2013 and 2014. Results of the integrated management studies revealed that all treatments were found effective in controlling Alternaria blight disease. However, comparatively least average disease intensity (14.34%) and its highest reduction (74.36%) were recorded with the combination seed treatment and foliar spray in treatment of *T. viride* ST @ 10 g/kg + Garlic clove extract ST @ 10 ml/kg + Hexaconazole FS @ 0.1 %, followed by treatment of Hexaconazole ST @ 1 ml/kg + It's FS @ 0.1% (Av. PDI : 15.46%, Av PDC : 72.37%) and of *T. viride* ST @ 1 ml/kg + Garlic clove extract ST @ 10 ml/kg + Mancozeb FS @ 0.25% (Av. PDI : 17.25%, Av. PDC : 69.16%). Significant increase in seed yield up to 54.56 per cent and highest ICBR (3.22) was recorded in treatment (*T. viride* ST @ 10 g/kg + Garlic clove extract ST @ 10 ml/kg + Hexaconazole FS @ 0.1%).

P (S 09) 29: Suppressing fungal diseases of aroids in organic farming systems

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Tropical tuber crops comprise cassava, sweet potato; yams and aroids are rich in carbohydrate and serve as staple food for millions of people in different parts of the world besides used as a raw material for industrial use (or) animal feed. Fungal diseases are one of the important factors which reduce the yield and quality of tropical tuber crops. Taro leaf blight caused by *Phytophthora colocasiae* is the most devastating disease of taro and has become a major constraint for cultivation and causes heavy yield losses to the extent of 50% every year. Similarly, collar rot is the most common disease of *Amorphophallus* caused by *Sclerotium rolfsii* Sacc. Successful management of pest and disease is the major problem faced by organic growers. There are attempts to tap the potential of various aspects of disease management such as biological control and cultural methods to mitigate fungal diseases incidence of tuber crops individually. But, no concrete effort has been made to integrate these strategies for an effective, cost effective and eco-friendly management package. At ICAR- CTCRI, attempts were made to locate resistant genes in taro and elephant foot yam accessions; epidemiology was studied and based on that cultural practices were modified to delay or reduce the incidence; the potential of *Trichoderma* spp, *Piriformospora indica* and *Bacillus* spp and organic amendments like vermicompost and vermitea were utilized to mitigate the crop losses in both crops due to fungal pathogens. Field screening as well as challenge inoculation with the pathogens could identify 10 accessions of taro 3 of elephant foot yam with resistance. Epidemiological studies on TLB showed that the leaves touching the soil gets infected first and from there it spreads to other leaves, hence mulching can delay the onset of disease development. Application of *T. asperellum* in elephant foot yam and *Bacillus amyloliquefaciens*, *B. subtilis* and *P. indica* in taro resulted in disease reduction as well as yield increase. Organic amendments, vermicompost and vermitea promoted plant growth; increased yield and reduced the disease incidence in taro and elephant foot yam. Later in an attempt to integrate the approaches, it was found that application of bio-agent amended vermicompost at the time of application can bring down taro leaf blight incidence considerably. Similarly, application of bio-agent amended vermicompost at the time of application as well as immediately after intercultural operations in elephant foot yam can significantly reduce the collar rot incidence. Thus, integration of these practices and its adoption may ensure healthy and pesticide free tuber crops for consumption.

P (S 09) 30: How do the foliar sprays against powdery mildew affect non-target microflora on the phylloplane?

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Effect of different fungicides (difenoconazole, tebuconazole, wettable sulphur), biocontrol agents (*Trichoderma viridae*, *Pseudomonas fluorescens*) and botanicals (neem oil) against powdery mildew and non-target phylloplane microbes was studied under poly house condition. The experiment was conducted on bell pepper and yard long bean separately. It was found that, biocontrol agent, *P. fluorescens* could give satisfactory control of the disease (up to 68.9 per cent) compared to 83 - 91 per cent reduction of the disease in the case of systemic fungicides. Study on the effect of foliar sprays on non-target phylloplane microflora revealed that, foliar spray with fungicides drastically reduced the population of non-target fungi, bacteria and actinomycetes on the phylloplane, immediately after the spray. However, the effect was not stable as the population was restored subsequently though to a limited extent. Sudden increase in plate count of fungi and bacteria was observed in the case of leaves sprayed with *T. viride* and *P. fluorescens* respectively, possibly an additive effect of the bioagents applied on them. In the case of bell pepper plants, increase in population of phylloplane microbes was observed in control also, indicating increase in population of phylloplane microflora as the plant gets older. However, the increase in plate count according to age of plant was conspicuous only in the case of phylloplane fungi and not for bacteria. Actinomycete population was very high on the leaf surface of young plants, which decreased as the plant grew older. For yard-long-bean, the phylloplane population didn't change much during the growth period of the plant. Sensitivity of the non-target microbes on the leaf surface could be an indicator of residual toxicity of the compound sprayed. Hence, treatments which does not harm the beneficial organisms may be preferred over toxic chemicals if efficacy against pathogens is on par.

P (S 09) 31: Management of fungal foliar diseases of groundnut (*Arachis hypogaea* L.) under organic cultivation

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Groundnut, the king of oilseeds, occupies an important position of being one of the most consumed food legumes of the world. It is cultivated primarily for oil, food and animal feed. Among nine oilseed crops grown in India, it ranks third in total area and second in the production. Even with such importance, fungal diseases such as, late leaf spot (*Phaeoisariopsis personata* Berk. and Curt.), early leaf spot (*Cercospora arachidicola* Hori.) and rust (*Puccinia arachidis* Spg.), poses major constraints in its production and productivity. These foliar diseases generally causes yield loss up to 50-70 per cent, deteriorating the productivity and the quality of seeds and fodder. Looking at the crop importance, losses caused by the diseases and the gradual shift towards organic production system, a field experiment was conducted in randomized complete block design at the bioresource farm of Institute of Organic Farming, University of Agricultural Sciences, Dharwad during *kharif* 2017 to manage fungal foliar diseases under organic groundnut production system. Highly susceptible variety JL 24 was taken for the study. Three foliar sprays were given at fifteen days interval starting with the onset of disease with bioagents @ 0.5 %, botanicals @ 5 %, sequential application of bioagents and botanicals and treated check (wettable sulphur @ 0.3 %). Results revealed that, minimum terminal disease severity (ELS-22.16 PDI, LLS-39.30 PDI, Rust-26.87 PDI) for fungal foliar diseases was recorded in sequential application

of bioagents (*Trichoderma harzianum – Pseudomonas fluorescens – Bacillus subtilis*) which was on par with wettable sulphur (20.10 PDI, 35.37 PDI, Rust- 23.80 PDI). Maximum terminal disease severity was recorded in untreated control (ELS- 37.87 PDI, LLS- 60.37 PDI, Rust- 50.93 PDI). Also, the sequential application significantly enhanced the plant growth and yield parameters, thereby recorded the highest B:C ratio (3.75).

P (S 09) 32: Evaluation of organic inputs and botanicals against *Sclerotinia sclertiorum* causing white mold of common bean

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The efficacy of various organic inputs (panchgavya, vermiwash, himsol, amritpani, tamerlassi, jeewamrit and dashparni) and botanicals (*Vitex negundo, Eucalyptus* sp., *Melia azedarach*, *Azadirachta indica, Lantana camara* and *Eupatorium adenophorum*) was tested against white mold pathogen (*Sclerotinia sclerotiorum*) of common bean using Poisoned Food Technique, additionally their impact on seed germination under greenhouse conditions was also recorded. Among various organic inputs, dashparni and jeewamrit resulted in 100 per cent mycelial inhibition at or above 6 per cent concentration, whereas vermiwash, himsol and amritpani were least effective. Amongst the aqueous extracts of botanicals, *E. adenophorum* was significantly superior over *L. camara* whereas *Eucalyptus* sp. was least effective. In case of alcoholic extracts, *Eucalyptus* sp. and *A. indica* resulted in more mycelia inhibition at different concentrations as compared to other treatments. Further evaluation of the organic inputs (at 6 and 8%) and botanicals (at 20%) found effective under *in vitro* conditions as seed treatment resulted in enhanced seed germination and reduction in disease incidence. Seed treatment with dashparni @ 6 per cent for 5 and 10 minutes was significantly superior to all other treatments resulting in 19.26 and 15.52 per cent disease incidence, respectively, followed by *A. indica* (alcoholic) at 20 per cent (26.95% and 19.26%). Present study concludes the use of dashparni and *A. indica* against *S. sclerotiorum* after field validation.

P (S 09) 33: Evaluation of wheat varieties against stripe rust disease of wheat under rainfed conditions in mid hill region of Jammu, India

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Modern crop farming has enhanced the food grain production but it has caused many problems to the environment and human health. Besides, it has contributed to global warming. The imbalanced use of agro-chemicals in soil and on plants is not only damaging the soil bacteria, fungi, actinomycetes etc. but has given rise to phenomenon like pest resistance and pest resurgence. Dependence on the external inputs like fertilizers, pesticides, machines etc. have increased rural indebtedness and created dependencies. Our farmers have indulged in indiscriminate use of chemical fertilizers and pesticides. In order to increase the agricultural production and control of insect-pests and diseases, our country is increasingly depending on agro-chemicals. Now the people are questioning the impact of modern agriculture on environment, economic and social aspects. Now many farmers are seeking the alternative practices that would make agriculture more sustainable and productive. Organic farming is the only alternative taking care of all ecological aspects. A natural balance needs to be maintained for sustainability of production system. The chemical fertilizers, pesticides and herbicides are not renewable and diminishing in availability. It may also cost heavily on our foreign exchange in future. Therefore, recycling of resources through organic farming approach is of paramount importance. The organic farming is based on organic relationship. The understanding of these relationships is the nucleus of organic farming. The organic farming is not only derived from organic matter but rather is a type of farming comprised of organic principles. Organic farming can be perceived as a system which should always be in search of natural alternatives suitable to the local specificity. The organic manures supply the nutrients in the soil, promote microbial activities and improve physical, biological and chemical properties of soils.

P (S 09) 34: Evaluation of different botanicals against *Colletotrichum capsici* causing ripe fruit rot of chilli

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Indian cuisine is renowned and celebrated throughout the world for its spicy taste. Chilli *(Capsicum annum* L.) is an important annual spice as well as vegetable crop belonging to *Solanaceae* family. Chilli possesses several nutritional and medicinal benefits to human health. It contains numerous chemical constituent such as fatty oils, steam-volatile oils, capsaicinoids, caretonids, protein, vitamin A, B, C, D, fibres and other minerals like Fe, Mg, Mn and Ca. It has the ability to boost the immune system and lower the cholesterol. Impact on economic loss posed by *Colletotrium capsici* as a devastating pathogen causing pre and post harvest disease in chilli. Adoption of disease management by use of botanicals is the need of current situation. Use of crude extracts of medicinal plants, as they posses antimicrobial activity, their feasibility and ecofriendly nature makes them popular. Therefore, easily available seven botanicals were evaluated under *In-vitro* and *in-vivo* condition against the pathogen *C. capsici*, causing ripe fruit rot of Chilli. Among the seven botanicals, Marigold*(Tagets* spp.), Congress grass *(Parthenium hysterophorus),* Tulsi *(Ocimum sanctum),* Nilgiri *(Eucalypts.* Spp) Drumstick *(Moringa oleifera)* and Ghaneri *(Lantana camara)* were tested @ 5, 10 and 15 per cent. *In-vitro* studied showed that among the seven botanicals, Neem @15 % was found to best followed by Tulsi@15 % with maximum growth inhibition. Neem @ 5% and 10% was also found superior as compare to other treatments. Whereas under field condition Neem @ 5%, 10% and 15% concentration exhibit minimum disease severity as compare to other treatments and among all the concentrations, Neem @ 15 % was found to best showed maximum yield of chilli with minimum disease incidence.The results showed the efficacy of botanicals in management of anthracnose disease of chilli.

P (S 09) 35: Mangement of powdery mildew of coriander through botanicals and organics

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Treatment involving panchagavya was very effective with 11.85 percent powdery mildew disease incidence compared to 44.44 percent disease in control plot and it was statistically on par with wettable sulphur (8.88%). Although azardichtin (19.26%)and cow urine (21.48%) reduced the disease moderately yield wise they were on par with panchagavya (5.58 q/ha).Similar trend was observed during 2010-11 also wherein,Spraying with 5% panchagavya resulted in least disease incidence of 11.81 percent compared to control with 45.33 percent incidence. Mean yield over the years was also highest with panchagavya spray (5.67 q/ha) which was statistically significant compared to control and on par with treated check sulphur (5.87 q/ha).

P (S 09) 36: Efficacy of organics against powdery mildew of mango under field condition

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Studies on management of powdery mildew of mango under organic situation was conducted in farmers field during 2013-14 in Dharwad district for two years and it was test verified in other districts through farm trials in other districts. Panchagavya with 1:10 dilution was most effective in checking the powdery mildew development compared to all other organic products with 33.33 PDI and its yield level was statistically on par with Sulphur (3gms/litre) with 3341.67 and 3445.00 kg / ha. However Tridemorph (1gms/litre) was the most effective in checking powdery mildew development with an highest yield of 4325.00 kg / ha. Observations on flower initiation , size and quality aspects of mango fruits indicated panchagaya to be the best treatment and commercially viable for sustainable mango cultivation.

P (S 09) 37: Ditrophic interaction of *T. koningiopsis* TRI 41 with *Fusarium oxysporum* f. sp. *cucumerinum* alters the metabolic profile of NVOC responsible for antifungal activity

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Cucumber (*Cucumis sativus* L.) is an important vegetable crop grown worldwide. However, the productivity of cucumber is hampered by wilt caused by *Fusarium oxysporum* f. sp. *cucumerinum*. Isolates of *Trichoderma* spp. were screened as the promising candidates for biological control of soil borne diseases. *In vitro* antagonism of *Trichoderma* against *F. o.* f. sp. *cucumerinum* revealed that *Trichoderma koningiopsis* TRI 41 effectively inhibited the mycelial growth of pathogen *in vitro* in comparison with other isolates. Further, scanning electron microscopy (SEM) analysis from the zone of hyperparasitism revealed the presence of cell wall lysis, coiling and ramification of hyphae. The secondary metabolites from the effective isolate *T. koningiopsis* TRI 41 inhibited the growth of pathogen upto 80.68 percent. The nonvolatile organic compound (NVOC) of antimicrobial nature was upregulated in the zone of hyperparasitism of *T. koningiopsis* TRI 41 rather than from the non hyperparasitised zone. The compounds, dl-Alanine-beta-naphthylamide, 1,4,7,10,13,16,19-Heptaoxa-2-cycloheneicosanone, Formic acid, 2-propenyl ester, Pyrazino[1,2-a]indole-1,4-dione, 2,3-dihydro-2methyl-3-methylene-, Propanamide, N-(1-naphthyl)-2-methyl-, Baicalein trimethyl ether and n-Hexadecanoic acid, 6-Isopropenyl-4,8-dimethyl, Hexadecanoic acid, methyl ester, 10-Octadecenoic acid, methyl ester, 1-Ethyl-3-(pyrrolidin-2-ylidene)-2-indolinone, 7,4'-Dimethoxy-3-hydroxyflavone, Heptanoic acid, docosyl ester, Palmitic acid, Octaethylene glycol and Cyclopropanebutanoic acid were upregulated. The upregulated compounds might be responsible for the suppression of *F. oxysporum* f. sp. *cucumerinum*. Hence, the present study suggests that, upregulation of NVOC during hyperparasitism by *T. koningiopsis* TRI 41 could be explored to manage the wilt of cucumber caused by *F. o.* f. sp. *cucumerinum*. However, *T.koningiopsis* TRI 41 also positively influenced the root architecture and increased the rootmetabolite production at the rhizosphere region of 35 days old cucumber plants. Moreover, the gel formulation of *T.koningiopsis* TRI 41 effectively controlled the incidence of *Fusarium* wilt of cucumber to about 13.45% compared to the untreated control (41.32%) under protected cultivation.

P (S 09) 38: Studies on comparative efficacy of botanicals and biochars for management of root and stem rot of cucumber caused by *Fusarium oxysporum* f. sp. *radicis cucumerinum*

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The present study was undertaken in cucumber root and stem rot disease caused by *Fusarium oxysporum* f.sp. *radicis cucumerinum* leading to rotting of stem, roots. The studies were aimed; Occurrence and pathogenecity of *Fusarium oxysporum* f.sp. *radicis cucumerinum* in field and polyhouse condition and develop management strategy through botanicals and biochars. The disease samples of cucumber were collected from severely affected field of RCA Horticulture farm and RCA Polyhouse during *Kharif* 2017-18 when crop was one month old. Eight Botanicals as water and ether extract such as *Ipomea carnea, Calotropis gigantean, Allium cepa, Datura stromonium, Catharanthus roseus, Azadirachta indica, Curcuma longa* and *Piper nigrum* were evaluated *in vitro* against mycelia growth of *F. oxy*sporum f.sp. *radicis cucumerinum* at three concentrations *viz*., 10, 20 and 30 per cent by poison food technique. Among the above botanicals water and ether extracts of *A. indica* found to have maximum per cent growth inhibition of the pathogen, 77.77% and 82.22 % with water and ether extracts, respectively. The biochar treatments were used to evaluate their influence on the growth parameters like germination shoot and root length. The biochar combination Eucalyptus wood (EW) + Citrus wood (CW) + Green house waste (GHW) showed maximum germination 100%, shoot length 7.73 cm and root length 12.10 cm. In order to device the efficient management strategy of the disease root and stem rot of cucumber under pot conditions seven treatments of biochar such as Eucalyptus wood (EW), Citrus wood (CW), Green house waste (GHW), Eucalyptus wood (EW) + Citrus wood (CW), Eucalyptus wood (EW) + Green house waste (GHW), Citrus wood (CW) + Green house waste (GHW) and Eucalyptus wood (EW) + Citrus wood (CW) + Green house waste (GHW) were evaluated against of *F. oxy*sporum f.sp. *radicis cucumerinum* at four concentrations *viz*., 1, 2, 3 and 4 per cent by per cent mortality. Among the above mentioned treatments the lowest mortality rate 4.17% was recorded with Eucalyptus wood (EW) + Citrus wood (CW) + Green house waste (GHW) at 3% concentration. The results obtained suggested that botanicals and biochars are good inhibitors of the disease *in vitro* and *in vivo*, respectively and thus can be recommended for the management of root and stem rot of cucumber in the field. The use of biochars would help the farmers get better yield and profit by reducing the cost of the fungicide and also the biochars improve the soil quality by maintaining the pH and EC of the soil.

P (S 09) 39: Antifungal efficacy of volatile organic compounds – carvone and citronellol against *Fusarium oxysporum* f. sp. *lycosperici* the incitant of tomato wilt

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Plant serves as a repertoire of volatile organic compounds with antimicrobial nature. The antimicrobial VOCs from different plant sources opens avenues for the management of soil borne pathogens. Considering its potential, research was undertaken to fish out the potential VOCs from the leaves of mint (*Mentha spicata*), lemongrass (*Cymbopogon citratus*), coleus (*Coleus amboinicus*), nochi (*Vitex negundo*), tulasi (*Ocimum tenuiflorum*), neem (*Azadirachta indica*) and vetiver (*Vetiveria zizanioides*) against *F. o.* f. sp. *lycospercisi.*

Leaves of mint, lemon grass and nochi effectively inhibited the mycelial growth of *F. o.* f. sp. *lycospercisi* by plate overlay method. Hence, the volatiles emitted from mint, lemon grass and nochi were trapped by air entrainment method and subjected to HS-GCMS analysis. It revealed the presence of 25 and 26 volatile organic compounds (VOCs) from mint and lemon grass, respectively. Among the diversified VOCs, carvone (MW: 150; 2.08 per cent area) from mint and citronellol (MW: 156; 5.27 per cent area) from lemon grass inhibited the mycelial growth of *F. o.* f. sp. *lycospercisi* upto 100 per cent through divided plate method. As carvone and citronellol were effective against *F. o.* f. sp. *lycospercisi* – a pellet formulation comprising 2g of dried leaf powder of mint and 2g of dried leaf powder of lemon grass were blended with 8g of vermiculite separately along with 2ml of castor oil and validated for the antifungal activity through olfactory chamber method. Pellet formulation of VM (vermiculite + mint) inhibited the mycelial growth to 54 per cent as against untreated control. Similarly, VL (vermiculite + lemon grass) pellet based formulation inhibited the mycelial growth to 87 per cent. Thus, soil application of pellet based formulation of mint and lemon grass can be effectively used for the management of wilt disease of tomato.

P (S 09) 40: Disease management in organic agricuture

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Organic farming is recognised globally as a priority area in view of the growing concerns on environmental pollution due to increased awareness about the fallouts of the indiscriminate use of agro-chemicals. Demand for safe and healthy food has been increasing with every passing day. The ill effects of plant protection chemicals on the flora, fauna, humans and environment as a whole are the major concerns. Though the use of chemical inputs in agriculture is inevitable to contain dreaded pests and meet the growing demand for food in a populous nation like India. Organic farming is recognised globally as a priority area in view of the growing concerns on environmental pollution due to increased awareness about the fallouts of the indiscriminate use of agro-chemicals. Demand for safe and healthy food has been increasing with every passing day. The ill effects of plant protection chemicals on the flora, fauna, humans and environment as a whole are the major concerns. Though the use of chemical inputs in agriculture is inevitable to contain dreaded pests and meet the growing demand for food in a populous nation like India, there are opportunities in selected high value fruit and vegetable crops where organic production can be encouraged to meet the domestic and export demand for fresh fruit and vegetables. There are several non-chemical environmentally techniques which can be prudently and strategically incorporated in a well crafted organic production technology module for specific crops. Modification in cultural practices, mechanical destruction of source of inoculum, clean cultivation use of organic amendment and bio-fumigation, developing pesticides of organic origin, encouraging natural biological agents, use of cover and trap crops, use of heat treatment, cold temperature, solar energy etc.

P (S 09) 41: Management of black scurf (*Rhizoctonia solani*) of potato through organic approaches

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Black scurf (*Rhizoctonia solani*) disease of potato is becoming prominent in many potato growing districts of Gujarat state which reduce quality and market value of the produce, resulting in economic losses. The field experiment was conducted during rabi season of 2014-15 in naturally infested field with scurf pathogen at

Potato Research Station, S. D. Agricultural University, Deesa (Gujarat) with the objective to find out suitable management strategies for black scurf throuh organic approches (bio- agents and organic amendements). Among different bio-agents (*Trichoderma viride, T. harzianum. Pseudomonas fluorescens* and *Bacillus subtilis*) tested against black scurf, the tuber treatment with 2 per cent boric acid spray along with tuber treatment with *T. viride* @ 10g/kg seed before sowing recorded the lowest disease incidence (15.33 %) and index (0.38) with highest total tuber yield (324.68 q/ha) with maximum income 2,57,414/ha.When price computed with healthy and diseased tuber yields among treatments, the maximum income variation was (92,986/ha) recorded by the same treatment followed by the tuber treatment with 3 % boric acid spray before sowing (68,440/ha). In case of various organic amendments tested, soil application of mustard cake @ 10 q/ha registered minimum disease incidence (37.33 %) and disease index (0.66) as compared to rest of the organic treatment with highest total tuber yield (327.20 q/ha) with maximum income 2,65,010/ha.When price computed with healthy and diseased 30 tuber yield among treatments, the maximum income variation was (1,12,990/ha) recorded by the same treatment followed by the neem cake @ 10 q/ha (56,660/ha).These organic treatments can provide an effective and economical management of black scurf of potato for cultivaters.

P (S 09) 42: Impact of seed treatment and soil application by using organic amendments and bio-agents on pigeonpea wilt

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Pigeonpea *Cajanus cajan* (L.) Millsp. is one of the important pulse crops cultivated in tropical and sub-tropical areas. It is very important pulse crop which is used predominantly in vegetarian Indian diet. Besides rich source of protein for human and animals, they are also important for sustainable agriculture, enriching the soil through biological nitrogen fixation and improving its physical conditions. Several bio-agents have been assessed and found capable of reducing plant pathogens. Thus, the use of biological agents in pigeonpea wilt management appears to be a potential approach. Six most efficient *Trichoderma* isolates *viz* 1 (*T. harzianum*), 3 (*T. harzianum,* 10 (*T. viride),* 16 (*T. viride*), 18 (*T. harzianum*) and 30 (*T. harzianum*) were assayed for efficacy using different methods of application. The treatments included different substrates for soil application, seed treatment and through irrigation water using Factorial Completely Randomized Design under pot conditions. The results of Ist crop indicated E (seed treatment with talc based formulation) had least wilt incidence (23.8 %) followed by D (29.3%) where *Trichoderma* was added in jaggery solution. and seed were primed. Next effective method was B (*Trichoderma* applied in soil through pre colonized FYM). Other methods of application were lesser effective. Among the isolates 30(26.6%), 10(29.4%) and 1(34.9%) were most effective followed by isolate 16(34.9%), 18(42.7%) and 3 (48.2).

P (S 09) 43: Solid state fermentation of cow manure for production of *Trichoderma harzianum* for management of soil-borne diseases

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Cow manure was used as a substrate in solid state fermentation to produce *Trichoderma harzianum* for the management of *Macrophomina phaseolina* and *Sclerotium rolfsii* in sunflower, sesame and groundnut were evaluated under greenhouse and field conditions. The antagonistic activity and growth promotion of *Trichoderma* isolates against above soil-borne pathogens under in vitro conditions. *Trichoderma* isolate T6 having potentially higher antagonistic efficiency along with high potential to secret lytic enzymes chitinase, â-1,3-glucanase and proteinase. T6 isolate was selected and characterized using morphological characters, scanning electron microscope studies and molecular characterization. Isolation and characterization of secondary metabolites from culture filtrate of T6 isolate. The biological assays indicate that these secondary metabolites may have a role in growth promotion and antagonistic activity. *Trichoderma* isolate T6 mass multiplied from sorghum grains fermentation. Trichoderma colonized sorghum grains mixed with well dried cow manure at 1:100 ratio. Shelf life of the Trichoderma enriched cow manure was evaluated up to nine months. Trichoderma enriched cow manure was stable up to two months of storage at field conditions. Seed treatment or soil application of Trichoderma enriched cow manure significantly reduced the disease incidence up to 90% and plant rhizosphere population of *T. harzianum* increased significantly and further increased the germination percentage, shoot length, root length and yield. Seed treatment with Trichoderma enriched cow manure alone was effective in controlling soil-borne diseases; but the combined seed treatment and soil application of *Trichoderma* enriched cow manure increased the efficacy. The investigations demonstrate that *Trichoderma* via solid state fermentation using cow manure have a potential role in organic farming.

Session 10

Breeding strategies for plant disease resistance

Keynote Papers

KN (S 10) 01: Citrus huanglongbing disease in Southern Vietnam and its management strategy

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In the Mekong Delta, Vietnam, Citrus Huanglongbing (HLB) was officially announced in 1994 and its causal organism was described by Bové et al., in 1995 to be Candidatus Liberibacter asiaticus, which is transmitted by citrus psyllid, *Diaphorina citri* Kuwayama, is a destructive citrus disease. Throughout the years, intensive works have been carried out for HLB management under small scale orchards and the achievements are discussed, the model for effective control of HLB under small scale which could elongate the life cycle of citrus tree for better and longer harvesting. The management mainly consisted of: 1) planting citrus young trees when the population density of the vector insect is low, and 2) controlling the vector by application horticultural oil, soft and systemic insecticides both ten to seven days before planting and once every two months after the planting for two years. The management also includes an option of interplanting guavas, *Psidium guajava*, between citrus trees. These techniques are included in a new integrated pest management (IPM) protocol for HLB in southern Vietnam. Following the establishment of the above IPM, the Japan International Cooperation Agency (JICA) has performed a project transferring appropriate cultivation techniques of King mandarin to citrus farmers in five provinces of Southern Vietnam. In addition, there were 130 rutaceae related accessions had been collected and screened for HLB tolerance; the results revealed that the serverity of HLB infection was less on Hanh/Tac/Quat (Citrus microcarpa) and Long Co co pummelo (Citrus maxima) than that on orange and mandarin. The wild Rutaceae species/clones such as Quyt Dang, Quyt rung, Cam rung, Buoi Rung, Buoi Dang, Buoi Bung, Mac Run, Mac Mat, Can Thang, Quach, Nguyet Que, Truc, Ca ri, Da tu bien and Gioi Lom were symptomless under transmission conditions and had a negative reaction by PCR tests. In a molecular study, 38 primers have been designed and used for screening of HLB tolerance capacity of 49 varieties/clones belonging to Rutaceae. The preliminary results shown that the tolerant varieties was grouped into Group D, which somehow matched with the tolerant group screened under screenhouse conditions.

KN (S 10) 02: Breeding for disease resistance in potato: a holistic approach in the age of climate change

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Report of the United Nation scientific panel said global warming due to climate change is already exacerbating food security by destroying crops yield and increasing pest and disease on farm lands. Water shortage, severe wet conditions, increase salinity, CO_2 and temperature rising curb the percentage of available agricultural land forcing growers to moves towards marginal lands and facing new disease threats. As global demand for food production escalates against a changing climate, traditional breeding looking at market and customer requirements dedicate to develop new varieties with improved agronomic, nutritional and quality traits such as higher yield per ha/nitrogen/water, nutrient-density, low calorie and of course disease resistant poses a great challenge seen the complexity of potato breeding. This approach that would be defined as “Sustaining Innovation” seeks to improve existing products. When applied to potato this translate in a time-consuming process that can take up to 10 years. At same time plant diseases are deeply influenced by environment and the change in CO_2 concentrations, temperature, and water availability can have positive, neutral, or negative effects on disease development and on the plant disease response. Consequently there is a great need for future research to implement dynamic environmental conditions to fully understand the multidimensional nature of plant-pathogen interaction and accordingly employ more dynamic, prompt technologies to produce disease-resistant potato varieties that are resilient to climate change. Therefore a “Disruptive Innovation” breeding approach that aim to apply new plant breeding techniques (NPBT) like TALEN and CRISPR/Cas9, nanoparticles immunization, could and should be employed to generate transgene-free products in a more precise, prompt and effective way that would better meets the demands for increasingly sustainable food production. Finally to respond adequately, we should optimally apply all existing and new technology niche tools to breed improved crops and reinventing phytopathology strategies to win in tomorrow disease management.

KN (S 10) 03: Marker-assisted breeding for rust management in wheat

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Wheat (*Triticum aestivum* L.) suffers from several biotic stresses like rusts, spot blotch, Karnal bunt, powdery mildew and head scab. Among all these diseases rusts are the most important because of their widespread occurrence. Leaf rust occurs in all the wheat growing regions of India while stripe rust is mainly confined to the cooler regions of north west India. Central and peninsular India provides the conducive environment for stem rust. Breeding for rust resistance is important for preventing the losses caused by the rust pathogen *Puccinia sp*. Over the years, judicious deployment of rust resistance genes have kept the rusts under control. However, continuous evolution of new virulent races of leaf , stem and stripe rusts have rendered many of the resistance genes ineffective. In view of the continuous evolution of new rust races, search and deployment of effective rust resistance genes is essential. Marker assisted breeding provides an effective tool to transfer new rust resistance genes in popular cultivars. Leaf rust resistance genes such as *Lr19*, *Lr24* and *LrTrk* have already been transferred in the background of different popular varieties such as HD2932, HD2733 and HD2967 in various combinations. Similarly, stripe rust resistance genes like *Yr5, Yr10* and *Yr15* have been transferred in different varieties. Apart from these seedling resistance genes some adult plant resistance (APR) genes such as *Lr34, Lr46, Lr67* and *Lr68* for leaf rust resistance has also been transferred into wheat varieties HD2733 and HD3059. Marker assisted backcross breeding can produce improved versions of the popular varieties or Near isogenic lines in shorter period of time. NILs may also be used effectively to deploy diverse genes in a given geographical area. Multiple NILs of a mega variety carrying different rust resistance genes can help managing the rust disease by preventing the build up and spread of inoculums.

Invited Papers

I (S 10) 04: Major biotic stresses of wheat in South Asia- an overview

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Spot blotch, caused by *Bipolaris sorokiniana* (Sacc.) Shoem syn.), has surfaced as a key production constraint in the North Eastern part of India and South Asia's intensive cropping system. The aggressiveness of spot blotch isolates is variable which explains why genetic resistance appears to be rather unstable apart from atmospheric conditions influencing pathways governing disease resistance. The genetic analysis of spot blotch resistance has been pursued by considering the trait as a quantitative trait locus, and to this end a recombinant inbred line (RIL) population has been developed from the cross cv. Sonalika (susceptible) x cv. BH1146 (resistant) to map the genomic regions responsible for spot blotch resistance in a large size population comprising of 1109 RILs resulting from the cross between 'Sonalika' and 'BH 1146', phenotyped under controlled and natural field conditions. It was highlighted that the QTL 'QSb.iiwbr-7B' and 'QSb.iiwbr-7D' are responsible for conferring resistance to spot blotch in resistant parent BH 1146. Beside this, some genotypes developed at IIWBR, Karnal, BHU, Varanasi and CIMMYT, Mexico was shown resistant in the Gangetic plains. During resistance to spot blotch attack, wheat strongly elicits SA signaling (SA biogenesis as well as the NPR1-dependent signalling pathway), along with WRKY33 transcription factor, followed by an enhanced expression of phenylpropanoid pathway genes. The occurrence of wheat blast caused by *Magnaporthe oryzae*, pathotype *Triticum* (synonym *Pyricularia oryzae*) in Bangladesh in 2016 has been a major concern in neighbouring countries including India considering its capacity of crop loss up to 100%. Considering the situation, the Indian Council of Agricultural Research and State Agriculture Universities along with State Department of Agriculture have taken initiative to restrict the entry of the pathogen from neighbouring country. Beside this, identification of resistant genotype against the pathogen in hot spots of Bolivia and Bangladesh is being carried out.

I (S 10) 05: Advances in vegetable breeding for disease resistance: way forward

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Vegetable crops are highly susceptible to biotic stresses caused by fungi, bacteria, virus and phytoplasma. Indiscriminate use of chemicals to manage diseases leads to increased cost of cultivation, environmental pollution, health hazards. The most sustainable approach is to develop resistant varieties. Plants are almost always resistant to certain pathogens but susceptible to other pathogens; resistance is usually pathogen species-specific or pathogen strain-specific. Breeding for the development of biotic resistant cultivars is major objective of vegetable breeder's. Attempts have been made to provide a description on resistant sources of different vegetable crops against major diseases, inheritance of resistance, genetic manipulations, biotechnological interventions and grafting which will be useful for the vegetable breeders for future breeding program. In the biotechnological approaches for vegetable breeding, most of the achievement has been to generate transgenic plants resistance to disease.

I (S 10) 06: Breeding strategies integrating genomic tools for harnessing host plant resistancein rice varietal improvement

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Rice is affected by bacterial blight (BB), blast, sheath blight and bakanae diseases. While prophylactic sprayshelp minimize crop loss, it increases production cost as well as risk of pesticide residues in grains. Several major genes governing resistance to these diseases have been mapped, of which selected genes were incorporated into popular varieties leading to development and release ofeight MAS (marker assisted selection) derived rice varieties with resistance to BB (IPB 1, PB 1718, PB 1728, Pusa 1592) and blast (PB 1637, PB 1609, Pusa 1612, Pusa Samba 1850). Augmenting molecular breeding for disease resistance, donors were identified through a novel high throughput screening protocol and QTLs governing bakanae resistance were mapped, genic markers for *Pi9* and near-isogenic lines with resistance to these diseases have been developed.Breeding strategy has been progressively refined to translate the potential ofgenomics through cost-effective integration of molecular tools in harnessing host plant resistance in rice varietal improvement.

I (S 10) 07: Present status and future research needs in identification of sources resistance against major diseases of soybean in India

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Soybean diseases are major stumbling blocks in successful raising of crop and achieving the highest productivity. Among the various management options available ,breeding for resistance a long term and sustainable approach.In this, we summarise here the efforts made in development of resistant varieties of soybean against major diseases mainly rust,purple seed stain and pod blight complex. Rust in Karnataka was severe and caused losses up to 20-80 per cent in JS-335 depending on its severity, stage of occurrence and favourable climatic conditions in northern Karnataka. In recent years, soybean anthracnose has become one of the major production constraints in all soybean growing areas of India. The loss due to this disease in India has been reported to an extent of 16-25 per cent in seed yield apart from affecting seed quality.The research efforts on development and release of rust resistant varieties in India over a decade has lead to development and release of first ever rust resistant and high yielding variety DSb 21 for the state of Karnataka and also south India during 2013. Later, DSb 23 and DSb 28-3 highly rust resistant and high yielding varieties which have recommended for cultivation for Southern Zone (Karnataka, Maharastra, TamilNadu, Andhra Pradesh and

Telagana States) during 2015and 2017.Out of 19 genotypes, the genotypes *viz.,* DSb 12, DSb 20, DSb 23-5 and Kalitur were found highly resistant with a disease grade of one to pod blight complex.. The genotype JS 335 was highly susceptible to anthracnose with a maximum disease grade of nine. Among the markers used, Satt 275 showed polymorphism for both the parents (EC 241780 and JS 335) as well as other genotypes. The amplified PCR product of genotypes with polymorphic marker Satt 275 was sequenced and most of the sequences scored an E value of 0.031 and an identity of 90 per cent with the mRNA sequence of the *Rpp*5 gene. The classification results revealed that the sequence of the advanced line DSb 30-2 showed the highest degree of identity with the concerned *Rpp5* like disease resistance mRNA sequence.

I (S 10) 08: Genetic and breeding strategies of wheat rust resistance in India – an overview

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Gene deployment: The gene deployment, therefore, aims at creating genetic diversity in large geographical tract. This would then prevent spread of virulence from one area to another and thereby causing a delay in the development and growth of epidemic. Gene Pyramiding: By systematically evaluating the pathogen virulence, the resistance genes against which the pathogen lacks virulence can be identified. When a widely grown variety becomes susceptible, then one such gene or genes against which the pathogen lacks virulence can be incorporated by a simple back cross programme. Multiple Disease Resistance: The other approach can be breeding for multiple disease resistance by using different genes. Gene Cycling: Gene cycling aims at cyclic shift in the resistance genes used for breeding for disease resistance. Gene cycling, therefore, possesses a temporal delay in the utilization and exploitation of resistance genes. Such a discontinuity minimizes the evolution of complex virulences and increase the utility of vertical resistance genes. Gene mosaic/ Varietal diversification: This would then create a varietal mosaic at village level which would buffer rapid disease spread. Loss due to disease, if occurs, would be minimal and must be confined to a few isolated farmers. This varietal mosaic creates diversity between fields of the next macro level management strategy. Multiline concept: Each multiline is conceived to be a mixture of a number of back crosses derivatives of a recurrent parent with each derivative carrying different genes for resistance. By introducing diverse genes for resistance in a population of isogenic lines, the strategy is to lower the load of inocula in the micro- environment of the host. Multigenic varieties: Use of multigenic varieties has been proposed to fight rust diseases. This approach aims at bringing together in a variety, several factors preferably previously, unused genes for resistance. By doing so, there is a chance that one can eventually exhaust the ability of the pathogen for adopting itself to attack to new varieties. Use of alien genes: If all the genes are exhausted, then the genes from distant or related species can be used in breeding programme. Most of Sr, Lr, Yr genes which have been exhausted in *Triticum* can be derived from wild species viz., *Aegilops, Secale* and *Agropyron* etc. Mutagenesis: This is another approach to combat rusts epidemics. Therefore, the genetic and breeding for rusts, resistance are the only strategies to prevent epidemics or pandemics.

I (S 10) 09: Breeding for disease resistance in maize

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Maize is a widely cultivated crop of the world, providing food, feed, and biofuel. Although maize production has increased steadily over the decades, an array of diseases is still causing heavy yield losses and reduction in grain and fodder quality. The disease epidemics can cause up to 100% yield loss in maize. The epidemic outburst of American rust, turcicum leaf blight and lethal necrosis in the past had nearly wiped out the maize crop. The average loss due to all the diseases taken together has been estimated to be 13%. Furtherore, climate change may cause unpredictable changes in the distribution, occurrence, and severity of infectious diseases. Fifteen of 61 diseases of maize recorded so far are major constraints. The major diseases are: four foliar diseases, two pre-flowering and three post-flowering stalk rots, four downy mildews and two sheath diseases. Of all the disease management strategies, use of host plant resistance is the most effective. Hence, disease resistance has become a part of any maize breeding programme. Initially breeders focused mainly on conventional breeding to evolve resistant cultivars, those include continuous germplasm collection, their evaluation to identify and to develop sources of resistance and incorporation of disease resistance into breeding populations before extraction of varieties from such populations. Although this approach has yielded promising results, most of the materials released as resistant to one disease turn out to be susceptible to another set of diseases. Hence, multiple disease resistance (MDR) is both practically and conceptually important and yet is also poorly understood. It can be noted that most disease resistance found in maize is quantitative disease resistance (QDR), and is oligogenic to polygenic. Nevertheless, qualitative resistance has been effectively used in maize. Resistant cultivars against the foliar diseases including maydis and turcicum leaf blights, gray leaf spot, polysora and common rust, and downy mildew were developed through conventional breeding. However, the progress in is limited in case of banded leaf and sheath blight, post flowering stalk rots, ear rots, etc. The progress in the understanding of the genetic and physiological processes underlying QDR has been slower due to their complex nature. Similarly, limited evidence is available regarding QTLs conditioning MDR, in which the same locus conditions resistance to multiple pathogens. The previous studies suggest that MDR QTL likely to exist, though they may be QTL of relatively small effect-possibly below the level of detection in those studies. In such cases, the larger-effect QTL tend to be disease specific. In some studies, only a single QTL was identified that conferred resistance to more than one disease such as resistance to both southern leaf blight and grey leaf spot. The analysis with molecular markers has provided insights into the basis of QDR in maize. The disease QTL (dQTL) mapping studies in maize thus far revealed information on the genetic architecture of disease resistance, including the number, location, and action of chromosomal segments. The past decade has witnessed significant progress in fine-mapping and cloning of genes controlling QDR. There has been successful tagging, validation and the transfer of dQTLs to susceptible genotypes in several studies. The association mapping and the use of SNP markers have greatly improved the power to dissect the inheritance of QDR. Use of high throughput genotyping platforms and precision phenotyping can provide the information needed to effectively use MAS in a breeding program on complex traits. The advent of CRISPR/Cas is expected to yield fruitful results in resistance breeding as well. Many inbred lines, hybrids, synthetics and populations resistant to the important diseases are now available and may be exploited to advantage by farmers. Level of resistance varies from disease to disease and among the varieties. There will be evolution of new races of pathogen. Therefore, breeding for disease resistance in maize must continue at the national and international institutes.

I (S 10) 10: Quantification of sheath blight resistance in rice germplasm

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Sheath blight (ShBl) caused by *Rhizoctonia solani* Kuhn [Teleomorph *Thanatephorus cucumeris* (Frank) Donk] is a major disease of rice (*Oryza sativa* L.) globally and it causes significant yield losses. The incidence of sheath blight is increasing over the years and genetic resistance for the disease is not available. Objective of the study was to identify potential donors for sheath blight resistance. A total of 16,854 entries comprising rice germplasm, land races, National Screening Nursery-1 (advanced variety trials), National Screening Nursery-2 (initial variety trials), Donor Screening Nursery, Replicated Yield Trials (elite breeding lines from Basmati and non-Basmati rice) and international rice germplasm from IRRI, were screened for sheath blight resistance under artificial inoculation conditions at Punjab Agricultural University, Ludhiana, India during the years 2009 to 2017. All the selected entries were further evaluated during the years 2018 and 2019 under artificially inoculation in field and *in vitro* condition using detached tiller technique. The relative lesion height and disease score (0-9) was recorded 15 and 21 day after inoculation in field and 7 day after inoculation *in vitro* conditions. None of the entry was found completely free from the disease. Accession no. 2443, acc. 2489, acc.2426 and acc.4736 from rice germplasm; IET 21299, IET 21601 and breeding ent no.3943 from National Screening Nursery-1 and 2; PAU5655-11-1-4-3 from Basmati rice and Lalua Kanda from international rice germplasm showed resistance to moderately resistance reaction against sheath blight during different years of testing under field and control conditions. Acc.2443 and IET 21299 showed the lowest disease score and slow progression of the sheath blight as compared to resistance checks Tetep and Jasmine 85 at 21 days after inoculation in field and in control conditions. These tolerant genotypes can be used as donors in disease resistance breeding program for developing rice cultivars resistant to sheath blight.

I (S 10) 11: High-throughput phenotyping for wheat breeding

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Plant Breeders are faced with the challenge of evaluating thousands of candidate varieties each season to identify the highest performing lines for advancement. New approaches that enable breeders to evaluation plant populations with increased speed and accuracy can result in increased genetic gain. We have developed several high-throughput phenotyping (HTP) platforms and associated data analysis pipelines for wheat breeding and applied these to improve selection in the breeding programs. These HTP approaches can be applied to any traits of importance in the breeding program, including disease resistance. We have demonstrated proof of concept using HTP for several diseases which will be presented as examples.

Oral Papers

O (S 10) 12: Studies on maize rust (*Puccinia sorghi* Schw.) under temperate agro-climatic conditions of Kashmir

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Common rust of maize is one of the most destructive diseases causing significant loss to maize production under temperate agro-climatic conditions of Kashmir. An extensive survey conducted during *kharif*, 2018 in major maize growing areas of Kashmir valley revealed the prevalence of disease in all the surveyed areas with varied levels of incidence and intensity. The fungus inciting the rust of maize disease was identified as *Puccinia sorghi* Schw. on the basis of its morphological and pathological characters. The disease appears on 2nd week of June as small yellowish flecks which turn into small tan spots and then round to elongated pustules on leaves. The pustules then enlarged to cover larger area of leaves resulting in premature desiccation. Maximum disease development in the field was observed during 2nd fortnight of august when the temperatures are moderate. Two hundred and twenty maize genotypes were screened for resistance against *S. oryzae* under artificially inoculated field conditions using 1-9 disease evaluation scale. The genotypes showed varied response from resistant to highly susceptible reaction. 3 inbreds lines (SMI-135, SMI-360, SMI-74) were found highly resistant with disease grade-1, 88 were categorised as resistant with disease score of 2 and 51 as moderately resistant. The remaining genotypes showed moderately susceptible to susceptible reaction. Experiment on the effect of fungitoxicants on the development of maize rust was conducted at Mountain Crop Research Station, Larnoo situated at an elevation of 2250m amsl. All the fungicides tested restrained disease incidence and intensity significantly compared to control. Propiconazole 25 EC was the most effective fungicide to control the rust disease of maize under temperate conditions of Kashmir. The resistant sources with varied levels of resistance exist against the common rust of maize. The determination of genetic basis of these sources and incorporation of their resistant genes into susceptible commercial cultivars may help in the development of high yielding rust resistant maize cultivars.

O (S 10) 13: Identification of resistant sources against white rust (*Albugo candida*) disease in rapeseed-mustard

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White rust (*Albugo candida*), is a destructive disease of oilseeds *Brassica*, causing great yield losses in India and elsewhere. Keeping importance of the crop as well as its disease(s) in view, present study was undertaken to find out putative resistance sources against white rust. Firstly, pathogen inoculation and germplasm screening technique was standardized under controlled environmental conditions at National Phytotron Facility, IARI, New Delhi. Thereafter, 35 accessions of *Brassica* spp. were screened using two isolates of *A. candida* from Pantnagar (*Ab-Pnt*) and Delhi (*Ab-Del*) at cotyledonary as well as true leaf stages. Out of 35 accessions tested, six accessions each of *B. juncea* (EC766192, EC766193, EC766164, EC766091, EC766230& IC20167) *B. carinata*(EC206641, EC206642, EC206651, IC555891, IC341164 & IC341170) were found resistant at both the crop stages against *Ab-Pnt* isolate. However, three accessions of *B. juncea* (EC766164, EC766230 & IC20167) and six accessions of *B. carinata*(EC206641, EC206642, EC206651, IC555891, IC341164 & IC341170) showed resistance against the *Ab-Del* isolate at both cotyledonary and true leaf stages. Among *Lepidium*species, only three accessions (IC508401, IC508406 & IC605224) were recorded as resistant against *Ab-Del* isolate at both the stages. Corresponding resistant reaction in the adult plant stage were also confirmed in field experiment in Delhi under artificial inoculated conditions. In addition, 35 released cultivars were also screened under controlled environment. Of which, two each of *B. juncea*(BIO-YSR & RLC-3) and *B. napus* (GSC-6 & GSC-7) and one variety of *B. carinata* (PC-6) were found resistant at both the stages against *Ab-Pnt* isolate. Whereas, only one variety each of *B. napus* (GSC-7) and *B. carinata* (PC-6) showed resistance against *Ab-Del* isolate. The identified resistant sources in *B. juncea*, *B. carinata* and *B. napus* could be utilized in breeding programme for development of resistant variety against the particular isolate(s) of white rust pathogen.

O (S 10) 14: Identification of yellow leaf resistance in indian sugarcane germplasm through genome wide association approach

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Yellow leaf disease (YLD) of sugarcane caused by *Sugarcane yellow leaf virus* (SCYLV) is an important viral disease affecting Indian sugarcane cultivars and causes 38.9 to 42.9% reductions in cane growth and 30.26 to 34.15% losses in juice yield in susceptible cultivars. Identification of varietal resistance is the most efficient strategy to manage the disease. ICAR-Sugarcane Breeding Institute, Coimbatore plays a predominant role in breeding of sugarcane varieties in India through National Hybridization Garden (NHG), where ~ 600 parental clones are being maintained every year for sugarcane breeding. To study the YLD resistance based on genome wide association approach, parental clones were screened during the last two years 2018 and 2019 using 0-5 YLD rating scale and categorized as R (0.0-1), MR (1.1-2), MS (2.1-3), S (3.1-4) and HS (4.1-5). Among the screened clones, 81% and 76.33% entries were identified as resistance; 5.6% and 2% entries were identified as susceptible to highly susceptible, respectively. Totally, 200 YLD free samples in R category and 143 samples under the MS, S and HS category representing all the major sugarcane growing places of India were collected and total RNA and DNA were isolated following the standard protocols for genome wide association study (GWAS). RT-PCR assays using the SCYLV-CP gene specific primers were performed for all the samples, in that all the susceptible samples had shown the expected positive amplification of 615 bp whereas 99 of 200 apparently resistant samples including *Sachharum spontaneum*, *S. barberi* and *Erianthus* sp. were negative to the SCYLV. GWAS based on linked disequilibrium in diverse genetic samples is a relatively new approach which offers higher resolution mapping that under optimal conditions can pinpoint causal genes underlying quantitative trait variation. Earlier work on the GWAS from CIRAD, France for YLD, two resistant markers was identified. Further, through SNP genotyping of resistant and susceptible DNA samples collected from NHG, the true YLD resistance parents can be identified and can be effectively utilizedin the future breeding programmes to develop resistant varieties to sustain the sugarcane productivity.

O (S 10) 15: Identification and development of blast resistant rice hybrids

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Rice is the predominant food for a majority of the people in India and the crop plays a crucial role in the Indian economy. Hybrid rice developed using the “three-line” hybrid breeding system boosted higher grain yield sufficiently. Due to changing climatic conditions, hybrid rice is severely affected by various diseases and insect pests. Utilization of superior and disease resistant restorer and male sterile parent in CGMS based hybrid breeding could develop a disease resistant high yielding rice hybrid. By following this concept, an experiment was conducted in the year 2018 at Department of Genetics and Plant Breeding, IGKV, Raipur in collaboration with ICAR-Indian Institute of Rice Research, Hyderabad for developing Blast resistant rice hybrid with higher grain yield. The experimental material comprised of three CMS lines *viz.,* CRMS 31A, IR 58025A , IR-79156A and eight restorer lines *viz.,* PAU 3761-26-3-1, KAGR 424, RP 5207-Bio-Bk 49-77-31, RP 5207-Bio-Bk 39-164-2-1, NSG-421, PAU 3761-26-3-1, RP5898-138-14-9-8-4-2 & PAU 2769-20-2-3-3-2-2-2-M-9. All parental lines were screened for blast resistance through two dominant genes *Pi2* and *Pi54* with their linked markers Pi2 pro 9 and Pi54 (MAS). Five restorer lines *viz.,* PAU 3761-26-3-1, KAGR 424, RP 5207-Bio-Bk 49-77-31, RP 5207-Bio-Bk 39-164-2-1, PAU 3761-26-3-1 and all three CMS lines *viz.,* IR-58025A, CR MS-31A, IR-79156A had Pi54 gene which showed there blast resistance feature. However none of the parents had Pi2 pro 9 marker. Eight restorers were crossed with three CMS lines in LxT fashion for generating 24 $F_{1's}$. All the 24 $F_{1's}$ were also screened for blast resistance through two dominant genes *Pi2* and *Pi54* with their linked markers *Pi2 pro 9* and *Pi54 (MAS)*. Out of 24 $F_{1's}$, total 15 were showing different dominant reactions. However, progenies of CRMS31A/ PAU 3761-26-3-1; CRMS31A/ KAGR 424 and CRMS31A/ PAU 3761-26-3-1 were showing highly resistant reaction. Grain yield of hybrid CRMS31A/ PAU 3761-26-3-1 was significantly higher than their parents. Further evaluation of blast resistance on field conditions are under process.

O (S 10) 16: Evaluation of finger millet hill germplasm collections against blast resistance in Uttarakhand hills

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Finger millet is a major rainfed crop of Uttarakhand hill farmers and it is circumvented by many biotic and abiotic factors, among biotic factors blast (*Magnaporthe grisea*) disease (Leaf, Neck and Finger) major limiting factor for production and productivity of the crop. In the present study, 205 finger millet hill germplasm collections were evaluated under field conditions from 2016-2018 during *Kharif* season against leaf, neck and finger blast resistance. Based on the average percent values for three consecutive years, it was found that none of the entry was highly resistant to leaf blast disease but it was observed that majority of germplasms were in moderate resistant category (4-6 score). The frequency distribution for leaf, neck and finger blast ranged from 37.5-82.5, 0-36 and 0-28 respectively. Germplasms like VHC 3637, VHC4085, VRB-MF-1817, VRB-MF-1819, VHC 4180, VHC 4087 entries were completely immune to neck blast with high degree of resistance to finger blast and moderate reaction to leaf blast. Entries *viz*., GUP-45, VRB-MF-1 and VRB-MF-12 were highly resistant to finger blast with (<1%) incidence and resistant to neck and moderately resistant to leaf blast disease. The identified resistant source utilized for blast resistant breeding program and they can be utilized for mapping of R gene/s for blast resistance.

O (S 10) 17: Genetic analysis of Fusarium wilt resistance in brinjal (*Solanum melongena* L.)

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Brinjal is one of the most important vegetable crops in India. Fusarium wilt (*Fusarium oxysporum* f. sp. *melongenae*), soil borne fungal disease is one of the most devastating disease of brinjal causing heavy yield loss. The development and use of resistant varieties is the most economic and sustainable approach to overcome this problem using identified resistance source. The present study was carried out at Division of Vegetable Science, ICAR-IARI, New Delhi to study the genetics of Fusarium wilt resistance. Susceptible variety (Pusa Uttam) was crossed with resistant genotype (DBR-160) to develop F_1 (30 plants), F_2 (210 plants) and backcross populations ($BC_1P_1F_1$, 84 plants; $BC_1P_2F_1$, 90 plants). All the populations including parents were evaluated for wilt reaction in sick plot using rootdip inoculation methods. The data was analysis using Chi square (÷^{2}) test. All the F_1 plants were resistant to Fusarium wilt which indicated dominant nature of inheritance. Out of the 210 F_2 plants, 164 plants were resistant and 46 plants were susceptible which clearly segregated in 3: 1 (R:S) Mendelian ratio with $\div^2$ value of 1.073 (P=0.03). This result suggests that resistance is governed by single dominant gene in the resistant parent DBR-160. The finding was also confirmed by the result of backcross population ($BC_1P_1F_1$) which was segregated in 1:1 (R:S) Mendelian ratio. This study will be very useful in brinjal breeding programme to transfer this resistant gene into desirable but susceptible variety through backcross breeding.

O (S 10) 18: Inter specific hybridization (*Brassica carinata* x *Brassica oleracea*) and development of advanced back-cross progenies for introgression of black rot resistance genes into cauliflower

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Indian cauliflower (*Brassica oleracea* var. *botrytis* L.; C genome) is highly susceptible to black rot caused by *Xanthomonas campestris* pv. *campestris* (Pam.) Dowson. Till now no durable resistance genes have been identified in C genome of *Brassica*. Two *B. carinata* genotypes, NPC-9 and HCA-6 were found highly resistant to *Xcc* race 1 and 4, most prevalent throughout the world. Inter-specific hybridization was attempted for introgression of resistance genes from *B. carinata* into Indian cauliflower using three different embryo rescue approaches. Reciprocal crosses were made between two *B. carinata* and 7 lines of Indian cauliflower. Very low rate of success was observed when *B. oleracea* lines were used as female parents. Among the three different approaches of embryo rescue, direct embryo culture was the most successful for development of F_1, BC_1, BC_2 and BC_3 population. Therefore, direct embryo culture could be used as the improved toll in developing inter-specific hybrids in brassicas. Through ovule culture and direct embryo culture 58 F_1 hybrids were developed. Success rates for hybrid plant development through ovule culture and direct embryo culture were 1.04% and 11.33%, respectively. All the F_1 hybrids were found to be highly resistant to *Xcc* race 4 and 1. Eleven NPC-9 based F_1 hybrids were used for development of BC_1 population and later on selected BC progenies with *Xcc* resistance were advanced to develop BC_2 and BC_3 progenies through direct embryo culture. Genome specific and AAFC SSRs were used to analyze the F_1 and successive back-cross progenies. Molecular analysis revealed successive elimination of B genome in the advanced back-cross progenies. Several BC_3 plants were recovered with effective resistance to *Xcc1* and *Xcc4*. These back-cross introgressed lines with resistance against *Xcc* would be very useful in future resistance breeding of Indian cauliflowers. They will also be useful in genetics and molecular studies to reveal the genomic components of B genome responsible for black resistance and identification of molecular markers for R genes for their introgression into desirable nuclear back-grounds.

O (S 10) 19: Screening of different genotypes of rice and accessions of wild rice, *Oryza rufipogon* against sheath blight disease caused by *Rhizoctonia solani* Kuhn

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Sheath blight of rice caused by *Rhizoctonia solani* Kuhn {teleomorph: *Thanatephorus cucumeris*) Frank (Donk)} is a major biotic constraint next to blast in almost all the rice growing areas, reducing both grain yield and quality degradation (Lee and Rush,1983; Manibhusanrao,1989; Nagarajkumar *et al*., 2004).The sheath blight disease generally appears at maximum tillering stage and affects all the parts of the rice plant above the water line. The yield loss due to this disease has been reported to range from 5.2-50% depending on environmental conditions, crop stages at which the disease occurs, cultural practices and cultivars used (Marchetti and Bollich, 1991). Species other than *Oryza sativa*, *O. nivara* and *O. australiensis* were found highly susceptible to the sheath blight pathogen, *Rhizoctonia solani* Kuhn, whereas *O.rufipogon* and *O.barthii* were found moderately resistant (Kannaiyan and Prasad, 1978). It has been reported that wild rices are the important sources of resistance to different rice diseases and insect, pests (Heinrich *et al.,*1985; Vaughan, 1994).Therefore, attempts have been made here to screen available genotypes of rice alongwith accessions of wild rice, *Oryza rufipogon* for resistance/tolerance against *Rhizoctonia* sheath blight pathogen under artificial inoculation condition. Six genotypes of rice namely, , Jasmine 85, TN1, Annapurna, Maudamani, CR 1014, Naveen and three accessions of wild rice *Oryza rufipogon* namely, AC 100005, AC 100015, AC100444 were taken up during *kharif*, 2017 and 2018; artificially inoculated with the virulent isolate (ShbSL4) of the sheath blight pathogen. The development of disease symptoms was critically recorded along with recording of time taken for expression of sheath blight symptoms. Reaction of sheath blight in different genotypes of rice and accessions of wild rice were taken based on 0-9 SES scale for rice. All the six rice genotypes and three accessions of *Oryza rufipogon* were found infected by the virulent isolate of *Rhizoctonia solani* with taking 4 to 7 days for producing sheath blight symptoms. Out of six rice genotypes, CR 1014showed moderately resistant reaction with least disease score of 1 while, the genotypes Maudamani and Naveen showed tolerant reaction with disease score of 3.Other two genotypes Jasmine 85 and TN1 were found to be moderately susceptible with recording of disease score 5.The genotype Annapurna showed susceptible reaction with disease score 7.In case of wild rice accessions of *Oryza rufipogon*. The accession AC 100444 showed moderately resistant reaction with least disease score of 1, whereas, AC 100015 was found to show tolerant reaction with disease score of 3.The accession AC 100005 of *Oryza rufipogon* was found to be moderately susceptible with disease score of 5.From this finding, the rice genotype CR 1014 along with Maudamani, Naveen and accession AC 100444 followed by AC 100015 can be retested for confirmation of resistance/tolerance against the sheath blight pathogen after which they will be used in resistance breeding programme.

O (S 10) 20: Viral disease scenario of major vegetable crops in Maharashtra and efforts toward developing effective management practices

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Vegetables are important component of nutritional security in India. Several commonly cultivated vegetable crops belonging to family Cucurbitaceae and Solanaceae are highly remunerative to farmers in the western region of Maharashtra. Among them tomato, capsicum, chilli, cucumber and melons are widely grown in the region which are prone to several viral diseases mainly due to favorable climatic conditions for viruses and their vectors multiplications. This condition is further aggravated with the erratic changing climate scenarios. Moreover, the intensive agriculture practices with imported genotypes and use of excess pesticides along with changes in climatic conditions have resulted into more complex problems of new emerging and reemerging viruses. Therefore, the study was undertaken to understand the present status of viruses infecting major vegetable crops grown in Western Maharashtra and to develop the effective and ecofriendly solutions for farmers to minimize the losses. Serological and molecular characterization indicated that the occurrence of viruses belonging to Potyvirus, Geminivirus, Cucumovirus, Tospovirus, and Tomamovirus groups was common and in most of the cases complex mix infection resulted into severe symptoms and crop loss in various areas surveyed in the state. The incidence of viruses varied from 30 to 100 percent and indicated an increasing trend of emergence of viruses and their vectors in recent years. Therefore, field experiments were conducted to develop integrated viral disease management strategies in major vegetable crops grown in western Maharashtra using various combinations of silver mulching (SM), crop cover (CC), insecticide/bio-pesticide/ (I/B) applications. The expression of disease symptom of major viruses was delayed up to 3 weeks in SM + I/B and maximum delay of 6-7 weeks in disease onset was in CC+SM+I/B. The best treatment (CC+SM+ I/B) was able to reduce viral diseases significantly and maximize the marketable yield.

O (S 10) 21: Genetic sources for *Fusarium* wilt resistance and molecular markers for resistance gene in garden pea (*Pisum sativum* L.)

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Wilt caused by *Fusarium oxysporum* Schlecht end.Fr. f. sp. *pisi* is a devastating disease of garden pea in India and worldwide. The early sown crop of garden pea fetch higher profit but it is more vulnerable to wilt which causes severe seedlings/plants mortality due to prevailing high temperature and yield losses up to 13.9-95%. The pathogen being soil-borne fungus and quite difficult to manage by chemical methods and the development of resistant varieties seems to be the only alternative. Thirty four genotypes of garden pea were screened under wilt sick plot to identify genetic sources of resistance against *Fusarium* wilt. Three genotypes GP-6, GP-55 and GP-942 were found to be highly resistant, four genotypes GP-17, GP-48, GP-473, GP-941 were resistant and identified as new source for *Fusarium* wilt. It was interesting to record that all the popular cultivated varieties (Arkel, Pusa Pragati, AP-3, VRP-6, VL-7, VL-10, PSM-3 and Arka Ajit) were highly susceptible to wilt. Recently the genetics was worked out at IARI, New Delhi using the identified novel source of resistance. With a view to identify molecular marker associated with *Fw* resistant gene, F2 population derived from a cross between Arkel (susceptible) and GP-6 (resistant) genotype used. Both parents and F1, F2 generations were phenotyped by artificial inoculation as well as wilt sick plot screening. Segregation analysis of 160 F2 progeny indicated that a single dominant gene governed resistance in 'GP-6'. Initially 122 markers (61 SSR, 60 ISSR and 1 SCAR) were screened for polymorphism between parents but only 29 ISSR markers were amplified. Among amplified markers 11 markers showed polymorphic band between susceptible and resistant parents but only one ISSR primer UBC-812 differentiated resistant and susceptible bulk by generating resistant bulk-specific amplicon. Earlier reported *Fw* resistant gene specific SCAR (Y15_999*Fw*) marker could also be validated in resistant parent. These two markers were used for genotyping of 160 F2 progeny. Marker analysis results revealed that genetic distance of two markers *viz* Y15_999*Fw* and UBC-812 were 25.76 cM and 5.01 cM, respectively. Thus, ISSR marker UBC-812 could be identified as novel marker which was found very close to the target resistant locus (*Fw*) and can be used for MAS (marker assisted selection) to develop *Fusarium* wilt resistant genotypes.

O (S 10) 22: Identification of defense genes /QTLs associated with stem rust resistance in wheat

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Stem rust caused by (*Puccinia striiformis* f. sp. tritici; Pst), is an important disease of wheat worldwide. To characterise loci conferring resistance to stem rust in bread wheats, we conducted a genome-wide association study (GWAS) with a panel of 400 accession using the wheat 35K Axiom® array. A total of 25 SNPs on 15 chromosomes (1DL, 2AS, 3AL, 3DL, 3DS, 4DL, 4DS, 5AL, 5BS, 5DL, 5DS, 6AS,6DL,7AS and 7DS) showed significant association with Compressed Mix Linear Model (CMLM) in GAPIT, R-package where each SNP explained 12.10 to 14.26% of the total phenotypic variance. The five most significant SNP (AX-95093852, AX-94582834, AX-95123669, AX-94997377, AX-94512213) on chromosome (1D, 3A, 3A, 5B And 7D) detected by CMLM showed significant association where each SNP explained 13.52 to 14.26% of the total phenotypic variance with (CMLM) corrected for population structure, kinship relatedness and adjusted for false discovery rate (FDR<0.01), where each SNP explained 6.6% to 28.8% of the total phenotypic variance. 25 candidate genes were identified by mapping the markers for the QTL to the available genome sequence of Wheat. Three of these genes, *TraesCS2A02G087200*, *TraesCS5D02G059300*, and *TraesCS6A02G089400* are annotated as leucine-rich repeat receptor-like, STPK & protein kinase like domain superfamily which have a role in pathogen recognition and disease resistance.

O (S 10) 23: Comprehensive patho-phenotyping and molecular mapping of RIL population of Wazuhophek/Improved Samba Masuri against sheath blight of rice

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Sheath blight is one of the important fungal diseases occurring in the most of the rice growing regions of the world and causes yield losses up to 70%. In India, it appears as an epidemic and endemic form in all the six rice growing eco-system. Till date, no absolute resistance has been identified for the disease in any rice line due to nectrotrophic nature of the pathogen and chemical control is the viable option at present to manage the disease. Through repeated artificial and natural screening at multiple hot-spot locations across the country, we have identified a sheath blight tolerant land race, Wazuhophek. A recombinant inbred line (RIL) population consisting of 330 lines was developed by crossing Wazuhophek and the variety, Improved Samba Mahsuri, which is highly susceptible to sheath blight. Patho-phenotypic screening of the F_2 population derived from the above mentioned cross revealed that sheath blight tolerance in Wazuhophek is quantitatively inherited. Later, intensive augmented screening under field conditions during three season and multiple parameters associated with tolerance/susceptibility *viz*., relative lesion height, lesion number, lesion boarder color and thickness, number of infected leaves, severity in leaves, number of infected tillers, sclerotial production, flag leaf and panicle infection, and yield were measured. In the RILs also, the quantitative nature of tolerance was confirmed. About 60 RILs showed tolerant reaction (<5 score) for three seasons i.e. KR-11, KR-38, KR-76, KR-86, KR-89, KR-90, KR-109, KR-113, KR-154, KR-162, KR-175, KR-177, KR-181, KR-183, KR-185, KR-187, KR-237, KR-257, KR-261, KR-262, KR-288, KR-296 etc. Linkage analysis and QTL mapping with a sub-set of RIL population using ICIM-additive method (version 4.2) revealed a major QTL associated with tolerance on chromosome 3 which explained > 30 % PV.

O (S 10) 24: Rapid phenotyping of stem and leaf rust diseases in wheat through speed breeding

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Rust diseases represent the most economically significant fungal diseases in wheat. Leaf and stem rust diseases continually pose a threat to wheat production at national and international level. Genetic/host resistance is the most economic, reliable, environmentally safest and sustainable way to manage rust diseases. Breeding for rust resistance involves field based phenotyping which is limited to one generation per year in conventional method. Moreover, field based phenotyping depends on environmental factors, plant growth stage, rate of disease development etc. These limitations slow down the progress in breeding and rust research programmes. With this background information, fifteen genotypes(10 cultivars + 5 susceptible lines) were subjected to rapid phenotyping of leaf and stem rust diseases seperately using speed breeding platform in a polyhouse and compared with the field screening. Speed breeding(SB) is a plant management system which uses constant light and controlled temperature to provide accelerated growth conditions, enabling 5 to 6 generations per year. In SB, plants reached booting stage in 4 weeks wherein artificial inoculation with the respective pathotypes of leaf and stem rusts were provided. Adult plant infection response type ranged from susceptible(S) to resistance(R) reaction in susceptible lines and cultivars respectively under SB which is comparable to the disease reaction for the same genotypes in the field. Rapid phenotyping method using SB could be completed in 10 weeks with optimum resource utilisation. This method has the potential to scaled-up for screening of large number of germplasm accessions, mapping population etc. Using this method, it is possible to conduct upto five consecutive rust phenotyping annually, compared to just one in the field. Breeding for rust resistance requires a continuous effort to stay ahead of the rapidly evolving pathogen which depends on the robust rust phenotyping. Method reported in this study provides a great tool for rust phenotyping similar to those observed in the field.

O (S 10) 25: Cowpea (*Vigna unguiculate* L.) germplasm resistant to root-knot nematode, *Meloidogyne incognita*

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Root-knot nematodes (*Meloidogyne* spp.), constitute a major group of plant-parasitic nematodes affecting crop production substantially worldwide. *Meloidogyne incognita* is a species of root-knot nematode commonly found on cowpea in most growing areas of the world. This nematode constitutes a major constraint to cowpea production symptoms of infection on roots are presence of galls, excessive branching of roots, and reduced root systems. Poor germination or death of seedlings may be observed in cases of heavy infestations. Root gall formation suppresses rhizobium nodulation and hampers nitrogen fixation in leguminous crops. The nematode resistant cultivars/accessions are an eco-friendly and economically feasible means for the management of root-knot nematodes. In the present work 400 accessions of cowpea germplasm were screened at ICAR-NBPGR, New Delhi during the years 2018-19 to identify new source of resistance to *M. incognita*. Preliminary screening was conducted in pots filled with nematode infected soil containing 3 second stage juveniles (J2) per gram of soil. After 40 days of sowing, plants were uprooted, root galls per plant root system were counted and a gall index (GI) of 0-5 was assigned using standard methods, where 0=no gall, 1=1-2, 2=3-10, 3=11-30, 4= 31-100, 5= >100 galls per root system. Host response of cowpea germplasm were determined using GI and designated as immune (GI= 0.0), resistant (GId”2.0) and susceptible (GI>2.0). Those accessions showing <10 root galls during preliminary screening were selected for rescreening with artificial inoculation under net house conditions to confirm their resistance consistency. Based on the number of root galls induced by *M. incognita*, four accessions (EC723870, EC724441, IC406512; IC550300) were found resistant with <10 root galls per root system. Nematodes penetration into roots were decreased drastically while none or very few egg masses were observed on resistant accessions. In conclusion, the drastic reduction in nematode penetration into the roots, reduction in root gall formation, and lower number of poorly developed egg masses suggest that resistance may be both pre-infectional as well as post-infectional in resistant cowpea accessions. These resistant accessions may be useful in cowpea plant breeding programs for nematode management.

O (S 10) 26: Identification and characterization of new sources of resistance to white rust and powdery mildew of Indian mustard at Wellington– a disease hot spot

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Rapeseed-mustard crops contribute 23 percent to the domestic edible oil production. The Indian sub-continent is endowed with rich diversity of oilseed *Brassica* species. So far, a total of 10,301 Indian mustard accessions are being collected and conserved at ICAR-NBPGR, New Delhi and ICAR-DRMR, Bharatpur. All these collections are not fully utilized in resistance breeding due to non-availability of ‘evaluation’ data. In this study,10,267 accessions were first evaluated at Bharatpur for white rust (caused by *Albugo candida*) resistance under natural epiphytotic conditions and 2,183 resistant accessions were identified, which were further evaluated at Wellington (Tamil Nadu), under hot spot conditions resulting in identification of 63 accessions with complete resistance. Molecular characterization of 63 resistant accessions with widely used two markers - At5g41560 and At2g36360, linked to white rust resistance loci AcB1-A4.1 & AcB1-A5.1, resulted in identification of seven “new” potential accessions expected to possess new resistance genes because of the absence of these two linked markers. Allelism test using F_2 populations also revealed the presence of new gene(s) governing resistance against *Albugo candida* isolate(s) occurring at Wellington. Secondly, powdery mildew of Indian mustard, caused by *Erysiphe cruciferarum,* is also emerging as a major disease leading to considerable economical losses and so far no resistance source has been identified. Therefore, a set of 1,020 Indian mustard accessions were evaluated against *E. cruciferarum* PMN isolate at Wellington, under hot spot conditions, which resulted in identification of one accession (PMW 18), for the first time, with high level of resistance, consistently for several seasons. Analysis of F_1, F_2 and backcross populations from cross Resistant (PMW 18) x Susceptible (PMW 25) accessions showed involvement of two genes with semi-dominant and gene dosage effect in governing resistance. A new disease rating system using five scale i.e. 0, 1, 2, 3, 4 and 5, has also been proposed in this study. Bulk Segrgant Analysis (BSA) of the F_2 population from the same cross identifed one closely linked SSR marker to one of the gene governing resistance to powdery mildew. By using the accession PMW 18 as a donor source, backcross breeding is now being undertaken at Wellington to transfer this important candidate gene to other popular Indian mustard cultivars.

Poster Papers

P (S 10) 01: Screening of pigeonpea genotypes against sterility mosaic of pigeonpea

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Pigeonpea (*Cajanus cajan* L.) belonging to family leguminosae is an important leguminous pulse crop of semi-arid tropic and subtropic regions (Asia and Africa). It is also known as red gram, arhar, tur dal. The crop is affected by several phytopathogens, of which, pigeonpea sterility mosaic disease/virus, and transmissible by eriophyid mites (*A. cajani)* has been major bottleneck. Yield losses up to 95 per cent or even 100 per cent in severe Sterility Mosaic Disease incidence were reported. Therefore, present investigation on screening of pigeon pea genotypes against the sterility mosaic disease was carried out during *Kharif,* 2018 at the Department of Plant Pathology, College of Agriculture, Latur. In present study, about 27 entries of pigeonpea were screened under natural epiphytotics against pigeonpea sterility mosaic disease. Of these GRG-152, ICP-2376, BRG-5, BRG-4, ICPL-15048, BSMR853, BSMR-736, BRG-1and BRG-3 were resistant; MPV-106, RVSA-16-1, IPA-16-8 and BRG-2 were moderately resistant, whereas, PUSA-2017-01, TDRG-58, ICP-8863, PUSA-2018, PUSA-2018-1, PUSA-2018-2, PUSA-2018-3 ,PUSA-2018-5, AKTE-12-04, KRG-244, PADT-16, RKPV-912, JKM-189 and TJT-501 were susceptible to Sterility Mosaic disease.

P (S 10) 02: Validation of SSR markers linked to BCMV resistance in F_2 population

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BCMV (Bean Common Mosaic Virus) of cowpea is a poty virus with yield losses ranging from 35-98 per cent respectively. SSR (Simple Sequence Repeats) are codominant markers used to study genetic diversity among crops. Hence studies were carried out on avialable four SSR primer pairs (M15, M135, M80 and Y96) found to be linked to BCMV resistance in cowpea. Markers were used to detect polymorphism between ten selected resistant and susceptible F_2 cowpea plants of crosses IC39916 x IT38956-1 and IC39916 x KBC-2. Genotype IC39916 was moderately resistant and genotypes IT38956-1 and KBC-2 were found to susceptible to BCMV. Polymorphic markers were then used to carry out PCR for selected resistant and susceptible F_2 cowpea plants linked to BCMV in cowpea. Genomic DNA of parents and selected F_2 plants phenotypically identified as resistant and susceptible were initially used as template for PCR amplification using SSR markers. Later they were validated using SSR markers reported to be linked to BCMV resistance. It was found that among four markers, Y96 marker showed amplification and polymorphism. Phenotypically susceptible ten F_2 plants of both the crosses showed similarity in banding patterns with susceptible parents but the results varied for the resistant F_2 plants. Cross IC39916 x IT38956-1 showed that except F_2 plants 1 and 2, the remaining plants showed similarity with IC39916. The similarity of 1 and 2 with susceptible parent revealed that, both the plants 1 and 2 were susceptible in nature, even though they were identified to be resistant phenotypically. In cross IC39916 x KBC-2 except plants 2, 8 ,9, the remaining plants showed similarity with IC39916. Susceptible parents and selected F_2 plants of cowpea were distinguished as resistant and susceptible with a difference in DNA fragment size ranging from 280-320 bp in the 4 per cent agarose gel.

P (S 10) 03: Prebreeding and population improvement for disease resilience in crop plants

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Pre-breeding refers to all activities designed to identify desirable characteristics and/or genes from unadapted (exotic or semi-exotic) materials, including those that, although adapted have been subjected to any kind of selection for improvement. Plant pathogens cause considerable yield losses in cereal production, reducing crop quality and threatening food safety. Disease prevention and control is thus a prerequisite for competitive cereal production with the breeding of genetically disease resistant crops being one of the most environmentally and economically desirable ways to manage plant diseases.The prevalence of different plant diseases is changing due to changing environmental conditions, including global climate change, but also changes in agricultural production with trends towards larger areas planted to fewer and/or genetically more uniform varieties, reduced crop rotation and soil tillage, loss of biodiversity, changing use of pesticides, and global trade. In such a changing environmental and economic context, plant diseases will inevitably appear and compromise crop production in regions where they did not represent a problem before, as is already being seen with the emergence of a new strain of heat tolerant wheat yellow rust and increasing problems with Fusarium head blight and Ramularia leaf spot. Understanding the host-pathogen biology is the first step towards minimizing the risks represented by plant diseases. Durable, both race non-specific and race-specific, resistance incorporated into high yielding genotypes is the main method to manage diseases of cereals. New durable and efficient sources of resistance will have to be sought, in the case of cereals, from landraces and from wild relatives of the crops.The recent progress in biotechnology has opened up enormous possibilities, both for introgression of specificdisease resilience traits and for base broadening in pre-breeding. Molecular techniques and bioinformatics allow more precise andfaster selection methodologies as well as providing a much more detailed understanding of the underlyinggenetics. Such efficient tools are a crucial element in the modern plant breeding process to handle complicated disease specifictraits efficiently.

P (S 10) 04: Screening against chrysanthemum wilt disease in natural epiphytotic field condition

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The field experiment was conducted to find the source of host resistance against wilt under the natural epiphytotic field condition located at Agricultural Research Station, Badnapur, during *Kharif* 2018-19 by screening chrysanthemum varieties. The eleven commercial varieties of chrysanthemum were evaluated for their reactions against *Fusarium oxysporum* f. sp. *chrysanthemi.* Observation on per cent disease incidences were recorded. Based on the disease incidence, test lines were categorized in Resistant, Moderately Resistant, Susceptible, Moderately Susceptible and Highly Susceptible group. The wilt disease incidence was calculated and scored on 0-5 scale. After screening of eleven commercial varieties of chrysanthemum including highly susceptible variety *viz.,* Aishwarya, it was concluded that none of the variety was found to be wilt disease free. However, two varieties *viz.,* Pournima White and Star of India were observed resistant to wilt. Whereas, three varieties *viz.,* Mums Pink, Valiant and Crimpson Tide were found moderately resistant and two varieties *viz.,* Bhagyashri and Ishwari were observed moderately susceptible. The two varieties *viz.,* Alfred Wilson and Alfred Simpson were shown susceptible reaction against wilt disease. Remaining two varieties *viz.,* Aishwarya and Thai Ching Queen were found highly susceptible to wilt disease.

P (S 10) 05: White rust disease resistance source in wild cruciferous genotypes against sixpathotypes of *Albugo candida*

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Most of the cultivars have narrow genetic base leads to a major bottleneck for crop improvement efforts and, therefore, the use of crop wild relatives is a promising approach to enhance genetic diversity of cultivated crops. All cultivated *Brassica* species including other crucifers attacked by a biotrophic pathogen *Albugo candida* causing the disease known as white rust or crucifers blister. Management of white rust is mainly through use of chemicals pesticides which are neither cost-effective nor safe to environment. The present study was designed to utilize these wild germplasm resources to develop white rust resistant genetic stocks of oilseed *Brassica* for crop improvement. Accordingly, the objective of the present investigation was to screen wild relatives of *Brassica* againstsixpathotypes of *Albugo candida* to identify resistant source. Total 39 wild relatives cruciferous including *Brassica chinensis, B. fruticulosa, B. fruticulosa (spain), B. oxyrrhina, B. tournefortii* (*RBT 2002*), *B. tournefortii (RBT 2003), Camelina sativa, Capsella-bursapastoris* (*early*),*Capsella-bursapastoris* (late), *Diplotaxis assurgens, D. catholica, D. cretacia, D. erucoides, D. Gomez-campoi, D. muralis, D. siettiana, D. tenuisilique, D. viminea, Enarthrocarpus lyratus, Erucastruma byssinicum, E. canariense, E. cardaminoides, E. gallicum, Lepidiumsativum, Sinapis alba,Crambeabyssinica* (EC400058), *C. abyssinica* (EC694071), *C. abyssinica* (EC694138), *C. abyssinica* (EC694144), *C. abyssinica* (EC694145), *C. abyssinica* (EC694147), *C. abyssinica* (EC694159), 6 genotypes of *Erucastiva* and *Oxycamp*were selected for screening against six pathotypes of *A. candidai.e*., Ac- Dli, Ac-Wltn, Ac-Pnt, Ac-Ludn Ac-Rnchiand Ac-Amblunder artificial epiphytotic conditions. Results indicated that thirteen crucifers were susceptible to white rust pathotypes. However, pathogenic reaction to many crucifers (08, 06, 06, 05, 05 and 03) were found susceptible to Ac- Dli, Ac-Pnt, Ac-Ambl, Ac-Rnchi, Ac-wltn and Ac-Ludnpathotypes, respectively. Though, three crucifers were susceptible to allsixpathotypes and remaining crucifers exhibit variable resistant type reaction rendering to individual pathotype(s).

P (S 10) 06: Phenotypic screening and molecular characterization of wheat germplasm for rust resistance

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Wheat (*Triticum aestivum L.)* is a staple crop and bears global significance considering its consumption and commercial uses. Hence increase in its production is very much essential to meet the demand of ever increasing population. Wheat crop is affected by different biotic and abiotic stresses. Among biotic stresses foliar diseases like rust, powdery mildew and spot blotch cause considerable damage to the crop and affect wheat yields. Climatic changes have led to the resurgence of new races of rust pathogens as well as movement of pathogens to the new areas. Stripe (yellow) and leaf (brown) rusts of wheat are a matter of major concern in wheat grown in north western plains zone (NWPZ) of India. Three pathotypes of stripe rust (*Puccinia striiformis)* namely, 46S117, 110S119 and 110S84 and two pathotypes of brown rust (*Puccinia recondita*) namely, 121R60 and 121R63 are major threat Indigenous and exotic germplasm accessions received from ICAR-NBPGR, New Delhi were subjected to screening for stripe and leaf rust under epiphytotic conditions. The accessions

showing resistance were subjected to molecular characterization with gene linked markers viz., *Cslv34* for Lr34/Yr18/Sr57/Pm38, *Xpsp3000* for Yr10, *Xgwm175* and *Xgwm273* for Yr15. The findings of the study revealed some of the accessions were found possessing single as well as multiple resistant genes. The accessions possessing multiple resistant genes could be used in breeding programme for the development of wheat varieties possessing durable disease resistance.

P (S 10) 07: Novel approach for selection of banana suckers with the decline of *Fusarium oxysporum* f. sp. *cubense* population in bihar

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Banana wilt caused by the fungus *Fusarium oxysporum* f.sp. *cubense* (Foc) is the most devastating disease affecting theproduction.Foc isolation was performed by infected plant diseased soil samples were collected from banana plants of different micro plots. It revealed that Foc population and disease incidence of new plantlets obtained from the first sucker of the tissue culture mother plant were 22.00%, 20.50%, 18.00%, 14.50% and 12.00% per plant, respectively in five district of Bihar *viz*., Katihar, Purnea, Khagaria, Kishanganj and Bhagalpur whereas it was 58.50%, 56.00%, 52.00%, 42.00% and 40.50% per plant in the sucker of the local cultivar mother plant micro plots. Overall, anegative correlation was determined about distance of sucker plant from mother plants and Foc population. In addition, PDI were declined because of lower Foc population. The suckers next to the local cultivar of mother plants were unable to grow due to the higher Foc density and high susceptibility of the plants. The efficiency of suckers can be enhanced against fusarium wilt by replacing the local cultivar with the tissue culture plant and incorporating integrated wilt management strategies.

P (S 10) 08: *In vitro* evaluation of different Plant extract against *Fusarium oxysporum* f. sp. *virguliforme*

S.S. Gote, V.S. Mete, P.H. Ghante, S.P. Pudke and S.K. Deshmukh

The pathogen was isolated successfully from the naturally diseased soybean plants specimens collected from farmers' fields as well as research fields which were purified and maintained for further studies. The typical symptoms were noticed on plants *i.e*. chlorosis of leaves. Early symptoms of sudden death syndrome are diffuse chlorotic mottling and crinkling of the leaves. Later, leaf tissue between the major veins turns yellow, then dies and turns brown. Green leaves turned into yellow in colour. Plants loss their vigourness. Xylem tissues have shown brownish to black colour apperence. Whole plant loss their turgidity and finally death of plant occurs. Pathogenicity of *Fusarium oxysporum* was proved by adopting sick soil inoculation method by using SDS (wilt) susceptible soybean variety *viz.,* JS 20-34 under pot culture. A critical review of the literature reveals that very little work has done on eco-friendly management of *Fusarium oxysporum.* The investigations were carried out to find the intensive and eco-friendly methods of controlling *Fusarium oxysporum,* by using plant extract in laboratory during the year 2018-19. The result obtained on mycelial growth and inhibition of *Fusarium oxysporum f. sp. Virguliforme* with eight plant extract. The antifungal activities of eight phyto-extracts Neem, Tulsi, *Parthenium,* Ghaneri, Garlic, *Gliricidia,* Onion, Drumstick were assessed at 10% concentration in the laboratory for evaluation of their efficacy against *Fusarium oxysporum* f. sp. *virguliforme* by using poisoned food technique. *In vitro* treatments of phyto-extracts *viz*., Garlic clove extract and Neem leaf extract showed effective mycelial growth inhibition *i.e.* 74.81 and 70.36 per cent which were significantly superior over the untreated control. However, significantly the highest mycelial growth inhibition was recorded 74.81 per cent by Garlic. It was followed by botanicals *viz*., Neem leaf extract (70.36 %), Tulsi leaf extract (65.92 %), Onion bulb extract (59.25 %), Ghaneri leaf extract (55.18 %), *Parthenium* leaf extract (43.32 %). *Gliricidia* leaf extract (39.99 %) and Drumstick seed extract (38.14 %). The lowest mycelial growth inhibition was recorded with Drumstick seed extract (38.14 %) which was at par with *Gliricidia* leaf extract (39.99 %), still these two plant extracts significantly superior over the control.

P (S 10) 09: Bulk segregant analysis for blast resistance in F_2 population derived from two contrasting rice genotypes of north eastern hill region

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Northeast India is considered to be a center of diversity for rice genotypes. Several wild species and landraces of rice found in this region have been characterized for blast resistance, but there is very little or no comprehensive information available regarding major resistant genes effective against blast pathogen of this region. Moreover, many of the landraces found in this region which show potential to resistance against the fungal pathogen are still unexplored. Therefore, the present study involved use of Bulk Segregant Analysis (BSA) technique on bi-parental population (F_2) derived from two contrasting rice genotype LR5, also known as Lal jangali (a local landrace of rice resistant to blast) and LR26 (Manipuri black rice traditionally known as Chakhao, susceptible to blast) in order to know the genetic basis for blast resistance in LR5. Disease assessment for blast on progenies and parental genotype was carried out under natural disease occurrence. F_2 progenies showing extreme phenotype were selected and subjected to genotyping with the polymorphic markers obtained from polymorphism survey on the parental genotype in order to identify markers linked to blast resistance. Association of the markers with phenotypic trait in the selected progenies was identified by several statistical analyses which revealed that significant markers for blast resistance found, were mostly present on chromosme12. In future more such markers can be used for further mapping of the segment of chromosome 12 in larger population for blast resistance, and the F_2 progenies found promising for desired traits can be further studied in the next generation to design better breeding approach for blast resistance relevant to North Eastern Hill region of India.

P (S 10) 10: Induction of sporulation in *Bipolaris oryzae* inciting brown spot disease of rice

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Brown spot disease caused by *Bipolaris oryzae* (*syn-Helminthosporium oryzae*; telemorph=*Cochliobolus miyabeanus*) is known to cause yield losses varying widely from 4 to 52% and is again becoming a serious threat to rice cultivation in India. Since the identification of disease from early 1950s, the disease has been managed effectively by spraying of fungicides; however host plant resistance to disease is considered to be an effective and economical way to manage the brown spot disease. The pathogen *B. oryzae* rarely sporulates on the artificial/natural media and requires specific culture and nutritional conditions. Since the pathogen does not sporulate well in culture, many workers have employed mixture of conidial and mycelial dust as inoculums in varietal resistance screening programmes. However it was observed that, conidia were 10 times more effective than mycelial dust in developing infections. Hence in the present work efforts have been made to obtain a good sporulation by manipulating the light and nutritional sources. The two isolates of *B. oryzae* (IIRR, Hyderabad and Lonavala) cultured on PDA for two weeks under dark condition were exposed to different regimes of light sources to induce the sporulation. It was found that, exposure of fungus to different NUV light regimes could induce the sporulation in fungus; however the maximum sporulation (22.8 x104 and 15.5 x104 in IIRR and Lonavala isolates respectively) was obtained when fungus was exposed to 12 hours of NUV light followed by 12 hours of incubation under dark conditions at 26 0C. Neither the complete NUV (24h) exposure nor complete dark (24h) condition could induce the sporulation in the fungus. The exposure of fungus to different durations of ultra violet (UV) and visible light did not trigger sufficient sporulation in fungus. Among the different nutrient sources tested for better sporulation of *Bipolaris oryzae*, Rabbit food agar (RFA) followed by corn meal agar could induce good vegetative growth and excellent sporulation in fungus after exposure of fungus to 12h of NUV and 12 h dark condition. Broken sorghum and maize grains were also found to induce better sporulation among the different natural media tested for the sporulation of the fungus. Hence, it was concluded that culturing of *B. oryzae* on RFA, with the treatment of 12 hours of NUV followed by incubation for 12 hours at 26 0C under dark conditions for 12 days resulted in maximum sporulation of the fungus. This technique is being standardized for obtaining sufficient number of conidia to screen large number of genotypes.

P (S 10) 11: Identification of resistant source against pod blight disease of soybean caused by *Colletotrichum truncatum* (Schwein) Andrus and W. D. Moore

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Soybean [*Glycine max* (L.) Merrill] is an internationally recognized crop as it is a rich source of protein and oil. The crop is being attacked by different pathogens due to changing climate. In recent years, there is a drastic increase in the incidence of pod blight disease( ) caused by *Colletotrichum truncatum* (Schwein) Andrus and W. D. Moore. In view of managing this disease, the study was undertaken to identify the source of disease resistance during *kharif* 2018 & 2019 under epiphytotic condition by infector row method. A total of 164 germplasm and advanced breeding lines along with released varieties were evaluated. The disease severity of pod blight was recorded at weekly interval. During *kharif* 2018 among 164 genotypes, 6 genotypes were Absolutely Resistant (AR), 43 showed Resistant(R) Reaction, 108 were Moderately Resistant (MR) and 7 showed Moderately Susceptible (MR) reaction. During *kharif* 2019 absolute resistant, resistant, moderately resistant and moderately susceptible reaction were expressed by 2, 38, 95, 28 and 1 genotypes respectively. AGS 31 and EC 125738 germplasm lines were found to be promising source of pod blight resistance as they showed absolute reaction in 2018 and 2019.These can be use in contemporary resistant breeding programme.

P (S 10) 12: Screening of wheat germplasms against loose smut disease

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Wheat enjoys status of staple food among the cereal crops globally. It is attacked by a large number of diseases among which rusts and smut are highly destructive and cause enormous damage. Loose smut caused by *Ustilago segetum tritici* is prevalent throughout the world. The mycelium remains dormant in the embryo, and developing kernels are replaced by black teliospores. No seeds develop in infected heads. The disease is spread by windblown teliospores. Cool, humid weather favours the development of this disease. Based on surveys conducted in northwestern India, 2-4% yield reduction of wheat from loose smut is estimated every year. Though this disease can easily be controlled by seed treatment from Vitavax but it assumes high importance particularly in hilly region where the fungicide availability in inaccessible areas is highly impossible. Under such situation the host resistance is the best. Therefore, the present study was planned to detect the resistant genotypes against loose smut under artificial inoculated epiphytotic conditions so that these identified genotypes can be used as donors in breeding programmes for developing loose smut resistant varieties. Experiment was conducted at ICAR-VPKAS Experimental farm, Hawalbagh, Almora during 2015-16 and 2016-17. One hundred twenty four wheat lines were used for screening. GO-GO method was adopted to inoculate the spikes with fungus spores at leaf boot stage. Inoculated spikes tagged separately were harvested and threshed separately. These inoculated seeds were kept for next sowing season. Each line was planted in single row. When all the lines completed spiking, the diseased and healthy spikes were counted and disease incidence was calculated. The result revealed that out of 124 wheat lines, 69 lines viz. VW 0716, VW 0739, VW 0751, VW 0765, VW 0920, VW 0933, VW 1348 etc. showed immune reaction (no symptoms on any plant), 22 lines showed highly resistant (VW 1507, VW 1533, VW 1542, VW 1545) to moderately resistant (VW 0738, VW 1501, VW 1502, VW 1511, VW 1515, VW 1534, VW 1535, VW 1539, VW 1541, VW 1544, VW 1552, VW 1553, VW 1562) reaction whereas, 33 lines were found moderately susceptible (VW 1508, VW 1509, VW 1514, VW 1526, VW 1528, VW 1529) to highly susceptible (VW 1516, VW 1518, VW 1520, VW 1527, VW 1555, VW 1558) to loose smut disease.

P (S 10) 13: Search for resistant sources in wild crucifers against *Alternaria brassicicola* causing *Alternaria* blight disease in Brassicas

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Narrow genetic base in cultivated Brassicas is a major bottleneck for trait improvement.Use of crop wild relatives is a promising approach for enhancing genetic diversity in the cultivated crops. All cultivated crucifers, including *Brassica* species,are attacked by a necrotrophic pathogen *Alternaria brassicicola* causing Alternaria blightdisease. Management of *Alternaria* blight is mainly achieved through use of chemicals which are neither cost-effective nor environment friendly. Present investigation was carried out to screen wild relatives of *Brassica* for *Alternaria* blight disease and identify resistant sources. A total of 39genotypes of wild species including *Brassica chinensis, B. fruticulosa* (2 genotypes)*, B. oxyrrhina, B. tournefortii (RBT 2002), B. tournifortii (RBT 2003), Camelina sativa, Capsella-bursapastoris (early), Capsella-bursapastoris (late), Diplotaxis assurgens, D. catholica, D. cretacia, D. erucoides, D. Gomez-campoi, D. muralis, D. siettiana, D. tenuisilique, D. viminia, Enarthrocarpu slyratus, Erucastrum abyssinicum, E. canariense, E. cardaminoides, E. gallicum, Lepidiumsativum, Sinapis alba* (6 genotypes)*, Crambea byssinica* (EC400058), *C. abyssinica* (EC694071, EC694138, EC694144, EC694145, EC694147, EC694159), *Erucastiva* and *Oxycamp* were used for screening against *Alternaria brassicicola* under artificial epiphytotic conditions. Results indicated that two genotypes of crucifer's species viz., *Capsella-bursapastoris* and *Diplotaxis cretacia* were showing resistant reactions against *A. brassicicola* (Delhi isolate), whereas, rest of 37 genotypes observed susceptible reaction against this pathogen. Resistance reaction observed by the above mentioned two species shall be reconfirmed by inoculating these with isolates collected from different parts of the country before their used in crop improvement programmes.

P (S 10) 14: Studies on variability of *Sarocladium oryzae* [(Sawada) Gams & Hawksworth] causing sheath rot disease of rice and identification of sources of resistance against the pathogen

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Sheath rot disease of rice is one of the most destructive diseases causing significant loss to rice production under temperate agro-climatic conditions of Kashmir. An extensive survey conducted during *kharif*, 2018 in major rice growing areas of Kashmir valley revealed the prevalence of disease in all the surveyed areas with varied levels of incidence and intensity. The main fungus inciting the sheath rot disease was identified as *Sarocladium oryzae* [(Sawada) W. Gams and D. Hawksworth] on the basis of its morphological and pathological characteristics. *Fusarium fujikuroi* and *Chalara aurea* were also found associated with sheath rot disease of rice. Twelve single spore isolates of *Sarocladium oryzae* were obtained from different locations of Kashmir valley which were designated as SO-1 to SO-12. During the present study a wide variation among the isolates of *S. oryzae* was observed in terms of cultural characteristics, morphology and pathogenicity. Growth of four isolates *viz*., SO-10, SO-12, SO-11 and SO-3 was profuse and fast with excellent sporulation. Pathogenic variability study of twelve isolates of *S. oryzae* was recorded on a set of eleven putative differential rice lines. Cluster analysis on the basis of similarity or dissimilarity in reaction types exhibited by these differential hosts grouped the isolates into 3 pathogenic groups. The isolates SO-9 and SO-7 have been found most aggressive isolates showed susceptible reaction with 10 and 9 genotypes respectively. The genotypes SK-406 and SR-4 showed resistant response with maximum number of isolates while as Aromatic Zag was found susceptible to all the isolates of *S. oryzae.* The isolates of *S. oryzae* tested in the present study exhibited considerable variation in the per cent disease intensity, virulence index, incubation period and lesion size. Among the 12 isolates, the maximum per cent disease intensity, virulence index, lesion length and shortest incubation period was observed in isolate SO-9 from Khudwani, district Anantnag, followed by SO-7 from Sheeri, district Baramulla. Three hundred and twenty one rice genotypes were screened for resistance against *S. oryzae* under artificially inoculated field conditions using 0-9 evaluation scale. The genotypes showed varied response from highly resistant to highly susceptible reaction. In order to validate the resistance, 42 genotypes which showed resistant reaction were further evaluated under controlled conditions against all the twelve isolates of *S. oryzae* along with highly susceptible genotypes. Out of 42 test lines, 11 genotypes (SK-98, SK-354, SK-415, SK484, SK500, GS-135, GS-145, GS-169, GS-183, GS-324, GS490, GS-357) were found resistant 24 genotypes were found moderately resistant and 7 genotypes showed moderately susceptible to highly susceptible disease reaction.

P (S 10) 15: Scope of endophytes in tropical tuber crops for disease management

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Tropical tuber crops are known for its role in food and nutritional security along with climate resilient nature, which contribute substantially for sustainable global development goals. Though the crops are less prone to biotic and abiotic stresses, few viral diseases and some fungal diseases, viz., taro leaf blight and anthracnose in greater yam are serious concerns. Though, it is a fact that synthetic chemicals save crop in adverse situations, the dreadful consequence led the researchers for mining various organic approaches for sustainable management through bio products. Endophytes are one among them, which has tremendous potential in managing the diseases by maintaining the plant health and fighting with pathogen through various mechanisms. Fungal and bacterial endophytes were isolated from different tropical tuber crops and medicinal plants and screened against *Phytophthora colocasiae* causing taro leaf blight and *Colletotrichum gloeosporioides* causing greater yam anthracnose. Generally, bacterial endophytes were more potential than fungal, which were identified at species level and the host pathogenic microbes were not used further. The effect of potent endophytes on disease suppression was tested *in vivo* in pot trial as well as field. Different potent *Bacillus* spp, viz., *Bacillus subtilis* , *Bacillus cereus*, *B. amyloliquefaciens* and *B. licheniformis* reduced the intensity of anthracnose in greater yam, whereas *B. pumilis* and *B.subtilis* reduced taro leaf blight. Apart from direct confrontation, the antibiosis nature of some endophytes was deciphered by characterizing the secondary metabolites and the compounds which showed inhibition were identified through different mass spectrometric techniques. The studies showed that endophytes have great potential to manage the diseases of tropical tuber crops, which are normally grown organically. However, the basics on the impact of endophytes on pathogenecity and induction of resistance mechanism ;for strategic application, the dose and delivery system have to be contemplated.

P (S 10) 16: Development and release of first commercial variety of *Momordica balsamina*: An asset for root Knot nematode sick soils

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The genus *Momordica* bear edible, tender green fruits of high commercial value.*Momordicabalsamina* locally known as Jhaarkarela in Punjab state of India is persumed to possess anti diabetic properties. It is a climbing annual wild plant with striking orange to red spindle shaped ribbed fruits and found climbing on bushes in sandy areas of Punjab, Rajasthan and Gujarat. There is long practice of using it as a vegetable in these areas. It has been used as a traditional medicine in many countries. Demand of the immature fruits of jhaarkarela has increased tremendously as it is considered good for diabetic patients. Local landraces of *M. balsamina* have been grown at some places but this crop of high economic importance have never been bred following systematic breeding programme. Assessing the importance of the crop, varietal development research programme on *M. balsamina* has been initiated at Department of Vegetable Science, Punjab Agricultural University, Ludhiana, Punjab with the germplasm collections from different parts of Punjab and Rajasthan.

Selection over years in *M*. *balsamina* following mass selection resulted in the development of a high yielding variety "Punjab Jhaar karela-1" in 2017, which, out yielded the local check (unimproved JhaarKarela grown by farmers) by 19.6%. New variety Punjab Jhaark karela-1 was found to be resistant to root knot nematode (RKN) disease both under artificial and natural epiphytotic conditions. RKN disease cause up to 48% of yield losses in bittergourd. To the best of our knowledge, Punjab Jhaar karela-1 is the first systematically developed and commercially released variety of *M*. *balsamina*.

P (S 10) 17: Screening of maize (*Zea mays* L.) locally available landraces for resistance against Turcicum leaf blight (TLB) under temperate conditions

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Maize is the leading cereal worldwide with wide adaptability and higher productivity potential. It has notable productive potential among the cereals and is the third most important grain crop after wheat and rice. Turcicum leaf blight (TLB) affects the maize crop from the seedling stage to maturity. The present study involved field evaluation of seventy maize landraces for resistance against TLB disease under artificially inoculated field conditions in an augmented design using 3 checks at Mountain Crop Research Station, Larnoo during *kharif,* 2017. Among seventy landraces, forty-three lines were categorised as resistant, eighteen moderately resistant, five moderately susceptible and landrace Tral 3 recorded highest percent disease index (PDI) as 78.91 per cent and rated as susceptible. Thus the genotypes identified to possess low disease severity score against TLB would be helpful for their deployment in future breeding programs and eventually could be used in developing promising genotypes having desirable level of resistance in disease endemic areas to aim for sustainable productivity.

P (S 10) 18: Evaluation of barley germplasm/cultivar against spot blotch of barley caused by (*Bipolaris sorokiniana* Sacc. Ex. Sorok.) Shoe

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One hundred forty three barley germplasm/cultivars obtained from various sources were evaluated against spot blotch(*Bipolaris sorokiniana)* under field conditon by creating artificial epiphytotic conditions during Rabi season 2018-19 at Nawabganj Research Farm, C.S.A. University of Agriculture & Technology, Kanpur.the experiment was laid out in Randomized Block Design with three replicates.Each cultivar was sown in two meter row spaced 22.5 cm apart in last week of December.The spore suspension of *Bipolaris sorokiniana* was prepared from 21 days old cultivar.The inoculation with the pathogen was made by spore suspension (4.3 × 10^4 spore/ml of water) on barley genotypes. The progress of the disease in all Barley genotypes was monitored from 2nd fortnight of March and disease severity at 10 days interval was recorded. Maximum disease severity was observed in RD 2935 , RD 2937 , RD 2938 (78.00%). However ,the minimum disease severity was recorded in barley genotypes *viz*; BH 1001, BH 1003, BH 1015,BHS 450, DWRB 123, DWRB 136, DWRB 158(35-36%).

P (S 10) 19: Cross infectivity of *Albugo candida* isolates causing white rust in *Brassica juncea* on different cruciferous host

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Brassic juncea, commonly known as Indian mustard is the second largest oilseed crop in India next to groundnut and it occupies nearly 90% of the total cultivated area amongst other six cultivated *Brassica* species. But all the available varieties of mustard are susceptible to white rust, or white blister rust caused by *Albugo cadida*. Even though, resistant lines of *B. juncea* are reported, it is not effective due to lack of information regarding the availability and distribution of *A. candida* pathotypes and its degree of host specificity. Seven isolates of *A. candida* and one isolate of *Albugo bliti* were cross inoculated to nine cruciferous host and test for its pathogenicity. *A. candida* isolate collected from Baghpat region was found to be pathogenic to *Brassica oleracea* var. *capitata,* Delhi isolate was pathogenic to *Brassica oleracea* var. *capitata*, *Brassica rapa* subsp*. rapa* and *Brassica oleracea* var*. botrytis*, Wellington isolate was found to be pathogenic against *Brassica oleracea* var. *gemmifera*, Meghalaya and Pantnagar isolates were pathogenic to *Brassica rapa* subsp. *rapa*. But the *A. bliti* isolate collected from Bhubaneswar region was found not to infect any of the cruciferous host. It was concluded that different *A. candida* isolates collected from different geographical regions have the ability to cross infect to other related cruciferous host and these can act as an alternate host in the field condition. A single nucleotide change in the pathogen can change its virulence spectrum and make the host susceptible which are previously reported to be resistant. Therefore, the screening for genotypes in the breeding program for white rust resistance should not be limited on a single host; rather it should include other differential host also where the pathogen has been reported.

P (S 10) 20: Charcoal rot and aerial blight of soybean in soya state of India: status, resistance and integrated management

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Survey (2017 and 2018) of soybean crop in different districts of Madhya Pradesh has revealed that varieties i.e. JS 335, JS 93-05, JS 95-60, JS 97-52, JS 20-29, NRC 86, RVS 2001-4, RVS 2001-18 were found to be affected by Charcoal rot (*Macrophomina phaseolina* (Tassi) Goid) and Rhizoctonia aerial blight (*Rhizoctonia solani*) with the range of 3.0-84.0 and 1.5 to 24.0 per cent, respectively. During 2017 and 2018, seventy six initial varietal trial entries from all over the country were evaluated under sick plot condition wherein NRC 133, AMS 100-39, JS 21-17, PS 1611, JS 21-71, SL 1191, JS 21-72, Himso 1689, KDS 1009 showed absolute/ highly resistant against both Charcoal rot (CR) and Rhizoctonia aerial blight (RAB) and maximum entries (thirty five) reacted as susceptible to highly susceptible against CR. Likewise, out of one hundred ninety germplasm accession, only twenty seven i.e. Cat 87, AMS 264, AMS 269, B 1664, Cat 2126B, CAT-489A, Cat 2310, EC 250608, EC 280129, HARDER, NRC 99, PS 1225, PS 1469,PI 210178, TG X 325 3F, JS 20-18, JS 20-19, JS 20-20, JS 20-25, JS 20-34, JS 20-36, JS 20-40, JS 20-84, JS 21-17, JS 21-18, JS 21-71, JS 21-72 were found to be absolute resistant against CR and most of these were also exhibited highly to moderately resistant reaction against RAB. In twenty two released varieties, only JS 20-34, JS 20-98, NRC 86, JS 20-69, MAUS 162 and MACS 1188 showed absolute to moderate resistant reaction against CR and RAB with good yield under hot spot condition at Jabalpur where incidence and severity varied from 0.0 to 92.0 and 0.8 to 28.3 per cent for CR and RAB, respectively. However, integration of various treatment like Soil application of FYM 10 t/ha plus *Trichoderma harzianum* 10 kg/ha plus seed treatment with Thiophanate methyl + Pyroclostrobin

50% @ 2 ml or Carboxin + Thiram 75 WP 3 g/kg seed were found to be effective in management of CR as reduced mortality up to 53.0 per cent.

P (S 10) 21: Development of donor specific SSR markers to identify alien introgressions in substitution lines derived from *Sinapis alba + Brassica juncea* hybrids

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Sinapis alba is a wild member of brassicacae family and reported for carrying resistance against *Alternaria brassicae*, *Sclerotinia sclerotiorum* with tolerance for high temperature, drought, seed shattering and bearing yellow seed colour. Because of its wild nature, this genus is still uncovered at genomic level. However, some transcriptomic information is available for expression of few important genes. Therefore, we have developed first genomic assembly of *S. alba* in the form of contigs from raw Illumina sequence data available in NCBI. The assembly has 445,086,869 base pairs composed in 382,969 contigs. The largest contig has 29,081 bp while the smallest contig possess 200 base pairs. The average size of contig was recorded 1162.2 bp while N50 was 1776 bp. To develop donor specific SSR markers, we have locally BLASTN this genomic assembly with *B. juncea*, *B. rapa* and *B. nigra* assemblies to identify contigs with dissimilar sequences. A total of 65,536 non-hit contigs were identified in *S. alba* assembly. These unique contigs were used to identify potential SSR loci by MISA software. A total of 5646 SSR loci were identified that designed 1604 (28.41%) SSRs and 1400 unique primer pairs were selected after removing redundant SSRs. The substitution lines of somatic hybrid showing phenotypic variations from *B. juncea* were used to evaluate by donor specific SSR markers. A total of 103 SSR primer pairs were used in this study. All primers selected showed polymorphism between *S. alba* and *B. juncea*. Out of total primer pairs in study, 87 were successfully amplified in 59 substitution lines and gave expected amplicon size.

P (S 10) 22: Introgression of *Alternaria* blight resistance from alien donor to *Brassica juncea*, their confirmation through *Sinapis* specific markers

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Sinapis alba (a wild member of Brassicacae family) is known to possess resistance for major biotic and abiotic stresses of *Brassica juncea*. The genus is still uncovered at genomic level due to their wild nature. The whole genome constitution of *S. alba* was used to develop stable somatic hybrids with *B. juncea* through protoplast fusion. These somatic hybrids showed high degree of resistance against *Alternaria* blight. Therefore, we have used these somatic hybrids to develop introgression lines through backcross breeding. The introgression lines were found morphologically variable from *B. juncea* as they had thick leathery leaves with prominent trichomes, rough stem with trichomes, long beak siliquae and differential response for *Alternaria* blight resistance. Simultaneously, we have developed first draft genome assembly of *S. alba* from raw Illumina data.

The assembly has 445,086,869 base pairs composed in 382,969 contigs. The largest contig has 29,081 bp while the smallest contig possess 200 bp. This genomic assembly was locally BLASTN with *B. juncea*, *B. rapa* and *B. nigra* reference assemblies to identify dissimilar contigs for development of donor specific SSR markers. A total of 65,536 non-hit unique contigs were identified in *S. alba* assembly. These contigs were used to identify potential SSR loci by MISA. The software identified 5646 SSR loci in contigs and designed 1400 unique SSR markers by Primer3 software. A total of 103 SSR markers were selected to track alien introgressions. The selected SSR markers were first checked in parent for amplification. All the SSR markers gave expected size amplicons in S. alba but not amplify in B. juncea. Out of 103 SSR markers, 87 were successfully amplified in 59 introgression lines showed resistance for *Alternaria* blight and variable morphological characters. The donor specific SSR markers gave expected size amplicons in differentially expressed resistance introgression lines conferred the alien introgressions.

P (S 10) 23: Generation mean analysis to study inheritance of plant disease resistance: a case study of cercospora leaf spot in mung bean

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Mung Bean has gained popularity worldwide due to its impressive nutritive value, health benefits, soil health enricher, short duration and prospects in bioenergy. In wet tropics and scenario of climate change, Cercospora leaf spot (CLS) disease of mung bean is an emerging disease with significant impact on grain yield. Understanding the genetics underlying disease resistance is a prerequisite for deployment of efficient disease resistance breeding and selection strategies. The present investigation, employed Generation mean analysis (GMA) for Inheritance study of Cercospora leaf spot resistance, for interspecific cross *viz.,* KG (mungbean, susceptible to CLS) x PU31 (Urd bean, non host to CLS). Traits namely, Area under disease progress curve (AUDPC), Days to flowering (DTF), Days to maturity (DTM), Plant height (PH), Pods per plant (PPP), Seed per pod (SPP) ,100 seed weight (100SW), Seed yield per plant (SYPP), Harvest index(HI),Incubation period(IP),Latent period(LP),Lesions 25 DAI(LDAI),Sporulation 35 DAI(SDAI) and Normalized difference vegetation index(NDVI) were studied. The experimental material consisting of six generations (P1, P2, F1, F2, BC1 and BC2) was laid out in a randomized block design with two replications. ANOVA showed significant difference ($p < 0.01$) between the generations for different traits under study. Non- allelic interaction was observed. Additive (*d*) dominance (*h*) gene effects and different types of interallelic interactions (*i*, *j*, *l*) contributed towards the inheritance of traits. Duplicate epistasis was observed for AUDPC, DTF, DTM, IP, LP, LDAI, SDAI and NDVI. The h/d ratio indicated the presence of the over dominance gene action for different traits. The resulting genetic information would aid deployment of proper breeding strategies in plant disease management against mung bean CLS disease. Phytopathology interlinked with breeding studies ensures healthy agriculture, and for Indian economy Agriculture and UN Sustainable Development Goals 2030 goes hand in hand .So present case study ensures a small but decisive step towards strengthening and shaping our agrarian economy.

P (S 10) 24: Identification of elite chickpea (*Cicer arietinum* L.) genotypes as source of multiple disease resistance

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Chickpea, one of the major pulse crops of Haryana as well as India and is sown as a *rabi* crop. It can be early sown (first fortnight of October), timely sown (1-15 November) and late sown (first fortnight of December). Wilt incidence is usually more in early sown crop which gradually decreases as the sowing time is delayed. The delay in sowing is usually coupled with decrease in yield due to availability of shorter grain filling span. Therefore, there always remains the need for genotypes that perform better in terms of yield as well as resistant to diseases under wide range of conditions.Management of diseases through chemical means is difficult as well as not ecofriendly, therefore, development of resistant varieties is the best remedywhich is also a great challenge for Plant Breeders and Plant Pathologists. Two such higher yielding *desi* chickpea genotypes namely H 08-18 and H 12-55have been identifiedas new sources of resistance for various biotic stresses prevalent in chickpea. In addition to their high yielding potential, theyare resistant.H 08-18 was identified for release with the name HC 6 in 2017 for general cultivation in Haryana State under irrigated areas for timely and late sown conditions. The average grain yield of this variety is about 26.3 q/ha under irrigated timely sown conditions; and 25.7q/ha under irrigated late sown conditions. This variety has shown resistant/tolerant reaction against *Fusarium* wilt with comparatively less infestation of gram pod borer (*Helicoverpa armigera)*.However, H 12-55 also named as HC 7 has been identified for release at National Level in 2018.This variety is suitable for cultivation in irrigated and late sown conditions in North West Plain Zone of India (Punjab, Haryana, Delhi, North West & Central Rajasthan, Western UP, Uttrakhand and Jammu).The average grain yield of this variety is 24q/ha. HC 7 has shown better tolerance against most prevailing diseases like *Fusarium*wilt, Dry Root Rot, Ascochyta Blight, Collar Rot and Stunt with relatively less infestation of gram pod borer (*Helicoverpa armigera)*. These genotypes having multiple resistance /tolerance to various diseases and insect pests, emerge as new sources for use in chickpea improvement programmes.Their use in chickpea genetic enhancement programmes will ensure incorporation of high yield with appreciable resistance which is generally difficult to achieve simultaneously in a single genetic background.

P (S 10) 25: Evaluation of rice genotypes against *Xanthomonas oryzae* pv. *oryzae* causing bacterial blight

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Bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* is one of the most important disease of rice due to its wide spread and destructive nature and lack of understanding about its management. It is a serious problem during south west monsoon in India. The disease is causing yield losses up to the extent of 50–80% in India, depending on the variety, severity and stage of the infection; whereas 70–80% yield losses have been reported from Gujarat state. Host plant resistance is an ecofriendly and economical alternative for the management of bacterial blight disease. The present study was carried out for the screening of rice genotypes against *Xanthomonas oryzae* pv. *oryzae.* A total number of sixty one rice genotypes found promising against bacterial blight during previous years in different trials were selected as maintenance. These genotypes were again evaluated during three years against the bacterial blight under artificial inoculation conditions in the field. Out of these rice genotypes, none of the genotype was immune towards the disease. Whereas five genotypes were showed resistant reaction, forty eight genotypes were showed moderately resistant reaction and seven genotypes showed moderately susceptible reaction. While susceptible checks GR-11 and TN-1 were showed susceptible and highly susceptible reactions, respectively. The consistent resistant reactions presented in five genotypes *viz*., IET- 24486, IET- 25400, IET- 25421, Chittimuthyalu and Sabita against bacterial blight. These genotypes can be used in breeding programme for developing bacterial blight resistant varieties.

P (S 10) 26: Disease severity of *Bipolaris maydis* on various white maize genotypes and yield performance

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A study was carried out involving 15 maize genotypes to identify the new sources of resistance against maydis leaf blight or southern corn leaf blight (*Bipolaris maydis*) under artificial epiphytotic condition at Main Maize Research Station, Anand Agricultural University, Godhra. The experiment included white maize genotypes namely CML-186, CML-293, GWL-8, GWL-12, GWL-27, GWL-28, GWH-1405, GWH-1005, GWH-712, GWH-1230, GWHQPM-916, GWHQPM-922, GWHQPM-929, GWC-1210 and GWC-1258 were tested against maydis leaf blight under laboratory and field conditions. According to disease severity scale (1-9), the white maize genotypes GWHQPM-922, GWHQPM-929 and GWHQPM-916 were found highly resistant, while GWL-8 and GWL-12 moderately resistance and rest of the genotypes were least resistance in *in vitro* analysis. In field screening, GWHQPM-916, GWHQPM-922, GWHQPM-929, GWC-1210 showed highly resistance followed by moderately resistant CML-186, CML-293, GWL-8, GWL-12, GWL-27, GWL-28, GWH-1405 and GWH-1005 maize genotypes. Whereas, GWH-712, GWH-1230 and GWC-1258 showed least resistance during field evaluation. *Bipolaris maydis* showed considerable effects on yield performance of crop. The results clearly indicated that the effect of maydis leaf blight on white maize genotypes and their yield performance showed that the significant difference was found in grain yield, plant height, ear height whereas ear weight, ear per plant and infected ear data were non-significant.

P (S 10) 27: Genetic variability studies and resistance to *Alternaria* blight in tomato (*Solanum lycopersicum* L.)

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Tomato (*Solanum lycopersicum* L.) is one of the most important solanaceous vegetables grown widely all over the world. Mid hills of Himachal Pradesh has emerged as the leading supplier of high quality fresh vegetables to the plains during summer and rainy seasons, thus, bringing lucrative returns to the growers. Considering its economic importance and demand as a high value crop, there is a continuing need to develop and identify varieties with improved production potential coupled with resistance to *Alternaria* blight. *Alternaria* blight causes severe losses to crop of tomato in rainy season. The present investigations were carried out in thirty four diverse genotypes of tomato including check variety, Solan Lalima.The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications at the Experimental Farm of Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal during Kharif season 2018, to ascertain the extent of variability and resistance to *Alternaria* blight disease. The genotypes were evaluated under field conditions. The results concluded that minimum disease severity was

recorded in genotype, EC-620378 (15.53 %).Twenty three genotypes viz., BT-10-12, BT-1-1, BT- Best, BT-12, 97/754, EC-191531, EC-620410, EC-174913, EC-620398, EC-14078, EC-915353, EC-620424, EC-620378, EC-620374, EC-16465, EC-620435, EC-526146, EC-620402, EC-620396, EC-37239, EC-620397, EC-620370 and Solan Lalima were also found moderately resistant to *Alternaria* blight. BT- best genotype also performed better in terms of yield and other important horticultural traits as compared to all the genotypes understudy.. Therefore, these genotypes can further be used in crossing programme to develop horticulturally superior and disease resistant hybrids in tomato.

P (S 10) 28: Screening and genetics of downy mildew [*Hyaloperonospora parasitica* (Pers. Fr) Constant] resistance in mid-early group of Indian cauliflower

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Cauliflower(*Brassica oleraceae*var. *botrytis* L.) is one of the leading vegetable crops in the world. However, its production and quality is often affected by various diseases and insect-pests, among them downy mildew often attains epidemic proportions causing huge economic losses to growers. The infected leaves can prematurely senesce, causing a reduction in photosynthetic area and energy reserves that can lead to low curd yield; sometimes even leading to plant death. It also results in poor market quality and storability of curds. Downy mildew in cauliflower is caused by Oomycete *Hyaloperonospora parasitica* Constant (Pers. Fr) Fr. (Syn. *Peronospora parasitica*). It is favoured by day temperature varying from 20 to 24°C, high humidity (>80%) and frequent rains. It appears during November - December in north Indian plains and severely affect mid-maturity group of cauliflower. It also affects seed and main crop in hill regions of North India. Chemical control of downy mildew is often practiced but many of the mutant isolates of downy mildew pathogen are reported to be insensitive to the fungicides. The most effective and environmentally sound means of combating diseases is through the use of host resistance. The study aimed to screen available cauliflower germplasm for downy mildew reaction and to investigate the genetics of resistance in mid maturity group of Indian cauliflower using F$_2$ population derived from two susceptible (S) backgrounds ('PusaHimjyoti' and 'PusaSharad') and three resistant (R) sources ('BR-2', '3-5-1-1' and CCm'). For screening, 356 genotypes were screened and identified BR-2, BR-202, Lawyana-1, PCF-165, BR-207, DC-431, DC-Maghi-1, DC-SM, KT-2, VV, DC-42 and DC-18 as resistant genotypes. Six population sets (P$_1$, P$_2$, F$_1$, F$_2$, B$_1$ and B$_2$) were developed from six S x R cross combinations. The F$_1$ population from all the combinations (S x R) were resistant to downy mildew. Pooled data from four F$_2$ populations of S x R crosses revealed the monogenic and dominant control of resistance in all the three donors. Segregation pattern of individual F$_2$ population also fitted well with the expected Mendelian ratio of 3:1 with high p value (0.3-0.7). The F$_2$ population generated from confirmatory crosses viz. 'PusaHimjyoti' (S) x 'PusaSharad' (S) (3 R: 106S; $\div^2$ = 0.08; *P*=0.7 - 0.8) and '3-5-1-1' x 'CCm' (143R : 2S; $\div^2$=0.03; *P* = 0.8-0.9) also confirmed the single dominant gene for downy mildew resistance in cauliflower. Further, the individuals from F$_2$ of PS x BR-2 and BR-2 x PusaHimjyoti were advanced by selfing to recombinant inbred lines (190) for fine mapping of the target gene *Ppa3*. The information is useful for breeding downy mildew resistant varieties/hybrids in cauliflower.

P (S 10) 29: Studies on occurrence and severity of white rust (*Albugo candida*) of rapeseed-mustard

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The survey was carried out at all blocks of Ayodhya (Milkipur and Bikapur block), Amethi (Raniganj block) and Sultanpur district (Baldirai block) for white rust severity and it was varied from 11.49 to 29.87 per cent. The maximum severity was recorded in village Mitaura (29.87%) followed by Jajwara (26.58%), Soraon (22.69%), Raniganj (21.14%) and Tendha (19.55%), respectively. While minimum severity (11.49%) was recorded at GPB form at Kumarganj, Ayodhya. Three hundred genotypes were screened under natural epiphytotic condition during 2018-19. In different genotypes, first symptom of disease was noted between 60-70 Days After Sowing. The disease severity ranged from 0% (GSL-1) to 60.26% (DIVYA-88), respectively. Out of three hundred genotypes, the 0 per cent disease severity was recorded in genotypes namely DRMR-32, DRMR-40, DRMR-17, DRMR-100, KGS-35, KGS-32, AKMS-8141, AKMS-8131, GSL-1, DLSC-1, DRMRHJ-2503, Shital, GSL-2, GSL-5, which were rated as disease free. On the basis of maximum severity and maximum grade of the disease reaction of each genotype was recorded and classified into different categories. Four genotypes were found highly resistant namely PAB-14-5, PRD-14-6, PRD-14-18, and RMM-09-04 (<5% leaf area covered by lesion). Twelve genotypes were found resistant namely RMWR-09-2, RMWR-09-1, DRMRSJ-31, PRD-14-11, PRD-14-16, PAB-14-14, PAB-14-17, PBZ-4, PHR-240, PRD-2013-8, RTM-314, RGN-323 (5-10% leaf area covered by lesion). Fifty genotypes were found moderate resistant namely Pusa Mustard-25, PHR-3278, PT-2015-3, RMT-10-13, TKM-17-1, BAUT-08-01, DRMRCI-72, RH-1518, TM-143, AKMS-8138, Kranti, Pusa MH-9, BIOYSR, PT-303, DRMR-1165-40, TS-38, TH-1402, RAUDT-10-33, PHR-2, EC-399299, CS-700-2-1-4, TS-46, PT-2010-5, PRD-14-1, DRMR-2019, PDZ-2, DRMR-5206, RH-1372, EC-399301, RMT-15-29, NPJ-201, SKM-1104, T-9, Jhumka, Vardan, PT-30, T-27, DRMRCI-59, DRMR-4005, TM-179, LES-55, DIVYA-99, TH-1502, NPJ-208, KMR-16-3, DRMRCI-70, RH-1326, RH-0725, DRMR-1153-12, CS-1100-1-2-2-3 (11-25% leaf area covered by lesion), One hundred ten genotypes were found susceptible (26-50% leaf area covered by lesion) and one hundred ten genotypes were found highly susceptible (>50% leaf area covered by lesion).

P (S 10) 30: Screening of sugarcane genotypes against yellow leaf disease in tropical and sub-tropical conditions in India

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Yellow leaf disease (YLD) is one of the major constraints in reducing production and productivity of sugarcane in India. Globally, YLD is known to be caused either by single or mixed infections of *Sugarcane yellows phytoplasma* (SCYP) and/or *Sugarcane yellow leaf virus* (SCYLV). In the present study, 189 sugarcane genotypes were evaluated against YLD during 2016 – 17 and 2017 – 18 crop growing seasons which comprised of 47 tropical and 142 sub-tropical sugarcane genotypes. Of the total 142 genotypes screened during 2016 – 17 crop growing season, the 86 genotypes showed HR reaction, whereas rest of the 56 genotypes showed MR to HS reaction based on the 0-5 disease rating scale. Moreover, incidence of YLD on these 56 sugarcane genotypes ranged from 1.17% to 65.38%. Similarly, during 2017-18 crop growing season, of the total 189 genotypes screened the 94 genotypes showed HR reaction while, 95 genotypes showed MR to HS reaction based on the same disease rating scale. Moreover, incidence of YLD on these 95 genotypes ranged from

2.38% to 67.44% on cane basis. YLD affected genotypes exhibiting mild to prominent yellowing of the midribs followed by spreading of yellowing towards leaf lamina, leaf tip necrosis and complete drying of the leaves.

P (S 10) 31: Evaluation of introgressed pre breeding material from *Solanum torvum* and *S. insanum* against root knot nematode in brinjal

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Brinjal is an important solanaceous vegetable crop consumed as a staple food in Asia and the Mediterranean region due to its high nutritive value. China and India are contributing the maximum share of its global production. Among the different pest and diseases, root-knot nematodes of *Meloidogyne* spp. are considered as the major constraint for sustainable production of the crop. These nematodes are reported to causes 16.67% yield reduction in brinjal, which amounts to almost 23$ million annual monetary loss. Use of host resistance is the most economical, ecofriendly and robust strategy to manage these obligate pests. Introgression of resistance genes from wild crop relatives could be valuable for strengthening elite cultivated brinjal cultivars. The present study deals with the evaluation of interspecific hybrids with *Solanum torvum* (Cross-I) and *Solanum insanum* (Cross II) and their progenies. Overall, 109 and 235 plants of cross I and cross II were screened, respectively and further 120 and 830 plants of F_2 progenies of Cross-I and cross –II, respectively, were screened in root knot nematode, *Meloidogyne incognita* sick plot (initial population 296.33 nem/250ccsoil). Observations were recorded on root gall index (0-5 scale) after uprooting the plants. Among the F_1 plants, for cross-I, categories of plants obtained were; resistant (36 plants), moderately resistant (15 plants) and susceptible (60 plants) and for cross –II, as resistant (45 plants), moderately resistant (15 plants) and susceptible (172 plants). From 120 F_2 plants of cross-I, two plants showed reaction as immune, one as resistant, 4 as moderately resistant, 4 as moderately susceptible, 78 as susceptible and 25 as highly susceptible to root knot nematode. However, out of 830 F_2 plants of Cross–II, 5 plants were found as immune, 32 as resistant, 42 as moderately resistant, 103 as moderately susceptible, 532 as susceptible and 224 as highly susceptible to root knot nematode. Selected immune, resistant and moderately resistant plants from both the crosses were again transplanted in the field, evaluated for their morphological traits. For cross-I, F_2 plants were variable for plant height (53.4-76.2 cm), fruit weight (30-85gm) and number of fruits per plant (13-55), while all the plants showed cluster bearing of black purple fruits. For cross-II, F_2 plants were variable for plant height (44-117.4 cm), fruit bearing (single to heavy cluster), fruit colour (variegated green, shining purple, purple, dark purple, variegated white and light green), fruit weight (26.5-145 gm) and number of fruits per plant (4-74 fruits). The selected plants from different reaction classes were maintained by selfing and, in future, plant progenies from each class will be screened to conclude the genetics of the trait under investigation.

P (S 10) 32: Inter-specific derivative lines with *Cicer pinnatifidum* specific segments imparting resistance against botrytis gray mold

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Chickpea is a cool season legume crop mostly grown in soils poor in fertility with less moisture retention capacity. It is an important source of protein in human food and is cultivated world-wide. Chickpea is prone to no. of biotic stresses of which botrytis gray mold, caused by (*Botrytis cinerea* Pers. ex. Fr.) is an important foliar disease of chickpea and its epidemics can cause grain yield and quality losses up to 100 percent. Presently resistance against botrytis gray mold in cultivated chickpea is lacking and interspecific material is being exploited for stable resistance as good amount of resistance is available in wild spp. One hundred and ten SSR primers were used to amplify genomic DNA of three parents (*C. pinnatifidum* 188, ICCV 96030 and PBG 1) of inter-specific derivative lines and only twelve primers showed polymorphism between parents. Twenty seven inter-specific derivative lines when amplified by these twelve primers, only ten primers (GA-9, GA-13, GA-22, GA-24, GA-26, GA-105, NCPGR-127, NCPGR-141, NCPGR-17 and TS-58) showed *C. pinnatifidum* 188 specific segments in a panel of these twenty seven interspecific derivative lines. Out of twenty seven lines, only twelve lines (10001, 10003, 10004, 10006, 10007, 10008, 10009, 10011, 10013, 10016, 10018 and 10019) showed *C. pinnatifidum* 188 specific segment. When compared with the screening data, only three lines (10008, 10009 and 10011) having *C. pinnatifidum* 188 specific segment showed moderately resistant reaction with disease score of 3.1- 4.0 to botrytis gray mold on 1-9 scale. The line 10008 was flanked by primer GA-22, line 10009 was flanked by GA-24 and line 10011 by GA-105 (Plate 6a), NCPGR-127 and NCPGR-141. The resistance in these three inter-specific derivative lines might have been derived from inter-specific cross PBG 1/ICCV 96030 × *C. pinnatifidum* which must have been contributed by *C. pinnatifidum* 188 parent. The primers flanking their segments are possibly associated with botrytis gray mold resistant gene.

P (S 10) 33: Characterization of wheat germpalsm lines grown under different environments

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Wheat is the second most important food crop after rice in India, accounting for 12 per cent of global production. But still the country needs to produce 109 million tonnes of wheat by 2020 to feed its growing population. Major factor contributing to the low and declining crop responses to fertilizer nutrients are because of continuous nutrient mining. Nutrient imbalance leads to depletion of major, secondary and micronutrients in wheat crop. The judicious combination of chemicals and organics are helpful in achieving enhanced and sustainable product. The relationship between the yield of grain and the uptake of nutrients by wheat is linear in nature. An experiment was conducted at wheat farm experimental area to study the characterization of diverse wheat germplasm with fertilizer and without fertilizer conditions. The experimental setup consist of 2 plots (one for fertilizer and other for without fertilizer wheat germplasm lines). Each plot have 285 wheat germplasm lines in augmented design. Data was recorded for number of days to heading, number of days to maturity, biomass, 100 grain weight, grain yield. Number of days to heading and number of days to maturity were almost same in both conditions, biomass was more in without fertilizer wheat germplasm lines and yield was more in fertilizer wheat germplasm lines; with a less significant difference between the two. Wheat germplasm lines were identified with high yield in low input conditions. Identified wheat germplasm lines will help to reduce inputs and hence protect the environment.

P (S 10) 34: Genetical and molecular status for resistance to wilt in cotton : A short review

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*Cotton (*Gossypium *spp.) which belongs to the Malvaceae family, is one of the most important natural fiber crop in the world. Fusarium wilt (FW) is caused by the soil-borne fungus* Fusarium oxysporum *f. sp.* vasinfectum *(FOV) that leads to Verticillium wilt which is one of the most serious diseases in cotton, deleteriously influencing crop's production and quality. Verticillium Wilt has become a major restriction in cotton production since Helicoverpa armigera, the cotton bollworm, became effectively controlled in recent years. The wilt had become a key subject of research in cotton-resistance genetics, breeding and plant pathology. This work consists of a literature review that provides a comprehensive synthesis of research progress in breeding, genetics, and molecular mapping of the cotton genome with molecular markers for identification of fusarium wilt. Enrolment of Fusarium wilt resistant cultivars has proven to be the most cost-effective method to control the disease. It is anticipated that new breeding methods and new varieties resistant to Verticillium wilt will be developed in the very near future which can combat Fusarium wilt.*

P (S 10) 35: Endophytic Fungi: Application for plant disease management

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Endophytes are the microoganisms residing in the internal tissues of the plants without causing any detectable symptom of disease to their host. Endophytes are very diverse and almost plant species studied till date, are found to harbor one or more endophytes. Most of the studies mainly targeted endophytes for the production of novel bioactive compounds with varied activities like antibacterial, antifungal, anticancer, immunosuppressive, insecticidal, antioxidant, etc. Fungi are the most studied endophytic organisms that produced plethora of biologically active compounds. In addition to bioactive compounds, some of them are known to produce toxic alkaloids which protect their hosts from grazing animals. Their role in crop protection and disease management gained a keen interest after some endophytes associated plants were found to show resistance for certain plant pathogens. This chapter discusses the roles and possibilities of endophytic fungi in the arena of phytopathogens control and management.

P (S 10) 36: Screening of mungbean (*Vigna radiate* (L.) Wilczek) for resistance against mungbean Yellow Mosaic Virus (MYMV) under field condition

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Mungbean (*Vigna radiata* L.) is also known as mung, moong, mungo. In India it is third most important pulse crop after chickpea and pigeonpea. It is an important short duration grain legume which is grown in different parts of the country, for grain and green manuring. It is an outstanding source of easily digestible protein with low flatulence, Which balance the staple rice diet in Asia. Mungbean Yellow Mosaic Disease (MYMD) caused by mungbean yellow mosaic virus (MYMV) and virus is transmitted by whitefly (*Bemisia tabaci*). Virus is an important constraint of mungbean cultivation in India. Use of resistant genotypes is the best method of avoiding the occurance of the disease. Keeping this point in view, out of fifty two genotypes of mungbean were evaluated for resistance against MYMV during *kharif* 2015 in field conditions. The percent disease resistance (PDI) of MYMV varied from 0 to 79.68% out of 52 mungbean genotypes five were found resistance, eight were moderately resistant, seventeen genotypes were recorded moderately susceptible and twenty two genotypes were noticed susceptible, five genotypes namely, PM 10-18, PUSA-1371, BM 2012-09, DGGV-2 and MH-810 found resistant during present investigation which can be used for the development of mapping population for the development of MYMV resistant varieties.

Session 11

Bio-prospecting in disease management

Keynote Papers

KN (S 11) 01: The good, the bad and the ugly in the shades of green: the genus *Trichoderma* in the spotlight

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The ascomycetous filamentous fungal genus *Trichoderma* has at least two faces, like Agni, the God of fire in Hindu mythology. Or is it even three? The Good, the Bad and the Ugly? In fact, *Trichoderma* species can be considered: Good – both as powerful producers of cellulolytic enzymes useful in the biotechnological industry, and as plant-beneficial microorganisms in agriculture due to a plethora of antagonistic mechanisms acting against plant pathogenic fungi, e.g. inhibiting them through the production of antifungal metabolites or by direct mycoparasitism, or indirectly promoting the growth of crop plants and inducing their immune system. Bad – as devastating agents of green mould diseases in the cultivation of mushrooms (champignon, oyster mushroom, shiitake, etc.) destroying crops and thereby causing serious economic damage world-wide and Ugly – as opportunistic pathogens of mainly – but not exclusively – immunocompromised humans, capable of causing serious, sometimes even life-threatening or deadly infections. Is the Good able to overcome the Bad and the Ugly, or rather ready to join the dark side? Are industrial and biocontrol *Trichoderma* strains representing a risk to mushroom production or human health? Is the biotechnological and agricultural application of *Trichoderma* strains safe or rather risky? Modern molecular taxonomy can provide assistance in answering these questions. The preparation of this lecture was supported by projects by projects K-116475 (Hungarian Scientific Research) and GINOP-2.2.1-15-2016-00006 (Széchenyi 2020 Programme). LK is grantee of the János Bolyai and Bolyai+ Research Scholarships of the Hungarian Academy of Sciences and the New National Excellence Programme, respectively.K (S11) 03: Microbes in consortim and their rhizospheric interactions

KN (S 11) 02: RNA based biopesticides for sustainable crop protection

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Can we really feed ten billion people as we head towards the next century? The current world population of 7.3 billion is expected to rise to 9.7 billion in 2050 and 11.2 billion in 2100. In this globalized world and interconnected economies, we need to address to ensure that our food crops are protected from pests and diseases as they account for 20-40% losses in productivity. The ongoing usefulness of chemical pesticides suffers from issues such as residual toxicity, run off, specificity and resistance. Genetic modification (GM) is not available for all crops/pathogens, and it is not the preferred choice for all producers and consumers. The development of a new chemical crop protection product can take 10 years of R&D at a cost of $250million. The discovery of

RNAi as a natural regulatory mechanism that plays critical roles in growth, development and host defence against viruses and transposons, has proved to be a powerful strategy to engineer disease resistance against viruses, viroids, nematodes, insect pests and fungi in plants. At present the use of RNAi for disease resistance is limited to engineering transgenic disease resistance plants. The aim to deliver transformative clean green technologies is the key driver to delivers pest targeting RNA interference (RNAi) as a topical application. Double stranded RNA, the key trigger molecule ofRNAi, has been shown to provide protection without the need for integration of dsRNA-expressingconstructs as transgenes. Consequently, development of RNA-based biopesticides is gainingmomentum as an alternative to chemical-based control measures, with pests andpathogens targeted with accuracy and specificity.Series of papers have shown that exogenous application of dsRNA can induce RNAi-mediated defence against viruses, fungi and insect pests. Real world application of RNA based biopesticides will be governed by factors such as cost effective production of dsRNA, stable delivery, risk identification and mitigation strategies,regulatory landscape and community acceptance.

KN (S 11) 03: Microbes in consortim and their rhizospheric interactions

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Biocontrol microbes in agriculture used as biopesticide, biofertilizer, biopesticides and biostimulants for the management of biotic and abiotic stresses of plants. Beneficial microorganisms plays an important role in plant protection, plant growth promotion and improve the soil health. The individual use of biocontrol microbes for plant disease management is not more efficient in comparison to use of consortium of microorganisms that include different efficient strains. Microbial strains which are compatible with other microorganism and does not have any suppressive or inhibitory effect on strains of other microorganism if co-cultured in a common media can then promote growth of plants or may suppress diseases. There are various positive factors of using variety of microorganism in a consortium as they may increase the efficiency of BCAs due to the nature of occupying different surroundings in the rhizosphere and thus are able to decrease competition among them. Further, enhancement of suppressing types of diseases is also regulated by a variety of biological controlled mechanism that are offered by an individual microorganism component. Earlier various microbes such as *Trichoderma, Glomus, Rhizobium, Bacillus, Pseudomonas* etc. were major microbes those were used in order to develop a consortium of microorganism. The efficacy of microbial consortium will depend on the synergistic effects of two or more biocontrol agents. Based on theoretical definitions of Bliss independence or Loewe additivity, the combination of biocontrol agents will be formulated. The additive and synergistic effect of microorganisms in consortium for growth promotion and triggering of defense systems, metabolic pathways against pathogen have been reported. The study on host response to such microbial effects is in continuation. The case studies on the statistical analysis for the independence-synergistic-antagonistic interactions were found very rarely among the biocontrol agents.

KN (S 11) 04: Bioprospecting microbial metabolites for the management of plant diseases

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It is a well established fact that continuous and indiscriminate use of chemical pesticides poses serious health hazards in human and also heavily pollutes the environment, particularly air, soil and water pollutions are common and is a serious environmental issue globally. In addition, non-target effects, residual toxicity in the plant produces and development of resistant against pesticides in target organisms such as insect pests, pathogens and weeds are the associated problems. In this scenario, adapting alternate safe methods of plant protection is the need of the hour. Therefore, biological control using beneficial microorganisms emerged as the best option for the eco-friendly disease management practice among other alternate disease control options. Several bacterial and fungal biocontrol agents were identified formulated, evaluated and some of them were commercialized and available for the farm use worldwide. However, short shelf life, lack of knockdown effect, inconsistent performance and non-availability of quality productsare the hindering factors for the large scale adoption of biological control. Alternatively, identification of effective microbial metabolites would be worthwhile for the management of plant diseases, as these metabolites are natural products, considered safe to the environment and also mostly specific in their activity against target organisms. Several actinobacterial, bacterial, and fungal strains have been reported to produce a variety of secondary metabolites, which are toxic to plant pathogens even at very lowconcentrations. Hence, our research has been focused on identification of antimicrobial metabolites for the management of plant diseases. Interestingly, six different antifungal metabolites and an azole and a phenazine compounds were isolatedfrom species of *Streptomyces, Bacillus, Pseudomonas*and*Trichothecium*, purified and tested against *Macrophomina phaseolina* and *Rhizoctonia solani*. Results of our various experiments have revealed that these microbial metabolites would be promising natural sources for the management of plant diseases and it is worth to investigate the microbial diversity in this line, which would eventually lead to discovery of useful antimicrobial metabolites.

Invited Papers

I (S 11) 05: Potential of botanical pesticides for disease management in organic agriculture

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Globally, over 2500 plant species belonging to 235 families have been reported to have biological activities against pests. The active compounds in plants include phenols, quinones, alkaloids, steroids, terpenes, alcohols and saponins. The terpenes, phenols, alcohols, alkaloids, tannins and other secondary metabolites found in botanical pesticides induce toxicity to fungal cell walls, cell membranes and cell organelles. These metabolites also inhibit spore germination, mycelial development, germ tube elongation, delayed sporulation and also inhibit production of important enzymes, DNA and protein synthesis. Homemade botanical pesticides have good potential in plant disease management in India. India has more than 18 million trees of neem with seed potential of 4,14,000 MT which can yield 85,000 MT of oil and 3,30,000 MT of oilcakes. There are number of other plants like *Bougainvillea glabra, Artemisia roxburghiana, Ocimum sanctum, Roylea elegans, Cryptolepsis buchanani, Melia azadirachta* which have shown a lot of potential against different diseases and pests of different crops. Homemade botanical formulations have been found effective against number of foliar diseases including fruit rots of strawberry, apple and citrus. Apple trays impregnated with cow urine based botanical formulation reduced post-harvest losses caused due to fungal pathogens and also increased the shelf life of the fruits. Botanical Formulations were found effective with 84.2 per cent reduction in the disease index of buck-eye rot of tomato caused by *Phytophthora nicotianae* var. *parasitica* and 4.74 times increase in yield. Cow urine based botanical formulation was also found effective against Phytophthora leaf blight and fruit rot of capsicum with 70.5 per cent reduction in disease index of leaf blight, 81.9 per cent reduction in the incidence of fruit rot along with 3.58 times increase in marketable fruit yield. Botanical formulations based on the local plants were also found effective against black rot of cauliflower with 74.8 per cent reduction in the disease index. The recent years have witnessed the introduction of nanotechnology mediated bio-pesticides. Nano-formulations of botanicals have been found more effective. Efficacy of pure silver nano-particles was found approximately 10,000 times higher than the water-based botanical formulations. Foliar spray of pure formulation of neem SNPs (150 ppm) was found most effective and incidence of buckeye rot was reduced by 82 per cent with 31.7 per cent increase in the fruit yield compared to control. Tomato plants sprayed with neem-based SNPs harvested indicated highest content of ascorbic acid, lycopene content and total phenolics in the fruits. The bio-pesticide market in India has registered growth at remarkable CAGR of 16.4 per cent in terms of consumption volume between the years 2013-2019 and highest growth of 19.0 per cent in consumption was observed during the year 2018. Use of botanical pesticides in plant disease management is an important component in organic farming and increased emphasis on organic and natural farming will broaden its consumption base in the country.

I (S 11) 06: *Trichoderma harzianum and Pseudomonas flourescens*: Micoorganisms with multiple beneficial effects in crop plants

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Enhancing food grain production has been a prime concern in agriculture. To fulfill this target, farmers, scientists and policy makers'together are doing great efforts at their respective fronts. Adopting improved crop varieties, use of certified seed, appropriate inputs like fertilizers for fertigation, pesticides for disease and pest management and proper irrigation etc. has been sincerely followed to achieve the level of food grain production to feed the ever increasing human population. However all these aspects have certain limitations? In the timeto come in future, there is every possibility of shrinking natural resources like cultivated land and irrigation water. It is also expected that atmospheric temperature will also be increased than what it is today. Availability of farm labors will also be reduced. Thus for ever increasing human population, we are compelled to enhance the food grain production on reduced area of cultivated land, reduced amount of irrigation water and that's too in a little unfavorable environment with less dependence on farm labors. Hence we will have to develop the ways and means to accelerate the growth rate of agriculture without sacrificing the natural resources and ecosystem. Certain micro organisms have shown the potential to enhance the level of water stress in the crops which requires very huge amount of water like rice along with inducing systemic resistance to diseases. These microorganisms have also been found to increase the seed germination, seedling vigor and reproductive ability of several crops .A bacterium namely, *Pseudomonas fluorescens* and a fungus namely *Trichoderma harzianum,* both have been found to enhance the level of tolerance to drought or water stress in certain rice varieties. These two have also been found to enhance heat tolerance in wheat crop in addition to enhancing the level of resistance against some important diseases. In addition to wheat and rice crop, some vegetable crops like tomato and chili have also been found to be benefited due to application of these microorganisms.

Application of these microorganisms have been found effective for better root growth ,shoot growth, root biomass and shoot biomass in several crops. Several isolates of *Pseudomonas fluorescens* and *Trichoderma harzianum* have been found to enhance the plant growth, hence potentially can be used to enhance the food grain production in future. Keeping the strong need of pesticides these microorganisms have also been tested for their compatibility with some of the most commonly used fungicides, insecticides and herbicides, so that they can be used in integration with these agrochemicals. Some selected strains of *Trichoderma harzianum* were found to be quite helpful in improvement of physiological parameters like total chlorophyll content, leaf area index, relative water content, membrane stability index along with reduction in free proline content in important food crops. These attributes are the positive indicators for drought tolerance. However there is an strong and urgent need to identify and classify these microorganisms on the basis of various activities they perform specifically. All these attributes have been discussed at length

I (S 11) 07: Emerging technologies for tackling pernicious soil borne diseases in apple with special reference to white root rot in India

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Himachal Pradesh is recognized as an “apple state” of India because its cultivation has emerged as remunerative venture that has revolutionized the socio-economic conditions of the growers. The area under apple cultivation has increased manifolds during the last few decades but the production has not increased proportionally and the productivity is quite low in comparison to advanced countries. In order to unravel the biological threats of *D. necatrix,* latest strategies of disease management have been evaluated and validated under field conditions. Amongst seven IR chemicals tested, maximum disease control in pot conditions was recorded with Salicylic acid (SA) at 300ppm (83.90%), which also provided maximum disease control of 78.14 and 74.11 per cent in virgin and sick fields, respectively and also effective in improving plant health as compared to other treatments. The induced resistance through SA persisted in seedlings for more than two years leading to permanent resistance as the plant survival in virgin and sick field was 68.89 and 59.44 per cent, respectively. The Calcium cyanamide, PGPR and AM fungi evaluated individually and in combination, revealed maximum disease control (100%) in combination treatment i.e. Calcium cyanamide + *Bacillus subtilis* + *Bacillus licheniformis* + AM fungi and Calcium cyanamide + *Bacillus subtilis* + *Bacillus licheniformis*) with maximum plant growth parameters, soil microbial population, root colonization by AM fungi, and physicochemical properties both under pot and field conditions. Out of 34 endophytic fungi isolated from symptomless roots of apple, wheat, maize, marigold, cherry, and garlic plants, only nine isolates which showed inhibitory effect. Subsequently, six most promising isolates were further subjected for root colonization assay. Under *in vitro* conditions, maximum mycelial inhibition of 81.48 per cent was obtained with isolate C2 followed by C1 (75.19%). Microscopic studies on interaction between fungal endophyte with hyphal tips of *D. necatrix* at interaction zone revealed various morphological abnormalities in the hyphae. In glasshouse conditions, seed treatment followed by soil application with M8 isolate was highly effective exhibiting 93.55 per cent disease control. The treatment M1 was next best which provided 89.25 per cent disease control. Similarly, under field conditions, the overall maximum disease control was exhibited by M8 (84.95%). The M1 was the next best and provided 81.72 per cent disease control. Six most promising fungal root endophytes were identified based on morphological, microscopy and rDNA internal transcribed spacer regions sequence analysis. Root colonization assay was performed which revealed maximum colonization. In case of seedlings treated with fungal root endophytes, maximum endosphere and rhizosphere count was recorded with *Crinipellis tabtim* strain M8. Additionally, confocal microscopic images of transverse sections of root cells colonized by fungal root endophytes varied to a greater extent. Thus, abundant tissue colonization by root endophytes as compared to untreated control suggested the establishment and persistence of inoculated strains in endosphere of apple seedlings. Our findings are the first report of colonization of apple roots by fungal root endophytes which suggest an alternative and sustainable approach for management of white root rot disease.

I (S 11) 08: Ecofriendly strategies for management of major diseases of nutricereals

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Small millets are the small- grained cereals belonging to the family Poaceae. The small millets comprising six species, namely, finger millet (*Eleusine coracana*), little millet (*Panicum sumatrense*), Italian or foxtail millet (*Setaria italica*), barnyard millet (*Echinochloa crusgalli*), proso millet (*Panicum miliaceum*) and kodo millet (*Paspalum scrobiculatum*) are grown in about 2 million ha area in India. These millets are good source of carbohydrates, micronutrients, vitamins, minerals *etc*. Apart from being nutritionally rich, low input requirement, sol rejuvenating capacity after stress alleviation, and ease in cultivation, have made these crops as indispensable component of dry land farming, tribal and rainfed hill agriculture. Although, small millets are known to cope up with abiotic and biotic stresses, nevertheless, under vulnerable conditions some of the diseases cause heavy losses and can damage entire crop. Blast and banded blight are the major diseases causing considerable yield loses. Application of chemical fungicides to control the diseases have drastic effects on the soil biota, pollute the atmosphere and environmentally harmful. The fungicides also causes phytotoxicity effect on the crop. In order to avoid such problems ecofriendly strategies is implied with the use of biocontrol agents which includes *Bacillus subtilis, Pseudomonas flourescens*and *Trichoderma asperellum.* Seed treatment (0.6%) and foliar application (0.6%) of *Pseudomonas flourescens*is effective in controlling blast and soil application of value added *P. flourescens* + *T.asperellum* + *B. subtilis*(one kg talc formulation mixed in 25 kg FYM or vermicompost, incubated for 15 days) per acre at time of sowing is effective against banded blight.The application of bioagents not only reduced disease severity but also increased yield significantly.

I (S 11) 09: Immunodetection of fungal pathogens and induction of phytoimmunity using bioinoculants

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Disease diagnosis is an art as well as science. We use the scientific method to perform and interpret tests for the detection of pathogens. The art lies in synthesizing information on symptom development, case history and the results of laboratory tests to determine the most likely cause(s) of disease. Understanding the difference between the terms ‘diagnosis’ and ‘detection’, which are mistakenly used interchangeably, is crucial. Choice of diagnostic test(s) can greatly influence the diagnosis. Many techniques that differ in sensitivity, specificity, reliability and cost effective are available for the detection of plant pathogens. Over the past few decades, immunological formats (ELISA,DIBA,Western blot, indirect immunofluorescence) and PCR based molecular diagnostic methods have increasingly received attention or complement to conventional methods. Innovative strategies have been developed using agriculturally important microorganisms for alleviation of biotic stress in cereals, pulses, horticultural and plantation crops. Induced immunity in plants using bioinoculants (BCA,AMF,PGPR) have been demonstrated. Time course accumulation of chitinase (CHT), b-1,3 glucanase (GLU) and phenylalanine ammonia lyase (PAL) increased markedly in treated plants in comparison to healthy control following challenge inoculation with fungal pathogen. Immunolocalization of chitinase and glucanase in bioinoculant treated and pathogen inoculated root and leaf tissue was further confirmed by indirect immunofluorescence using PAbs of chitinase and glucanase labelled with FITC conjugate as well as by transmission electron microscopy using PAbs of chitinase, glucanase labelled with gold conjugates. Microarray analysis were done to compare up regulated and down regulated gene expression among untreated pathogen inoculated, bioinoculants treated and pathogen inoculated plants as well as untreated uninoculated ones. Enhanced accumulation of phytoalexin(s) following induction of phytoimmunity were also documented. This may lead towards efficient bioformulations and delivery system which could become important inputs leading to a resilient agriculture.

I (S 11) 10: Bioprospecting of endophytes and botanical for the management of downy mildew in pearl millet

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Crop plants are affected by many biotic and abiotic constraints. Many biostimulants of plant- and microbial-origin have been identified as an alternative or supplement to the conventional disease management strategies. These environment-friendly bioagents not only promote growth and enhance yield but also suppress the effect of pathogens directly or indirectly. Pearl millet is an important food crop of semi-arid tropics. The downy mildew disease caused by *Sclerospora graminicola* is an important biotic constraint in pearl millet production. A study was undertaken to isolate the fungal endophytes and screen the bioagents and their solvent extract for their potential in controlling the downy mildew disease of pearl millet. Overall, 202 endophytic fungal isolates representing different pearl millet growing areas and host tissue have been enumerated. The isolates have been identified by morphotyping and ITS sequencing. Endophytic fungal isolates of pearl millet *Fusarium oxysporum, Trichoderma asperellum* and *Acremonium* reduced the downy mildew incidence in greenhouse conditions. The anti-mildew assay revealed that methanol extract of *Acremonium* sp. inhibited the sporulation and zoospore release in *S. graminicola.* The bioactive TLC fraction has shown Acremine F in UP-LCMS profile, which is a known sporangicidal agent. The aqueous extract of a plant *Eclipta alba* was subjected to ultrafiltration, the 50 kDa fraction rich in saponins including Eclalbasaponins, showed disease protection ability. The bioagents and botanical treatment have enhanced the HR response in host seedlings, higher callose and lignin deposition, higher accumulation of defense-related enzymes like PAL, POX, LOX and PPO, and over-expression of defense-related genes. The saponin-rich fraction of aqueous extract of *E. alba* was used to synthesize Zinc oxide nanoparticles. Treatment with ZnO-NP at 50 ppm concentration caused plasmolysis and inhibition of zoospore germination of *S. graminicola*. The biofabricated ZnO nanoparticles could promote growth and induced defence-related responses in pearl millet seedlings.

I (S 11) 11: Biocontrol ability and present research scenario of *Catenaria anguillulae* Sorokin: a facultative endoparasite of nematodes

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The integrated management of plant parasitic nematodes using biological control agents is an ecologically safe practice for sustainable better human life. There are several fungi in nature to regulate nematode population in soil. *Catenaria anguillulae* is one such fungal endoparasite of nematodes has attracted attention of large number of researchers after it was first reported by Sorokin in 1876 that caused a disease in epidemic form in nematodes eventually killing most of them. This blastocladian chytrid has several attributes what an efficient biological control agent must have. These attributes include its facultative endoparasitic ubiquitous nature, fast multiplication at high rate, epidemic causing ability, compatibility with agrochemical and fertilizers, growth over a wide range of temperature and pH and selective stimulation in its population in response to amendment with oilcakes and root exudates of various crops. The techniques for its selective isolation, semi-quantification, rapid virulence test, purification and maintenance of the fungus are developed. We report the different media knowing their nutritional requirements using cheaper and easily locally available substrates for various purposes, viz., residue free growth, mass culture, maintenance and morphometrical variation. It has also been found that *C. anguillulae* survives in the mass culture over a period of six month. Our preliminary work clearly reflects great potential in *C. anguillulae* as an appropriate biological control agent. However, the extensive work on its nutritional requirement, refinement of its mass culture technique including formulation development, ecological aspects and performance evaluation against agriculturally important plant parasitic nematodes is still required for its field application.

Oral Papers

O (S 11) 12: Biological control of *Sclerotium rolfsii,* causing stem rot of groundnut (*Arachis hypogaea* L.)

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Groundnut (*Arachis hypogaea* L.) is one of the widely cultivated oilseed- legume crops, in India. The crop is succumb to a number of pathogens *viz.,* fungi, viruses, phytoplasmas, bacteria and nematodes, which contributes in overall quantitative aswell as qualitative losses. Hovewer, stem rot disease caused by *Sclerotium rolfsii* Sacc., a soil borne fungus having a wide host range and inflicting about 15-50 per cent yield losses in groundnut crop. The pathogen, being exclusively soil borne, seems to be uneconomical and hazardous to manage with alone chemical fungicides. Among various ecofriendly disease control measures, bioprotection with biocontrol agents has been emerging as one of the promising means. Therefore, the present study was attempted to assess the bioefficacy of nine biocontrol agents, applying CRD and all the treatments replicated thrice, during *Kharif*, 2018, at the Department of Plant Pathology, Dr.BSKKV, Dapoli. The results revealed that the test biocontrol agents as potential antagonists, which significantly inhibited mycelial growth of *S. rolfsii*, over untreated control. However, *T. virens* was found most effective with significantly highest mycelial growth inhibition (91.58%), followed by *T.harzianum* (81.03%), *T. hamatum* (66.27%), *T.viride* (63.21%) and *A. niger*

(57.21%). Rest of the test bioagents were found to be least effective. Thus, the bioagents *T. virens, T. harzianum* and *T. hamatum* could be exploited for biological control of groundnut stem rot disease.Poster

O (S 11) 13: Characterization of bioactive metabolites from *Trichoderma* sp against Major soil borne pathogens

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Chemical control of plant diseases can be impressive but this is comparatively a short term measure and additionally, the accumulation of harmful chemical residues sometimes causes serious ecological imbalance. In recent years, the increasing use of potentially hazardous chemicals in agriculture has resulted in growing concern of both environment and public health properties The strains of *Trichoderma* used as biocontrol agents show different mechanisms of action in their antagonistic interactions with fungal pathogens. These include antibiosis, through production of a variety of compounds with antibiotic activity Metabolites can be the starting materials, intermediate materials, or end products of these chemical reactions. There are two types of metabolites *viz.*, primary and secondary metabolite. A primary metabolite is a kind of metabolite that is directly involved in normal growth, development and reproduction. The primary metabolites are carbohydrates, proteins, nucleic acids and lipids The secondary metabolites (SMs) are small molecules that are not directly essential for growth yet have important roles in signalling, development and interaction with other organisms Based upon chemical and analytical reports, the *Trichoderma* spp. are prolific producers of secondary metabolites (peptaibols, non-ribosomal peptides (NRPs), volatile and non-volatile terpenes, pyrones, siderophores and nitrogen containing compounds) as 373 different molecules have been identified, but in many cases the specific activity of these molecules is unknown An attempt was made to characterize the secondary metabolites from efficient *Trichoderma* isolates Tri-4 (*T. viride*) which was identify by inverted Petri plate technique. Detection secondary metabolites were done by ethyl acetate extract of liquid chromatography mass spectrometry (LCMS) analysis methods The aim of present investigation was to develop a metabolomic method and which can be utilized to identify potential *Trichoderma* spp. LC-MS techniques were explored to identify antifungal compounds produced by *T. viride*. It was revealed that, the culture filtrate of isolates Tri 4 (*T. viride) showed* the presence of antifungal compound at different retention time. LCMS chromatographic profiling TOF MS spectrum of Tri-4 isolate showed three prominent peaks correspondingly three compounds were tentatively identified as Ferulic acid ($C_{10}H_{10}O_4$) at 195.11 m/z, Harzianic acid ($C_{19}H_{27}NO_6$) at 366.31 and Viridiofungin A ($C_{31}H_{46}O_{10}N$) at 592.31 m/z ratio with retention time 1.94, 3.46 and 3.15 min.

O (S 11) 14: Microbial surfactants from plant growth promoting microorganisms as potential biocontrol agents

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Biosurfactants are multifunctional amphiphilic molecules produced by microorganisms either extra-cellularly or as a part of the cell membrane. Biosurfactants are categorized into rhamnolipids, trehalose lipids, lipopeptides, phospholipids, fatty acid salts and polymeric biosurfactants. These biomolecules have been harnessed in numerous studies to enhance nutrient availability, soil flushing efficiency and biocontrol ability in addition to pharma applications. We are working on microbial surfactants with agriculture applications for more than a decade. We have isolated more than 1000 bacteria (Pseudomonas, Bacillus, Actinobacteria, Rhizobium, Azospirillum) from different sources and screened for plant growth promotion and biosurfactant activity. Strains of *Pseudomonas aeruginosa* are known to produce rhamnolipid and showed antifungal activity. Bacillus strains (*Bacillus amyloliquefaciens* RHNK 22, *Bacillus subtilis* R 72, *Bacillus subtilis* MAH84, *Bacillus velezensis* MHNK1, *Bacillus velezensis* MS 20, *Bacillus safensis* SE4, *Bacillus siamensis* SE 16, *Bacillus mojavensis* RHPR 20) are known to produce surfactin, fengycin and iturin lipopeptides. These lipopeptides inhibited *Sclerotium rolfsii, Rhizoctonia solani*, *Macrophomina phaseolina*, *Fusarium oxysporum f. sp. ricini* (IIOR strain) and *Fusarium oxysporum f. sp. lycopersici* MTCC 10270. Microscopic analysis using scanning electron microscopy revealed condensation of fungal hyphae using lipopeptides produced by Bacillus. Strains of Actinobacteria (*Streptomyces* sp. RHPR3, *Streptomyces puniceus* RHPR9, *Streptomyces* sp. RHPR14 and *Streptomyces mediolani* RHPR25) produced trehalose lipids and inhibited *Phytophthora nicotianae* and *Macrophomina phaseolina*. Biosurfactant formulations are developed and antifungal studies are done *in vitro* and *in planta*. Efficacy of the above mentioned biosurfactants to control fusarium wilt and charcoal rot has been evaluated under greenhouse conditions and the results will be presented. These biosurfactant formulations can be used as alternatives to chemical fungicides and can be potential biomolecules for sustainable agriculture.

O (S 11) 15: Exploring endophytic microflora from North-Western Himalayas

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North Western Himalayas is rich in medicinal wealth repository, occupying an important place in Vedic treatise. This region has wide range of altitudes, topography and climatic conditions most suited to natural habitats for wild medicinal plants that are threatened by over-use and environmental and geopolitical instabilities. About 800 valuable medicinal species found in this part of India are extensively used by the locals since time immemorial for curing various human diseases. Medicinal plants sector possesses great potential to uplift the economy of India, however, various developmental and anthropogenic pressures on the forests, unscrupulous/ unscientific exploitation of medicinal plants in the wake of their increasing national and a global trade demand have caused severe depletion of the medicinal plants resource base thereby affecting the health and livelihood options of the people. Medicinal plants are gaining global attention owing to the fact that the herbal drugs are cost effective, easily available and with negligible side effects. Bioactive natural products of medicinal plants have long been and will continue to be an important source of medicinal raw materials. Phytochemicals reported in plants are cyanogenic glycosides, protease inhibitors, lectins, alkaloids, non-protein amino acids, saponins, steroids and tannins that can be derived from any part of the plant like bark, leaves, flowers, fruits, roots, seeds etc. Endophytes represent a potential source of novel natural products for medicinal, agricultural and industrial uses, such as antibiotics, anticancer agents, biological control agents, and other bioactive compounds. Common endophytes include a variety of bacteria, fungi and actinomycetes, and they can be isolated from wild or cultivated cropsof either the monocots or dicots. Among the microbial group the most frequently isolated endophytes are the fungi. Endophytic fungi are considered as an outstanding source of bioactive natural products because there are so many of them occupying millions of unique biological niches growing in different types of environment. The search for new and effective antimicrobial agents has become a necessity due to rise in the number of super resistant strains and failure of currently used antibiotics against them leading to the increased global health concern. Various traditionally used medicinal plants for their ability to host endophytic fungi having antimicrobial potential have been undertaken world-wide.

O (S 11) 16: Nematode-trapping fungi: Strategic life style transitions and their role as bio-control agent in crop protection.

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Nematode-trapping fungi are fascinating group of soil living microorganisms that suppress the population of plant-parasitic nematodes. These fungi are known to form specialized traps to capture the motile nematodes in soil through adhesion or mechanical trapping and then extracts nutrients from killed and parasitized nematode. These fungi have been studied over several decades and have marveled the researchers and students due to their spectacular action of capturing and killing of nematodes. These fungi are also known to parasitized some fungi. Plant parasitic nematodes and *Rhizoctonia solani* cause severe damage to Indian agriculture every year. Environmental and health concerns over the use of chemical pesticides spurred the search of alternatives for management of plant diseases. Nematophagous and mycoparasitic ability of *Drechslerella dactyloides*, *D. brochopaga*, *A. conoides*, *A. eudermata*, *Dactylellina gephyropaga*, *D. phymatopaga,* were studied against several plant parasitic nematodes and against *Rhizotonia solani* infecting rice under lab and pot conditions. These fungi were also found to grow well in various agricultural soils by forming germ tube and after capturing of nematodes by conidial traps. *Drechslerella dactyloides* was found to grow and parasitized the nematodes in soil environment infested with lower concentration of chemical fungicides. Delivery of nematode-trapping fungi in nematode infected soil caused a significant reduction in root-knot disease of tomato and rice. *Arthobotrys conoides, A. eudermata and Dactylellina gephyropaga* were observed to form hyphal coils around hyphae of *Rhizoctonia solani* within 24 hours of hyphal interface. *A. eudermata* was found most virulent against all four isolates of *R. solani* followed by *A. conoides* and *Dactylellina gephyropaga.* Treatment of *R. solani* infested soils with *A. eudermata, A. conoides and D. gephyropaga* decreased sheath blight infection in rice tillers by as compared to *R. solani* inoculated plants. Results indicate that nematode-trapping fungi could be used as potential microbial tool for management of plant-parasitic nematodes and *Rhizoctonia solani*.

O (S 11) 17: Biological control of *Ustilaginoidea virens*, causing false smut of rice

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False smut of rice caused by *Ustilaginoidea virens* has recently gained attention due to its widespread occurrence. Amongst the methods available for management of diseases, biological control is by far the most practical and eco-friendly method. Therefore, experiments were conducted both in vitro and field conditions to evaluate and validate the bio-agents having best potential to manage the false smut pathogen, *Ustilaginoidea virens*. The preliminary evaluation of the bio-agents in vitro conditions revealed that *Trichoderma harzianum* showed the most promising control of the pathogen as it indicated 68.82% inhibition percentage, followed by *Trichoderma atroviride* (54.04%), *Dendryphiella sp* (44.94%), *Bacillus amyloliquefaciens* (40.29%) and *Bacillus subtilis* (40.15%). The efficacy of the five potential bio-agents against *Ustilaginoidea virens* was validated in field condition on Maudamani variety. All the treatments showed lesser disease severity than the control indicating that the bio-agents have potential to manage the disease. The number of grains per panicle was much higher in all treatments when compared with that of controls indicating that bio-agents have beneficial impact on rice yield. The chaffiness was much lesser in *Trichoderma atroviride* and *Bacillus subtilis* treated plants with respect to the control. Therefore, *Bacillus subtilis* and *Trichoderma harzianum* are the most potent bio-agents against false smut of rice. The next challenge is to develop formulation and if possible commercialize the product for distribution to farmers affected by false smut disease.

O (S 11) 18: Biological management of diseases of tomato grown in poly house under organic production system

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Among various bioagents tested with different concentrations to manage powdery mildew and early blight of tomato grown under protected condition *Pseudomonas fluorescence* and *Bacillus subtilis* were found to be the most efficient organisms over the years and their combinations with 10 gram per liter concentration helped to manage diseases of tomato (up to 60 % reduction) in poly house with highest mean yield of 3.12 ton / 5 Gunta. These bioagents also had growth promoting characters with 18 days earliness, 40 % increase in height, 45 percent increase in number of fruits. Crop period was extended by 20 days with 3-4 additional pickings with highest cost benefit ratio.

O (S 11) 19: Novel microbial consortia for holistic management of serious wilt complex disease problem in pomegranate cultivation

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Pomegranate wilt disease caused by different soil borne pathogens in pomegranate adversely affecting crop cultivation in all major growing regions of India. At present, the crop is severely affected by wilt pathogen and day by day, the wilting severity is increasing at faster rate even at initial stage. Soil borne diseases through chemical is not possible because chemical fungicides it will react up to 15 days to control the pathogens growth later same pathogens survive to other places for time bound and regain survive and attack on the root system in pomegranate. Biological control is a nature friendly approach that uses specific microorganisms, which interfere with plant pathogens to overcome the problems caused by chemical protection methods. Different bioagentsviz, fungal based bacterial based actinomycetes have the ability to control a range of pathogens under a variety of environmental conditions particularly in horticulture crops is being well worked. In search of novel strains of microbial consortia, containing Trichoderma strains bacterial strains and actinomycetes were isolated from rhizospheric soil of Pomegranate orchards in different pomegranate cultivation south-western region of Maharashtra and identified and developed microbial consortia. Initially bioagents inoculated on 5 days old grown pathogen because *C. fimrbiata* is slow growing pathogen and observation taken after 7 days. There are significant differences between the bioagents tested. On the whole bioagents were found better except *B. subtilis*. Among the different bioagents(strains) *T. harzianum*showed the maximum inhibition of the test fungus (100%) but remains on par with T. reesei (100%), *T. hamatum*(100%) and *Penicillium* sp.(100%). Whereas, *P. fluorescens* (32.33%) showed lower inhibitory effect over pathogen but restricted the growth, while the B. *subtilis* was recorded zero inhibition on pathogen growth. In case of Actinomycetes 5 days old grown culture of pathogens restricted the growth (100%) within 24 hrs. This microbial consortium were used for partially wilt affected Pomegranate plants and is being assessed in farmers orchards and results revealed that in experiment plot covered 87 per cent and farmers field rejuvenated 80 per cent infested plants due to wilt complex pathogens. The enormous potential of these novel microbial consortia as an effective biological control agent for wilt complex problem in Pomegranate would be discussed.

O (S 11) 20: Studies on effect of different strains of *Trichoderma viride* and *Trichoderma harzianum* on plant growth promoting activity and disease controlling potential against collar rot of chickpea

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Experiment was conducted under in vivo condition to study the plant growth promoting and disease controlling potential of Trichoderma harzianum / T. viride strains against collar rot of chickpea caused by Sclerotium rolfsii. All strain used as seed treatment @10g/kg seed along with recommended dose of fertilizer and agronomical practices. Data on observation of plant growth promoting parameters i.e plant population, root and shoot length, fresh and dry shoot and root weight, number of nodules, weight of nodules and yield component i .e, mortality percentage number of pod /plant, test weight (100 seed weight), yield quintal / ha, yield in g /plot. All strains of T. harzianum and T. viride were found significantly effective in promoting plant growth, reducing mortality% and enhancing yield and yield components over control. However, Trichoderma strains i.e T. viride (T 18), T. harzianum (T 28) were more effective in controlling collar rot of chickpea. Plant population was significantly higher on (T7,188.50), least (T3,108) over control. However maximum plant population was recorded from Trichoderma strain number T28 (188.50) followed by T18(176.66) and T8(165.00). Trichoderma strain number T1 (25), T18 (23) , and T6 (23) were significantly more effective in increasing shoot length over other Trichoderma strains whereas Trichoderma strain number T7 (22), T8 (22) including control ,which are statistically at par among themselves. Significantly higher root length was recorded in Trichoderma strain number T1 (14.66cm) followed by T6 (12.33cm), T7 (12.33cm), T18 (12.33cm) over control (8.33cm) and statistically at par among themselves. Whereas least root length was observed in T.harzianum strain number T28 (11) over control (8.33cm) Significantly higher fresh and dry shoot weight were recorded from different Trichoderma strains over control (1.90g,). However both fresh and dry weight of shoot were significantly higher in Trichoderma strains number, T5 (3.92g, 0.92g) followed by T6 (3.02g, 0.94g), T7 (3.06, 0.88g) over other strains. Similarly, significantly higher fresh root weight were recorded from strain number T7 (0.37g) followed by T2 (0.32g), T3 (0.32g) and dry root weight was recorded significantly higher in all strains over control (0.01g) maximum dry root weight was observed in Trichoderma strains number T8 (0.07g) followed by T28 (0.07g) and T3 (0.04g).

O (S 11) 21: Rejuvenation of drying *Prosopis cineraria* through biocontrol agents in arid region

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Prosopis cineraria (Indian Mesquite) locally called as *Khejri* is an indigenous tree, which effectively stabilizes sand dunes and can withstand periodic burial. It offers lifeline to human beings during famine, as its powdered bark can be mixed with flour and made into cakes for consumption. Growers are maintaining 30-60 trees in a hectare because crops grown under *Khejri* trees perform better than those grown without it. In last two decades, large scale mortality of *P. cineraria* has been observed in certain pockets of the region due to species of Ganoderma, basal rot causing soil borne plant pathogen. During survey two species are prevalent in arid region viz., *Ganoderma lucidum* and *G. tsugae* where G. *tsugae found* more aggressive in nature for causing mortality in *Khejri* compared to *G. lucidum.* The disease is more prevalent in sandy soils where trees grow under rain fed conditions. Soil moisture stress coupled with high temperature (55°C) during summer months predispose the host to fungal infection. The spread of the disease from diseased plant to healthy is through root to root contacts. Mechanical ploughing and tractorization injured the lateral roots of *P. cineraria* in that condition the tree gets easy predispose for entry of the infection. The association of an insect *Acanthophorus serraticornis* aggravated the root rot incidence due to weakening effect it imparts on the trees leading to increased infection by *Ganoderma.* The protection technique involves digging a pit during rainy season around the trunk until the lower portion of the branching roots become visible and applying phorate granules (20 gm) or Choloropyrifos (20 ml) is applied in order to protect the tree from the attack of *Acanthophorus* and termite at the base of the pit. After layering a cover of soil over this application *Trichoderma longibrachium and T. harzianum* amended with *Prosopis juliflora* compost (2 kg) and farmyard manure (5 -7 kg) is applied. Irrigation is also given to spread *Trichoderma* in the whole pit and to provide additional moisture. After layering biocontrol agent (BCAs) one more layer of another BCA, *Aspergillus nidulans* amended with onion residues (2 kg) is applied to protect the tree from the attack of Ganoderma, again irrigation is also given to spread BCAs and residue in the whole pit and to provide additional moisture to establish the bio-agent beneath the tree collar region. A major problem experienced in this management strategy is that *Trichoderma* may not establish in the soil due to lack of sufficient food substrate. Therefore, *Trichoderma* was multiplied on compost prepared from *Prosopis juliflora* leaves, which was found a rich food substrate for survival and multiplication of bio-agent. In subsequent field demonstrations, application of native strains of *T. longibrachitum* and *A. nidulans* along with onion residues and FYM was found more effective than *T. harzianum* in restricting *Ganoderma* infection on mesquite trees. *T. longibrachatium* is having better saprophytic ability to multiply rapidly in a rich food substrate like *Prosopis juliflora* compost and onion residues, which itself are having antifungal properties. This technology applied to infected *Khejri* trees at our CAZRI campus and found that trees falling in the category of 3 and 3+ before treatment are now under the scale of 1+ and 2. The technology has been found more effective in rejuvenating the partially infected *Khejri* trees. During rainy season it was observed that soil working helped in collecting more rainy water in infected trees leading to better growth.

O (S 11) 22: *Streptomyces* spp.: Promising biological agent for the management of cotton bacterial blight caused by *Xanthomonas citri* pv. *malvacearum*

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Cotton is affected by bacterial blight disease caused by *Xanthomonas citri* pv. *malvacearum* (*Xcm*). Biocontrol agents are the best alternatives for disease management. Actinobacteria are very effective against plant bacterial diseases. Study was conducted to manage the cotton bacterial blight using *Streptomyces* spp. under *in vitro*, pot culture and field conditions. Actinobacteria were isolated from cotton rhizosphere soil from different parts of Tamil Nadu. Their efficacy against *Xcm* was evaluated under *in vitro* by agar well diffusion technique. Fifteen actinobacterial isolates were selected from seventy five isolates through preliminary screening and five effective isolates were selected by further screening using crude metabolites. These best five isolates were identified through molecular characterization of 16S rRNA gene phylogenetic tree was constructed using MEGA 6. Among them, *Streptomyces luteus* strain RAL2 effectively inhibited the growth of *Xcm* with an area of 1036.50 mm^2 followed by *Streptomyces rochei* strain RAS1 (955.30 mm^2) under *in vitro* and these two isolates were further used for pot and filed study. Glasshouse experiment and two field trials were conducted in black cotton soil types in Coimbatore. Delivery of both the *Streptomyces* strains as seed treatment and foliar spray was found promising for the management of bacterial blight of cotton in pot and field study. Results revealed that application of *S. luteus* RAL2 recorded lowest PDI and highest per cent disease reduction over control followed by *Streptomyces rochei* RAS1. The effectiveness of these strains was identified as the presence of antibacterial compounds such as aromatic hydrocarbons, phenols and fatty acids in crude metabolites analysed by GC-MS. In pot and field experiments, disease control efficiency, maximum plant growth promotion and seed cotton yield were higher in the plants treated with *S. luteus* strain RAL2, followed by *S. rochei* strain RAS1 compared to chemical control agents and chemical plant defense inducers.

Poster Papers

P (S 11) 01: A novel method for preparation of *Trichoderma* formulation with increased shelf life

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In recent years, a greater knowledge of chitin chemistry and the increased availability of chitin-containing waste materials from the seafood industry, have led to the testing and development of chitin-containing products for a wide variety of applications in the agriculture industry. A number of modes of action have been proposed for how chitin and its derivatives can improve crop yield. Keeping this in view, sorghum based medium supplemented with colloidal chitin was prepared for the production of Trichoderma formulation in bio-fermenter. Colloidal chitin was obtained from sea shells. The,sea shells were crushed into a fine powder with help of mortar and pestle, the powdered sea shell mixed with concentrated HCl in 1:2 ratio incubated overnight with continuous stirring. After incubation equal volume of 95% of ice cold ethanol was added and again incubated at 28°C for 24 hour. After 24 hour the mixture was centrifuged at 3000 rpm for 30 minute at 4°C. Supernatant was discarded and pellet was washed with distilled water and again centrifuged with the above said RPM, this process continues till the smell of alcohol was removed. Obtained white colour pellet was the sole source of colloidal chitin. For the production of Sorghum based medium, sorghum grains were washed thoroughly, soaked in 2% sucrose solution for overnight. After incubation complete grains were dried and crushed into fine powder. Sorghum grain powder is mixed with distilled water @ of 40g per liter and again autoclaved. Such production media was supplemented with colloidal chitin @1%, 2% and 3%. A final volume of 5 litres was prepared for each concentration. *Trichoderma viride* (01PP) MTCC 12450 inoculum @ 5 ml containing 2x10^8 cfu/ml was added in each medium. In biofermenter acclimatized conditions were shaking speed – 150 rpm, pH-7.0, temperature 25±2°C. The whole process was continued for 5-7 days until greenish colour was obtained. After incubation complete content was filtered and mixed in sterilized talc powder in the ratio of 1:9. The prepared bioformulations with @ 1%, 2% and 3% colloidal chitin were dried into the vacuum drier to remove moisture and were examined for cfu level upto 14 months. The results of present studies indicated that *Trichoderma* formulation with 2% colloidal chitin showed maximum cfu level @ 2x 10^6 cfu/ml even after 14 months of incubation. This is first report on the use of colloidal chitin in bioreactor for increasing shelf life of *Trichoderma viride* based bioformulation. This may be used for extension of shelf life in solid state and liquid fermentation based commercial production of *Trichoderma*.

P (S 11) 02: Biological control of Alternaria blight disease of Indian mustard using PGPR

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Indian mustard (*Brassica juncea* Coss. & Czern) is an important oilseed crop in India. Among various diseases infecting mustard crop, Alternaria leaf spot also known as Alternaria blight is incited by fungus *Alternaria brassicae*, which majorly affects the crop production leading to a yield loss of up to 70%. The disease is controlled by application of different fungicides prior to winter rains but it is costly and also cause pollution in the environment. This investigation was designed to explore the potential of rhizospheric bacteria to use as bio control agents for suppression of the disease. Total of sixteen bacterial isolates were isolated from the rhizosphere of mustard, tomato and brinjal and they were screened for their antagonistic activity against *A. brassicae in vitro* and *in vivo* conditions. Out of sixteen isolates, two bacterial isolates (B3 and B12) showed maximum inhibition (35% and 38.6 5 respectively) against the pathogen and also displayed high degree of secondary metabolite formation. These two bacterial isolates molecularly characterized as *Pseudomonas fluorescens* were further tested in green house and field conditions through seed bacterization treatment for disease suppression. Mustard seeds were treated with the bacterial solution overnight and were sown in pots and fields the next day. It was found that the disease incidence percentage of B3 and B12 was 32 % and 35 % respectively compared to control with 62.8%. The results of the above study were highly significant in evaluation of PGPR against *A. brassicae*.

P (S 11) 03: GC–MS analysis of antifungal compounds extracted from actinomycete isolates obtained from Uttarakhand limestone rock

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Present study was aimed to evaluate the metabolites produced by actinomycete isolates, RK-302 and RK-320 obtained from lime stone rock of Uttarakhand (India) for bio control of head scab of wheat caused by *Fusarium graminearum* and its compounds analysis through GC-MS. Ethyl acetate extracts of isolates RK-302 and RK-320 was fractionated and factions namely RK-302 (21-23), RK-302 (15-17), RK-320 (2-7) and RK-320 (14-18) inhibited the growth of *F. graminearum*, causal agent of head scab of wheat. Data on inhibition zone obtained with fraction of ethyl acetate extract of RK-302 and RK-320 revealed that three fractions of RK-302 (15-17) and (21-23) resulted into maximum inhibition of *F. graminearum* as compared to control (no ethyl extract). Thus these fractions for RK-302 were selected for GC-MS profiling. Likewise, fractions (2-7, 14-18) of RK-320 which showed better inhibition of *F. graminearum* were selected for pooling for GC-MS analysis. In present study, data obtained through GC-MS revealed many compounds in extract of isolate RK-320 (2-7) and RK-320 (14-18). GC-MS analysis of ethyl acetate extract of RK-302 revealed major compounds; 1-tridecanol, undecane, 1-tridecene, dodecane, 1-pentadecene, tetradecane, eicosane, 1-hexadecene, hexadecane, heptadecane, 1-heptadecene, tetracosane, heneicosane, 1-nonadecene, tetracontane, tetracosane. Fourteen common compounds revealed from RK-302 and RK-320 by GC-MS analysis were: undecane, 1-tridecene, dodecane, 1-pentadecene, tetradecane, eicosane, 1-hexadecene, hexadecane, heptadecane, 1-heptadecene, heneicosane, 1-nonadecene, tetracontane, 3-hexen-2-1. Three compounds, tetracosane, hexatricontane and tristearin were found in ethyl acetate extract of RK-320 but these compounds were not found with RK-302. In present study, extracts were found effective against wheat head scab pathogen, *F. graminearum* thus results indicated that extracts contain diverse compounds and present GC-MS analysis substantiated that as many compounds were detected.

P (S 11) 04: Management of *Macrophomina phaseolina* (Tassi.) Goid. causing dry root rot of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]

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Disease control efficacy of three selected bioagents *viz*., *Trichoderma viride*, *Pseudomonas fluorescens* and *Bacillus subtilis* used as seed treatment (ST) and soil application (SA) along with or without organic amendment and two botanicals was evaluated against *Macrophomina* dry root rot of clusterbean under field conditions. The combined treatment of *T. viride* and *P. fluorescens* used as seed treatment and soil application provided maximum control of clusterbean dry root rot. The disease control efficacy of *T. viride* and *P. fluorescens* was improved when these two were used in combination with FYM, plant extracts *viz.,* neem seed kernel extract (NSKE) or Calotropis leaf extract (CLE).

P (S 11) 05: Exploiting phosphate solubilizing bacteria as biofertilizer cum biofungicide for controlling wilt causing fungi

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Efficiency of 50 phosphate solubilizing bacterial (PSB) isolates belonging to Bacillus and Pseudomonas groups including two national checks (*Bacillus polymyxa* and *Pseudomonas striata*) were evaluated against wilt causing fungi (*Fusarium oxysporum)* under controlled conditions. Local PSB isolates belonging were isolated from upland soils of districts Raipur, Durg and Baster of Chhattisgarh state. Out of 50 PSB isolates tested only local isolate No. 3640, 3910, 4467 and two national checks PSB H5 and PSB H27 showed complete inhibition of growth of *Fusarium oxysporum* in broth medium. The PSB isolates also showed significant growth inhibition of the *Fusarium.* Results were reproducible when these PSB isolates were tested for their antifungal properties against the *Fusarium* on agar medium (Modified Martin and Pikovsakya media). During identification of these promising local PSB isolates, it was found that isolate No. PSB 3421 belongs to the genera *Bacillus* whereas other 49 isolates belong to the genera *Pseudomonas*.

P (S 11) 06: Prospecting for the endophytes from mango against *Colletotrichum gloeosporioides* causing anthracnose of mango

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Endophytes associated with the internal plant tissues without showing any external symptoms are one of the less exploited and less studied group of microorganisms. The endophytes associated with *Mangifera indica* which can suppress the anthracnose causing pathogen *Colletotrichum gloeosporioides* is less understood. In the present study we aimed to isolate endophytic fungi from leaf and stem tissues of ten varieties of mango test for their antagonistic activity against *C.gloeosporioides*. A total of 55 endophytes were isolated from ten different mango varieties *viz.*, Alphonso, Totapuri, Neelam, Anfas, Willard, Khaderi, Pancharasi, White Sari, Badam Model and Kisan Bhog. Out of the total, 35 were endophytic fungi and 20 were endophytic bacteria. Maximum number of endophytes were isolated found the stem tissue followed by leaf samples. Out of 35 fungal isolates, 17 showed septate mycelium which was dark coloured and remaining 18 endophytes showed aseptate mycelium and were hyaline. Further, ten endophytic bacteria were isolated from leaf tissues and ten from stem tissues. Among the isolated endophytic fungi EFWDS-A isolated from the stem tissue of Willard showed maximum inhibition of 83.70% followed by EFAL-C and EFAS-D with inhibition of 72.32%, 71.11% respectively. Most of the bacterial endophytes isolated were gram positive and rod shape except two EBPL-1 and EBWDS-1 which were gram positive and spherical in shape. All the bacterial endophytes were negative for indole test. All the isolates showed positive for citrate utilization. The study indicated that endophytes can be exploited as potential antagonists against *C. gloeosporioides* (Penz.) causing anthracnose of mango. Endophytic fungi EFAL-C, EFAL-D, EFAS-A, EFAS-B, EFAS-D, EFTS-E, EFWS-1 and endophytic bacteria EBANL-1, EBAS-1, EBKS-1, EBPS-1 associated from mango varieties were found promising for the suppression of *C. gloeosporioides.*

P (S 11) 07: Evaluation of efficacy of nano-particles on seed health status of soybean seeds with respect to seed borne pathogens

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Nanotechnology is a multidisciplinary and rapidly growing field in the area of science and technology which involves the manufacture, processing and application of nanometer scale assemblies of atoms and molecules. Nanomaterials are generally defined as materials with at least one dimension less than 100 nm. Due to their extremely small size and greater surface activity, they possess unique physical and chemical characteristics which deviate vastly from those of individual atoms or molecules and also the same material at bulk scale. Therefore, their reactivity enables them to have novel applications in different sectors. In lieu of this, the present study was conducted to investigate the effect of nano-particles in enhancing seed quality and their role in controlling various seed borne fungi in soybean. The experimental material consisted of two soybean varieties viz. Pusa 9712 and DS 2614. The seeds of both varieties were coated with nano and bulk formulations of three nano-particles viz. zinc oxide, titanium dioxide and silicon dioxide in five dosages for each treatment viz. 100ppm, 250ppm, 500ppm,750ppm and 1000ppm. The study revealed non-significant differences with respect to germination percentage and seed vigour indices for different concentrations for both the nano and bulk form of all the nano-particles. However, significant differences were recorded in the nano formulations for field emergence percentage, both nano and bulk formulations with respect to electrical conductivity and nano formulations for dehydrogenase activity. Hence, nano and bulk formulations of silicon dioxide @ 500-750 ppm, followed by titanium @750 ppm and zinc oxide @ 1000ppm were found to be the most effective treatments for enhancing seed quality. Four different seed borne fungi were isolated from seed samples of the two varieties viz. *Aspergillus niger, Aspergillus flavus, Rhizoctonia bataticola and Cercospora kikuchi.* High incidence of storage fungi (*Aspergillus* sp) reduced seed germination potential in-vitro. The field fungi causing reduction in seed germination or seedling emergence was *Cercospora kikuchii*. All seed samples of both the cultivars were found infected to some degree. The results revealed that in case of both the varieties, as compared to control, nano formulations of silicon dioxide at three different dosages viz. 500 ppm, 750 ppm and 1000 ppm was the most effective treatment in controlling these fungi. Hence, efficacy of nano-particles on seed health status of soybean seeds with respect to seed borne pathogens needs to be further investigated since it shows considerable promise.

P (S 11) 08: Bio-efficacy of microbial agents against anthracnose disease of yard long bean

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Anthracnose caused by *Colletotrichum lindemuthianum,* is one of the major limiting factors for yard long bean (*Vigna unguiculata* sub sp. *sesquipedalis*) production in Kerala. Most of the cultivated varieties of cowpea are found to be susceptible to this disease. The symptoms initially appear on the lower portion of vines as necrotic lesions, later extending to the whole stem and leaves resulting in the drying of the whole plant, causing considerable yield losses. With this in view, a field trial was laid out in October 2018 to test the efficacy of certain biocontrol microbial isolates against this disease. Biocontrol yeast isolates *Pichia guilliermondi* (Y-12), *Hanseniaspora uvarum* (Y-73) and *Trichoderma harzianum* (Th-3), *Trichoderma viride* (KAU strain), *Pseudomonas fluorescens* (KAU strain) were tested through seed treatment (10g or 10 ml / kg) and foliar spray ($2x10^8$ spores/g for fungal and yeast isolates and $1x10^8$ cfu/g for bacterial isolate at 15, 30 and 45 DAS). The fungicide carbendazim @ 2g/kg (seed treatment) and 2g/L spray was used as check. The results showed that the yeast isolate *Hanseniaspora uvarum* (Y-73) gave 59 percent control of the disease and was on par with chemical check. *Trichoderma harzianum* (Th-3), *Trichoderma viride* (KAU strain) and *Pseudomonas fluorescens* (KAU strain) were the next best effective treatments. The finding provides a valuable microbial component to be included in the integrated disease management strategy in combating the anthracnose disease, thus helping to reduce the use of chemical fungicides.

P (S 11) 09: Investigations on fungal biocontrol agents against root knot disease of tomato caused by *Meloidogyne incognita*

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Root knot nematodes (*Meloidogyne* spp.) are one of the top five most devastating plant pathogens affecting food production globally. They are adapted to parasitize on many vegetables, cereals, pulses, oilseeds and fibre yielding crops, fruit trees, plantation crops and ornamentals worldwide and estimated crop loss due to *Meloidogyne* species in major geographical regions of the tropics ranges from 5-43 per cent. In the present investigation, an experiment was conducted to test biological activity of seven fungi on tomato infected with root knot nematode disease caused by *Melidogyne incognita* under pot culture conditions. The evaluation was carried out under glass house conditions following the completely randomized design consisting of 09 treatments with 3 replicates including a negative and a positive control. Soil was collected from ICAR - IARI fields and mixed with sand (soil: sand :: 3:1). It was autoclaved in a polythene bag at 15 psi, 120 °C for 3 hours. After cooling, pots were filled with 1 kg soil per pot (earthen pot, 16 cm dia) and kept undisturbed. On the next day, tomato seedlings (variety- Pusa Ruby) were subjected to root dip treatment with seven fungus bio-agent @10u -10v conidia/propagules individually for two hours and then transplanted in the pots containing sterile soil. After 2 days, root knot nematode juveniles (*M. incognita*) were inoculated by a pipette in soil by boring small holes around the plant (inoculation rate was 2 J_2 g-1 of soil). Before inoculation, the nematode suspension was bubbled with air to prevent settling of nematodes at the bottom. Proper irrigation with water was given to each pot daily. After 39 days of transplanting, plants were uprooted and data on number of galls per plant, shoot length, root length, shoot weight, root weight of each plant recorded and statistical analysis was done. Results indicated that among seven fungi, one strain of *Verticillium lecanii* exhibited significant plant growth promotion and biological control activity followed by *Aspergillus niger* 4991. However, *Fusarium chlamydosporum* showed higher plant growth promotion activities and also considerable reduction in gall formation. Rest of fungal agents such as *Metarhizium anisopile, Nematoctonus robustus*, *Hirsutella thompsoni*, and *Verticillium lecanii* were effective in plant growth promotion but not promising in control of gall formation. The present study reports *V. lecanii, A. niger* 4991 and *F. chlamydosporum* can be consider for evaluation on a larger scale in field.

P (S 11) 10: Bioefficacy of *Paecilomyces lilacinus* against *Meloidogyne incognita* and its growth promoting ability in tomato

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In vivo studies indicated that talc based formulation of *P. lilacinus* was most effective in enhancing the plant growth along with higher antagonistic activity against *Meloidogyne incognita* (89.14% egg hatching inhibition). Seed treatment with *P. lilacinus @6g/kg* resulted in more than 82 per cent germination. Shoot and root length were increased with enhanced vigor index of 1331.0 after 7 days. It also increased root and shoot length by 125 and 51.13 per cent over the control. Nematode multiplication was significantly reduced when *P.lilacinus* was applied along with organic amendments such as FYM and Neem cake to soil . Apart from nematode management increase in root length and shoot length was significantly higher in *P.lilacinus* treated plants than the plants in untreated control. Total (100 percent) reduction of RKN index was recorded in tomato seedlings grown in soil applied with FYM + *P.lilacinus* and Neem cake + *P.lilacinus*. The pot experiments revealed a significant increase in plant growth parameters, *viz.* plant height, shoot and root weight, number of branches as well as yield per plant in tomato treated with *Paecilomyces* strains.

P (S 11) 11: Prospects of *Pseudomonas fluorescence* for the management of red rot disease of sugarcane

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Pseudomonas fluorescence has been extensively studied for its plant growth promoting and disease suppressing properties. For maximum utilization of disease suppressing potential of *Pseudomonas fluorescence,* there is need to standardise an effective dose and method of application. A study was conducted to observe the effect of different doses and application methods of *Pseudomonas fluorescence* on *Colletotrichum falcatum* causing Red rot disease of sugarcane using commercially available talc based formulation of *Pseudomonas fluorescence* (Pant Bioagent-2). The sugarcane cultivar Co1148 which showed susceptible reaction to *C. falcatum* pathotype Cf 09 was used for planting. Three doses 15, 20 and 25 gm/l were taken for sett treatment and 50, 75 and 100 g/row for soil application. The results obtained were compared with untreated control. Three methods of application- sett treatment, soil application and combination of both were studied. Out of three methods of application, combination of the sett treatment with two soil applications in the field showed the least disease severity (4.2).

P (S 11) 12: *In vivo* evaluation of bioagents/ consortia on turmeric rhizome rot caused by *Pythium aphanidermatum*

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Turmeric (*Curcuma longa* L.) is one of the most important spice crop cultivated in India. Field efficacy of bioagents and their consortia was assessed against rhizome rot. Effect of different bioagents/ consortia on *P. aphanidermatum* revealed that, consortial treatment 4 (Biomix) recorded maximum germination (96 %) followed by consortium 1 (92.0 %) whereas minimum germination found in control treatment (42.00 %). Maximum average mortality found in total control treatment (63.00 %) and minimum mortality recorded in consortial treatment 4 (4.00 %) followed by consortial treatment 1 (8.50 %). Maximum average reduction over control found in consortium 4 (93.61%), followed by consortium 1 i.e. 86.49 per cent.

P (S 11) 13: Bacterial volatile organic compounds: Unexplored antimicrobial and defense signalling molecule for the management of rice blast disease

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Volatile Organic Compounds (VOCs) typically occur as a complex mixture of low-molecular weight lipophilic compounds derived from different biosynthetic pathways. Bacterial volatile compounds are one among them. They are generally produced by catabolic pathways. To describe their complexity the term “volatome” has been recently proposed. In nature, VOCs are responsible for inter and intra organismic communication, partaking in innumerable interactions between plants, antagonists and mutualistic symbionts both below and above ground. They are able to exert important ecological services such as plant growth-promotion and bio control activity when the microorganisms are associated with the beneficiary host plant. They showed the ability to induce plant resistance against pathogenic fungi, bacteria and several viral diseases. Plant associated bacteria of endophytic *Pseudomonas putida* BP25 endophytic bacteria *was* shown to suppress the plant pathogen rice blast fungus *Magnaporthe oryzae* Isolate 1637. Pyrazine groups of BVCs such 2-Methyl pyrazines was shown to inhibit all developmental stages of the fungus. In order to validate the observed *in vitro* antifungal activity of 2-Methyl pyrazines on blast disease, series of *in planta* experiments were conducted on rice seed and seedlings. Seed priming was adopted on rice during germination as well as early seedling growth. Blast disease incidence and disease severity on volatilized seedlings were significantly reduced as compared to un-primed seedlings. Reduction in blast disease severity was observed with 2-Methyl pyrazines. Among the defense related genes, *Os*EDS1, *Os*PDF2.2, *Os*PR3 and *Os*OSPR1.1 were found to be either non-responsive or slightly responsive but significant induction of *Os*PAD4 gene was observed. This study clearly indicates the defense induction by seed priming with bacterial volatile compounds, which can be use as an alternative method for rice blast management.

P (S 11) 14: Assessment of pearl millet root bacterial endophytes for biocontrol activities

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Plants are potential inhabitants of indigenous microbes principally recognized as endophytic microbes which can reside inside their tissues without giving any visible external symptoms and live in mutualistic association with plants for at least a part of their life cycle. Endophytic microbes may be bacteria, fungi and actinomycetes. Bacterial endophytes have an advantage over bacteria residing the rhizosphere because they are within plant's tissues and have an opportunity to always be in contact with the plant's cells and therefore, to readily exert a direct beneficial effect. They are known for their potential to improve plant growth by direct and indirect mechanisms. Direct mechanism includes the microbial synthesis of phytohormones for example, production of Indole-3-acetic acid (IAA), ethylene, cytokinins and gibberellins. In indirect mechanism, bacterial endophytes produce secondary metabolites *i.e.* siderophore, antibiotics, hydrogen cyanide (HCN) and enzyme like 1-Aminocyclopropane-1- carboxylate (ACC) deaminase, cellulase and protease that play an important role in conferring tolerance to biotic and abiotic stresses. A total of 30 pearl millet root bacterial endophytes (PMRBE) were obtained from roots of pearl millet streaked on nutrient agar plates and these were assessed under laboratory conditions by examining their potential for siderophore production, HCN production, ACC utilization and cellulolytic activity. Sixteen isolates *viz.*, PMRBE1, PMRBE2, PMRBE4, PMRBE5, PMRBE6, PMRBE7, PMRBE9, PMRBE10, PMRBE16, PMRBE17, PMRBE18, PMRBE20, PMRBE23, PMRBE25, PMRBE26 and PMRBE28 were positive for siderophore production, three isolates *viz.* PMRBE6, PMRBE25 and PMRBE28 were found positive for HCN production, 30% of the bacterial endophytes showed good growth on ACC supplemented plates and cellulolytic activity was found in bacterial endophyte PMRBE18. Pearl millet root bacterial endophytes exhibiting biocontrol activities could be exploited in friendly, sustainable organic agriculture.

P (S 11) 15: Compatibility of *Pseudomonas fluorescens* isolates with agrochemicals

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Pseudomonas fluorescens is a Plant Growth Promoting Rhizobacteria (PGPR) as well as broad spectrum biocontrol agent for integrated disease management. A study was carried out to evaluate the compatibility of *P. fluorescens* strains PfAhC and PfAP with commonly used nine fungicides, nine insecticides and seven herbicides at their recommended field dosages 50%, 100% and 125% RD by inhibition zone technique. Among nine fungicides Carbendazim 50% WP, Propiconazole 25% EC, Mancozeb75% WP, Carbendazim 25%+Mancozeb 50% WS and Tebuconazole 50% + Trifloxystrobin 50% WG were found highly compatible and Hexaconazole 5% EC, Copper oxychloride 50% WP, Chlorothalonil 75% WP and Carboxin37.5% +Thiram37.5% WP were non-compatible with PfAP isolate. Mancozeb 75% WP found to be noncompatible with PfAhC and other fungicides same as compatible with PfAP. Among the nine insecticides Acephate 75% SP, Monocrotophos 36% SL, Profenophos 50% EC, Imidacloprid 17.8% SL and Spinosad 45% SC were found highly compatible and Quinolphos 25 % EC, Dimethoate 30% EC Chloropyriphos 50% +Cypermethrin 5% EC Chlorantraniliprole 18.5 % SC were non-compatible with (isolate PfAP and PfAh-C) expressed varied inhibition zones. Among the seven herbicides Imazethypr 10% EC, Atrazine 50% WP, Glyphosate 41% SL and Pendimethalin 30% EC were found highly compatible and 2,4-D Sodium salt 58% SL, Metribuzin 70% WP and Quizalofop ethyl 5% EC were non-compatible with Pseudomonas fluorescens (isolate PfAP and PfAhC). Thus, based on inhibition zone technique different chemical pesticides viz. fungicides, insecticides and herbicides were found to be compatible with bioagent (Pseudomonas fluorescens isolates). Present studies indicated the possibilities of compatible pesticides could be incorporated along with bioagents for effective and sustainable disease management with lesser disturbance to agro-ecosystem.

P (S 11) 16: Encapsulation of *Pseudomonas fluorescens* in sodium alginate beads enriched with additives

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Inoculation of plants with microorganisms to control plant diseases has been practiced for several decades. *Pseudomonas fluorescens* is one such biocontrol agent, is used to combat many phytopathogens. The success of potential biocontrol activity depends on the development of appropriate formulations. For the commercial use, microbial inoculum should be supported by an appropriate formulation preventing a rapid decline of introduced microorganisms and extending their shelf-life. Microencapsulation is one such formulation which is prepared by using sodium alginate as a polymer. To date, most formulations encompass several disadvantages like less viability of microorganisms during storage. A study was conducted for the enrichment of alginate beads with different additives to provide satisfactory viability of the microorganisms and quality of the product. The basal media King's B broth, supplemented with sugar source (mannitol 2%, trehalose 15 Mm), wetting agent (PVP 2%, PEG 0.25%), adhesive (CMC 1%, liquid paraffin 1%) and surfactant tween-80 (0.5%) in eight different combinations was prepared. The population of bioagent was studied at monthly intervals. Results showed that mannitol combined with PVP, CMC and tween-80 was found promising, where the population of bioagent was noticed as 23.5x106 even 240 DAI. Thereafter, the beads were prepared using a separating funnel containing the bacterial suspension and sodium alginate solution in the ratio of 1:10. This solution is allowed to pass through the slowly stirred calcium chloride solution, keeping variable concentration of sodium alginate and CaCl2 solution. Population of P.fluorescens was noticed as 12x1036 cfu/g in the beads. It was observed that there was a two-fold increase in bacterial population in the beads after secondary multiplication, when kept in additives enriched KB broth for additional 24h (26x 1036 cfu/g). From the study, it is clear that additives enhance the population and shelf life of the alginate beads of *P. fluorescens* compared to control.

P (S 11) 17: Efficacy of different isolates of *Pserdomonas fluorescens* and plant extracts on the management of Anthracnose disease in chilli

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Anthracnose disease of Chilli caused by *Colletotrichum capsici* is one of the most common and damaging disease occurring nearly every season, wherever chillis are grown, is a threat to chilli cultivation. Six different isolates of *P. fluorescens* were tested against *C. capsici* among which the native isolate Pf$_2$ was found to be most inhibitory to *C. capsici*. The isolates Pf$_2$ recorded the maximum germination per cent, shoot length, root length and vigour index. Among the aqueous extracts of five plant products *viz*., *Allium sativum, Allium cepa, Azhadiracta indica*, *Eucalyptus globules* and *Prosopis juliflora*. *Allium sativum* extract at 15 per cent conc. recorded 100 per cent inhibition of the mycelial growth of *C. capsici* in *Invitro* condition. In pot culture experiments, application of *P. fluorescens* as seed treatment @ (10ml /kg of seed) plus a prophylactic spray with the extracts of *Allium sativum* @ 15 per cent concentration as foliar spray on the 60th and 75th DAT plus soil application with mushroom spent compost @ 5tonnes/ ha was found to be on par with the test fungicide Mancozeb 75% WP in reducing early blight disease incidence and recording a significant increase in the fruit yield when compared to control.

P (S 11) 18: Evaluation of biocides against fenugreek powdery mildew (*Erysiphe polygoni)*

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Fenugreek (*Trigonella foenum-graecum* L.) is an important seed spice crop of Rajasthan. It is belonging to the family *Fabaceae.* It has medicinal value due to presence of diosgenin that is used for the synthesis of sex hormone and oral contraceptive. Powdery mildew is a serious disease limiting the productivity of fenugreek. To evaluate the efficacy of biocides like plant extracts (NSKE, garlic cloves, datura, tulsi and lantana leaves extract @ 5%), animal by-products (cow urine and cow milk @5%) and bioagents (*Trichoderma viride* 4g/lit and *Pseudomonas fluorescens* @ 8g/lit) on powdery mildew of fenugreek, a field experiment was conducted during *Rabi* 2012-13 and 2013-14 in randomized blocked design with susceptible fenugreek local cultivar (Rmt-1) at Sri Karan Narendra Agriculture University, Jobner. The crop was sown in the last week of October in both the years with plot size of 2.0 x 2.0 m^2. The per cent diseases intensity was recorded after 15 days of last spray by examining 20 leaves from 10 randomly selected plants in each treatment by using 0-5 disease scoring scale. Among the nine biocides tested for the management of fenugreek powdery mildew, foliar application of neem seed kernel extract recorded 18.94 per cent disease intensity with a seed yield of 21.68q/ha. Foliar application of cow urine recorded 38.75 per cent disease intensity as against 41.30 per cent disease intensity with cow milk. Foliar application of *Trichoderma viride* and *Pseudomonas fluorescens* recorded 26.63 and 29.97 per cent disease intensity.

P (S 11) 19: Antimicrobial activities of rice phyllosphere and spermosphere microbiome associated *Pantoea* species on rice foliar pathogens, *Magnaporthe oryzae* and *Xanthomonas oryzae* pv. *oryzae*

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The major constraints to rice production are biotic stresses such as blast disease caused by *Magnaporthe oryzae* and bacterial leaf blight caused by *Xanthomonas oryzae* pv. *oryzae*. Current method of rice blast and blight disease management exploits Resistance gene based host resistance and tricyclazole based agrochemical formulations. While host resistance is short lived, the agrochemicals are not acceptable in international trade due to chemical residues on the product of commerce. In order to develop an alternative ecofriendly option for rice disease management, bacterial flora of rice phyllosphere and spermosphere microbiome was explored. The phyllosphere and spermosphere bacteriome of basmati and non-basmati rice cultivars, namely PB1 and VLD85 were analysed using polyphasic tools including NGS based metagenomic and culture media based conventional methods. Bacterial species like *Pantoea ananatis, P. vagans, P. dispersa, P. deleyi, P. anthophila* and *P. agglomerans* were not only found dominating on rice cultivars but also suppressed foliar pathogens of rice, *Magnaporthe oryzae* and *Xanthomonas oryzae* pv. *oryzae. Pantoea dispersa*, *P. agglomerans*, *P. ananatis*, *P. vagans* and *P. deleyi* were found effective against *Magnaporthe oryzae* by showing showing >60 percent inhibition*. Pantoea anthophila, P. ananatis* and *P.vagans* were found effective against *Xanthomonas oryzae* pv. *oryzae* by forming zone of inhibition around 15mm. This study culminated in identification of potential *Pantoea* species for bacteriome transplantation on rice phyllosphere for mitigation of foliar diseases.

P (S 11) 20: Biosynthesis, characterization and evaluation silver nanoparticles from fungal antagonists and entomopathogens against major pests of groundnut

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Groundnut crop is an important oil seed crop, mostly affected by root rot complex fungal pathogens *Aspergillus niger* (Collar rot), *Sclerotium rolfsii* (Stem rot/Sclerotium wilt) and *Macrophomina phaseolina* (Dry root rot/dry wilt) and also white grubs (*Holotrichia consanguinea*) which infects roots and pods of groundnut.The highly effective fungal antagonists and entomopathogenic fungi viz. *Trichoderma harzianum*(Th3), *T. asperellum* (Ta13)*, Metarhizium anisopliae* (Ma1) and *Beauveria bassiana* (Bb1)were morphologically and molecularly characterized based on the sequence analysis of ribosomal DNA (rDNA) region (ITS1 and ITS4). The compatibility among the fungal biocontrol agents were tested by co cultivation plate method. The lab studies proved that fungal antagonists and entomopathogens were compatible to each other and bioefficacy of biological formulations and silver nanoparticles were evaluated against root rot complex pathogens and white grub. Biosynthesized silver nanoparticles (25, 50, 75, 100 ppm) were tested against root rot complex pathogens revealed that *T. harzianum* (Th3) and *T. asperellum* (70- 75%) was effective against major fungal pathogens of groundnut at 100ppm. Different spore concentrations of *M. anisopliae* Ma1 and *B. bassiana* Bb1at $2x10^9$, $3x10^9$ and $4x10^9$ CFU/ml were tested against healthy second and third instar of white grubs. The mortality rate of the insect larva was highest 70-72% in second and 60-62% in third instars at $4x10^9$ CFU/ml and colonization of these fungus were also observed. The preliminary investigation of the efficacy of AgNPs of *M. anisopliae* (Ma1) and *B. bassiana* (Bb1) revealed that these strains were highly effective against healthy white grubs (Second and third instars larva).

P (S 11) 21: Screening of suitable biocontrol agents and plant extracts against *Fusarium solani* causing root rot of papaya

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Research in the past few years have clearly shown that selected strains of the fungi provide an eco-friendly well balanced plant health management system through systemic resistance to diseases of biotic and a biotic nature, increasing seed vigour, improving enhancement of root area and aqueous plant extract suppressed the growth of pathogen. *Fusarium solani* was established as a causal organism of root rot of papaya. Use of Bio-control agents is eco-friendly approach and a good option to manage the soil borne phyto-pathogens. Among native and commercial bioagents tested against the pathogen, *Trichoderma viride* (native) was found most effective in suppression of the pathogen. Antagonistic effect of native and commercial on *Fusarium solani in vitro* was also studied by dual culture technique and found that the growth of the pathogen was much faster in the control plate than in dual culture. The highest inhibition of growth of *Fusarium solani* was exerted by *Trichoderma viride* (native isolate) after 240 hrs (76.8%). Among plant extracts two different concentrations (8% and 10%) of aqueous extract of wild garlic (*Adenocalymma alliaceum*), neem (*Azadirachta indica*), garlic, tulsi and makoi were tested against root rot incidence on papaya under artificial condition in pot. All the plant extracts significantly inhibited root rot incidence on papaya (caused by *Fusarium solani*). The Lowest root rot incidence was recorded in case of treatment with wild garlic with 43 per cent and 45 per cent incidence at 10 per cent and 8 per cent concentration respectively followed by neem showing 47per cent incidence and garlic (49%) incidence, respectively at their 10 per cent concentration. Thus, the native isolates of Trichoderma spp*.* were superior to commercial ones suppressing the pathogen growth. Wild garlic (*Adenocalymma alliaceum*) was identified as the most effective plant extract where root rot disease symptom was not observed upto 67 days at 10 per cent concentration.

P (S 11) 22: Inhibitory effect of *Bacillus* spp. against *Rhizoctonia solani* causes Banded leaf and sheath blight of maize

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Inhibitory effect of *Bacillus* spp. were evaluated against *Rhizoctonia solani.* Five strains *viz. B. licheniformis* B-02, *B. pumilus* B-07, *B. amyloliquefaciens* B-16, *B. subtilis* B-20 and *B. amyloliquefaciens* UI tested against *R. solani.* Effect of volatile secondary metabolite produced by five potential *Bacillus* spp. antagonist on inhibition of mycelial growth of *R. solani* was recorded on inverted plate. Maximum inhibition was recorded in the volatile secondary metabolite of *B. pumilus* B-07 (78.18%) followed by *B. subtilis* B-20 (65.89%), *B.*

licheniformis (61.77%), *B. amyloliquefaciens* UI (57.66%) and *B. amyloliquefaciens* B-16 (56.48%). Effect of culture filtrate on inhibition of mycelial growth of *R. solani* was recorded on dual plate. Maximum inhibition was recorded in the culture filtrate of *B. subtilis* B-20 (51.75%) followed by *B. licheniformis* (50.01%), *B. pumilus* B-07 (46.80%), *B. amyloliquefaciens* B-16 (38.26%) and *B. amyloliquefaciens* UI (29.05%).In dual culture plate, maximum inhibition of mycelial growth of *R. solani* was recorded in *B. subtilis* B-20 (50.59%) followed by *B. amyloliquefaciens* B-16 (46.67%), *B. amyloliquefaciens* UI (40.79), *B. licheniformis* (35.30%) and *B. pumilus* B-07 (32.17%).

P (S 11) 23: Bio efficacy of soybean fungal endophytes against *Alternaria* and Target leaf spot diseases of soybean under field condition

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Soybean crop is threatened by many fungal diseases.Seed borne plant pathogens significantly reduce yield and quality. Among these, *Alternaria* and Target leaf spot diseases are the most prevalent in recent years.Fungal endophytes benefit to plant by promoting plant growth, improving resistance to multiple stresses and diseases. In present investigation, efficient fungal endophytes isolated from root (*Daldinia eschscholzii*), stem (*Neofusicoccum parvum* & *Diaporthe phaseolorum*) and leaf (Fungal endophyte isolate 994) of healthy soybean plant were evaluated against *Alternaria* and Target leaf spot diseases in field condition during *Kharif* 2019 at MARS,Dharwad. Endophytes were evaluated through seed treatment (talc formulation), soil drenching (30 DAS) and foliar spray (45 DAS).Among endophytes evaluated, *Daldinia eschscholzii* showed lowest *Alternaria* leaf spot disease severity (27.00 PDI) followed by *Neofusicoccum parvum*(28.30 PDI) when compared to untreated control (51.00 PDI) and *Neofusicoccum parvum* showed lowest target leaf spot disease severity (28.60 PDI) followed by *Daldinia eschscholzii* (29.00 PDI) when compared to untreated control (57.60 PDI). The standard checks viz., Corboxin+Thiram and *Trichoderma harzianum*(IOF strain) showed least disease severity of *Alternaria* leaf spot (23.00 PDI & 25.00 PDI respectively) and Target leaf spot (23.00 PDI & 27.30 PDI respectively). Significant difference in growth parameters *viz.,* plant height, number of branches and number of pods set that resulted in higher yield level. Treatments with *Neofusicoccum parvum* yielded 2788 kg/ha, *Daldinia eschscholzii* recorded the yield of 2766 kg/ha which are significantly higher compared to untreated control (2548 kg/ha). Yield levels of standard checks viz., Carboxin+Thiram and *Trichoderma harzianum*(IOF strain) showed 2750 kg/ha and 2877 kg/ha respectively.Hence,the study opened a new window of opportunity in application fungal endophytes for suppressing seed borne fungal pathogens of soybean.

P (S 11) 24: Comparative evaluation of of fungal and bacterial endophytes of soybean (*Glycine max* (L.) Merrill) against the soil-borne pathogens in northern Karnataka

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A total of 30 fungal and 30 bacterial endophytes were isolated from healthy soybean plants during *kharif* 2017 from major soybean growing areas of northern Karnataka *viz*., Belagavi, Haveri, Bidar, Dharwad and parts of Maharashtra *viz.*, Kolhapur and Sangli districts. Maximum number of endophytes were obtained from Belagavi district (21) followed by Dharwad district (15). Mean maximum endophyte association was observed in irrigated condition (1.38 for fungal and 1.63 for bacterial endophytes), black soil (1.31 for fungal and 1.46 for bacterial) and at vegetative stage (1.73 for fungal and 1.27 for bacterial). In dual culture method of screening, the endophytes RF-BV-3, SF-DM-8, RB-KK-6, SB-BS-6 and LB-BU-1 were effective against *Sclerotium rolfsii* and the isolates SF-DM-8, SB-DG-11 and LB-BiN-8 were effective against *Rhizoctonia bataticola.* The effective endophytes against *Fusarium oxysporum* were RF-BV-3, SF-BV-3, SF-DM-8, SF-DS-10, LF-HH-5, LF-DM-10, LF-DD-13, LF-KK-14, RB-HS-1, SB-BiJ-9, LB-BU-1 and LB-BV-2. Based on cultural, morphological and molecular methods, the effective fungal endophytes were identified as *Daldinia eschscholtzi* (RF-BV-3), *Fusarium solani* (SF-BV-3 and LF-KK-14), *Neofusicoccum parvum* (SF-DM-8), *Diaporthe phaseolorum* (SF-DS-10 and LF-HH-5), *Phomopsis* sp. (LF-DM-10) and *Colletotrichum aenigma* (LF-DD-13). The effective bacterial endophytes were identified as *Acinetobacter* sp. (RB-HS-1), *Alcaligenes faecalis* (RB-KK-6), *Stenotrophomonas* sp. (SB-BiJ-9), *Bacillus pumilus* (SB-DG-11 and LB-BiN-8), *Paenalcaligenes* sp. (LB-BU-1), *Bacillus cereus* (SB-BS-6) and *Brevibacillus* sp. (LB-BV-2). Under glasshouse studies, SF-DM-8 was effective against all the three pathogens (less disease incidence of 21.88 % against *S. rolfsii*, 27.50 % against *R. bataticola* and 25.00 % against *F. oxysporum*) and showed enhanced growth promotion activity (increased plant height, leaflet number *etc.*) with maximum disease incidence of 100 per cent in untreated check. The endophyte RB-KK-6 was effective against *S. rolfsii* with less disease incidence (31.25 %). The endophytes RF-BV-3 and SB-BiJ-9 were effective against *F. oxysporum* with minimum disease incidence of 16.67 per cent.

P (S 11) 25: Probiotic potential of Lactic acid bacteria.

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Probiotic are (bacteria and yeast) good for our digestive system. Probiotic must compete with thousands of species already in the gut and help in digestion, improve the bowel movement and prevent the multiplication of harmful bacteria, that's by they are friendly bacteria or good bacteria. In the present study total six isolates were isolated from different food (dosa batter, chocolate and pickle) and milk products (curd, cheese and kaladi). These isolates were studied for their antimicrobial properties against human pathogens viz. *Eschericia coli* (MTCC1697), *Pseudomonas aerugonisa* (MTCC741) and *Salmonella typhimurium* (MTCC98). The results revealed that out of six isolates, five isolates viz L1, L2, L3, L4 and L5 had good antimicrobial potential against human pathogens and among them L1 with 41.00mm, 39.00mm and 45.00mm zone of clearance respectively showed significant potential followed by L2 with 38.00mm, 26.00mm and 28.00mm zone of clearance respectively. Further all these isolates were evaluated for their probiotic potential viz, pH tolerance, bile salt tolerance, temperature sensitivity, lactose utilization and NaCl tolerance and the result showed that all the isolates from curd (L1), cheese (L2), kaladi (L3), and dosa batter (L4) showed good probiotic potential than that of the isolates from chocolate (L5) and pickle(L6). Morphological and biochemical studies revealed that all the isolates had characters similar to the genus *Lactobacilli*. This study concluded that the isolate L1 and L2 had best antimicrobial and probiotic potential and these isolates can be further studied for their identification at species level.

P (S 11) 26: Efficacy of potential antagonists against *Phytophthora infestans* on potato in India

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Potato late blight caused by *Phytophthora infestans* (Mont.) De Bary is one of the most destructive diseases of potato world over including India. Treatments of seeds (tubers) and foliar spray with of fungicides applied at regular intervals or scheduled according to late blight forecasting system are effective in reducing infection, but uses of chemicals are hazardous, harmful for beneficial micro-organisms. Biological control of plant pathogens offers an exciting opportunity to manage plant diseases. In the present study, the efficacy of four bio-agents, *viz., Penicillium viridcatum, Trichoderma harzianum, T. viride* and *Myrothecium verrucaria* were evaluated for the control of potato late blight. All the four biocontrol agents provided good control of late blight development both on detached leaves and whole plants of potato cv. Kufri Chandramukhi. *T. viride* followed by *P. viridicatum* were most effective in controlling late blight (lesion area 3.48 and 3.66 cm^2 respectively as against 9.96 cm^2 in untreated control). *T. harzianum* and *M. verrucaria* were at par with each other but showed significant reduction of the disease over control (lesion area 5.93 and 5.06 cm^2 respectively). Similar results were achieved when bioagents tested on whole plants, *P. viridicatum* and *T. viride* were most effective in controlling the disease (43.18 and 39.63 % DI respectively as against 90.10 % in untreated control). *M. verrucaria* was next in order (56.46 % DI) followed by *T. harzianum* (59.05 % DI).

P (S 11) 27: Plant growth promoting activity of indigenous strains of *Trichoderma harzianum/Trichoderma viride* as seed treatment in groundnut.

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Experiment was conducted *in vivo* to study the plant growth promoting activities of strains of*Trichoderma harzianum* and *Trichoderma viride* used as seed treatment@ 10 g /kg seed in groundnut. Various observations of growth parameters and yield components i.e. plant height (cm), no. of branches, no. of pods / plant, unfilled pods/ plant, filled pods/plant and pod yield/ plant (g) were recorded maximum in *Trichoderma* strains T2 (34.0cm, 4.8, 9.6, 6.2, 12.6g) respectively, followed by T3, T4 and minimum unfilled pod was recorded in strain T4(1.8) *Trichoderma harzianum* strain number T 3 (5.6cm), T5 (5.6cm), T8 (5.6cm), T1 and T2 were significantly more effective in increasing number of branches/ plant over other strains and control. Numbers of pods / plant were significantly higher in treated plots over control (8.4) with maximum number of pods from T18 (10.8), T2 (9.6), T1 (9.6) and T3 (9.0).). However, significantly higher number of filled pods were recorded from *Trichoderma viride* T18 (6.6), T7 (6.4) and T2 (6.2) over other strains. Pod yield (g) / plant recorded from plots treated with different isolates shows significantly higher pod yield (g) from *Trichoderma harzianum* strain number T2 (12.6 g), T1 (12.4 g), T3 (12 g), *Trichoderma viride* T18 (11.8 g), T6 (10.8 gm), T4 (10.8 gm) and T28 (10.6 gm) over control (6.6gm).

P (S 11) 28: Characterization of endophytic fungi associated with roots of *Capsicum chinense* and assessment of their bioactive potential *in vitro*

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Fungal root endophytes establish a mutualistic relationship with the host plant and protect them from the soil borne pathogens. In this study, we isolated a total of 86 fungal strains belonging to 14 different morphotypes from 125 root segments of indigenous Naga King Chilli (*Capsicum chinense* Jacq.) during flowering stage (90 days) of crop i.e. April, 2017, grown under shifting cultivation system of Manipur, North Eastern India and identified them based on cultural morphology and rDNA ITS sequence analysis. The percentage isolation rate (IR %) and colonization frequency (CF %) of the root endophytic fungi were 68.8% and 43.2%, respectively. The highest relative abundance (RA %) was recorded with *Phoma* sp. i.e. 16.3%, whereas the maximum isolation frequency (IF %) was observed with *Cladosporium tenuissimum* (32%). The bioactive potential of *Phoma* sp. was evaluated in vitro by dual culture tests against *Aspergillus flavus*, *Colletotrichum capsici*, *Curvularia lunata* and *Fusarium oxysporum* isolates which showed strong (Class 1) to moderate (Class 3) antagonistic activity. Further, the ethyl acetate extracted crude metabolites of *Phoma* sp. was assessed against some human pathogenic bacteria i.e. *Salmonella typhi* (*MTCC* 733), *Staphylococcus aureus (MTCC 96), Escherichia coli (MTCC 1697)* and *Bacillus subtilis* (*MTCC* 441), which exhibited good inhibitory activity. Maximum inhibitory zone (21 ± 2 mm) was recorded with *Bacillus subtilis followed by Staphylococcus aureus.* Thus, the present findings reveal the importance of root endophytic fungi for their role in antimicrobial activity and biocontrol potential against pathogenic microorganisms that could be exploited by the biotechnological and agricultural industries.

P (S 11) 29: Bio-prospecting in management of charcoal rot of *Rabi* sorghum in field conditions.

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Bio-management of charcoal rot comprised of seven treatments including control *viz. Trichoderma asperellum* Liquid formulation, *T. harzianum* Liquid formulation, Biomix Liquid formulation, *T. asperellum* powder formulation, *T. harzianum* powder formulation and Biomix powder formulation were evaluated against charcoal rot disease in variety CSV 29 R were undertaken at All India Co-ordinated Research Project on Sorghum Research Station,VNMKV,Parbhnai during *Rabi* season 2018-19. Results revealed that mean number of nodes crossed by *Macrophomina phaseolina* were ranged from 1.8 to 3.2. The highest (3.2) mean number of nodes crossed by *Macrophomina phaseolina* was observed in control whereas lowest (1.8) mean number of nodes crossed was recorded in *Trichoderma harzianum* liquid formulation which was significantly superior over rest of the treatments. Mean length of spread by *Macrophomina phaseolina* ranged from 12.7 to 29.0 cm. Highest mean length (29.0 cm) of spread by *Macrophomina phaseolina* was observed in control whereas lowest (12.7 cm) mean length of spread was recorded in *Trichoderma harzianum* Liquid formulation which was significantly superior over all other treatments. The highest Charcoal Rot percentage (28.60%) was recorded in control followed by *Trichoderma asperellum* and Biomix powder formulation (18.67 %) whereas lowest Charcoal Rot percentage was recorded in *Trichoderma harzianum* Liquid formulation (10.33%) which was significantly

superior over all other treatments. The highest Charcoal Rot Index (28.60 %) was recorded in control followed by *Trichoderma asperellum* powder formulation (19.67%) whereas lowest Charcoal Rot Index was recorded in *Trichoderma harzianum* liquid formulation (11.73%) which was significantly superior over all other treatments.

P (S 11) 30: Ecofriendly management of pea wilt caused by *Fusarium oxysporum* f. sp. *pisi*

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Pea wilt, a soil borne disease caused by *Fusarium oxysporum* f. sp. *pisi* is an emerging problem of pea growing areas in Himachal Pradesh. It causes huge losses by reducing yield upto 25-50 %. Though often chemical management are able to manage pathogen at certain degree but their adverse effect on soil beneficial microorganism and the environment cannot be ignored. In this study, different management components viz., organic compost, bioagents and botanicals were evaluated against *F. oxysporum* f. sp. *pisi.* Among organic compost, vermicompost showed *in vitro F. oxysporum* f. sp. *pisi* mycelial inhibition of 39.7% followed by farm yard manure (29.7%) and minimum inhibition of mycelium was found with NADEP (18.1%). Among biocontrol agents, all bioagents were found to be effective against the pathogen but maximum mycelial inhibition of 77.4% was obtained with *Trichoderma harzianum* strain SMA-5 which was followed by *T. viride* (76.7 %) and minimum mycelial inhibition obtained with *T. koningii* (JMA-11). The pure extract (100%) of all test botanicals found to be cent percent effective against the pathogen. However, at 25% concentration *Eucalyptus* sp. yielded maximum mycelial inhibition of 25.2% followed by *Eupatorium adenophorum* with 24.1% and was statistically at par with each other. While *Melia azedarach* was found least effective against the pathogen at 25% concentration. Therefore ecofriendly management practices can become an effective alternative of the fungicides application.

P (S 11) 31: Antagonistic activities of local cyanobacterial Isolates against fungal phytopathogens

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Cyanobacterial antagonistic activity is the significant factors influencing their presence in diverse habitats and as unique producers of a variety of secondary metabolites that can be utilized as eco-friendly biocontrol agents. In present work Several Cyanobactrial isolates obtained from various Agrofields were screened for activity against some major fungal phytopathogens such as Fusarium oxysporum, and Rizoctonia solani. The crude extracts of three Cyanobacterial isolates (*Oscilatoria okenii, Anabaena sphaerica and Nostoc carneum*), were capable of diminishing the growth and further development of phyto-pathogenic fungal isolates. Whereas Oscilatoria okenii showed more toxic activity compared to other cyanobacterial strains. crude extract (100% in Methanol) of *Oscilatoria okenii*, was found more efficient against local isolates Fusarium oxysporum (% MI – 88.46 ± 0.24), as compared *Rizoctonia solani* (78.33). *Oscilatoria okenii*, was found most promising to be developed as biocontrol agent for agronomic fields. It was observed that Antagonistic potential of cyanobacteria have need to be further investigated that can offer promising solutions in bio-control against pathogenic fungi.

P (S 11) 32: Isolation and characterization of Potassium solubilizing microorganisms from Sri Lankan soils

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Potassium is the third most important plant macronutrient that contributes to the steady and high quality crops. However, a high percentage of potassium in soil exists in insoluble form in rocks and minerals such as muscovite mica and orthoclase. Levels of soluble potassium are low in Sri Lankan soils. Some soil microflora has an ability to dissolve soil nutrients present in soil enhancing crop growth and yield. This study isolated microorganisms with potassium solubilizing ability from soil samples collected from 4 sites in Sri Lanka. Pure cultures of bacterial, fungal and actinomycetes colonies were obtained from randomly collected soil samples by subsequent streaking on NA and PDA media. Among 79 different fungal and bacterial isolates, two fungal strains (FU2 and FU10) and one bacterial strain (CRa) were able to solubilize potassium giving a hyaline zone around the inoculum on modified Alexandrov medium. The fungal isolate FU10 showed the highest and rapid potassium dissolving ability with an average hyaline zone diameter of 6.7 cm. The fungal isolate FU2 showed an average diameter of 3.4 cm while 0.8 cm was the maximum zone diameter formed by the bacterial isolate CRa. Improved growth characteristics were shown by seedlings of T-245 tomato variety grown in CRa inoculated natural soil compared to uninoculated natural soil. These suggest that the FU2, FU10 and CRa can be potentially developed as plant growth promoting inoculants and probably to increase disease resistance of high potassium demanding crops. Greenhouse assays are underway to further investigate their ability for growth promotion and disease resistance of some selected vegetable crops.

P (S 11) 33: *In vitro* antagonism of biocontrol agents against *Sclerotium rolfsii* causing collar rot of chilli

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Chilli collar rot caused by *Sclerotium rolfsii* is a serious soil borne disease. For devising an effective management strategy, the efficacy of different bioagents, *viz*., *Trichoderma viride*, *T. harzianum*, *T. hamatum*, *T. koningii*, *Pseudomonas fluorescens* and *Bacillus subtilis* were conducted under *in vitro* conditions. All the six antagonists have shown the potential of parasitizing the growth of *S. rolfsii in vitro*. The rate of inhibition was fastest in *T. harzianum* (81.33 %) followed by *T. viride* (78.31 %) and *T. hamatum* (75.40 %). Least inhibition was recorded in *B. subtilis* (62.59 %) after 72 hours of incubation. The antagonists such as *T. harzianum* and *T. viride* can be used as a bio-control agent against *S. rolfsii* of chilli.

P (S 11) 34: Evaluation phosphate solubilizing bacteria on chickpea nodulation

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Virtually all major metabolic processes in plant and soil Phosphorus plays a vital role but the least mobile element contrary to other macronutrients. Phosphorus deficiency in the soil leads to a deleterious effect on nodule formation ultimately growth parameters. A total of thirty-three phosphate solubilizing bacterial strains were isolated from the rhizosphere of chickpea. *In vitro* evaluation, out of thirty-three isolates potential ten isolates showing a remarkable phosphate solubilizing index and reduction in pH of the medium were selected for morphological and biochemical study. The morphological and biochemical characterization of ten isolates concludes that the isolates belong to *Bacillus* sp. and *Pseudomonas* sp. A pot trial experiment with eight treatments was conducted to investigate the role of phosphate solubilizing bacteria in nodulation and growth parameters of Chickpea. The potential native phosphate solubilizing strain *Bacillus* sp. which showed the highest phosphate solubilization index and reduction in pH of the medium used as inoculants for pot experiment. The treatment includes Rhizobium, phosphate solubilizing bacteria (*Bacillus* sp.) and Fertilizer alone and in combination with inoculants and control. The treatment co-inoculation with Rhizobium + Phosphate solubilizing bacterial shown the highest germination, increase in nodule number, fresh nodule weight and it was at par in plant height, No. of branches, shoot and root dry weight/plants over the best treatment Rhizobium + Phosphate Solubilizing Bacteria + Fertilizer. Co-inoculation of Rhizobium + Phosphate Solubilizing Bacteria shows significant enhancement in nodulation and nodule fresh weight as compare to Rhizobium alone, it indicated the role of phosphorus nutrition responsible for increased nodulation and nodule fresh weight of Chickpea. The native *Bacillus* sp. could be considered proficient candidates used as biofertilizers for improving nodulation and shows a positive effect in improving growth parameters and development in Chickpea plants due to the production of plant growth-promoting substances in a more environmentally friendly application besides sustaining soil health.

P (S 11) 35: Effect of additives in microencapsulated formulation of *Trichoderma asperellum*

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Trichoderma spp., the most prevalent culturable fungi with potential biocontrol activity, has been widely used to combat fungal pathogens. For the commercial production, the inoculum of *Trichoderma* spp. should be supported by an appropriate formulation. Till date, several formulations with diverse carrier materials have been developed and one among them is sodium alginate bead based formulation. However, the erratic performance and reduced shelf life is one of the major concerns in the formulation. Hence, to tackle the situation, a study was conducted to evaluate the effect of different selected additives on the shelf life of the bead formulation of *T. asperellum*. Sugar (mannitol 2%, trehalose 15 Mm), wetting agent (polyvinylpyrrolidone (PVP) 1%, polyethylene glycol (PEG) 0.25%), adhesive (carboxy methyl cellulose (CMC) 0.5%, liquid paraffin 1%) and surfactant tween 80 (0.5%) was used in eight different possible combinations. Fifty ml potato dextrose

broth amended with these additives was inoculated with *T. asperellum* and was subjected to serial dilution and plating on PDA medium and the population was studied at monthly intervals. Results showed that trehalose in combination with PVP, CMC and tween 80 was found promising, where the population of the bioagent varied from 12.6 - 39x10v from 7 - 180 DAI. Further, sodium alginate and additives were dissolved in distilled water and was extruded dropwise into $CaCl_2$ solution. Thereafter, population of *T.asperellum* entrapped in beads was estimated by dissolving in potassium phosphate buffer (pH 7) and plating on PDA medium. It was observed that the colony count varied from 23.0 - 34.0x10v cfug^{-1} bead, two months after storage in comparison to control. Likewise, it was also noticed that the number of beads formed per ml of sodium alginate solution amended with additives ranged between 16-26, whereas only 8 bead/ml was formed in control, when the additives were not used.

P (S 11) 36: Exploring the antagonistic potential of rhizospheric *Trichoderma* isolates for stem and crown rot management in Berseem (*Trifolium alexandrinum* L.)

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Among various fodder crops, *Trifolium alexandrinum* L. (commonly called as Berseem), is popular among livestock farmers of India due to its multicut nature (4-8 cuts), long duration of green fodder availability, better yield, high nutritional quality, digestibility and palatability. It has wider adaptability to the Northern and Central Indian conditions and possesses good nitrogen fixing ability. However, incidence of stem and crown rot (*Sclerotinia trifoliorum*) in berseem reduces crop establishment, forage quality and green fodder as well as seed yield. Management of stem and crown rot based on biocontrol strategies is of utmost importance as fodder is directly consumed by livestock and use of chemicals might have deleterious effects on entire food chain arising out of livestock products. Based on above facts, in order to develop a disease management strategy based on biocontrol in berseem, twelve isolates of *Trichoderma* (TBR-1 to TBR-12) from berseem rhizosphere were obtained, purified and characterized. Antagonism studies of *Trichoderma* isolates against target pathogen revealed that among all isolates tested, best isolates was TBR-7 and TBR-9. Plant growth promotion studies revealed that some of the *Trichoderma* isolates (TBR-7, TBR-8, TBR-9) were found to have growth promoting effect on berseem (in terms of increased root weight, shoot weight, primary root length, lateral root number). Among all isolates, TBR-7 provided better protection than others to berseem plants against clover rot disease under controlled conditions. Field trial conducted with most promising *Trichoderma* isolate (TBR-7) shows that, among different treatments, seed treatment with *Trichoderma* @ 0.05 % followed by foliar spray of Chitosan @ 0.05 % was at par with chemical check i.e. seed treatment with carbendazim @ 0.02 % followed by foliar spray of carbendazim @ 0.01 % in managing stem and crown rot disease along with providing good fodder as well as seed yield. Therefore, this *Trichoderma* isolate could be further utilized on large scale along with chitosan for disease management in berseem in an eco-friendly and sustainable way.

P (S 11) 37: Antagonistic activity of bacterial endophytes against *Bipolaris sorokiniana* isolated from wheat

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Wheat is the second largest cultivated crop in the world mainly due to its presence in the diets of most nations. Wheat is a major staple food crop being consumed by 30 percent population of the world and is grown in all the continents**.** The present investigation was carried out at division of Crop Protection, Indian Institute of Wheat and Barley Research, Karnal to exploit diverse endophytic bacteria from 8 recommended wheat varieties. Total 101 endophytic bacteria were isolated 40 from leaf, 30 from stem and 31 from root tissues of wheat on nutrient agar, *Pseudomonas* and *Actinomycetes* selective media and were assayed using dual culture techniques and examined for the effect on growth, sporulation and antifungal activities against *Bipolaris sorokiniana* under in vitro conditions. Among all, 8 bacterial endophytes were effective, but HD3272-18 (73.70%), UP2950-7 (62.50%) and WB2-5 (45%) were found to be more effective. Based on molecular characterization 3 bacterial endophytes were identified as *Bacillus subtilis* subsp. *subtilis.* (HD3272-18), *Bacillus cereus* (UP2950-7) and *Bacillus subtilis* (WB 2-5).

P (S 11) 38: Biochemical characterization and Antimicrobial activity of *Pleurotus* spp.

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Biochemical analysis of five different *Pleurotus* spp. revealed that highest phenol content (903.11 mgGAEs/100 g dry wt.), tannin content (35.42 mgCAEs/100 g dry wt.), alkaloid content (675.42 mgBOEs/100g dry wt.) and saponin content (36.32 mg/100g dry wt.) was reported in *Pleurotus sapidus*. Consequently, extracts of these species was also evaluated for its antimicrobial activity against prevelant plant pathogens like *Fusarium oxysporum*, *Alternaria alternata*, *Rhizoctonia solani,* and *Bipolaris maydis*. Correlation among biochemical constituents and antimicrobial activity of mushrooms revealed highly positive correlation among antimicrobial activity and phenol as well as tannin while moderately positive correlation was observed among antimicrobial activity and alkaloid as well as saponin. Regression equation showing the role of biochemical components in antimicrobial activity was also recorded.

P (S 11) 39: *In-Vitro* evaluation of native isolates of *Trichoderma asperellum* against *Fusarium oxysporum* f. sp. *gladioli* causing *Fusarium* wilt of gladiolus

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Gladiolus (*Gladiolus grandiflorus* Ness) the “queen of bulbous flowers”, is an important commercial flower crop fetching high returns in national and international markets. *Fusarium oxysporum* f. sp. *gladioli* causes corm rot, wilt and yellows in gladiolus. *Fusarium* wilt is a major constraint to flower industry with respect to quality and yield. Use of fungicides for the management of *Fusarium* wilt has been found to be inconsistent. Application of biocontrol agents constitutes an effective option for the management of *Fusarium* wilt. The present study was carried out to analyze the efficacy of *Trichoderma asperellum* against *Fusarium* wilt. Three *Trichoderma asperellum* isolates i.e, Pune (Ac no. MK041249), Vadaj (Ac no. MN372214) and Kusur (Ac no. MN386231) which were isolated from rhizospheric soil of gladiolus from Pune region, were tested *in vitro* for their efficacy against *Fusarium* wilt pathogen of gladiolus. Isolates of *Trichoderma asperellum* were found effective and will be further evaluated *in vivo*. The biocontrol mechanism studies revealed that selected *Trichoderma* isolates possessed good competitive saprophytic ability. The isolate *Trichoderma asperellum* “Pune” was found to be the best as 72% inhibition was found through volatile compounds. Besides isolate *Trichoderma asperellum* “Vadaj” possessed strong mycoparasitic ability against *Fusarium oxysporum* f. sp. *gladioli i.e,* 75% inhibition was found in dual culture assay. The biocontrol activity involving mycoparasitism, antibiotics and competition for nutrients, also induces defence responses or systemic resistance responses in plants. Biocontrol agents should not be considered as an independent tool, but should be adequately implemented in an integrated management framework. The promising isolates of *Trichoderma asperellum* will be further evaluated *in vivo* for incorporation in integrated wilt management in gladiolus.

P (S 11) 40: Evaluation of bacteria isolated from nodules of various leguminous plants for the biological control of soil borne pathogens of chickpea.

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Biological control of plant pathogens occurs in several ways, the most common mechanisms being parasitism and predation, competition for nutrients or space, production of antimicrobial substances and induced resistance. In the present investigation a total of 30 bacteria were isolated from the nodules of different leguminous plants and were characterized for their antagonistic potential by dual culture assay against Fusarium oxysporum f.sp. ciceri (FOC) Sclerotium rolfsii, Rhizoctonia bataticola causing wilt, collar rot, and dry root rot in chickpea. Simultaneously, they were also screened for plant growth promoting and biosurfactant activity. All the 30 bacteria were further evaluated for their production of â-1,3-Glucanase, chitinase, cellulase, lipase, protease, siderophore, hydrocynanic acid (HCN) indole acetic acid (IAA). Two potential antagonistic bacterial isolates (Rhizobium sp, IHNO-2, IHCP-2) evaluated for biological control of wilt disease of chickpea is evaluated under greenhouse conditions and the data of same will be presented.

P (S 11) 41: Efficacy of bioagents against *Sclerotium rolfsii* causing chickpea collar rot

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Collar rot of chickpea caused by *Sclerotium rolfsii* has a major constraint and potential threat to successful chickpea cultivation. Therefore efforts were made to evaluate the different bioagents in *in vitro* condition against *Sclerotium rolfsii*. Among seven bioagents were evaluated *in vitro* against *S. rolfsii* by dual culture technique. However, *Trichoderma harzianum* was found most effective with significantly least linear mycelial growth (02.66 mm) and significantly highest mycelial growth inhibition (97.04 %) of the test pathogen. This was followed by *T. longibrachiatum* (20.75 mm and 76.94%), *P. fluoeroscens* (22.91 mm and 74.54%), *T. hamatum* (24.16 mm and 73.15%) and *T. asperellum* (27.25 mm and 69.72 %). However, the bioagents found least effective with minimum mycelial growth inhibition were *B. subtilis* (61.66%) and *T. koningii* (59.91%).

P (S 11) 42: Isolation, screening under *in vitro* and identification of phyllosphere microflora from maize

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Twenty-two bacterial cultures (P_1 to P_{22}) and six fungal cultures were isolated from the phyllosphere by leaf imprint method and dilution method. The colony characters of isolates of bacteria and fungi pertaining to their shape, size, elevation, margin, texture, appearance and pigmentation were recorded. Grams' staining and endospore staining revealed that P_1, P_4, P_6, P_7, P_{12}, P_{14} and P_{16} were Gram positive, endospores and rod shaped. Biochemical tests revealed that all the twenty-two isolates were positive for the catalase and oxidase test. Isolates $P_{1,}$ P_6, P_7, P_{14}, P_{16}, P_{17} and P_{22} showed positive results to Voges prausker's test. Isolates of phyllosphere bacteria $P_{2,}$ P_3, P_5, P_8, P_{10}, P_{11}, P_{13}, P_{15} and P_{21} revealed positive results to Indole test. Whereas, isolates P_1, P_4, P_6, P_7 and P_{22} showed negative reaction to methyl red test. The phyllosphere bacterial isolates P_8, P_{15}, $P_{17,}$ P_{18}, P_{19}, P_{21} and P_{22} recorded negative reaction to gelatin liquefaction. Screening of phyllosphere microflora against *E. turcicum* was conducted following dual culture technique for all the isolates. Phyllosphere bacterial isolate P_9 recorded maximum growth inhibition of 24.09 per cent radial growth of the test pathogen. Fungal isolate *Aspergillus niger* showed highest inhibition 60.6 per cent compared to other isolates. Compatibility of six fungicides with potential bacteria and fungi were tested by turbidometry and poisoned food technique. The growth of phyllosphere bacterial isolate of P_9 and isolate P_{16} was highest in carbendazim + mancozeb showing OD value of 3.14 and 2.54 respectively, indicating that carbendazim + mancozeb was compatible with the phyllosphere bacterial isolates. Propiconozole was compatible with *Aspergillus niger* fungal isolate. The potential phyllosphere isolate P_9 and isolate P_{16} along with compatible fungicide were tested for their growth promoting activities under laboratory conditions. Seed treatment with (carbendazim + mancozeb) + isolate P_9 + isolate P_{16} not only increased germination percentage by 95.22 per cent but also enhanced seedling vigour (2394.78). The potential isolate P_{16} of phyllosphere bacteria were sent to Eurofins for further characterization at molecular level by 16S rRNA gene sequencing for identification. Based on the sequencing, the phyllosphere isolate P16 identified as *Bacillus amyloliquefaciens*.

P (S 11) 43: Evaluation of biopriming potential of *Trichoderma* and *Pseudomonas* against seed and soil borne diseases of safflower

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A field experiment was conducted for two consecutive *rabi* seasons from 2017-18 to 2018-19 to evaluate the biopriming potential of *Trichoderma* and *Pseudomonas* as a seed dressers for management of seed and soil borne diseases of safflower. Among the different priming treatments, seed biopriming with *Trichoderma harzianum*

@ 10g/litre water for 12 hrs was found to be the most effective as it recorded significantly highest germination (95.3%) and least incidence of Phytophthora seedling blight (4.9%), Fusarium wilt (4.4%) and Macrophomina root rot (4.7%). The next effective treatments as regards Phytophthora seedling blight, Fusarium wilt and Macrophomina root rot control were seed treatment with *Trichoderma harzianum* @ 10g/kg seed 1 hr before sowing (6.5%, 8.6% and 7.5%, respectively) and seed biopriming with *Pseudomonas fluorescens* @ 10g/litre water for 12 hrs (8.6%, 12.1% and 9.5%, respectively). Moreover, seed biopriming with *Trichoderma harzianum* @ 10g/litre water for 12 hrs recorded significantly highest seed yield (1023 kg/ha), net monetary returns (Rs.21260/-) and B:C ratio (2.21) followed by seed treatment with *Trichoderma harzianum* @ 10g/kg seed 1 hr before sowing (867 kg/ha, Rs.15332/- and 1.87, respectively) and seed biopriming with *Pseudomonas fluorescens* @ 10g/litre water for 12 hrs (781 kg/ha, Rs.12064/- and 1.68, respectively). The overall results showed that seed biopriming with *Trichoderma harzianum* @ 10g/litre water for 12 hrs was found most effective and economical for management of the seed/soil borne diseases of safflower.

P (S 11) 44: *In vitro* evaluation of different bio agents against *Fusarium oxysporum* f. sp. *chrysanthemi*

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The pathogen (*Fusarium oxysporum* f. sp. *chrysanthemi*) was isolated successfully from the naturally wilted chrysanthemum plants specimens collected from farmers' field as well as research field which were purified and maintained for further studies during the year 2018-19. The typical symptoms were noticed on plants *i.e.* the chlorosis of leaves. Green leaves turned into yellow in colour. Plants loss their vigourness. Xylem tissues shown brownish to black colour appearance. Whole plants loss their turgidity and finally death of plant occurs. Pathogenicity of *F. oxysporum* was proved by adopting sick soil inoculation method by using wilt susceptible chrysanthemum variety *viz.*, Aishwarya under pot culture. A critical review of the literature reveals that very little work has done on eco-friendly management of *Fusarium oxysporum.* The Investigations were carried out to find the intensive and eco-friendly methods of controlling *F. oxysporum,* by using bioagents in laborat ory during the year 2018-19. The result obtained on mycelial growth and inhibition of *F. oxysporum* f. sp. *chrysanthemi* with six fungal antagonists and one bacterial antagonist. Results revealed that all the evaluated bioagents were exhibited fungistatic cum antifungal activity against *F. oxysporum* f. sp. *chrysanthemi* and significantly inhibited its growth over untreated control. The six fungal biocontrol agents *viz*., *Trichoderma viride, Trichoderma harzianum, Trichoderma hamatum, Trichoderma koningii, Trichoderma longibrachiatum, Aspergillus niger* and one bacterial biocontrol agent *viz*., *Pseudomonas fluorescens* were evaluated *in vitro* for their efficacy against *Fusarium oxysporum* f. sp. *chrysanthemi* by applying dual culture on PDA as basal medium. All the antagonists were significantly superior over the untreated control. The *Trichoderma viride* and *Trichoderma harzianum* were at par with each other but significantly superior over all other treatments.The average mycelial growth of test pathogen was ranged from 24.66 mm in treatment of bioagent *viz*., *Trichoderma viride* to 45 mm *Aspergillus niger* as against untreated control (90 mm). Whereas, average per centage mycelial growth inhibition was in the range of 49.99 per cent (*Aspergillus niger*) to 72.59 per cent (*Trichoderma viride*) as against 00 per cent in untreated control. Amongst the tested anatagonists, *Trichoderma viride* was found the most effective and recorded least mycelial growth of *F. oxysporum* f. sp. *chrysanthemi i.e.* 24.66 mm with the highest per cent mycelial inhibition *i.e.* 72.59 per cent over the test pathogen.It was followed by *Trichoderma harzianum* which was shown 26.66 mm mycelial growth of test pathogen and 70.36 per cent inhibition of test pathogen. The maximum mycelial growth 45 mm of test pathogen with least mycelial growth inhibition *i.e.* 49.99 per cent were recorded in *Aspergillus niger*, still it was significantly superior over untreated control.

P (S 11) 45: Evaluation of new strain of *Trichoderma* along with combination of fungicide for the management of collar rot (*sclerotium rolfsii*) of lentil

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Several diseases are known to infect lentil (*Lens culinaris* Medik) during its growth stages. Among them, collar rot caused by *Sclerotium rolfsii* Sacc., is very common in all the major lentil growing areas. The disease causes appreciable loss in yield due to which, area under this crop is consistently decreasing. For restoring the area production and productivity of lentil, it is necessary to reduce the loss caused by this disease. Seeds of lentil cultivar-Bragg were dipped in bioagents / fungicidal solution for 10 minutes dried in shad and planted 4×3 m sized plot with 30 x 10 cm spacing. Control plots were maintained without seed treatment. Percent disease incidence was recorded in all treatment by counting the number of infected plants. The yield per plot was also recorded. Different *Trichoderma* stains including mutant **(**T-1—*Trichoderma herzianum* T-6, T-2—*Trichoderma herzianum* T-28 , T-3—*Trichoderma viride* T-18 , T-4—*Trichoderma mutant*, T-5—Propineb(Antracol) , T-6—Hexaconazol+Zineb (Avtar), T-7—*Trichoderma herzianum*T-6 + Propineb**)** obtained from IGKV, Raipur (CG) have been used as seed treatment and compared with chemical seed treatment and also observed different plant characters of lentil crop. *Trichoderma harzianum* T-6 + Propineb (@10g + 1.5g/kg) seed was significantly effective in minimizing collar rot incidence at field condition. Significantly higher yield (1970.12kg/ha.) was also observed in this treatment at compared to control (1721.32kg/ha.). This treatment was also significantly superior to other treatment is increasing the yield of lentil crop.

P (S 11) 46: *In vitro* evaluation of different bioagents against *Fusarium oxysporum* f. sp. *lycopersici* causing wilt in tomato

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Tomato (*Lycopersicon esculentum* Miller) crop suffers from several diseases, among which wilting caused by *Fusarium oxysporum* f. sp. *lycopersici* is one of the serious diseases observed regularly in tomato growing areas. Therefore, efforts were made to evaluate bio efficacy of the different bioagents *in vitro* condition against *F. oxysporum* f. sp. *lycopersici*. Among five fungal and two bacterial bio-agents tested *in vitro*, exhibited significant inhibition of mycelial growth of *F. oxysporum* f. sp. *lycopersici.* However, *Trichoderma koningii* recorded significantly highest inhibition of mycelial growth (92.22%) followed by *T. longibrachiatum* (90%), *T. harzianum* (87.60%), *T. asperellum* (67.22%), *T. hamatum* (60.93%), *Bacillus subtilis* (53.52%) and *Pseudomonas flurorescens* (42.41%) over control.

P (S 11) 47: Effect of fungicides and bioagents on *Fusarium oxysporum* f. sp. *udum*, seed germination and seedling vigour in cultivar ICP-2376 in pot

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The fungicides and bioagents taken in the study could be able to reduce the mycoflora associated with seeds and thereby increase germination percentage, root and shoot length and ultimately seedling vigour index and also reduction in mortality per cent. Various fungicides and bioagents i.e. carbendazim 50% WP @ 0.1%, thiophanate methyl 70% WP @ 0.1%, carboxin 37.5%+ thiram 37.5% 75WP @ 0.25%, carbendazim 12%+ mancozeb 63% 75WP @ 0.25%, *T. asperellum, T. harzianum* and *T. hamatum* were tested against *Fusarium oxysporum* f. sp. *udum* in pot. The cultivar ICP-2376 was used for experiment. The maximum seed germination per cent was observed in carboxin 37.5%+ thiram 37.5% 75WP @ 0.25% which recorded 96.90% germination, followed by carbendazim 12%+ mancozeb 63% 75WP @ 0.25% which recorded 93.80% germination. The shoot and root length were ranged between 20.68 to 32.63 cm and 7.52 to 10.51 cm, respectively. The maximum seedling vigour index was observed in carboxin 37.5%+ thiram 37.5% 75WP @ 0.25% which recorded 4180.2. The maximum pre-emergence and post-emergence mortality was observed in control (untreated) which recorded 46.86% and 4.41%, respectively. The maximum fresh and dry weight was observed in carboxin 37.5% + thiram 37.5% 75WP @ 0.25% which recorded 13.36 g and4.97g, respectively.

P (S 11) 48: Investigations on abiotic stress tolerance and antagonistic potential of *Pseudomonas* isolates from Kerala

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Pseudomonas spp. are one among the most extensively utilized biocontrol agents in sustainable agriculture. However, prevalence of abiotic stresses such as drought, high temperature, salinity and acidity may affect the field performance of the bacteria, which necessitates isolation of native strains from stressed soils. A total of 26 representative soil samples were collected from four districts *viz.*, Ernakulam, Palakkad, Thrissur and Alappuzha. Subsequent soil analysis confirmed that samples procured were abiotically stressed. When soil samples were subjected to serial dilution and plating technique on King's B medium, maximum population of *Pseudomonas* spp. was recorded in samples procured from Moncombu (1.3-7.8x10^{6}cfu g^{-1}) and minimum population from Vyttila (3.14- 6.01 x 10^{4}cfu g^{-1}). A total of 13 isolates were purified and designated with sample codes based on location *viz*., M (Moncompu of Alappuzha), V (Vyttila of Ernakulam), T (Thrissur) and P (Palakkad). These isolates were screened for *in vitro* abiotic stress tolerance and compared with reference culture of KAU. The isolates P2, M4 and T5 were selected as temperature tolerant (50 ^{o}C), M4 and V4 as salt tolerant (1.5 M NaCl), P4 and T4 as drought tolerant (30% poly ethylene glycol 6000) and M4 and M5 as acid tolerant (pH 3.5) strains. Thereafter, isolates were evaluated for *in vitro* antagonistic potential against *Phytophthora capsici, Pythium aphanidermatum, Sclerotium rolfsii, Rhizoctonia solani* and *Fusarium oxysporum* using Bangle method. Four isolates *viz*., P2, P4, M4 and M5 were selected as the potential antagonistic strains with per cent growth inhibition ranging from 62.21 to 91.00. Further biochemical studies revealed higher ACC deaminase (M4, M5) , exopolysaccharide(M4, P4), cellulase (P4) and â-1, 3 glucanase (M4) activities of these strains. Moreover, all the isolates higher plant growth promoting potential and biocontrol potential under pot culture experiment using cowpea- *R. solani* system. Based on molecular characterization, promising isolates were identified viz., P2 as *Pseudomonas putida*, P4 as *P. fluorescens* and M4 and M5 as *P. aeruginosa.*

P (S 11) 49: Population dynamics of liquid formulation of *Pseudomonas fluorescens* and its *in vitro* and *in planta* studies against soil borne fungal pathogens

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Carrier liquid based formulations of *P. fluorescens viz*., P I, P II and P III supplemented with different adjuvants were prepared and were serially diluted to record the population at 10^8 and 10^9 dilutions. It was observed that the formulation P I supplemented with carboxy methyl cellulose (CMC) and mannitol recorded the highest count of 18.85 x10^8cfu ml^{-1} and 8.8x 10^9 cfu ml^{-1} followed by P II [CMC and polyvinyl pyrrolidine (PVP)] of 18.95 x 10^8 cfu ml^{-1} and 16.8 x 10^9 cfu ml^{-1} at 48 h after inoculation. It was noticed that in general, the population decreased gradually on storage and among the three media, the maximum population was observed in P II closely followed by P I and P III (coconut water, mannitol, CMC) at 8 MAI. The antagonistic efficiency of these liquid formulations was evaluated *in vitro* by poison food technique against important soil borne fungal pathogens. It was noticed that all the three formulations of *P. fluorescens* at all three concentrations showed cent per cent inhibition against the soil borne pathogens, *Pythium aphanidermatum* and *Phytophthora capsici.* An *in planta* experiment was conducted with nine treatments where these treatments were applied 10 days before challenge inoculation and thereafter twice on symptom appearance as soil drench and foliar spray. Incidence of collar rot caused by *R. solani* was noticed at 40 days after sowing (DAS). Results showed that all three formulations at 0.5 and 1 per cent showed an increase in biometric characters and can reduce the severity of collar rot infection caused by *Rhizoctonia solani*. Among the various formulations of *P. fluorescens,* maximum yield was recorded in P I (0.5%) followed by P III (1%) and P II-(0.5%) with the minimum in absolute control.

P (S 11) 50: Studies on efficacy of aqueous seed extracts against *Pectobacterium carotovorum* causing black leg and soft rot of potato

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The use organic farming is now gaining popularity. Different parts of many plants have antimicrobial properties. In this context the seeds of some medicinal plants were tested agaist *Pectobacterium carotovorum* causing black leg and soft rot of potato. The seeds used in the studies were *Terminalia chhebula*(Chhebulic myrobalan),*T. belerica* (Beleric myrobalan),*Emblica officinalis* (Indian goose berry),(*Azadirachata indica*(Neem), (Greater cardamom),*Raoulvtia serpentina*(Snake root),*Coriandrum sativum* (Dhania),*Cuminum cyminum* (Cumin),*Nigella sativa*(Black cumin),*Foeniculum vulgare*(Fennel),*Piper nigrum*(Black pepper,*Cassia fistula* (Indian laburn),*Cassia tora* (Senna tora). The healthy seeds were collected washed several times in sterilized water and air dried. Fifty grams from each selected plant part along with 50ml of double distilled water were taken band grinded with the help of pestal and mortar to a fine pulp.The pulp was filtered through two layers of muslin cloth and gently pressed to get maximum filterate.The filterate from each plant part was collected and kept separately in different sterile specimen tubes and centrifused at 1500rpm for 15 minutes. The supernatant liquid was drawn carefully into a 5ml syringe and then passed through membrane filter of 0.45nm size to sterilize the extract . The filter sterilized extract of each part collected in sterilized specimen tube with screw cap and stored in deep freeze maintain ed at -20^0 C. The extracts were evauated *in vitro* following the inhibition zone technique. In this technique, two drops of bacterial suspension of each test bacterium was transferred on to the petriplate containing NSA medium and spreaded over the surface of the medium with the help of a sterilized glass spreader. Three sets of Hi-media discs (5mm), soaked for one minute in each plant extracts were placed on the media surface of each petriplate at the equidistance from the centre. In each set four numbers of discs were used to hold sufficient quantity of the plant extract. Two sets of petridishes were used for testing each plant extract petriplates were incubated at 27±1^{0}C for 24 hours in a BOD incubator. After the incubation period, the petriplates were examined for development of inhibition zone around the discs. The diameters of each zone of inhibition was measured and recorded to assess the antimicrobial properties of plant extracts against each test bacterium. In control the paper discs were soaked in sterilized water.The experimental results revealed all the seeds possess antibacterial peoperties.Significantly maximum zone of inhibition (11.33mm) was observed in *A. subulatum* followed by *T. chhebula* and *S. caryophyllus (10mm)*. Minimum zone was recorded in *P. nigrum* and *C. fistula*. In control no inhibition zone was recorded.

P (S 11) 51: Exploring the potentiality of novel rhizospheric bacterial strains against *Ralstonia solanacearum* and promoting tomato plant growth

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Bacterial wilt caused by *Ralstonia solanacearum* is the world's most economically important destructive disease of crop plants. In the current study, we aimed to evaluate the novel bacterial isolates from Tomato rhizosphere for biocontrol of *Ralstonia solanacearum.* One eighty bacterial strains from the Tomato plant's rhizosphere were isolated from the Tomato rhizosperic soils collected from different regions of Uttarakhand state and evaluated for their biocontrol activity against *R. solanacearum* under *in vitro* and *in vivo*. Among them, six isolates were found to be highly effective in inhibiting the growth of *R. solanacearum.* The isolate Gp2NA8 produced the highest inhibition zone followed by that of Gp3NA6 and Gp4NA8. They were also tested for their ability to promote growth and induce resistance of tomato plants against the bacterial wilt in the green house conditions. Bacterization of tomato seed with these isolates was found to be effective in controlling the tomato wilt. Compared with the control most of the isolates promoted plant growth that was measured by seed germination, plant height, fresh weight and dry weight. Likewise all isolates significantly reduced the infection percentage compared with non-treated control, however, the rate of growth enhancement and disease suppression varied considerably with isolates. The isolate of Gp2NA8 besides being best biocontrol agent also shown higher plant growth promotion.

P (S 11) 52: Bio- prospecting of native bio-agents against common soil borne pathogens of bellpepper nursery

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Bell pepper (*Capsicum annum* L.) is the most popular and highly remunerative vegetable crop grown for fresh fruits throughout the world. It is utilized for home consumptions, catering and industries round the year. In India, Himachal Pradesh is the second largest producer of capsicum contributing 19 per cent of its total production. The quality of yield is affected by various fungi like *Pythium, Phytophthora, Fusarium, Rhizoctonia, Sclerotium, Phomopsis, Colletotrichum,* etc. causing diseases in nursery. Since the crop is highly remunerative, farmers make non-judicious use of the fungicides for managing these diseases and their persistence in soil leads to human health hazards and environmental pollution. An eco-friendly and sustainable strategy is required for management of these diseases. In search of native bioagents, soil samples were collected from eight different healthy and diseased nurseries of bell pepper grown in Solan and Sirmaur districts of Himachal Pradesh. Repeated isolations were made from soil samples by serial dilution technique. The media used for isolations were Potato dextrose agar (PDA), Nutrient agar (NA) and Starch Caesin Agar (SCA) for fungi, bacteria and actinomycetes, respectively. The number of isolates were enumerated by viable count method. Among various locations, site 7 of Solan district had highest fungal count (28×10^2 cfu/g soil) whereas site 6 had the lowest. Site 1 of Sirmaur district had highest bacterial and actinomycetal population (191×10^5 cfu/g soil) and (175×10^3 cfu/g soil), respectively whereas site 8 of Solan district had lowest bacterial count (6×10^3 cfu/g soil) and site 5 and site 8 had lowest actinomycetal population. Based on morphological and cultural keys 40 (16 fungal, 18 bacterial and 6 actinomycetal) isolates were purified and selected for further potential antagonistic activity test by pathogen at centre method against three soil borne pathogens viz. *Pythium, Rhizoctonia* and *Fusarium* responsible for causing nursery diseases. Among various isolates, the maximum per cent inhibition of the pathogens were observed with fungal isolate 5 i.e., 88.24, 91.85 and 92.59 against *Rhizoctonia* and 75.00, 83.33 and 86.67 against *Fusarium* after 4, 6 and 8 days of incubation, respectively. Fungal isolate 5 showed maximum per cent inhibition of *Pythium* i.e., 100 even after 72 hours of incubation. Six fungal, six bacterial and five actinomycetal isolates were found effective in inhibiting these soil borne pathogens significantly. Therefore, these isolates were selected and maintained for further studies.

P (S 11) 53: The potential of antagonistic yeasts and bacteria isolated from tomato phyllosphere and fructoplane in the control of Alternaria fruit rot of tomato

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Tomato (*Solanum lycopersicum* Mill) is the most important vegetable crop in Oman, grown across the entire country. *Alternaria* fruit rot caused by the filamentous fungus *Alternaria alternata* is one of the major constraints in tomato production in Oman. This fungus invades the tomato fruits through injured or weakened tissues. The pathogenic infection of fruits occurs during crop growth in the field, harvesting, postharvest handling and storage. Ripe fruits are more susceptible to fungal infection because of high content of moisture and nutrients, and no longer protected by the intrinsic factors, which confer resistance during their development. Biological control by using naturally available antagonistic microorganisms has been preferred for the control of post-harvest diseases of fruits and vegetables because it is environmentally safer than other control methods. The objectives of this study were to isolate antagonistic yeasts and bacteria from tomato phyllosphere and fructoplane and to evaluate their ability to suppress Alternaria fruit rot of tomato. A total of 24 yeast and 48 bacterial isolates were isolated from tomato leaves/fruits collected from Barka, Muscat Governorate of Sultanate of Oman. These microorganisms were tested for their antagonistic activities against *A. alternata* by using an *in vitro* dual culture technique. Among the 72 bacterial and yeast isolates tested, one yeast (*Meyerozyma guilliermondii*) and two bacteria (*Cronobacter sakazakii* and *Pseudomonas aeruginosa*) showed inhibitory activity against *A. alternata*. Scanning electron microscopic observation of the hyphae of *A. alternata* at the periphery of the inhibition zone in dual culture assay plate showed morphological abnormalities such as shrinkage, distortion and loss of turgidity. *P. aeruginosa* and *C. sakazakii* were found to grow well at temperatures ranging from 25°C to 35°C and the optimum temperature for the growth of *M. guilliermondii* was between 25 and 30°C. Postharvest dip treatment of tomato fruits with *M. guilliermondii*, *P. aeruginosa* and *C. sakazakii* significantly reduced the incidence of Alternaria fruit rot.

P (S 11) 54: Development and testing of termiticidal botanical formulations

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Termites in their habitat are one of the most important organisms which help in organic matter decomposition, creating nutrient balance in soil besides providing good aeration due to their tunneling behavior. But when their habitat encounters with areas of human use, they are one of the most problematic and destructive insect pest species that causes losses in the agriculture as well as in the wooden structures of buildings and households. For the termite management many physical, chemical and biological practices are in use. Use of chemical insecticide is one of the most widely used practice. Many chemical insecticides are being used with negligence which causes soil and water pollution as well as toxicity to humans through ingestion via chemically sprayed food crops and in some cases through inhalation. Thus, the chemical insecticide usage for termite management needs to be eliminated. The present study focuses on developing botanicals-based formulations which can prove to be good alternative to chemical insecticides. In this study, 6 plant based microemulsion formulations were developed, all differing in their contents and ratios of their components. In no-choice bioassay performed for testing the efficacy of these microemulsions against termites, microemulsion formulation K5 and TWI showed 96.7% and 80% mortality, respectively, after 11 hours. All the data pertaining to this study will be presented in the conference.

P (S 11) 55: Standardization of media of *Trichoderma asperellum* for commercialization of biocapsules with and without adjuvants

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Present day agriculture encourages the use of biocontrol agents as an alternative to chemical fungicides because of its safety to humans, environment and nonpathogenic organisms. *Trichoderma* sp., a very effective biocontrol agent meant for plant disease management is known to promote plant growth and induce biotic and abiotic stress tolerance in plants. The ability of *Trichoderma* to sense, invade and destroy other fungi has

been the major trait behind their commercial success as biopesticides. Commercialization of biopesticide products is primarily hindered due to poor shelf life. This limitation can be addressed by improving the shelf life of the organism through standardization of media of *Trichoderma asperellum* with adjuvants. Hence, a study was conducted to check the effectiveness of adjuvants on population of *Trichoderma* in different media. The culture was grown in potato dextrose (PD) broth and Trichoderma selective medium (TSM), with and without adjuvants. Both media were supplemented each with a sugar source (mannitol 3% and trehalose 15mM), wetting agent (PVP 2% and PEG 0.25%), adhesive (glycerol 3%, CMC 1% and liquid paraffin 1%) and surfactant (tween-80 0.5%). Twelve different combinations of these additives were used in both media and thereby standardized for maximum conidial production. The population of bioagent was studied at monthly intervals. Results showed that trehalose in combination with polyethylene glycol (PEG), glycerol, tween 80 and polyvinylpyrrolidone (PVP), glycerol, tween 80 in potato dextrose broth were the best, where the population of the bioagent was observed as 19 × 1016 and 10.66 × 1016 respectively at 60 days after inoculation (DAI). Also it was observed that all the treatments in potato dextrose broth showed higher population of the bioagent when compared with the treatments in TSM. From the study it is clear that both media along with additives could enhance the shelf life of *Trichoderma asperellum*..

P (S 11) 56: Biochemical characterization of *Trichoderma* species isolated from temperate region of India

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Recently, the environmental contamination caused by excessive use of chemical pesticides has increased the interests in integrated disease management, where chemical pesticides are substituted by bio-pesticides to control plant diseases especially soil borne diseases. *Trichoderma* species are potential fungal bio-control agents used against a wide range of soil borne plant pathogens. The major issues involved in mass production a biocontrol agent are selection of effective strains, development of cost effective methods, effective methods for storage in order to retain maximum shelf life. In the present study a total of 20 *Trichoderma* isolates were isolated from rhizospheric soil samples collected from various commercially grown chilli fields and kitchen gardens of district Anantnag and Baramulla of Kashmir valley by using *Trichoderma* specific medium. In order to evaluate a potential *Trichoderma* isolate, different biochemical tests such as carbohydrate metabolization, ammonia production, phosphate solubilization, chitinase production, HCN production and IAA production were done. Among all the isolates *Trichoderma* isolate (AT3) was found to be the best. After that shelf life of potential *Trichoderma* isolate (AT3) was checked on ten different cheap and locally available substrates including charcoal, ash, sawdust, cowdung, vermicompost, maize seeds, wheat seeds, rice seeds, dal weed and talc. These substrates were supplemented with 5% molasses, 5% yeast extract and 5% glycerol and were then stored at three different temperatures viz., 10°C, 20°C and 30°C. From the present study it is concluded that *Trichoderma* isolate (AT3) isolated from commercial field of Bangidhar Anantnag was the best as far as biochemical and enzymatic activity is concerned, among various substrates used, maize seeds and wheat seeds were found best for retaining the growth of *Trichoderma* species, among different temperatures 10°C was found best for retaining the growth of *Trichoderma* formulation and among different supplements used, molasses was found to be the best.

P (S 11) 57: Screening, identification and colonization by bacterial root endophytes against *Dematophora necatrix*, ubiquitous pathogen of fruit trees

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The objective of this study was to find out the potential root endophytic bacteria against *Dematophora necatrix,* Hartig, the causal pathogen of white root rot of apple; however it has a very wide host range across different fruit trees. Out of 74 endophytic bacteria isolated from symptomless roots of apple, only nine isolates which showed inhibitory effect during preliminary screening were further evaluated under *in vitro*, pot and nursery conditions against white root rot pathogen/disease*.* The most promising isolates were identified on the basis of morphological, biochemical and 16sRNA sequence analysis. Six most promising isolates were further subjected for root colonization assay. Under *in vitro* conditions, maximum mycelial inhibition of 80.37 per cent was obtained with isolate EK6 followed by ES8 (76.67%). Microscopic studies on interaction between bacterial endophyte with hyphal tips of *D. necatrix* at interaction zone revealed various morphological abnormalities in the hyphae. Nine most promising root endophytes proved effective after initial screening, were evaluated again under *in vitro*, glasshouse, and nursery conditions as seed dip treatment + soil application and root dip treatment + soil application. Out of nine bacterial endophytes screened under glasshouse and nursery conditions (virgin and sick fields), maximum vigour index, disease control and plant health parameters were recorded in *Stenotrophomonas maltophilia* strain EK6 followed by *Enterobacter* sp*.* strain EA7 and *Pseudomonas aeruginosa* strain ES8. Root colonization assay was performed with six bacterial root endophytes which revealed maximum colonizing behaviour of successful colonization. In case of seedlings treated with bacterial root endophytes, maximum endosphere and rhizosphere count was recorded with *Stenotrophomonas maltophilia* strain EK6. Additionally, confocal microscopic images of transverse sections of root cells colonized by promising bacterial root endophytes varied to a greater extent. Thus, abundant tissue colonization by various root endophytes as compared to untreated control suggested the establishment and persistence of inoculated strains in endosphere of apple seedlings. These findings are the first report of non-targeted colonization of apple roots by bacterial root endophytes against most devastating white root rot pathogen. This study highlights and explored the inner plant values with unique root symbiotic microbes. The multifarious activity of these microbes suggested them as an alternative approach for management of soil borne plant pathogens.

P (S 11) 58: Effect of bioagents on the incidence of *Macrophomina phaseolina* causing stem and root rot of sesame

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Sesame (*Sesamum indicum* L.) is one of the most ancient oil seed crop cultivated in tropical and sub-tropical countries. Irrespective of the agro-climate conditions, sesame is liable to be infected by various pathogenic fungi. Among the fungal diseases, stem and root rot of sesame caused by *Macrophomina phaseolina* affects severely at all stages of crop growth. *Macrophomina phaseolina* is a diverse, omnipresent soil borne pathogen. The present study was planned to evaluate the efficacy of various biocontrol agents against *Macrophomina*

phaseolina causing stem and root rot of sesame. Among the tested biocontrol agents against *Macrophomina phaseolina*, *T. viride* was found the most effective against the fungus followed by *T. harzianum*, *Bacillus subtalis* and *P. fluorescens* was the least effective in reducing Stem and root rot incidence.

P (S 11) 59: Development of *Trichoderma* formulation utilizing agri-waste rice husk biochar for mass multiplication and long-term storage

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Most of the substrates/culture media that are presently in use for mass culture of *Trichoderma* contain expensive ingredients (e.g. wheat, sorghum, maize, foxtail millet, molasses and brewer's yeast, etc.) and they do not support the biocontrol agent after its application in the field. Since these media are highly enriched, inoculum produced on them has relatively poor parasite fitness, therefore, a process for mass multiplication and long-term storage media for *Trichoderma species* on jaggery amended rice husk biochar has been developed that can be directly used for seed and soil application and avoid the tedious steps of drying, grinding, sieving and mixing of mass multiplied bioagent. Improved bio-efficacy of biochar-based *Trichoderma* formulation under field condition may be attained as higher and increased *Trichoderma* growth (10^{16}cfu/g biochar) was observed under storage.The present technology would greatly facilitate utilization of easily available agri-wastes for inexpensive and efficient production of bioagent formulation.

P (S 11) 60: Efficacy of bio-fungicides fungicides *Pseudomonas fluorescens* against blast (*Magnaporthe grisea*) disease in rice

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Organic farming is essence of agriculture in order to minimize chemical management of rice diseases an On Farm Trails were conducted on "Assessment of efficacy of bio-fungicides *Pseudomonas fluorescens* against blast (*Magnaporthe grisea*) disease in rice*"* conducted at KVK Rewa. Three treatment viz; T1- Farmers practice, T2: Foliar application of *Pseudomonas fluorescens* @ 5ml/ lit. and T3 : Seed treatment @10 ml/ kg and foliar application of *Pseudomonas fluorescens* at 10 different locations during 2016-17 and 2017-18 at Amara and Rithi village of Rewa District among all treatment T3 shows best result in which disease incidence was observed least 4% followed by T2 13% and T1 23%. Similarly maximum yield was obtained in T3 39.40 qtl./ha followed by 36.40 qtl./ha in T2 and 28.90 in T1. Maximum cost benefit ration was shown by T3 (2.48) followed by T2 (2.38) and T1(2.11).

P (S 11) 61: Management of cucumber powdery mildew caused by *Erysiphe cichoracearum* (DC)

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Cucumber (*Cucumis sativus* L.) is one of the oldest cultivated vegetable crop belongs to family cucurbitaceae. Powdery mildew is a serious disease of cucumber, caused by *Erysiphe cichoracearum* (DC). Symptoms first appears as white nearly or fluffy somewhat circular patches or spots which appear on the upper surface of the leaves and spreads to petiole, stem and fruits. Severely infected leaves become brown , shrivelled and defoliation may occur. Yield loss due to powdery mildew disease was estimated to be 50-70 per cent. Field experiment was conductedat at MARS, Raichur to evaluate various fungicides, botanicals and bio agents which are found to be efficient under laboratory studies. Fungicides, botanicals and bio agents spray was taken after disease appearance three sprays given at an interval of 15 days. The results revealed that minimum disease severity of 6.67 per cent was recorded in trifloxystrobin 25 % + tebuconazole 50 % after the third spray and recorded highest yield of 11.20 t/ha followed by azoxystrobin 23 % SC which showed the disease severity of 9.53 per cent with yield of 10.42 t/ha . While, *Pseudomonas flourescens* has shown least disease control with disease severity of 28.26 per cent compared to control plot which recorded highest disease severity of 75.67 per cent. Result indicated that combi fungicide trifloxystrobin 25% + tebuconazole 50% (0.30%) has proven to be most effective followed by azoxystrobine 23 % SC (0.15%) in management of disease.

P (S 11) 62: Characterization of *Fusarium* species causing bakanae disease of rice under temperate conditions of India

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The present work was conducted to identify *Fusarium* species affecting different varieties of rice under temperate conditions. A total of thirty-two *Fusarium* isolates were isolated not only from different locations but also from different seeds of pre-released and released varieties of rice. Out of thirty-two *Fusarium* isolates, seventeen isolates viz., *Fusarium* A1 to A17 were isolated from different locations of rice growing areas of Kashmir namely Khudwani, Larnoo, Tolinowpora, Nagam, Khull, Sopore and Wadura. Fifteen isolates viz., *Fusarium* A18 to A32 were isolated from different pre-released and released varieties of rice namely, SKUA-494, Mushbudji, SKUA-504,SKUA-525, Nunbouel, SKUA-516, Pusa Sughand-3 and SKUA-508. Among different isolates, highest indole acetic acid was produced by A29 isolated from variety Nunbouel and lowest was produced by isolate A6 isolated from variety K-39 grown in Tolinowpora (1650m amsl). Similarly out of sixteen *Fusarium* isolates which produce Gibberellic acid, highest was produced by isolate A7 isolated from variety China-1039 grown in Tolinowpora and lowest was produced by isolate A25 isolated from variety SKUA-494. The isolates were identified as *Fusarium fujikuroi* (*Fusarium* isolate A1, A7, A15, A17, A29 and A30), *Fusarium proliferatum* (*Fusarium* isolate A3, A11, A13, A14, A20 and A24), *Fusarium equiseti* (*Fusarium* isolate A6 and A9), *Fusarium nanum* (*Fusarium* isolate A10, A22 and A27), *Fusarium commune* (*Fusarium* isolate A16, A19, A25, A28 and A31) after nucleotide blasting under NCBI by targeting elongation factor 1 and 2.

P (S 11) 63: Management of *Macrophomina phaseolina* (Tassi.) Goid. causing dry root rot of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]

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Disease control efficacy of three selected bioagents *viz*.,*Trichoderma viride*, *Pseudomonas fluorescens* and *Bacillus subtilis* used as seed treatment (ST) and soil application (SA) along with or without organic amendment and two botanicals was evaluated against *Macrophomina* dry root rot of clusterbean under field conditions.The combined treatment of *T. viride* and *P. fluorescens* used as seed treatment and soil application provided maximum control of clusterbean dry root rot. The disease control efficacy of *T. viride* and *P. fluorescens* was improved when these two were used in combination with FYM, plant extracts *viz.,* neem seed kernel extract (NSKE) or Calotropis leaf extract (CLE).

P (S 11) 64: Assessment of pearl millet root bacterial endophytes for biocontrol activities

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Plants are potential inhabitants of indigenous microbes principally recognized as endophytic microbes which can reside inside their tissues without giving any visible external symptoms and live in mutualistic association with plants for at least a part of their life cycle. Endophytic microbes may be bacteria, fungi and actinomycetes. Bacterial endophytes have an advantage over bacteria residing the rhizosphere because they are within plant'stissues and have an opportunity to always be in contact with the plant's cells and therefore, to readily exert a direct beneficial effect. They are known for their potential to improve plant growth by direct and indirect mechanisms. Direct mechanism includes the microbial synthesis of phytohormones for example, production of Indole-3-acetic acid (IAA), ethylene, cytokinins and gibberellins. In indirect mechanism, bacterial endophytes produce secondary metabolites *i.e.* siderophore, antibiotics, hydrogen cyanide (HCN) and enzyme like 1-Aminocyclopropane-1- carboxylate (ACC) deaminase, cellulase and protease that play an important role in conferring tolerance to biotic and abiotic stresses. A total of 30 pearl millet root bacterial endophytes (PMRBE) were obtained from roots of pearl millet streaked on nutrient agar plates and these were assessed under laboratory conditions by examining their potential for siderophore production, HCN production, ACC utilization and cellulolytic activity. Sixteen isolates *viz.*, PMRBE1, PMRBE2, PMRBE4, PMRBE5, PMRBE6, PMRBE7, PMRBE9, PMRBE10, PMRBE16, PMRBE17, PMRBE18, PMRBE20, PMRBE23, PMRBE25, PMRBE26 and PMRBE28 were positive for siderophore production, three isolates *viz.* PMRBE6, PMRBE25 and PMRBE28 were found positive for HCN production, 30% of the bacterial endophytes showed good growth on ACC supplemented plates and cellulolytic activity was found in bacterial endophyte PMRBE18. Pearl millet root bacterial endophytes exhibiting biocontrol activities could be exploited in friendly, sustainable organic agriculture.

P (S 11) 65: Biocontrol potentiality of native proteobacteria against *Ralstonia solanacearum* under potato growing regions of Bankura, West Bengal

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Bacterial wilt caused by pathogenic *Ralstonia solanacearum* has become a severe problem mainly on potato in West Bengal and no effective control measure is available yet. Random sampling of soil was done in different Blocks and Mouzas of Bankura district of West Bengal and it was found that there are 7mouzas of Bankura which are affected by this lethal pathogen. To explore possibilities for the development of biological control for the disease 17 Proteobacteria were isolated from rhizosphere of plants growing in the local field of Bankura 5 were selected which were antagonistic to the pathogen. These were identified as *Pseudomonas aeruginosa*, *Pseudomonas putida* and *Pseudomonas plecoglossicida*. These were assessed for their potential to biocontrol the manifestation of the pathogen on potato by, Vigour of the germinated seedlings and survivability of the seedlings following their transplantation. Among the strains *Pseudomonas plecoglossicida* was found to be promising to combat the pathogenic effect of *R. solanacearum*in bioassays. Among the isolated Proteobacteria, there are 8 isolates which were antagonistic to other three soil-borne fungal pathogen i.e. *Rhizoctonia solani*, *Sclerotium rolfsii* and *Sclerotinia sclerotium*. Combination of the antagonist *Pseudomonas plecoglossicida*with the pathogen improved the percentage of the seedling emergence and the value (70%) was almost similar to that of the control. It was concluded that biocontrol organisms could be isolated from rhizosphere and applied to bacterial wilt infested field to combat the disease infestation.

P (S 11) 66: Management of mosaic disease of bottle guard (*Lagenariasiceraria* (Mol.) Stand) through integrated approaches

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Mosaic disease of bottle guard [*Lagenariasiceraria* (Mol.) Standl] is one of the most important foliar diseases, causing significant loss in India. The pathogen has wide geographical distribution and has been reported in over 100 countries, including environments ranging from semi-arid to tropical. It is the most widely distributed and important viral disease of cucurbits. The field trial was conducted during *Kharif* season of 2015 to 2018 at RARI, Durgapura for the integrated disease management of mosaic disease in bottle gourd through different means and combinations among seven treatments. The minimum disease incidence (6.56 %) and maximum yield (338.5 q/ha) were observed in treatment T_5(T_0+ Seed treatment with carbendazim 12%+ mancozeb 63% @ 3 g/kg and drenching of Captan 70 % +Hexaconazole 5% WP @ 0.1% 15 days after germination followed by spraying of Tebuconazole 50% + Trifloxystrobin 25% @1g/l + spray with (Imidacloprid 17.8 SL @ 7.5 ml/ 15 l + Neem oil 0.2%) followed by Fosetyl-Al @ 0.1% followed by spraying of Tebuconazole 50% + Trifloxystrobin 25% @1g/l + spray with (Imidacloprid 17.8 SL @ 7.5 ml/ 15 l + Neem oil 0.2%) followed by Fosetyl-Al @ 0.1% at 10 days interval) while maximum disease incidence (40.13 %)and minimum yield (225.7 q/ha)were observed in treatment T_7(Control). Natural products such as herbal extracts may provide alternatives to synthetic fungicides.

P (S 11) 67: Eco-friendly management of web blight disease of cowpea through bioagents

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Cow pea (*Vignaunguiculata* (L.) is attacked by many fungal, bacterial and viral diseases. Among the diseases, web blight caused by *Rhizoctoniasolani* Kuhn is the most serious soil borne disease in cow pea growing areas due to environmental conditions like high temperature and humidity causing severe yield loss. A field trial was conducted during 2016*kharif*season to manage web blight disease of cow pea. Combination of *T. harzianum*(Th-BKN) plus *B. subtilis*(Bs-BKN) used as seed treatment (5 + 5 g kg^{-1}) and soil application (5+5 kg ha^{-1}) proved to be most effective against web blight incited by *R. solani* in field conditions and provided maximum disease control (79.5%). Seed emergence, plant survival, , fresh and dry weight, root and shoot lengths and grain yield was higher and per cent cowpea plant mortality was lower in treatment *T. harzianum*(Th-BKN) plus *B. subtilis* (Bs-BKN) used in combination as seed treatment (5 + 5 g kg^{-1}) and soil application (5+5 kg ha^{-1}). The bioagents studied in the present investigation could be therefore, used as part of Integrated Disease Management (IDM) strategy for web blight of cowpea in areas where the disease is reported to cause yield loss.

P (S 11) 68: RNA-seq reveals dynamic expression of genes in *Chaetomiumglobosum* antagonistic to *Bipolaris sorokiniana* causing spot blotch of wheat

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Chaetomium globosum Kunze, is a ubiquitous filamentous fungus that commonly colonizes the soil and cellulose-containing substrates. The fungus has been reported to be a potential antagonist of various plant pathogens, most of which are soil borne and seed borne. Improved understanding of microbe- microbe interaction in the rhizosphere would assist in the development of potential bio-formulations. The molecular events and patterns of gene expression are not yet explored in *C. globosum.* In this study, we performed global transcriptome profiling of *C. globosum*strain Cg2 during interaction with phytopathogen *Bipolaris sorokiniana* isolate BS112 using RNA- seq in order to gain insights into the potential mechanism underlying the antagonism. Dual-culture technique was done to study bipartite interaction and was followed by isolation of total RNA from pooled samples of individual treatment at different intervals. The two paired end cDNA sequencing libraries were prepared and sequenced using IlluminaHiSeq 2×151 bp Chemistry. Approximately 20 million reads were obtained from three libraries with each in duplicate (Cg2 control, BS112 control and Cg2-BS112). Transcriptome analysis showed significant differential gene expression in *C. globosum*during challenge with *B. sorokiniana.* A total of 14366 (log2FC and pval0.01) differentially expressed genes (DEGs) were detected. Among them 7145 were up-regulated and 7221 were down regulated. Functional classification of DEGs based on gene ontology enrichment analysis and KEGG pathway annotations revealed that, 271 Antibiotic biosynthesis genes, 68 enzymatic Genes and 249 signaling genes were expressed in interaction. We identified various genes of biological function such as biosynthesis of secondary metabolites, polyketide synthase, antibiotic, hydrolytic enzymes, putative fungistatic metabolites, carbohydrate and protein metabolism related genes and some of signaling genes like protein kinases (PKs).This RNA-seq profiling will generate a novel dataset for further studies and will provide a blueprint for further research in biocontrol mechanism of this fungus.

P (S 11) 69: Triple combination of “Cu-Chi-Tri” exhibits a relay of mechanisms in managing late blight disease of potato

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Late blight had surpassed the annual management cost of $4 billion worldwide. Threat of emerging pesticide resistant races and excessive usage of pesticides calls for an effective and ecofriendly management strategy. A triple combination “Cu-Chi-Tri” consisting of reduced dosage of $Cu(OH)_2$, an antimicrobial and defence inducing biopolymer chitosan and a *Trichoderma* exhibiting copper-chitosan tolerance, was found effective against late blight in earlier researches. Therefore, this study was conducted to decipher the underlying operative mechanisms. The polymeric chitosan was found to form a chemical barrier between host and pathogen leading to reduced sporangial germination and sporangiophore production on leaf surface. The *in-vitro* and microscopic observations revealed anti-*Phytophthora* activity of chitosan in terms of extensive mycelial inhibition and morphological alterations, the larger oligomers (DP=5-7) being more effective. However, *Trichoderma* was found to depolymerize larger chitosan fragments (DP>6) to smaller oligomers resulting into mixture of monomers to hexamers in 72 h, both *in vitro* and *in planta*, hence, leading to a switch-over of defense mechanism from being a barrier to antimicrobial to a defense inducer. The defense induction was evident from activity of defense enzymes catalase and lipoxygenase, that was activated earliest by smaller oligomers (DP<5) and most prolonged by the ‘triple combination’ containing monomeric (DP=1) to hexameric (DP=6) oligomers of chitosan. The totality of different mechanisms was summed up with reference to disease severity that was found to be minimum for triple combination with *Trichoderma*, the depolymerized chitosan (i.e. oligomeric form) along with $Cu(OH)_2$ and thus establishing a resilient synergy for sustainable management of late blight disease.

P (S 11) 70: Evaluation of bacterial bio-formulations for the management of soil borne diseases in chilli

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Chilli is an important vegetable crop of Coastal regions of India. Productivity of chilli is affected by the incidence of insect pests and diseases. Soil borne diseases caused by various fungi and bacterium are important as they cause 30-40 per cent crop loss when the conditions are favourable. Chemical control of soil borne diseases is not effective and often results in the development of resistant strains. Three bacillus strains (RCh6-2b, STC-4 and RP-7) have been identified as potential biocontrol agents through various screening and evaluation process against many soil borne pathogens. These strains and the metabolites inhibited the growth of *Fusarium solani, Macrophomina phaseolina, Sclerotium rolfsii* under *in vitro* conditions. Further studies indicated that these strains produce antibiotics viz. iturin, surfactin, macrolactin, pumilacidin and amicoumacin. Application of talc formulations of these potential biocontrol strains in nursery and during transplanting reduced the incidence of soil borne diseases and increased the yield in the field evaluations. Further it was observed that the biocontrol efficiency was reduced wherever the incidence of bacterial wilt was recorded. Though the incidence of viral diseases was not reduced in the treatments, improved growth and increased yield was observed in biocontrol treatments compared to control.

P (S 11) 71: Survey of Nematode-trapping fungi in Bundelkhand region of India and test of their *in vitro* nematophagous and mycophagous ability against plant pathogens

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The Bundelkhand region covers an area of 7.08 million hectares (mha) and is located between 23020' and 26020' N latitude and 78020' and 81040'E longitude. The Bundelkhand region is rocky and mainly constitutes non-arable land. The soil of in the region is a mixture of black and red-yellow soils which are poor in organic nutrients. Bundelkhand has a hot and semi-humid climate. Usually the hottest days are in May and coldest days in December or January. Nematode-trapping fungi are a group of soil living carnivorous fungi that capture and kill the nematodes by their trapping. These fungi are most important because of their potential use as bio control agenet of plant and animal parasitic nematodes and some other plant pathogenic fungi. Since no work has been done on the presence of nematode trapping in fungi in Bundelkhand region of India, the present investigation was carried out to know the presence and dominance of nematode- trapping fungi in some region of Bundelkhand area. The soil samples were collected from Bundelkhand area. Soil samples were collected from the agricultural crop soil, forest plant soil and fruit orchard soil and processed for isolation and characterization of nematode-trapping fungi by soil plate technique. Each species attacking on nematodes were isolates, purified and characterized. The most important nematode- trapping fungi recovered from the soil were *Drechslerella dactyloides, D. brochopaga, A. conoides, A. eudermata, Dactylellina gephyropaga, D. phymatopaga, A. clododes and A. oligospora*. Orchard soil yielded maximum nematode-trapping fungi in comparison to other soils. The adhesive trap forming fungi was found more frequently in comparison to constricting forming fungi. These fungi were tested for their nematophagous ability against *Meloigodyne incognita* and mycophagous ability against *Rhizoctonia solani*. *Drechslerelladactyloides* and *Drechslerella brochopaga* were found more nematophagous against *M.incognita*. *R. solani* was found to susceptible againstmycoparasitic nature of *Arthobotrys conoides, A. eudermata, A. cladodes and A. oligospora.*

P (S 11) 72: Screening of soybean entries under AICRP trial against Yellow mosaic and bud blight disease

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Yellow mosaic disease (YMD), an important constraint in the production of soybean in India.The yellow mosaic disease (YMD), caused by whitefly transmitted begomovirus is one of the most important diseases of soybean.Besides YMD, recently, a thrips (*Thripstabaci*) transmitted tospovirus, groundnut bud necrosis virus(GBNV), appeared to be a serious concern causing budnecrosis disease (BND) in pulse crops in India. Though there is no absolute management option available against YMD and BND, deploymentof resistance is the most promising approach for their management. Breeding for resistance followed by release of new varieties through All India Coordinated Research Project (AICRP) on soybean showed promising result. In the present study we evaluated soybean entries under field condition in Delhi, a hotspot for YMV and BND. A total of 45 IVT, 19 AVT 1 entries and 20 AVT 2 entries of soybean were evaluated under epiphytotic field condition suitable for yellow mosaic and bud necrosis disease. For IVT entries two rows (5 m each) of individual entries were sown in non-replicated design while for AVT1 and AVT 2 entries evaluation was done in replicated trials. 12 entries in IVT showed highly resistant reaction against both yellow mosaic and bud necrosis.Among the AVT1 entries, NRC 138 and DS 3110 showed highly resistance against yellow mosaic disease. In AVT2 MACS 1493,NRC 128,NRC-137, NRC132,NRCSL-1 and PS 1611 showed highly resistant against yellow mosaic disease and KDS 992 is highly susceptible against Bud necrosis disease.

Session 12

Progress in chemical control of plant diseases

Keynote Papers

KN (S 12) 01: Integrated pest management of invasive shot hole borer and Fusarium dieback on agriculture and urban-wildland forest in California

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Integrated pest management is a strategy for addressing pest problems by combining control techniques to reduce the pest's impacts while minimizing impacts on people and the environment. This approach focuses on long-term management using a program of six components: pest identification, monitoring and assessing pest populations and damage, thresholds for when management action is triggered, prevention methods, control tools, and evaluating the effectiveness of management. Managing Fusarium Dieback (FD), a new vascular disease of hardwood trees ISHB-FD has proven to be a challenge. It is part of a highly invasive pest-disease complex threatening the agricultural crops, urban forests and native wildlands in California. This disease is vectored by two recently introduced invasive ambrosia beetles (*Euwallacea* spp.) known as Polyphagous Shot Hole Borer (PSHB) and Kuroshio Shot Hole Borer (KSHB) and collectively form the pest-disease complex known as Shot Hole Borer-Fusarium Dieback (ISHB-FD) complex. The range of options for the immediate term include direct control using contact insecticides, systemic insecticides, and fungicides to manage the beetles and their associated fungi. However, these options for chemical treatment are expensive, and not always effective. Based on current knowledge about ISHB-FD we developed an IPM program that takes into account cultural, physical, mechanical, and chemical and biocontrol strategies to control ISHB-FD in California. In this lecture, I will discuss those strategies and the metrics needed to evaluate the success of an IPM program to control ISHB-FD in urban-wildland forests and avocado groves in California.

KN (S 12) 02: Novel fungicides to overcome resistance and regulatory challenges in managing plant diseases

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The development of fungicide resistance in plant pathogenic fungi is a threat for many modes of action (MoA). This is an important motive driving the development of new fungicides. New fungicides might have new targets and forming new MoA-groups, or they can represent new actives within an existing MoA, which are not or only slight affected by already existing resistance mechanisms for the respective MoA. Recently introduced fungicides representing new MoA are e.g. the oxysterol binding protein inhibitors for control of oomycetes. New representatives from an existing MoA-group have been developed for demethylation inhibitors (DMIs, FRAC group 3), succinate dehydrogenase inhibitors (SDHIs, FRAC group 7) or complex III inhibitors (FRAC group 11, 31, 45). Within the DMIs, mefentrifluconazole has been developed with high efficacy on DMI adapted isolates of various pathogens such as *Zymoseptoria tritici* or *Erysiphe necator*. Other interesting candidates are complex III inhibitors like metyltetraprole, which binds in the outer quinone binding site, but is not affected by the main mutation (G143A) causing resistance to commercialised quinone outside inhibitors (QoIs) or inhibitors binding in the inner (matrix) site (QiI) such as fenpicoxamide. In the SDHI class, the development of target site mutations and presence of resistance mechanisms is quite complex; there are cases with complete cross resistance but also cases with an incomplete or lack of cross resistance. The elucidation, knowledge and interpretation of the effects of different resistance mechanisms in various pathogens to the representative fungicides of a particular MoA-group are mandatory for devising efficient resistance management strategies. Another important driving factor for the development of new fungicides are more restrictive regulatory requirements. Since different DMIs are under regulatory pressure, the development of DMIs with favourable regulatory profiles is mandatory to sustain this MoA. This has also played an important role in the development of the new DMI mefentrifluconazole and was achieved by inclusion of special tests which indicate the absence of undesirable side effects.

KN (S 12) 03: Recent progress and problems in chemical control of plant diseases

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Synthetic chemicals have contributed to sustaining quality food production through protecting a variety of crops from fungal diseases. However, the discovery of new chemical leads has decreased and there are more restrictions on chemical fungicides. Development of fungicide resistance in pathogens reduces fungicide efficacy and threatens food production. Under such circumstances, some new fungicides possessing unique property have been developed recently. Benzovindiflupyr (Syngenta), a succinate dehydrogenase inhibiting (SDHI) fungicide, is effective against various pathogens including *Colletotrichum* spp. which are less-sensitive to this class of fungicides in general. Mefentrifluconazole (BASF) has higher intrinsic activity against some pathogens such as *Zymoseptoria tritici* (Strobel *et al*., 2019), and *Monilinia fructicola* than preexisted sterol demethylation inhibiting (DMI) fungicides. Sumitomo developed a new quinone-outside inhibiting (QoI) fungicide metyltetraprole and its high control activity has been reported against QoI-resistant strains of *Z. tritici* and *Pyrenophora teres* ((Suemoto *et al*., 2019; Matsuzaki, 2019). Fungicide resistance will continue to impact global food security as long as ordinary type of 'fungicides' which triger pathogens directly are used. To breakthrough this situation, the use of broad-spectrum systemic acquired resistance (SAR) inducers will be promising because they induce resistance in plants based on and orchestrated by a number of defense mechanisms which are less likely to be broken down by pathogens. The three SAR inducers, probenazole, tiadinil, and isotianil effective to control blast disease caused by *Pyricularia oryzae*, now share over 80% of fungicides used for nursery box treatment common on rice in Japan. In the future, registration of conventional fungicides will become stricter than today. The progress of new technologies will assist the discovery of novel molecules and accelerate the integration of chemical control with biocontrol and resistance breeding in particular.

KN (S 12) 04: Strategic management of fungicide resistant *Cercospora beticola* in sugar beet using a holistic management strategy

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*Cercospora beticola*causes Cercospora leaf spot (CLS), one of the most damaging foliar diseases of sugarbeet grownin warm and humid regions.Growers usea combination of resistant varieties, crop rotation, incorporation of infected residue, and fungicides to manage CLS. Since the 1970s, growers have become more dependent on fungicides for effective control of CLS. Growers have used fentin acetate and triphenyltin hydroxide, benzimidazoles, demethylation inhibitors (DMIs), and quinone outside inhibitors (QoIs) with varying levels of success at controlling *C. beticola*. Over time, the pathogen, which has the ability to produce large numbers of conidia and multiple generations during a growing season, have developed resistance to most of the fungicides used for its control. In 2016, growers in the USA lost over $200 million because ofQoI resistance and a CLS epidemic. Currently, there are few fungicides that provide effective control of *C. beticola* when used alone and very few effective alternating partners. There is no new chemistry identified for CLS control in the near future. Sugar beet seed companies have been working at developing cultivars with improved resistance to *C. beticola*. Current field trials in the USA indicate that new cultivars have better resistance to *C. beticola* compared to the best current approved resistant cultivars. Fungicide applications were done on a calendar basis, and on an only when needed based on the presence of symptoms and favorable environmental conditions. Trials were harvested in September and the results indicated that a new generation of sugar beet without fungicide applications resulted in similar or higher recoverable sucrose compared to older varieties sprayed with fungicides. Strategies including incorporation of infected crop debris, crop rotation,planting away from previously infected field, new improved *C. beticola* resistant varieties, and when necessary, judicious use of fungicide mixtures are necessary for the sustainable and economic production of sugar beet.

KN (S 12) 05: Chemical control of major diseases in canola: Challenges and thrusts

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Canola is an important oilseed crop in Australia and area sown has exponentially expanded from 1.39M ha in 2009 to 2.3M ha in 2017. Both blackleg caused by *Leptosphaeria maculans* and stem rot caused by *Sclerotinia sclerotiorum* are serious impediments to sustainable canola production. Sclerotinia stem rot (SSR) had been present in Australia at low levels since the mid-nineties, however, the first major disease outbreak occurred in 2008. Currently, SSR is a yield limiting disease of canola in Australia particularly in years when conducive environmental conditions prevail during the cropping season. Lack of genetic resistance poses significant challenges in managing this disease and therefore, fungicides are the only means of managing SSR other than a few cultural practices such as crop rotation and isolation. Research conducted on the management of Sclerotinia in Western Australia over the last eight years has shown that while several fungicide products are effective against SSR, timing of fungicide application is critical and it should coincide with the onset of spore release but also taking into account whether subsequent seasonal conditions will be conducive for disease development.Blackleg is the most important disease of canola Australia-wide. Despite Australian commercial canola varieties having excellent resistance to blackleg, evolution of more virulent strains often compromise the genetic resistance. Therefore, management of blackleg with fungicides is an important tool in the integrated disease management strategies recommended to growers. Some fungicide products such as seed dressing with Jockey®, in-furrow application if Impact® and foliar application of Prosaro® had been used for successfully managing blackleg. However, recently, the evolution of the pathogen strains with reduced sensitivity in particular to the DMI fungicides have been detected across Australia. This highlights the need for continuous development of new chemistries for effectively managing blackleg in canola.Effective chemical control strategies and economics of chemical control to manage SSR and blackleg in canola will be discussed in detail.

Invited Papers

I (S 12) 06: Exploration of novel chemicals for management of post flowering stalk rot of maize

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Maize (*Zea mays* L) often faces yield loss problem due to adverse effect of biotic factors. Of these, post flowering stalk rot (PFSR) is an important one which is a ‘complex’ disease caused by *Macrophomina phaseolina* and *Fusarium verticillioides* alone and in combinations. The disease affects grain yield through plant dryness, reduced kernel filling and lodging. Cultural practice and fungicides are usually considered as effective management strategies for PFSR. In present investigation, five new chemical compounds namely Carbendazim 20, Prevent 107, Prevent 114, ALK Phosphoric acid and Thiram 7.5% developed by Micro Chemicals (India), Mandsaur (MP) were tested *in vitro* against important fungal pathogens *Rhizoctonia solani*, *M. phaseolina*, *Bipolaris maydis, F. verticilloides, F. oxysporum* and *Sclerotium rolfsii*. Carbendazim 20, Prevent 107, Prevent 114 and ALK Phosphoric acid exhibited excellent fungicidal activity against *R. solani*, *M. phaseolina* and *F. verticilloides* at 0.5 ml/l concentration. Evaluation *in vivo* during *kharif* 2016, 2017 and 2018 revealed three chemicals except Prevent 107 as superior in reducing PFSR incidence as compared to the commercial formulation Carbendazim 50WP. Although the performance of the new molecules was not significantly different, Carbendazim 20 @ 1 ml/l provided highest disease reduction (43.79%) followed by ALK Phosphoric acid @1.5ml/l (37.27%) and Prevent 114 @1.5 ml/l (32.08%). Performance of Prevent 107 @1.5 ml/l (30.07% reduction) was same with Carbendazim 50WP. With respect to grain yield, Prevent 114 contributed increased yield(19.17%) followed by Prevent 107 (15.95%), ALK Phosphoric acid (12.12%) and Carbendazim 20(10.35%), where as Carbendazim 50WP provided 0.69% increased yield over untreated (inoculated) control. The study showed a prospect of utilizing new chemical formulations as an alternative to the existing effective fungicides, especially for PFSR disease management.

I (S 12) 07: Morphological and molecular charecterization of blight causing pathogen in *Nerium oleander* and its management

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Nerium (*Nerium oleander*. L) is a fascinating, versatile flower crop of commerce and is a popular traditional loose flower belongs to the family Apocynaceae. It is commonly known as oleander, and is also an important medicinal plant in Indian folk medicine. It is one of the best pharmacognostic devices available now-a-days. The flowers are extensively used for making garland, religious offering and the plant is more popular for landscaping purpose. The leaf blight which induces brown coloured concentric ring symptoms on the leaves and the symptoms begin as small round spots, brown in colour with characteristic concentric rings. The spots may coalesce and form irregular spots as the disease progresses. Studies were conducted to isolate the pathogen from the infected nerium field. Morphological and molecular characterization and identification of the causal organism were carried out. Results obtained from that is the causal organism of the disease is *Alternaria chlamydospora* Mouch. This disease is observed first time in India on *Nerium* and the pathogen belongs to the family Pleosporaceae. During microscopic observations, it was observed that the mycelium is thread-like and septate. The conidia observed were brown and muriform. Sporulation was observed where the conidia were of about 20 micrometers in length. Among the recent molecules tested under *in vitro* condition, Tricyclazole (18%) + Mancozeb (62%) @ 0.3% was inhibitted 100 percent of the pathogen *Alternaria chlamydospora*.

I (S 12) 08: The Impact of Phytophthora diseases on crop production in Ghana

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Crop production plays an important role in the development of Ghana, through the provision of foreign exchange, food and income. Major crops grown in Ghana include cocoa, pineapple, root and tuber crops, legumes, cereals and vegetables. Cocoa production alone contributes about $ 2 billion annually to the GDP of Ghana with pineapple and other export crops also contributing significantly. The major factors affecting crop production include pests and diseases, with diseases caused by *Phytophthora* species having great impact. The black pod disease of cocoa, which is a major disease, is caused by two *Phytophthora* species; *Phytophthora megakarya* and *Phytophtora palmivora,* and have been reported to cause yield losses of between 30 to 100%. *Phytophthora parasitica* and *Phytophthora nicotiana* which also cause heart rot in pineapple result in yield losses of up to 100% on susceptible pineapple varieties like the MD2. As a result of the impact of these Phytophthora species on crop production in Ghana, especially on cocoa, government subsidizes the distribution of pesticides for their management, but not without its impact on the annual budget which forces it to go for loans annually in order to boost production. The level of damages caused by *Phytophthora* species on susceptible crops increases cost of production and thereby making crop production difficult in Ghana, which affects food security and income of farmers.

Oral Papers

O (S 12) 09: Green engineered Ag nanoparticles are effective against *Rhizoctonia solani* causing sheath blight of rice

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Silver (Ag) nanoparticle was synthesized by green approaches from *Trichoderma asperllum* and characterized by UV-Vis spectroscopy, Zetasizer, DLS, FTIR, SEM, TEM and NTA. These nnaoparticles were further evaluated at different doses against *Rhizoctonia solani* causing sheath blight of rice and found effective at 200 ppm with 73.39% of radial growth inhibition. Electron microscopy study for mode of cation showed that the nanoparticles accumulate inside the fungal cells, causes distortion that leads to death of the pathogen. Besides, Ag nanoparticles also found to produces ROS and causes death of fungal cell. Sclerotia of the pathogen could not able to germinate at 200 and 100 ppm. In green house, it was found that, application of Ag nanoparticles causes plant growth parameters as compared to control, with 20.00% disease incidence in treatment as compared to inoculated control *R. solani* (88.00%). Plants treated with Ag nanoparticles alongwith challenged inoculation of the pathogen showed highest concentration of vital secondary metabolites like phenols (20.58%), flavonoids (7.76%), terpenoids (28.09%) and total soluble sugars (16.12%).

O (S 12) 10: Management of bacterial leaf blight (*Xanthomonas axonopodis* pv. *cymopsidis*) of clusterbean in Rajasthan

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Rajasthan is major clusterbean producing state in India which contribute 70-75 % of total area and 60-62% of total production of country.Bacterial leaf blight (BLB) caused by *Xanthomonas axonopodis* pv. *cymopsidis* is an important disease of clusterbean, under severe infestation it cause 58-68 % losses in seed yield**.**Three-year field experiments were conducted in hot arid conditions at Bikaner, Rajasthan with the objective to find out suitable management strategies for BLB. The experiment was conducted on highly suscibtible cv. M-83 against BLB with five different treatment combination**s** of seed soaking with streptocycline and **/or** tetracycline and spraying against the blight and compared with an untreated control. Results of experiment showed that all the treatments brought significant decline in disease intensity and consequently enhancement of seed yield compared to control. The treatment having combination of seed soaking with streptocycline @ 500 ppm for one hour followed by two spray of streptocycline @ 250 ppm and copper oxychloride (0.2%) at 15 days interval had minimum (14.83%) BLB intensity, highest seed yield (11.18 q /ha) and net return (Rs. 16270 / ha). The seed soaking in streptocycline @ 500 ppm for one hour followed by two spray of copper hydroxide (0.2%) at 15 days interval was the next best treatment with 17.33 per cent disease intensity and 10.45 q/ha of seed yield. These treatments can provide an effective and economical management of bacterial leaf blight of clusterbean for cultivators.

O (S 12) 11: Evaluation of green synthesised zinc, sulphur and silver nanoparticles under *in vitro* and glasshouse condition against *Phakopsora pachyrhizi*

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Soybean rust caused by *Phakopsora pachyrhizi* Syd. is one of the major disease in soybean. The use of nanoparticles against soybean rust is merger. Hence three nanoparticles *viz.,* Chitosan based zinc oxide nanoparticles (Ch-ZnONPs), Pomegranate aril based sulphur nanoparticles (PA-SNPs) and Pomegranate aril based silver nanoparticles (PA-SNPs) were synthesised, characterised (by Particle Size Analyser and Scanning Electron Microscopy) and evaluated under *in vitro* and glasshouse conditions. The maximum per cent spore inhibition of 70.25, 74.70 and 86.68 per cent over control was recorded in Ch-ZnONPs (1250 ppm), PA-SNPs

(2000 ppm) and PA-AgNPs (500 ppm) respectively. The effective concentration of each nanoparticle under *in vitro* condition were evaluated in glasshouse along with their corresponding bulk materials. Among synthesised nanoparticles, the PA-AgNPs recorded lowest disease severity (6.67 PDI) at 250 ppm over untreated control (43.70 PDI) was found effective in reducing soybean rust under glasshouse condition. The synthesised nanoparticles have antifungal and antimicrobial activity resulting in lowest disease severity compared to the corresponding bulk materials and control.

O (S 12) 12: Role of crop protection chemicals in doubling farmer's income

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Agriculture is the backbone of the Indian Economy, as it employs nearly half of India's workforce and contributes 17% to the Nation's GDP. The Green Revolution led India from a food deficient country to a food surplus economy. It has not only helped increase exports of agricultural products but has also helped satisfy the demands of India's huge population. Although India has doubled its per hectare yield in the past decades it continues to be lower than the peer economies. One of the gravest problems faced by farmers is low level of income. The yearly average income earned by an Indian farmer is close to $ 1800 as compared to USA's $ 119,880, UK's 50,365 and Japan's $ 5,000. Farmers lose a significant part of their income as their crop and produce are attacked by pests and weeds. India's per hectare consumption of pesticides is significantly lower than countries with high yield. The per hectare consumption in India is 0.6 kg as compared to China's 17 kg, Japan's 12.5 kg, Germany's 3.7 kg, France's 3.7 kg and UK's 2.8 kg. Therefore, the crops get affected by pests at various stages in the farming value chain including pre-harvest and during harvest. As the productivity is directly hampered due to pest and weeds, it affects the income levels of farmers. It is essential to protect not only the crop but also the produce as on an average 25% of the yield is destroyed during storage and transportation. Crop protection chemicals play a vital role in two ways; protecting the crop and produce from pests and increasing the farm productivity. When judiciously applied, the damage of the crop is reduced and the output increases which directly impact the income generate per hectare. Hence, the crop protection chemicals will play a principal part in government's aspiration to double farmer's income by 2022. Integrated Pest Management (IPM) is one of the modern approaches to increase farmer income while protecting the environment. It provides a framework to undertake a step-by-step method in ensuring good crop health and higher productivity. IPM ensures reliable crop quality, decreased severity of pest infestations, reduced potential for problems of pest resistance or resurgence and increased consumer confidence leading to fair price of the yield. Chemical Crop protection products are often the most cost effective way of controlling infestations as part of an IPM strategy. To get the most out of these products, they must be applied correctly. Responsible use and good handling practices limit potential pesticide residues in crops and the environment as well as handling practices limit potential pesticides residues in crops and the environment as well as help avoid pest resurgence and resistance. Improved application techniques and equipment, such as reduced drift nozzles and spot spraying, help farmers protect untreated refuges and natural habitats for wildfire and pest enemies. The timing of treatment (season and time of day) as well as the type of products used is also critical factors. In short, doubling farmer's income cannot be guaranteed without the use of crop protection products. The present review paper will discuss about "Role of crop protection chemicals in doubling farmer's income"

O (S 12) 13: Effect of seed treatment and management of Cercospora leaf spot of marigold through chemicals and bioresources

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Floriculture is the art and knowledge of growing flowers to perfection. Marigold is one of the commercially exploited seasonal flower crop in India for multiple uses and ranks third in number after roses and chrysanthemum. Marigold (*Tagetes spp*.) is an Asteraceous plant and is native to South and Central America, specifically from Mexico. Cercospora leaf spot is caused by *Cercospora tageticola* Ellis & Everhart which causes heavy losses to marigold worldwide as well as in Himachal Pradesh during rainy season when the intensity is very high and an estimated loss upto 62 per cent to the crop was recorded due to the congenial climatic conditions. Therefore present detailed investigation were undertaken with the objectives i.e. effect of seed treatment with fungicides, bioresources and to evaluate the efficacy of chemical and non chemical methods against the disease for devising methods for its management. Since *Cercospora tageticola* is a seed borne pathogen, seed health testing studies were conducted by following standard method prescribed by International Seed Testing Association with desired amount of best fungicides, botanicals and bioresources to test their efficacy on different seed health parameters and seed infection due to seed borne nature of the pathogen, three treatments, Folicure 25% EC (tebuconazole), Score 25% EC (difenoconazole) and *Trichoderma harzianum* were found to be most effective by improving high germination percentage from 63.33 to 76.00 in comparison to other treatments, respectively. Different four non-systemic and six systemic fungicides and nine botanicals and bioresources were evaluated against *Cercospora tageticola* Both under in vitro and in vivo conditions. Amongest both types of fungicides, Folicure 25% EC (tebuconazole) (83.70 per cent) recorded maximum mycelial inhibition with minimum radial growth (14.67mm) of test pathogen. While in case of botanicals/bioresources, darak leaves extract (Melia Azedarach Makino) and beejamrit was most effective and significantly superior to all other treatments with 79.79 and 63.38 per cent inhibition in mycelial growth, respectively.

Poster Papers

P (S 12) 01: Management of gray mold disease of castor using fungicides

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Gray mold disease incited by *Botryotinia ricini* is a major constraint in castor growing areas of Telangana state resulting in yield losses. Use of chemical fungicides is an important tool to control the gray mold disease in castor. Investigations were carried out at ICAR -IIOR, Hyderabad, India during 2018 and 2019 with the aim to manage castor gray mold disease by using chemical fungicides under *in vitro* and *in vivo* conditions. An Experiment was conducted *in-vitro* by poison food technique to determine the effect of fungicides on radial growth of *B. ricini*. Propiconazole, Carbendazim and Pyraclostrobin + Fluxapyroxad were highly fungitoxic and Azoxystrobin has very low fungitoxicity against *B. ricini* under *in-vitro* conditions. These effective fungicides were tested in polyhouse and field conditions using highly susceptible castor hybrid DCH-519 in randomized

block design. The fungicides were sprayed on racemes (spikes) twice at fifteen days interval. Among the fungicides tested, Propiconazole at 0.03% was most effective giving a disease reduction of 89.3% followed by Pyraclostrobin + Fluxapyroxad at 0.03% with 81.8% disease control and Carbendazim were least effective. Propiconazole at 0.03% was found effective against castor gray mold and significantly increased the seed yield. Hence, two sprays of Propiconazole fungicide 0.03% at 60th and 75th days after sowing can be recommended for the management of castor gray mold disease.

P (S 12) 02: Management of cucumber mosaic virus (CMV) in cucumber (*Cucumis sativus*) in Bagalkot district.

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Cucumber (*Cucumis sativus*) is a widely cultivated plant in the gourd family, Cucurbitaceae. Cucumber mosaic virus (CMV) is most destructive disease in cucumber and its field management was carried out in the College of Horticulture, Bagalkot by using different combination of insecticides and botanicals during kharif 2018. Among the treatments imposed, seed treatment with imidacloprid 600 FS @ 9ml/kg followed by sprayed with acetamiprid 20% SP @ 0.2 g/lit and fipronil 5% SC @ 1 ml/lit has significantly less CMV incidence (25.56%), aphids population (9.73/plant). Seed treatment with imidacloprid 600 FS @ 9ml/kg followed by sprayed with acetamiprid 20% SP @ 0.2 g/lit was effective in the management of CMV incidence (46.67%). Further it was observed that seed treatment with imidacloprid 600 FS @ 9ml/kg followed by sprayed with acetamiprid 20% SP @ 0.2 g/L and fipronil 5% SC @ 1 ml/L observed higher yield compared to other treatments imposed. The maximum percent disease incidence (83.33%) was recorded in control.

P (S 12) 03: Management of coriander powdery mildew by new generation fungicides

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Coriander (*Coriandrum sativum* L.) is major an important seed spices in India used for flavor of food items. Coriander crop utilized from leaf to seed and affect many biotic and abiotic constraints limiting the quality and quantity of the crop. Apart from several crop management practices for good crop growth Powdery mildew of coriander is bottle neck for optimum production of coriander crop. Looking to importance of the crop and nature of the disease screen out some older and new generation fungicides for the management of the disease. The trail has been conducted for four years 2015-16 to 2018-19 in randomized block design, 3 m x1 m plot size , spacing 30cm x 20 cm with seven treatments *viz* Foliar spray of Tebuconazole (0.1%) (T_1), Foliar spray of Propineb(0.2%) (T_2),Foliar spray of Azoxystrobin(0.1%) (T_3),Foliar spray of Wettable sulphur (0.2%) (T_4), Foliar spray of Haexaconazole(0.1%)(T_6) Untreated control (T_7) on released coriander variety Chhattisgarh Dhaniya -1 .During the experiment applied best practices for good crop of coriander except fungicide application. The fungicide as treatment was applied when first appearance of the disease. The data on disease intensity recorded on the basis of 0-4 scale(0= Healthy plant),1=Whitish small spot on leaf, 2=Whitish growth covering on the entire leaf, 3= Growth on leaf and stem, 4= Growth on leaf, stem and umbel/pod before 25 days of crop harvest and yield data was taken at the time of harvesting and converted from per plot to q/ha. The pooled result of four year of experiment minimum disease intensity (%) found in the treatment when spray Wettable sulphur (0.2%) 4.25% PDI and maximum yield 14.25 q/ha. Next best treatment was spray of Hexaconazole (0.1%) disease intensity 7.13 per cent and 12.0q/ha.

P (S 12) 04: Management of blight disease complex of potato through novel fungicide combination Azoxystrobin + Mancozeb (Pluton)

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The potato (*Solanum tuberosum*) is one of the most important vegetable crops in the world, belonging to the family Solanaceae and is an important starchy food crop in both sub-tropical and temperate regions. The crop suffers from many diseases caused by fungi, bacteria, nematodes, viruses and nutritional deficiencies. Among these, Early blight and late blight caused by *Alternaria solani* and *Phytophthora infestanse* respectively is one of the most important disease prevailing all across the potato cultivation areas of India. The disease causes losses to crop productivity in the field and to tuber quality in storage. Average annual yield loss of potato due to this disease was apx. 60-75% of the total production depending upon the nature of the disease, weather conditions and type of variety grown (Dey and Chakraborty, 2012). For the management of this disease KRDC scientist have evaluated a novel pre mix combination fungicide coded as Azoxystrobin 11.5% + Mancozeb 30% WP (Pluton) in Wettable Powder (WP) formulation. The ratio of these two fungicides in premix combination is very important. Pluton is the mixture of 2 different groups of fungicide, one belonging to Dithiocarbamate group and second component of this mixture belongs to strobilurins each with different nature of mode of action. Recommended as foliar sprays under field conditions. This pre mix fungicide was found to be effective in reducing the blight complex intensity and resulted in highest yield as compared to recommended fungicides. The recommended dose for the disease management is 750-875gm per hectare. This novel fungicide mixture with good and stable (WP) formulation has become excellent alternatives to the currently available chemical tools for field level inhibition of this severe biotic threat of Potato. This is also an excellent combination to avoid or delay development of resistance by the fungi.

P (S 12) 05: Field management of purple blotch in onion through fungicides

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Onion (*Allium cepa* L.) is the oldest known important vegetable crop which is regarded as Queen of kitchen due to its highly valued flavor, aroma, unique taste, making the crop an important ingredient in all types of dishes. In spite of the increase in area planted, the production is estimated to be 4.5 per cent lower as compared to the previous years. Several abiotic and biotic factors hiders the production of onion. Among the various biotic factors diseases plays a predominant role in reducing the yield. Purple blotch is one such disease which is responsible for hindering the production in onion. Losses under field conditions vary from 30 to 100 per cent. The disease may reach epidemic state during the favourable conditions of high relative humidity (80-90 %) and optimum temperature (25°C). Field experiment was conducted in Main agriculture research station,(MARS)Dharwad during *kharif* 2017-18 by taking six different treatments including two treated check. The results revealed that seed treatment with *T. harzianum* @ 10 g/kg, furrow application of enriched

T. harzianum (*T. harzianum* 1 kg + vermicompost 100 kg) @ 250 kg/ha followed by spray of (tebuconazole 50 % + trifloxystrobin 25 %) @ 0.5 g/l proved to be significantly superior in terms of reduction in the disease and increasing in the bulb yield.

P (S 12) 06: *In vitro* evaluation of chemicals and antibiotics against bacterial leaf spot of Mango caused by *Xanthomonas campestris* pv. *mangiferae-indicae*

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Bacterial leaf spot of mango caused by *Xanthomonas campestris* pv. *mangiferaeindicae* is an important disease of mango worldwide. The severity of the disease in all the mango growing areas of Maharashtra resulting deteriorating losses to the farmers both in terms of quality and quantity. Chemicals *viz.* copper sulphate, copper oxychloride, streptocycline, mancozeb, 2 bromo 2 nitro propane 1,3-diol, carbendazim and antibiotic streptocycline and their combinations were evaluated *in vitro* by applying inhibition zone assay method by using Nutrient Agar (NA) as basal medium. The results revealed that the highest mean bacterial inhibition zone was made by Streptocycline treatment 22.40 mm in diameter followed by Carbendazim + Streptocycline (21.96 mm). The minimum mean inhibition zone was made by Copper sulphate treatment with 14.20 mm in diameter. Among individual concentrations the maximum inhibition zone was made by streptocycline (500 ppm) 27.6 mm in diameter followed by streptocycline + copper sulphate (250+2000 ppm) 25.3 mm in diameter. Streptocycline (500 ppm) and streptocycline + copper sulphate (250 + 2000 ppm) inhibited growth of the pathogen to the extent of 30.66 and 28.11 per cent over control followed by carbendazim + streptocycline (1000+500 ppm) with an inhibition growth of pathogen (24.60 mm) and per cent inhibition over control (27.33).

P (S 12) 07: Green synthesized *Trichoderma harzianum* based Zinc nanoparticles (Th-ZnNPs) in plant protection: One molecule with three benefits

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Nanotechnology is a frontier science in agriculture. Atomic level modifications of particles in the size range of 1-100 nm in any one of its three dimensions are classified as nanoparticles. Exploitation of metal nanoparticles is necessary of sustainable crop production. In the present investigation, zinc nanoparticles (Th-ZnNPs) were synthesized in ecofriendly manner using extract of *Trichoderma harzianum* as natural reducing agent. Briefly, 125 mg of zinc oxide was dissolved in distilled water and *Trichoderma harzianum* (Th) extract was added drop wise. The reaction mixture was kept under magnetic stirrer for 24 hr followed by microwave irradiation and ultrasonication. The synthesized Th-ZnNPs were characterized through various instruments. The UV-vis spectrophotometer analysis showed absorption maxima (peak) at 355 nm and particle size analysis revealed the 52 nm size of Th-ZnNPs. The Atomic Force Microscope and Scanning Electron Microscope revealed the circular to irregular shape of Th-ZnNPs with size range of 45-98 nm. The evaluation of Th-ZnNPs against plant pathogens revealed that, complete mycelial growth inhibition (100 %) of *Fusarium oxysporum* f. sp. *ciceri* (wilt of chickpea) was noticed at 500 ppm and maximum growth inhibition zone (23.33 mm) was noticed against *Xanthomonas axonopodis* pv. *punicae* (Bacterial blight of pomegranate) at 500 ppm. The soaking of chilli and maize seeds in Th-ZnNPs solution (1250 ppm) increased the seedling vigour and reduced the seed borne infection compared to Th-extract, bulk ZnO and water control.

P (S 12) 08: Evaluation of fungicides and bio-agents for integrated disease management of dry root-rot of sweet orange *Fusarium solani*

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Citrus belongs to the family Rutaceae, it is long-lived perennial crop and grown in more than 100 countries across the World. It is consider as one of the most important tropical fruit crop in India. The disease incidence of dry root rot is reported to be 5 to 50 per cent and nearly 10-15 per cent of the infected tress is being killed every year (Gopal *et al.,* 2000). Each treatment, three pots / replication were maintained and all the treatments were replicated thrice. All these pots were watered regularly and maintained in the screen house for further studies. The observations of disease incidence were recorded at different intervals *viz*., 20, 30, 40, 50, 60 Days after sowing. The total disease incidence of dry root rot with all the treatments were ranged from 20.97 (SAFF + *T. viride*) to 54.14 (Carbendazim) per cent. In Integrated disease management of dry root rot using Jambheri seed, using pot culture revealed that the treatment SAFF + *T. viride* recorded significantly highest reduction in total disease with maximum per cent reduction over the control (76.70%) followed by SAFF + *Trichoderma harzianum* ST (28.20% and 68.66%), Carbendazim + *T. harzianum* ST (33.36 and 63.04 %), Carbendazim + *Trichoderma viride* ST (33.79% and 62.45 %) and *Trichoderma harzianum* ST (40.85 and 54.61 %).

P (S 12) 09: Pragmatic management of causative agent of pomegranate wilt, *Ceratocystis fimbriata,* through *in vitro* assessment of fungicides and plant extracts

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Pomegranate is a vital fruit crop which is cultivated throughout the world. The crop having an essential role in the economy of farmers is scourged by various bacterial, fungal as well as viral diseases. In accordance to importance of various diseases associated with pomegranate, wilt disease, caused by *Ceratocystis fimbriata,* is the most rampant and devastating disease leading to massive losses to the farmers. Since farmers are heavily reliant on fungicides for combat against wilt disease, various fungicides and extracts of locally sourced plants known for their antimicrobial activity were therefore tested *in vitro* to formulate a strategic approach for management of the disease. Amongst systemic fungicides tested, absolute restraint was shown by carbendazim (100%), propiconazole (100%) and hexaconazole (100%) at all concentrations tested. Among non-systemic fungicide tested, mancozeb and propineb showed absolute inhibition of the mycelial development of *Ceratocystis fimbriata* at all concentrations evaluated. Amongst the combi-product fungicides, carbendazim 12%+ mancozeb 63% WP was absolutely efficient in all concentrations used against *Ceratocystis fimbriata*. All the combinations of fungicide + chemicals tested showed complete control (100%) of *Ceratocystis fimbriata* and were at par with one another. Amongst the plant extracts evaluated, the aqueous extracts of *Nerium indicum* at 30% concentration was noted to be most active in restricting mycelial growth of *Ceratocystis fimbriata* (40.98%). The efficacy of leaf extracts at 30 per cent was significantly superior over 10 and 20 per cent. However, the efficacy of most plant extracts tested against *Ceratocystis fimbriata* was intermediatory. The current studies were undertaken with an objective to articulate a plan of action against wilt disease of pomegranate by incorporating fungicides and plant extracts after a thorough *in vitro* evaluation.

P (S 12) 10: *In-vitro* efficacy of fungicides and bioagents against wilt of pigeonpea caused by *Fusarium oxysporum* f. sp. *udum*

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Pigeonpea wilt disease caused by *Fusarium oxysporum* f. sp. *udum* is one of most devasting seedborne disease. In this experiment total eight seed dressing fungicides at their recommended dosages were evaluated *in-vitro* by poisoned food technique, against *Fusarium oxysporum* f. sp. *udum* causing wilt. The systemic fungicides *viz*. Carbendazim 50% WP, thiophanate methyl 70% WP, tebuconazole 25% WG, pyroclostrobin 20% WG and combi fungicides *viz*. corboxin 37.5% + thiram 37.5% WP, carbendazim 12% + mancozeb 63% 75 WP and contact fungicides captan 75% WP were evaluated. However, the fungicides *viz.,* tebuconazole 25% WG, carboxin 37.5% + thiram 37.5% 75 WP and carbendazim 12% + mancozeb 63% 75 WP were found most effective with 100 per cent mycelial growth inhibition of *Fusarium oxysporum* f. sp*. udum.* The eight bioagents evaluated against *Fusarium oxysporum* f. sp. *udum* by dual culture technique. The most effective bioagent was *T. harzianum*, which resulted in significantly highest mycelial growth inhibition (85.62%), followed by *T. hamatum* (82.61%). *T. asperellum*, *A. niger, T. koningii*, *T. longibrachitum* which also caused mycelial growth inhibition in the range of 61.64 to 77.32 per cent.

P (S 12) 11: Management of wilt of pomegranate caused by the interaction of *Ceratocystis fimbriata* and *Meloidogyne incognita*

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Pomegranate is one of the important fruit crop of Karnataka and Maharashtra states in India. This crop is heavily suffering from the wilt disease caused by *Ceratocystis fimbriata* and *Meloidogyne incognita* either individually or by interaction of both the pathogens. The disease progression is so rapid and irreversible many times when both the pathogens are associated. To manage this disease under field conditions an experiment is conducted at a farmer's field at Tulsigeri village of Bagalkot taluk during 2017-18. The fungicides and bioagents against *Ceratocystis fimbriata* ; nematicides and oil cakes against *M. Incognita* were evaluated *in vitro* and effective 14 treatments in 3 replications were evaluated in filed along with control. Data revealed that propiconazole @ 0.2% + phorate @ 18 g/ plant recorded 66.6% of primary branches, 27.2% of secondary branches and 44.7% of tertiary branches infected followed by propiconazole @ 0.2% + neem cake @ 100 g/ plant + *T. harzianum* @ 100 g/plant recorded 50.0% of primary branches, 50.0% of secondary branches infected and 60.0% of tertiary branches infected. These two treatments found effective over all the treatments. This was followed by tebuconazole @ 0.2% which recorded 50.0% primary branches, 40.0% of secondary branches and tertiary 34.4% of tertiary branches infected and propiconazole @ 0.2% recorded 50.0% of primary branches infected, 60.0% of secondary branches infected and 66.6% of tertiary branches infected. In control complete wilt incidence was observed in primary, secondary and tertiary branches. The highest yield of 14.58 t/ha was recorded in propiconazole + phorate with net returns of Rs. 7,40,423 which was followed by propiconazole + neem cake + *T. harzianum* (12.99 t/ha) with net returns of Rs. 6,10,701.

P (S 12) 12: Efficacy of fungicides against *Fusarium solani* f. sp. *pisi* causing root rot of pea in Himachal Pradesh

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Pea root rot is a complex disease, mainly caused by *Fusarium solani* f. sp. *pisi* in Himachal Pradesh becoming a major threat to pea cultivation in the state. Since, the cultivars grown in the state are highly susceptible to this disease and as it affects the crop at its initial stages which ultimately leads to high yield losses. Fungicides application is highly effective and simple approach to reduce the disease at its initial stage due to its high accessibility. In the present investigation, six fungicides *viz.*, carbendazim 50 WP, propiconazole 25 EC, tebuconazole 2 DS, thiram 75 DS, carboxin 75 WP and carboxin 37.5% + thiram 37.5% were evaluated *in vitro* against the pathogen at different concentrations. Among the tested concentration of different fungicides inhibition percentage were increases with increase in concentration. At each concentration, carbendazim 50 WP was found highly effective. All test fungicides gave cent percent mycelial inhibition at 1000 ppm except carboxin 75 WP which showed 66.3 percent mycelial inhibition of the pathogen. Carbendazim 50 WP and carboxin 37.5% + thiram 37.5% gave cent percent mycelial inhibition at 500 ppm while at 750 ppm carbendazim 50 WP, propiconazole 25 EC and carboxin 37.5% + thiram 37.5% showed cent percent mycelial inhibition. So, these fungicides can be used as a seed dresser to reduce the incidence of pea root rot.

P (S 12) 13: Evaluation of fungicides for the management of northern leaf blight of maize

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Northern leaf blight caused by a fungal pathogen *Exserohilum turcicum,* is one of the most devastating diseases of maize. It is reported to cause 28 to 91 per cent reduction in grain yield. It is prevalent in almost all the maize growing areas such as Karnataka, Andhra Pradesh, Uttar Pradesh, Uttarakhand, Himanchal Pradesh, Orissa, and North Eastern hill states. Use of fungicides for the management of disease is an effective management strategy and thus various fungicides have been tested for field application. Eight fungicides Azoxystrobin, Tebuconazole, Propiconazole, Thiophenate methyl, Zineb, Captan, Curzate M8 (Cymoxanil+ Mancozeb) and Avtar (Zineb+ Hexaconazole) were evaluated at five different concentrations against *Exserohilum turcicum* under *in vitro conditions.* Systemic fungicides were tested at 5, 10, 20, 30 and 50ppm while non systemics were tested at 50, 100, 200, 500 and 1000ppm. Four fungicides (Propiconazole, Tebuconazole, Avtar and Captan) gave good results under lab conditions and were tested under glasshouse condition. Propiconazole 25% EC gave the best results compared to other tested fungicides both under *in vitro* and *in vivo* conditions.

P (S 12) 14: Management of Fusarium wilt of chickpea under rainfed conditions in mid hill region of Jammu, Jammu & Kashimir, India

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Chickpea is one of the most vulnerable crop to attack of pests and diseases causing huge production losses. Among the diseases, chickpea wilt poses a severe problem in rainfed areas of Jammu region. It was observed that chickpea seeds treated with *Trichoderma viride* (soil application) recorded 21.50% wilt incidence followed by *Trichoderma viride* (seed application) 35.25%, neem seed cake 47.00%, Carbendazim 48.90%, Thiram 50.14% and Captan 56.50%. While *Trichoderma viride* (soil application) gave 78.50% (highest) wilt disease control, followed by *Trichoderma viride* (seed application) 64.75%, neem seed cake 53.00%, Carbendazim 51.10%, Thiram 49.86%, Captan 43.50% and least in check. Recommendations of the results were repeated in the 4 farmers field in Reasi district, disease incidence were 25.40% but after applying of *Trichoderma viride* (soil application) diseases incidence reduced to 7.95% only and it was reduced to 6.75% (Table 2). While yield of chick pea was enhanced from 5.25 to 9.20 q/ha and maximum 9.80 q/ha against least farmers' practices i.e.5.25% only.

P (S 12) 15: Impact of seed priming with fungicides and biocides on germination of wheat caused by *Bipolaris sorokiniana*

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B. Sorokiniana is a most destructive fungus causing foliar disease of wheat and spreading all the wheat growing area, s of country. The present investigation were taken to evaluate the potentiality of different seven fungicides (Raxil 060 FS, Trifloxystrobin 500SC, Trifloxistrobin + Tebuconazole 080FS, Vitavax, Flint (Trifloxystrobin 50WG), Nativo 75WG (Trifloxystrobin 25% + Tebuconazole 50%) and Tebuconazole 2% D S), bioagent (*Trichoderma viride*) and botanical (Neemexcel) were tested against *B. Sorokiniana* on wheat seed in blotter paper method. It was revealed that seed treatment with fungicides and biocides significantly increased the germination percentage of wheat seed over the control except Nativo 75WG and Trifloxystrobin + Tebuconazole 080FS. The maximum germination with 100 per cent was recorded in the treatment of *Trichoderma viride* followed by Raxil 98.64%, Tebuconazole 2%DS 98.24 per cent and vitavax 96.00.Seed treatment with neem product (neemexel) gave(93.88 per cent) the superior result over the control(92.00 per cent) but inferior to other treatment *viz*. Trifloxistrobin +Tebuconazole 080FS (82.00 per cent), Nativo 75WG (Trifloxystrobin 25% + Tebuconazole 50%) 84.40 per cent, Flint (Trifloxystrobin 50WG), 90.40 per cent and Trifloxystrobin 500SC (91.20 per cent) .

P (S 12) 16: Efficacy of integrated management technologies against Phytophthora blight in sesame in Kymore Plateu and Satpura Hills agroclimatic zone of Madhya Pradesh

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Sesame (*Sesamum indicum* L.) is one of the oldest Indian originated, high value cash crop in oilseeds. India ranks first in world with 19.50 lakh hectare acreage and 8.507 lakh tonnes of production. The productivity (436 kg $^{--1}$ ha) of Sesame is less than the potential yield of recommended varieties in other countries of the world. Among the different biotic factors, Phytophthora blight is a major constraint for the productivity of Sesame and it causes up to 79.8 % yield loss due to non adoption of suitable integrated disease management modules for Phytophthora blight management. In the present investigation, on farm trials were conducted by KVK Sidhi in two adopted villages (Chhawari and Mamder) during year 2014-16 to evaluate the efficacy of four different treatments including farmer's practice for management of Phytophthora blight of Sesame. The results revealed that all three treatments were significantly superior over farmer's practice (T_1). The treatment no. four (T_4) comprising Seed Treatment with Apron(Metalaxy)-35SD @6 g /Kg seed + Soil treatment with *Trichoderma viride* @ 5 kg ha^{-1} + Foliar Spray of Ridomil gold MZ 68 WG @ 0.25% at early onset of disease found most effective in reducing Phytophthora blight disease incidence (86.69%), increasing yield (36.05 %), net return (Rs. 7439.75) and benefit- cost ratio (Rs. 0.45). This was followed by T_3 and T_2 where respectively seed Treatment with Apron (Metalaxy)-35SD @6 g /Kg seed + Soil treatment with *Trichoderma viride* @ 5 kg ha^{-1}) and seed Treatment with Apron (Metalaxy)-35SD @6 g /Kg seed. In this way, for effective management of Phytophthora blight in sesame, seed Treatment with Apron (Metalaxy)-35SD @6 g /Kg seed + Soil treatment with *Trichoderma viride* @ 5 kg ha^{-1} + Foliar Spray of Ridomil gold MZ 68 WG @ 0.25% at early onset of disease can be used for improved sustainable management.

P (S 12) 17: *Phytophthora* fruit rot - an emerging disease of brinjal

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Recently, a new fruit rot disease was seen widespread in brinjal. The disease was reported from Thrissur and Palakkad districts of Kerala state with disease severity upto 52 per cent. The symptoms observed were tan to brown lesions on the fruits which rot subsequently. The rotten parts became depressed and developed wrinkles. White cottony mycelium was also found on the lesions. Usually the infection begins from lower fruits. White cottony mycelium on the fruit surface produced lemon shaped sporangia with conspicuous papillae. Isolation of pathogen on carrot agar showed similar type of mycelium which developed in a distinct rosette pattern and later produced lemon shaped sporangia. The pathogenicity of the isolate was proved by inoculation on healthy brinjal fruits .Based on cultural and morphological characters it was concluded that the pathogen belongs to

the genus *Phytophthora.* Efficacy of different fungicides at different concentration and a bioagent against the pathogen was assessed under *in vitro* conditions. A total of seven fungicides and one bioagent were tested. It was found that, all the three concentrations of copper hydroxide (0.05, 0.1 ,0.15 per cent), metalaxyl + mancozeb (0.05, 0.1, 0.25 per cent), mancozeb (0.05, 0.1, 0.2 per cent), Fosetyl-Al (0.05,0.1 ,0.2 per cent), cymoxanil 8% + mancozeb 64% (0.05 ,0.1 ,0.25 per cent) showed cent per cent inhibition whereas, azoxystrobin at 0.025 and 0.05 per cent recorded 36.77 and 38.44 per cent inhibition respectively. The bioagent *Trichoderma sp* (KAU) also gave cent per cent inhibition of the pathogen.

P (S 12) 18: Spray scheduling of fungicides for the management of *Stemphylium* blight of onion caused by *Stemphylium vesicarium*

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Onion is one of the most important commercial crops grown all over the world. It is threatened by many diseases and pests which result in yield losses and also depreciate the quality and export potential of the produce. Stemphylium blight caused by *Stemphylium vesicarium* (Wallr.) Simmons is one such disease, which has emerged as a major economic threat to the onion crop in the past few years. It is also a serious problem throughout the country, especially in Northern and Eastern India. Generally, chemical management is chosen as a resort to manage field diseases like leaf blights owing to its quick and ensured effectiveness. But the use of chemicals without a well-structured strategy leads to injudicious use of fungicides, which is not only uneconomical but also poses environmental risks. Not only the fungicide itself, but also the effect of application frequency and spray interval on the disease severity and yield should be taken into account in order to formulate a well-rounded strategy. The present study was conducted to find out the optimum number of sprays and spray interval for managing the Stemphylium blight of onion. Six different spray schedules using two recommended fungicides *viz*. mancozeb 75% WP (1.5 kg ai/ha) and difenoconazole 25% EC (125 g ai/ha) used in alteration, were devised and tested under field conditions. An untreated check was also maintained and the disease severity was recorded for all the treatments. The various spray schedules were compared on the basis of disease management offered by them, their effect on yield and their economic feasibility was also taken into account. Spray schedule having 5 sprays of fungicides starting at 30 days after transplanting, at 10 days interval offered the highest per cent disease control as well as the highest net return due to treatment.

P (S 12) 19: Efficacy of fungicides as foliar spray with seed treatment by fungicides and bio agent separately on web blight severity and grain yield of moongbean

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A field trial was conducted during *kharif* season of 2018 in NEBCRC, Pantnagar having nine treatments including control with three replications using Kopergaon as a susceptible cultivar of moongbean. Nine treatments included (taken 4 fungicides, every fungicide sprayed on standing crops which seeds were treatment with fungicide combination *i.e.,* carbendazim + thiram (2:1) 3gm/kg seed and same fungicide sprayed on seed treatment with one bio agent *i.e.,* PBA-3, 6gm/kg seed) and control sprayed with water. Effect of foliar spray of four different fungicides *viz.* tebuconazole 50% + trifloxystrobin 25% WG (700g/500 lt. water), tebuconazole 25.9% EC (700g/750 lt. water), and pyroclostrobin 133 g/l + epoxiconazole 50 g/l (700ml/750 lt. water) and Fluxapyroxad 62.5 g/l + epoxiconazole 62.5 g/l (750ml/500 lt. water), were tested among these nine treatments and also observed the interaction of seed treatment and foliar spray of fungicides. Two sprays were done at 30 and 40 days after sowing at 10 days interval. Seed treatment with carbendazim + thiram and two foliar sprays of nativo (tebuconazole 50 % + trifloxystrobin 25% WG) at 10 days interval showed highest decline in disease severity (56.46 %) and highest grain yield (1388.6 kg/ha) over check followed by seed treatment of PBA-3 and two foliar sprays of nativo (tebuconazole 50 % + trifloxystrobin 25% WG) which gave 47.06 per cent decline in disease severity over check and 1321.50 kg/ha grain yield.

P (S 12) 20: Management of white rust in Indian mustard caused by *Albogo candida*

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Fungicides are alternatives of resistant varieties. In absence of resistant varieties it play major role in managing the disease. Therefore, fungicidal management trial was conducted to search effective and economically beneficial fungicides. All the test fungicides significantly reduced the disease severity in comparison to check. After third spray, the minimum per cent disease severity on leaf (12.96%) and on staghead (7.3%) were recorded on three foliar spray of Thiram 2.5 g/kg seed + Propiconazole @ 0.1%, which has highly significant with all treatments. The Maximum average yield (1677.77 Kg/ha) was recorded in Thiram 2.5 g/kg seed + Propiconazole @ 0.1% and followed by *P. fluorescen* @ 6.0g/kg seed + Propiconazole @ 0.1% (1633.33 Kg/ha), and minimum seed yield (988.88 Kg/ha) was recorded on control plot. The Maximum per cent increase in yield 69.66% was recorded with Thiram 2.5 g/kg seed + Propiconazole @ 0.1% followed by treatment *P. fluorescen* @ 6.0g/kg seed + Propiconazole @ 0.1% (65.16%). However, maximum yield loss (41.05%) was recorded on Thiram 2.5 g/kg seed + Propiconazole @ 0.1% followed by *P. fluorescen* @ 6.0g/kg seed + Propiconazole @ 0.1% (39.45%). Three foliar sprays of Thiram 2.5 g/kg seed + Propiconazole @ 0.1% were most effective reducing the disease severity and boost up the seed yield. Maximum yield loss of 41.05 was avoided with Thiram 2.5 g/kg seed + Propiconazole @ 0.1% but maximum cost-benefit ratio of 1:3.42 was recorded with foliar spray of Propiconazole @ 0.1%.

P (S 12) 21: Evaluation of bioefficacy of ametoctradin 300 g/l + dimethomorph 225 g/l sc against downy mildew disease of cucumber

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Cucumber is the most important Vegetable crop of Haveri district. The crop is suffering from many fungal and viral diseases. Among the diseases, downy mildew is the most deadly and causing severe yield loss. For this an experiment was conducted having eight treatments with three replications for the management of downy mildew disease. Before the treatment imposition all the treatments were nonsignificant to each other. After the first spray all the chemical treatments reduces the disease incidence drastically. Before second spray the treatments Ametoctradin 300 g/l + Dimethomorph 225 g/l SC at 1000 ml/ha and market standard Ametoctradin 300 g/l + Dimethomorph 225 g/l SC (Zampro) @ 1000 ml/ha recorded least Per cent Disease Index (6.34 and 6.94 % respectively) which was found to be on par with lower dose of Ametoctradin 300 g/l + Dimethomorph 225 g/l SC at 800 ml/ha and market standard Ametoctradin 300 g/l + Dimethomorph 225 g/l SC (Zampro) @ 800 ml/ha. Among the market standard, Cymoxanil 8% + Mancozeb 64% WP @ 1500 g/ha recoded the PDI of 9.16% which is followed by Dimethomorph 50% WP @ 1000 g/ha (10.83). Highest PDI was recorded in untreated control treatment (16.26%). Similar trend was noticed at 10 days after 3rd spray. Ametoctradin 300 g/l + Dimethomorph 225 g/l SC at 1000 ml/ha and market standard Ametoctradin 300 g/l + Dimethomorph 225 g/l SC (Zampro) @ 1000 ml/ha recorded highest fruit yield of 22.84 and 22.78 tons/ha respectively and which were found to be on par with Ametoctradin 300 g/l + Dimethomorph 225 g/l SC at 800 ml/ha (21.07 t/ha) and market standard Ametoctradin 300 g/l + Dimethomorph 225 g/l SC (Zampro) @ 800 ml/ha (21.00 t/ha). Lowest fruit yield was recorded in untreated control treatment (8.62 t/ha). There were no symptoms of phytotoxicity on Cucumber plants either on leaves or fruits after the application of Ametoctradin 300 g/l + Dimethomorph 225 g/l SC at 1000 and 2000 ml/ha. None of the treatments exhibited any phyto toxicity symptoms after 1,3,5,7 and 10 days after application of the chemical. Ametoctradin 300 g/l + Dimethomorph 225 g/l SC at 1000 ml/ha was found to be most effective for the management of downy mildew of Cucumber as it exhibited an on par performance with Ametoctradin 300 g/l + Dimethomorph 225 g/l SC at 800 ml/ha with respect to Percent Disease Index and yield.

P (S 12) 22: Screening of fungicides against *Ganoderma lucidum* for the management of basal stem rot of coconut

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Basal stem rot incited by the fungus *Ganoderma lucidum* is a lethal disease of coconut causing significant reduction in yield. A study was undertaken to assess the inhibitory effect of eight fungicides at 100, 250 and 500 ppm concentrations on the growth of *Ganoderma lucidum,* under *in vitro* evaluation by poisoned food technique. The virulent isolate of *Ganoderma lucidum isolated* from Coconut Research Station, Veppankulam was used for the study. Fungicides *viz.,* Thifluzamide 24 SC, Mancozeb 50% + Carbendazim 25% WS, Zineb 68% + Hexaconazole 4% WP, Myclobutanil 10% WP, Dodine 65% WP, Pyraclostrobin + Fluxapyroxad 250 SC, Kresoxymethyl 44.3% SC and Isoprothiolone 40% EC. Among the eight fungicides tested, Mancozeb 50% + Carbendazim 25% WS, Zineb 68% + Hexaconazole 4% WP and Pyraclostrobin + Fluxapyroxad 250 SC were found superior recording 100 per cent inhibition of *Ganoderma lucidum* at all the concentrations tested and showed superior over the other fungicides tested under *in vitro.*

P (S 12) 23: Efficacy of novel fungicide combination of Azotrix on sheath blight of rice caused by *Rhizoctonia solani*

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India has maximum area under rice cultivation at world level but productivity is low which is attributed to several factors like drought, lack of inputs, unfavourable weather conditions, lack of world standards, suitable varieties, poor seed quality, less availability of agro-chemicals and socioeconomic problems, non-adoption of modern production technologies and the most important are the losses caused by weeds, insect-pests and diseases. The rice crop suffers from many diseases caused by fungi, bacteria, nematodes, viruses and nutritional deficiencies. Among these, sheath blight caused by *Rhizoctonia solani* is one of the most important disease prevailing all across the paddy cultivation areas of India. This disease cause yield loss up to 69% and appears at maximum tillering stage. The disease is soil-borne in nature. The sclerotia produced by the fungus is the main source of survival of this pathogen. Once infection occurs, secondary spread take place through direct contact. For the management of this disease KRDC scientist have evaluated novel pre mix Patented combination fungicide coded as Azotrix (Azoxystrobin 16.7% + Tricyclazole 33.3% SC) in Suspension Concentrate (SC). Azotrix is the mixture of 2 different groups of fungicide, one belonging to trizole group and second component of this mixture belongs to strobilurins each with different nature of mode of action. Recommended as foliar sprays under field conditions. This pre mix fungicide was found to be effective in reducing Sheath blight intensity and resulted in highest grain yield as compared to recommended fungicides. The recommended dose for the disease management is 200-250 ml per acre. This novel fungicide mixture with good and stable suspension concentrate formulation has become excellent alternatives to the currently available chemical tools for field level inhibition of this severe biotic threat of rice.

P (S 12) 24: Determination of persistence of fungicide in seeds and seedlings of groundnut

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Persistence of carboxin fungicide in seeds and seedlings of groundnut was analyzed using Liquid Chromatography – Mass Spectrometry (LC-MS/MS). Groundnut seeds were treated with carboxin + thiram (Vitavax power @ 3g kg-1), stored in butter paper bags and the systemic component of the treated fungicide carboxin was analyzed for its residues upto one month period at weekly intervals. Treated seeds were sown in earthen pots and the seedlings raised were analyzed for the presence of carboxin residues at weekly intervals upto one month age. Maximum residues of carboxin were recorded in groundnut seeds stored for two weeks (332.83 mg kg-1). In case of seedlings, significantly highest residue of carboxin was recorded at immediately (zero days) after emergence (12.43 mg kg-1) and the least was found with one month old seedlings (0.04 mg kg-1). Fungicide residues were found to be very less in seedlings when compared to seeds and this can be attributed to degradation of fungicide at the time of seedling emergence and its further growth. Persistence of carboxin in the seedlings till one month indicates that the systemic fungicide (carboxin) may protect the crop till one month age against seed and soil borne diseases.

P (S 12) 25: Zinc nanoparticles and their antifungal activity against *Alternaria burnsii* causing blight of cumin

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Zinc nanoparticles (ZnNPs) produced were evaluated against *Alternaria burnsii* to observe the inhibitory effect of these ZnNPs on the mycelial growth. Physical characterization of synthesized ZnNPs was 68.04 nm in size, Pdi- 0.263, Keps-252.4. Among the twelve treatments, the best treatment was synthesized ZnNPs with concentration (750 ppm) proved most effective with 86.17 per cent average inhibition of mycelial growth of *A. burnsii.* The next effective treatment was synthesized ZnNPs with concentration (700 ppm) giving 83.40 per cent growth inhibition which was at par with treatments of synthesized ZnNPs with concentration 650 ppm with 82.49 per cent and 600 ppm, 550 ppm, 500 ppm giving 82.02 per cent growth inhibition, respectively. The next treatment was synthesized ZnNPs with concentration (250 ppm) giving 79.26 per cent growth inhibition. Followed by treatment commercial ZnNPs with concentration (1000 ppm) giving 53.46 per cent growth inhibition. The next effective treatment was commercial ZnNPs with concentration (500 ppm) giving 44.69 per cent growth inhibition. Followed by treatment of carbendazim 50 WP with concentration (500ppm) giving 11.51 per cent growth inhibition. The least effective treatment was commercial ZnNPs with concentration (100 ppm) giving 3.22 per cent growth inhibition. It was also noticed that as the concentration of the ZnNPs increased, there was corresponding increase in per cent mycelial growth inhibition of the pathogen. Further, methylene blue staining was done and the structural changes of fungal samples after ZnNPs treatment were studied. The hyphae lost their smoothness, unusual bulges were formed on the surface of fungal hyphae followed by reduction in the distance between two hyphae. Branched conidia turned round and conidial development was suppressed. These results suggest that ZnNPs not only distorted and damaged the conidia but also inhibited the fungal growth greatly.

P (S 12) 26: Evaluation of fungicides for the management of fruit rot in chilli caused by *Colletotrichum* species in Himachal Pradesh

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Fruit rot (chilli anthracnose) caused by a complex of five *Colletotrichum* spp. is one of the most important constraints in chilli (*Capsicum annuum* L.) production throughout the world and is known to cause both qualitative and quantitative losses. This group of fruit rot fungus also results in deterioration of seeds during storage conditions as well as causes the pre and post emergence damping off in nursery. In the present study, an attempt has been made to study the effect of some commercial formulations on the growth behavior of three *Colletotrcihum* spp. *viz., Colletotrichum truncatum*, *C. gloeosporioides* and *C. coccodes*, prevalent on this crop in Himachal Pradesh. Seven fungicides Carbendazim (Bavistin), Trifloxystrobin 25 per cent + Tebuconazole 50 per cent (Nativo), Copper oxychloride (Blitox), Propineb (Antracol), Captan, Hexaconazole (Contaf), and Difenoconazole (Score) were evaluated under *in vitro* conditions. The data recorded on mycelial growth inhibition of three species revealed differential behavior with respect to their sensitivity to the test fungicides. Only one fungicide Nativo showed 100 % mycelia inhibition of all the test species even at 50 ppm, whereas other fungicides were effective against one or the other species at different concentration levels.

P (S 12) 27: *In vitro* evaluation of fungicides and bioagents against tomato early blight pathogen *Alternaria solani*

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Early blight disease caused by *Alternaria solani* (L.) is one of the most destructive diseases of tomato in the tropical and subtropical regions. In the present study, efficacy of different fungicides at different concentration and bioagents against *A. solani* was assessed under in vitro conditions. A total of eight fungicides and seven bioagents were tested. Results of the experiments indicated a positive correlation between the concentration and per cent inhibition of growth of mycelium except propineb, hexaconazole iprodione 25% + carbendazim. It was found that, all the three concentrations of propineb (0.1%, 0.2% and 0.3%), hexaconazole (0.05%, 0.1% and 0.15%) and iprodione 25% + carbendazim (0.1%, 0.2% and 0.3%) showed cent per cent inhibition of *A.solani.* In addition to this, difenoconazole at 0.075 per cent concentration also resulted in total inhibition of the pathogen. Among remaining fungicides, all the three concentrations of difenoconazole was significantly superior over copper hydroxide, pyraclostrobin, azoxystrobin and trifloxystrobin 25% + tebuconazole in inhibiting mycelial growth and it ranged from 94.99-100 per cent. Among the bioagents, *Trichoderma viride* (KAU) and plant growth promoting microbial consortium (PGPM mix of KAU) were recorded cent per cent inhibition of pathogen. Among different bacterial antagonists *Bacillus subtilis* 1; an endophyte isolated from cocoa recorded maximum growth inhibition of 51.66 per cent.

P (S 12) 28: Efficacy of fungicides against wilt disease caused by *Fusarium solani* in cluster bean under field condition

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Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.], commonly known as *guar* is a member of (Fabaceae) family and use of cow fodder or otherwise fodder of the livestock .The present experiment was carried out during *kharif* season 2018-19 Department of Plant Pathology, S.K.N. College of Agriculture, Jobner (Jaipur) Rajasthan. The experiment consisted of six treatment of wilt management practices i.e., check, Carbendazim (Bavistin), Carbendazim + Mancozeb ,Tebuconazole + Trifloxystrobin, Fosetyal aluminium+ fluopicolide, Captan+ hexaconazole,Thiram +Carboxin, all treatment seed treated with 2g/kg seeds. The seed treatment were taken in randomized block design with four replication. The pooled data over two years revealed that all the fungicides practices for the management of wilt in *guar* resulted in significantly low disease incidence of wilt and significantly maximized seed yield over the check. The pooled analysis of data further revealed that seed treatment with Carbendazim (Bavistin) resulted in lower wilt incidence (5.71 and 11.42%) followed companion that showed wilt incidence (8.57 and 14.28%). Next effective seed dresser were captan and hexaconzole that showed wilt incidence of 11.42 and 17.14% , respectively. these fungicide were found to be at par with best fungicides. Seed treatment with fosetyl aluminium + fluopicolide were found to be least effective which showed wilt incidence of 20 and 34.28% and decrease.

P (S 12) 29: Management of stem and root rot of sesame caused by *Macrophomina phaseolina*

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Sesame (*Sesamum indicum* L.) is one of the oldest important oil seed crop and is under cultivation from ancient times. It is valued as quality food, nutrition, edible oil, biomedicine and health care, all in one. India contributes the highest sesame acreage of above 17.73 lakh hectares with the production 8 lakh tonnes and productivity of 445 kg/hectare. The low productivity is attributed to poor crop management and exposure of the crop to a number of biotic and abiotic stresses. Irrespective of the agro-climate conditions, sesame is liable to be infected by various pathogenic fungi. Among the diseases affecting Sesame, stem and root rot caused by *Macrophomina phaseolina* is the most serious one. It affects severely at all stages of crop growth. The sclerotia of pathogen survives in the soil, crop residues and on seed which cause characteristic symptoms such as sudden wilting, destruction of fibrous root, blackening of stem and roots. By keeping in view of the importance of crop field trials were conducted to combat this disease of sesame. Treatments comprising of combination of bioagents and fungicides were tested and evaluated for disease severity and crop loss. Of these eight treatments, minimum *Macrophomina* stem & root rotincidence and maximum seed yield was recorded in the spraying of Trifloxistrobin + Tebuconazole @ 0.5 g/l at capsule initiation and second spray of this combination after 15 days interval followed by Pyraclostrobin + Metiram @ 3g/l at capsule initiation and second spray after 15 days interval. There was substantial decrease in disease severity and increase in grain yield. Based on the findings it is concluded that spraying of Trifloxistrobin + Tebuconazole @ 0.5 g/l at capsule initiation and second spray after 15 days interval was very effective and economical for management of stem & root rot disease of sesame under hot and dry region.

P (S 12) 30: Trace analysis of fungicides in different IDM module of Basmati rice using high performance liquid chromatography

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India is the leading exporter of the basmati rice in the word. The country has exported 4056758.62 MT of Basmati rice to the world for the worth of Rs. 26870.17 crores during the year 2017-18. The area of Basmati rice across major states in India (J & K, H.P., Punjab, Haryana, Delhi, Uttarakhand and Western U.P.) is 1515.00 thousand ha with Production of 5027.00 thousand tones. During last few years the export of Basmati rice to USA and UK has been adversely affected due to the detection of tricyclazole and carbendazim residue in grains. Experiment having 18 IDM modules was conducted at Crop Research Centre of Sardar Vallabhbhai Patel University of Agri. & Tech., Meerut. In this experiment fungicides were sprayed in their recommended doge at different growth stages of Basmati rice variety PB-1121 for the management of major fungal diseases. The objective of this study was to develop an ideal IDM module for disease management with keeping the fungicide residue below the Maximum Residue Limit (MRL) in rice grains. Results determines that residue of tricyclazole was highest (3.88 ppm) in module 16 and lowest (0.56 ppm) in module 07. The residue of carbendazim was maximum (0.46 ppm) in module 01 and minimum (0.04 ppm) in module 03. The maximum (0.1 ppm) residue of hexaconazole was found in module 15 and minimum (0.05) in module 04 whereas; the residue of propiconazole was maximum (1.8 ppm) in module 17 and minimum (0.4 ppm) in module 05. Results revealed that the residue of hexaconazole and propiconazole has been found approx to their MRL while residue of tricyclazole (except module 07) and carbendazim were below to their MRL. Maximum (35.69q/ha) yield was recorded in module 02 while minimum (24.44 q/ha) in module 13.

P (S 12) 31: Evaluation of fungicidal efficacy of CuNPs synthesized by chemical and biological method *in-vitro* and *in-vivo*

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Conventional methods of pest management adversely affect the non target organism and environment as a whole. Due to its numerous setbacks, pesticides are brought to the limelight of criticism. Such detrimental effect of pesticides can be attributed to its high toxicity, non-biodegradable nature, and residual activity. Therefore an alternate avenue was realized to combat phytopathogens employing nanotechnology that could be a boon in agriculture. Such one application is use of nanoparticles (NPs) as nano-fungicides to manage phytopathogens. A nanoparticles by virtue of its high efficacy and durability may delay development of resistance in pathogens. Moreover NPs of Copper (CuNPs) and Silicon (SiNPs) exhibit synergistic effect when combined with bio-control agents, essential oil and biopolymers etc. Propitiously, biological method of synthesis of NPs satisfies the criteria of being eco-friendly and efficiency.Taking into consideration the aforementioned demerits of conventional method and prospects of nano-fungicides, an attempt was made to synthesize CuNPs by Chemical as well as Biological method which was further characterized by UV-Vis spectroscopy, Transmission electron microscope and Fourier transform infrared spectroscopy. TEM measured the NPs of average size ranging from 10-90 nm. FTIR revealed the presence of functional groups, possibly involved in capping of synthesised nanoparticles. The synthesised CuNPs was evaluated (*in-vitro)* for its efficacy against several fungi and bacteria. In case of maize pathogens *Rhizoctoniasolani* f. sp. *sasakii* and *Bipolarismaydis*complete inhibition was achieved at 300 ppm of CuNPs, whereas in *Macrophominaphaseolina*, complete inhibition was observed at 200 ppm.*In vivo* evaluation was conducted against *B. maydis* and *R.solani* f. sp. *sasakii.* Among the various treatments, seed treatment+spray @ 300 ppm exhibited statistically significant result with PDI of 27.61 and 29.81 respectively.

P (S 12) 32: *In Vitro* evaluation of some plant species extracts and fungicides against *Botryodiplodia theobromae* (Pat.) Griffon and Maube the pathogen of mango die back and gummosis

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Mango (*Mangiferaindica* L.) is one of the most important fruit of the tropical and subtropical world and cultivated extensively as a commercial fruit crop in India. Among the diseases infecting mango, the mango die back and gummosis is a major threat to the mango industry. This disease is incited by number of pathogens but *Botryodiplodiatheobromae* (Pat.) Griffon and Maube with its teleomorphic state *Botryosphaeriarhodina* is the major causal organism. In the present study, eleven indigenous plant species extracts viz., lantana, mint, onion, garlic, cannabis, parthenium, *Aloe vera*, eucalyptus and lemongrass, and seventeen fungicides (seven systemic, five contact and five combination fungicides) were tested against the mycelial growth of *B. theobromaein vitro* through poison food technique. Cannabis leaf extract was most effective in inhibiting the mycelial growth of *B. theobromae* at 20.49 per cent followed by garlic clove extract (17.40 %). Among the fungicides, carbendazim showed the maximum mean growth inhibition at 98.75 per cent followed by chlorothalonil (95.74 %), carbendazim + mancozeb (95.37%) and thiophanate methyl (86.66%). It is evident from the present investigation that systemic fungicides such as carbendazim and chlorothalonil are most effective against the mango die back and gummosis and plant species extracts have limited effectiveness against this disease. Therefore, the use of plant species extracts as control agent may need further investigation and refinement and chemical fungicides will continue to be a method of choice for the present.

Session 13

Workshop on wilt disease of solanaceous crops

Keynote Papers

KN (S 13) 01: Characterization and diversity of Indian isolates of *Ralstonia solanacearum* inciting bacterial wilt of tomato

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Tomato (*Solanum lycopersicum* L.) belongs to the family solanaceae is one of the most important protective food crops of India and grown in 0.458 M ha area with 7.277 M mt production and 15.9 mt/ha productivity. Low productivity of crops is due biotic and abiotic factors. Among various diseases, bacterial wilt caused by *Ralstonia solanacearum* is devastating soil borne plant pathogen to damage the tomato crop 4 - 95% depends on the seasons and cultivars. Ninety six isolates of *R. solanacearum* were isolated from tomato from different agro-climatic regions belonging states of Jammu & Kashmir, Himachal Pradesh, Uttarakhand, Jharkhand, Odisha, West Bengal, Karnataka and Goa. Based on carbon utilization, biovar of *R. solanacearum* was determined using set of carbon sources and it showed that biovar 3 of *R. solanacearum* were found most prominent (90.2 per cent) in all the states of India, whereas biovar 4 was found in Jharkhand and Himachal Pradesh only 9.8 per cent. All the isolates of *R. solanacearum* belong to phylotype I, which are found in most Asian countries. To study the genetic variation and different evolutionary dynamics among the strains BOX-PCR and multilocus sequence typing approaches were used. Amplification products yielded in BOX-PCR fingerprint pattern ranging from 500 bp-4 kb. Considerable genetic variation was observed among *R. solanacearum* isolates. Multilocus sequence typing of 18 isolates of *R. solanacearum* was done using house keeping pathogenicity and virulencegenes. A lot of genetic variability was found in Indian isolates of *R. solanacearum* irrespective of place of isolation and climatic conditions.

KN (S 13) 02: Formulation of the bacterial antagonist *Bacillus* spp. for management of bacterial wilt disease caused by *Ralstonia syzigii* sub sp. *indonesiensis*

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Bacterial wilt of tomato caused by *Ralstonia syzigii* subsp. *indonesiensis* (Formerly *R. solanacearum*) is one of the most economically important diseases of tomato in the world, especially in Indonesia. Biological agents such as Plant growth Promoting Rhizobacteria (PGPR) is considered as a potential biological control agent for the suppression of plant diseases such as bacterial wilt. Endophytic bacteria as PGPR considered one of the options to control vascular wilt disease because of its ability to live and colonized internal roots of plants. *Bacillus* spp. are one of the most potential genera of PGPR group used for controlling pathogens and promoting plant growth because of their spore-forming ability which increases their adaptation to the environment. Our previous study had acquired 4 best *Bacillus* strains which had ability to promote growth yields and increase resistance of tomato to bacterial wilt disease. Our current research purposed to develop the best

formula for the *Bacillus* strains to improve their ability to control *R. syzigii* subsp. *indonesiensis* and promote growth and yields. This research conducted in Factorial design with 2 factors, isolates (4 isolates: *B. pseudomycoides* SLBE1.1.SN, *B. thuringiensis* SLBE3.1.BB, *B. mycoides* SLBE1.1.AP dan *B. cereus* SLBE3.1.AP) and formulations (sugarcane waste, coconut water waste, bulk tofu waste, and liquid tofu waste) with 5 replications. Parameter observed are disease development (Symptom appear, severity), growth development (germination rate, plant height, number of leaves, root length), generative phase (Time of flowering and yields) and the isolates shelf life. Result shown that not all formulations can increase shelf life of endophytic bacteria. Bulk formulations such as sugarcane waste and bulk tofu waste had higher populations and longer shelf live compared to liquid waste formulations. Isolates *B. pseudomycoides* SLBE1.1.SN, *B. thuringiensis* SLBE3.1.BB had best ability to increase growth rate of tomato, which increased yields effectivity compared to control constructively (25.7%, 26.5% and 33.76%) and can suppress disease development of *R. syzigii* subsp. indonesiensis compared to control (80%) to 20%, 20% and 0%.

Invited Papers

I (S 13) 03: Bacterial wilt: diversity, virulence of *R. solanacearum* and management strategies

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Bacterial wilt poses a major threat towards the production of solanaceous vegetables *viz*. brinjal, tomato and chilli. The disease is caused by *Ralstonia solanacearum*, a soil bacterium and the pathogen affects several plant species. The pathogenicity and virulence of *R. solanacearum* is due to the presence of various virulence factors and effector proteins. Management of bacterial wilt has met with limited success due to the existence of diverse strains, survival ability of the bacterium in adverse conditions, wide host range including asymptomatic hosts and efficient mechanism of invading the host. In this article, brief account of the bacterial wilt disease, pathogen diversity, virulence factors and various strategies used to manage bacterial wilt disease are described. We have studied the genetic diversity of *R. solanacearum* infecting solanaceous vegetables and found that the isolates from brinjal and other solanaceous vegetable belong to phylotype I and biovar 3. Further, our studies indicated that Indian isolates clustered into two sub groups based on partial *egl, hrp* and *pga* sequences indicating the presence of two major population groups. Sub group 1 is the dominant group and consists of unknown/ newer sequevars, and sub group 2 consist mainly the isolates which are designated with previously described sequevars 17, 44, 47, 48. Draft genome sequence of two representative isolates *viz*. Rs-09-161 and Rs-10-244 was carried out. From the genome sequences, we analysed various virulence factors and type III effector proteins of *R. solanacearum*. Rs-09-161 and Rs-10-244 share more than 99 per cent similarity between them and are closely related to GMI1000. The virulence factors in *R. solanacearum* appear to be highly conserved in the *R. solanacearum* species complex. Various management strategies, including resistant varieties, grafting on resistant root stocks, soil amendments, use of biocontrol agents, bio-fumigants, plant products etc. had been developed with varying levels of success.

I (S 13) 04: Functional analyses of putative pathogenicity genes of *Fusarium* spp. inciting vascular wilt of tomato

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Fungal diseases of plants are one of the major concerns in cultivation world wide resulting in loss of billions of dollars. Like all other living organisms, fungi are able to perceive and respond to changes in the environment, including the presence of a host in the case of pathogens. The fungal plant interplay depends on mutual recognition, signaling, and the expression of pathogenicity and virulence factors, from the fungal side, and the existence of passive, preformed, or inducible defence mechanisms in the plant, resulting in compatible (susceptibility) or incompatible (non-host, basal or host specific resistance) interactions. The necessity to develop new strategies for control of *Fusarium* wilt of tomato signifies identification of potential pathogencity genes and ascertain their role to use them as molecular stooges for fungicide development or to develop transgenics. Semi-quantitative gene expression studies identified two effector pathogenicity genes, *FOW2* and *chsV* reported as Zn(II)2Cys6-type transcription regulator and class V chitin synthase, respectively as potential ones for being secreted all the time. The roles of these genes in pathogenicity of *Fusarium oxysporum* were established by RNA interference (RNAi) induced silencing (knockdown). The silencing vector encoding hairpin RNA of each of the gene fragment was constructed in a two-step PCR based cloning, and introduced into the fungal genomic DNA. Silencing of either of the genes resulted in less virulent fungal phenotypes with altered physiological characteristics like sporulation and growth on solid media and a reduction of mRNA expression. The results therefore demonstrate the applicability of these pathogenicity genes as useful molecular targets for exploitation in *Fusarium* incited vascular wilt control in tomato. RNAi is also emerging as an alternative genetic tool in development of pathogen resistant crops. Host delivered RNAi technology through expression of RNAi sequences of *FOW2* and *chsV* in tomato was therefore explored as a method to enhance resistance of tomato plants to *Fusarium* resistance. Co-expression of these two RNAi constructs in two independent elite tomato cultivar transgenic lines conferred high levels of stable, consistent resistance to *Fusarium* with delayed or reduced disease symptom development. The transgenic lines exhibited more than 75% survival, which was significantly higher than that of the control wild type plants. *F. oxysporum* infecting transgenic lines displayed substantially reduced mRNA levels of two targeted genes, *FOW2, and ChsV*. Confocal microscopy revealed profoundly restricted mycelia in *Fusarium* infected transgenic plants. There was efficient downregulation of the target genes in the colonizing *Fusarium* pathogens on tomato seedlings. These results demonstrate that host-induced gene silencing of potential fungal pathogenicity genes as an effective strategy for enhancing resistance in crop plants.

I (S 13) 05: Diverse strategies for management of bacterial wilt of solanaceous crops in Eastern coastal regions of India

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Bacterial wilt of solanaceous crops, caused by *Ralstoniasolanacearum,* has been a serious bottleneck for their commercial cultivation in particularly in eastern parts of India. The most affected crops in the region are tomato, brinjal and chili. The wilt incidence is almost ubiquitous in the coastal regions of Odisha during the main cropping season when the climate is hot and humid. There are no varieties available in market in the preferred segment like large round in brinjal, purple tinged green and bullet type segment in chilli for Eastern region, which can boast absolute immunity or resistance against bacterial wilt. Based on development in scientific research over past couple of decades, there is some information available now to enable us to devise multifarious and multipronged strategies to manage the disease losses within economic threshold. In this line we made efforts in collection of germplasm from Eastern and North Eastern parts of India for resistant sources and a total of around 140 accessions of chilli (*Capsicum annuum, C. chinense, C. frutescens* and *C. baccatum* and 42 accessions of brinjal and nine *Solanum* spp. were collected and being maintained at our center. In chill IIHR-H-HP 1, 7, 9, 41,54, 71, 89, 111, 112, 123, 125, 129 have been identified as resistant and IIHR-H-HP 130 as highly resistant accession. In brinjal viz., CARI-1, IIHR-B-B-51, IIHR-B-B-41, IIHR-B-B23, 37-36-4-4, IIHR-B-B-42, IIHR-B-B-34, IIHR-B-B-43 as resistant sources for bacterial wilt resistance as confirmed by artificial inoculation and sick plot screening. The wild species such as *Solanumtorvum* and *S. macranthum* which are highly wilt resistant are being successfully used as rootstock for grafting to combat the bacterial wilt in brinjal, tomato, chilli and capsicum. Incorporation of resistance from resistant sources in to different genetic backgrounds is being attempted with highly encouraging leads. Effect of soil amendments in different concentrations and combinations have also given some encouraging results. Experiments using biochar, lime, microbial consortium, cocopeat, green manuring etc. are being evaluated for their effect of bacterial wilt incidence under *in vivo* conditions.

I (S 13) 06: Cultural, biochemical and molecular characterization of *Ralstonia solanacearum*, causal agent of wilt of solanaceous vegetables

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Cultural characteristics of twenty isolates of *Ralstonia solanacearum* collected from brinjal,tomato,chilli and potato during survey were assessed by culturing each isolate on two media *viz*., Triphenyl Tetrazolium Chloride (TTC) and Casein Peptone Glucose Agar (CPGA). Study was taken up during 2015 and Isolates were designated as RS-1 to RS-20. Among the isolates tested against the media for their growth traits, RS-10 and RS-7 recoded significantly superior growth in CPGA medium by producing 73×10^5 cfu/ml and 60×10^5 cfu/ml respectively. Moderate growth of the pathogen ranged between 23x10^5 to 47×10^5cfu/ml was recorded by RS-1, RS-2, RS-5, etc. Significantly least growth was observed with 14×10^5 cfu/ml by RS-4 and RS-20 isolates. The isolates differed greatly in respect of colony size and shape as RS-12, RS-17 and RS-18 isolates produced medium sized colonies ranged between 3.47 to 3.69 mm and were circular to irregular in shape. Big colonies (4.32 to 4.43 mm) were produced by RS-4, RS-6 and RS-15 isolates. On the contrary, the isolates RS-1, RS-2, RS-3 and RS-5 produced small colonies in the range of 2.06 to 2.85mm. Variation in colour revealed that, a total of 13 isolates (RS-1, RS-2, RS-3, RS-4, RS-5, etc.) appeared absolute white, while the other isolates RS-9, RS-11, RS-12 and RS-13 etc. exhibited creamy white colour. Further, the colonies were flattened in 11 isolates, slightly raised and convex in six isolates. On TZC medium, the isolates differed greatly in respect of colony colour as the isolates RS-8 and RS-19 exhibited light pink colour, whereas the isolates RS-6, RS-11 and RS-14 appeared deep red. The rest of the isolates exhibited light pink with red tinge at the centre. In respect of size and shape, the colonies of RS-6, RS-8, RS-11, RS-14 and RS-19 were very small ranged bet ween 1.66 to 3.29 mm. whereas the other isolates RS-1,RS-3, RS-4, RS-5 etc., produced big colonies. Small to medium sized colonies were produced in some isolates. Isolates also differed in shape, either flattened/ slightly raised/convex. Most of the isolates are fluidal with whitish periphery except RS-8 and RS-19. Biochemical study revealed that, all the 20 isolates were positive for gelatin liquefaction, catalase, oxidase and KOH solubility test. Few isolates differed for hydrogen sulphide production and indole test In molecular characterization, highly specific primers OL 11 and Y2 were used in PCR amplification to identify the different isolates of *R. solanacearum*. The specific primers amplified DNA sequence at 300bp encoding 16SrRNA confirming that all the 20 isolates were of *R. solanacearum*. Further, RAPD technique was employed to detect to variations among the 20 isolates . A total of 15 primers belongs to OPA, OPH, OPE and OPF were used to determine the genetic diversity between the isolates. Results exhibited that a total of 94 DNA bands were detected using 9 primers. Eighty nine bands were polymorphic. The primers OPH-01, OPH-03 and OPH-11 and OPF 01 exhibited 100 per cent polymorphism indicating significant molecular variability between the isolates. Genetic similarity co-efficient of 20 isolates ranged from 0.46 to 0.80. The highest genetic similarity of 80 per cent was exhibited between RS-5 and RS-6 isolates. Least genetic similarity of 30 per cent was observed between RS-12 and RS-20 isolates.

I (S 13) 07: Efficacy of bio-agents and chemicals in managing *Fusarial* wilt disease in tomato in field condition

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Tomato (*Solanum lycopersicum*) is a popular vegetable crop in India. The crop suffers by many fungal, bacterial, viral diseases and among them, Fusarial wilt caused by *Fusarium oxysporum* f.sp. *lycoprsici* is a major problem in the crop. This disease is devastating all over the world. In India, there may be generally 30 to 40% yield loss and sometime upto 80% under favourable weather condition. An experiment was conducted at Central Farm, OUAT, Bhubaneswar using tomato cv. BT-10 in different combination and method of application of bio-agents, antibiotic and chemicals in integrated manner to manage Fusarial wilt disease in the field conditions in 2008-09 and 2009-10. The treatments were followed *i.e*. T1= Seedling root dip and soil treatment with *Trichoderma viride, T*2 = Seedling root dip and soil treatment with *Pseudomonas fluorescens*,T3 = Seedling root dip and soil treatment with *T. viride* + Seedling root dip and soil treatment with *P fluorescens,* T4= Seedling root dip with carbendazim and streptocycline and soil drenching with streptocycline, carbendazim and plantomycin, T5 = *T. viride* was applied as soil treatment and three times basal drenching with *T.viride* and *P. fluroscens* was practised, T6 = Control (neither seedling root dip nor soil application was adopted). Minimum wilt (2.89%) incidence and maximum yield (74.16qt/ha) was recorded in the treatment where seedling root dip with carbendazim @ 0.15% and streptocycline 0.015% + soil drench with carbendazim (0.2%), plantomycin (0.1%) and blitox- 50 (0.3%) were practised. It was followed by seedling root dip and soil treatment with only *P. fluorescen*s which produced (70.35q/h) was also higher than other three treatments. In control maximum wilt (12.35%) incidence and minimum yield (57.69q/h) was recorded.

Oral Papers

O (S 13) 08: Phenomenon of reversal of phenotypic conversion in *Ralstonia solanacearum* and a simplified protocol for reversing avirulent to virulent colony types for consistency in results during prolonged experimentation

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A protocol for inducing virulence in *Ralstonia solanacearum* for biocontrol studies was developed considering the problem of losing its virulence in laboratory conditions abruptly which causes inconsistency in results during prolonged experimentation. In our study, we observed that some of the factors enhance the occurrence of virulence colony type (fluidy with the pink centre). Two such factors were identified and based on which a methodology was developed to get virulent colonies. First factor is *Phyllanthus emblica* **(**Indian gooseberry) extract and second is the nutrient deprivation. *P. emblica* extract suppresses *R. solanacearum* initially in well diffusion assay, but after 2-3 days of incubation, it develops virulent type colonies. The test strains tend to develop fluidy colonies near to the agar well where extract was added. The effect of *P. emblica* extract was confirmed using ascorbic acid, the key organic acid present in *P. emblica* extract. Similar effects were seen from nutrient deprivation. Slanting of the medium in agar plates was found to induce virulent type colonies towards nutrient deprived area. Coupling these two phenomena of *P. emblica* extract and nutrient deprivation found to have synergistic effects. Therefore, based on these observations a protocol was developed for maintaining virulent colony types for biocontrol studies. In this protocol, *R. solanacearum* culture is swabbed in a slanting agar medium having low nutrient on the edges tend to form fluidy virulent colonies in 2-4 days based on its strain type. The tagging of *R. solanacearum* with green fluorescent protein confirmed that the fluidal colonies were induced out of non fluidal ones. Additionally, the method also has an impact on two other virulence factors *i.e.* production of cellulases and pectinases which help the pathogen in entering the xylem vessels and to cause wilting of the host. *In-planta* trial also showed enhanced pathogenesis. This method will be useful in the laboratories working on biocontrol of *R. solanacearum* to keep the culture virulent for the entire study period. Also, use of these PC mutants as biocontrol agents for cross protection without knowing the stability in natural environment is questionable and needs to be confirm.

O (S 13) 09: *In vitro* bio-efficacy of *Pseudomonas fluorescens* against *Fusarium oxysporum* f. sp. *lycopersici*

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Fusarium oxysporum f. sp. *lycopersici* was isolated successfully on Potato Dextrose Agar (PDA) medium, from tomato plant showing typical symptoms of wilt. An efficacy of all the ten native isolates of *Pseudomonas fluorescens viz.,* PfCB, PfCP, PfAT, PfAP, PfRB, PfRT, PfLT, PfLB, PfAhC and PfUC was evaluated *in vitro* against *Fusarium oxysporum* f.sp. *lycopersici* by dual culture technique. Among them, PfAh-C was found to be most effective and recorded least mycelial growth (2.28 cm) with highest mycelial inhibition (74.61 %) of *Fusarium oxysporum* f. sp. *lycopersici*. The next effective isolate PfAP in order of mycelial growth was (2.60

cm) with inhibition (71.08 %). The isolates PfAT (2.78 cm), PfRT (2.80 cm), PfRB (2.85 cm), PfUC (3.01 cm), PfCB (3.01cm), PfCP (3.05 cm), PfLB (3.13 cm) and PfLT (3.15 cm) were comparatively poor and resulted higher in growth of the pathogen. *In vitro* test showed that *Pseudomonas fluorescens* isolates were antagonistic to *Fusarium oxysporum* f. sp. *lycopersici*.

O (S 13) 10: Variability of *Ralstonia solanacearum* in different agro-ecological units of Kerala

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Ralstonia solanacearum, inciting bacterial wilt of solanaceous crops, is a complex species with broad physiological and genetic diversity. The disease is very severe in Kerala, mainly due to the acidic soil reaction coupled with humid tropical climate prevailing here. High genetic variability existing among different isolates of the pathogen collected from different locations of the state has been reported earlier. Since the bacterium is known to modify itself according to the soil environment in which it thrives, the present study was aimed at characterisation of the pathogen present in different agro- ecological units (AEUs) of Kerala, the AEUs being demarcated chiefly according to soil type. Purposive sampling survey was conducted in four AEUs of Kerala *viz.*, North Central laterite (NCL), Marayur hills (MH), Southern laterite (SL) and Palakkad central plains (PCP) and isolates of the pathogen were collected. The isolates were categorized into races and biovars based on pathogenicity on differential hosts and utilization of disaccharides and hexose-alcohols respectively. The results revealed that two isolates from Marayur hills (MH 1 and MH 2) belong to race 3, biovar II whereas two from Palakkad central plains (PCP 1 and PCP 2) belong to race 1 biovar III A. The other four isolates collected from Northern central laterite (NCL 1 and NCL 2) and Southern laterite (SL 1 and SL 2) were identified as race 1, biovar III. Molecular characterization of the isolates followed by phylogenetic analysis revealed that the eight isolates collected from different AEUs clustered on different branches of the tree while those from the same AEUs clustered together. This indicates considerable variation among the isolates in accordance with location which can be attributed to the difference soil parameters in these locations.

Poster Papers

P (S 13) 01: Identification of bacterial wilt/ brown rot (*Ralstonia solanacearum)* free areas in Uttar Pradesh for producing export quality potato: need scientific spproach in the regime of WTO-SPS agreement

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India's share in global export of potato is very low (0.7%). In order to stabilize potato market contributing to enhancing the potato growers income by 2022, it is necessary to formulate an effective policy for exporting table potatoes/ seed potatoes to the potential importing countries. The major bottleneck in the export of potato is occurrence of diseases which are of quarantine significance and one such disease is bacterial wilt/

brown rot disease of potato caused by *Ralstonia solanacearum*. There is zero tolerance for the in most international potato seed certification systems. Since, India is one of the signatories of WTO; it has to comply with all provisions of WTO agreement related to Sanitary and Phytosanitary (SPS) measures. Therefore, to promote export of potato it is indeed needed to be free from disease of concern to importing countries. To promote potato export without applying any phytosanitary treatment, the identification of free areas in accordance with global standard of International Plant Protection Convention (IPPC) *i.e*., International Standard for Phytosanitary Measures (ISPM-4) is the safest phytosanitary measure for importing countries. Identified disease free areas should be notified by the Ministry of Agriculture, Govt. of India. Notified free areas (brown rot pathogen) may be used in the establishment of potato export zones. The scientific approach may be provide justification for phytosanitary measures for identification of disease free areas in line with provisions of international agreements and thus facilitate trade thereby increasing income of potato growers.

P (S 13) 02: Green synthesis of silver nanoparticles, its characterization and study the efficacy against *Fusarium oxysporum*

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Nanotechnology is the art and science of manipulating matter at a scale of 1- 100 nm with some noble properties. In this study, Silver nanoparticles were synthesized by standardized protocol from a promising indigenous biocontrol agent *Trichoderma asperellum.* Characterization were made using UV-vis-spectrophotometer, DLS, zeta-sizer and electron microscope. The synthesized silver nanoparticles were tested against *Fusarium oxysporum* by agar well method and poison food method at 100% concentration. Mycelial growth of *F. oxysporum* at an interval of 24 hours was observed and comparison done with control. During the study silver nanoparticle was found to cause significant inhibition of the mycelial growth of the pathogen. The effect of silver nanoparticle on the inoculum was also studied with light microscopy and observed deformity and lysis after exposure to the nanoparticle. When the effect of silver nanoparticle on the protein content and biomass production of *F. oxysporum* was studies, it was also found to cause reduction in protein content and biomass production after exposure to the silver nanoparticles. This study showed encouraging result of using silver nanoparticle for growth inhibition of *F. oxysporum*. Further studies is necessary to come to a conclusion for its field application.

P (S 13) 03: *In vitro* evaluation of biocontrol agents against *Ralstonia solanacearum* causing bacterial wilt of tomato

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Bacterial wilt caused by *Ralstonia solanacearum* is one of the devastating diseases of tomato (*Lycopersicum esculentum*) crop. The pathogen/disease, being soil borne is very difficult and uneconomical to manage alone with chemicals. Therefore, the present study was undertaken to assess bio-efficacy of biocontrol agents *viz.*, *T. viride, T. harzianum, T. koningii, T. longibrachiatum, T. virens, Aspergillus niger, Bacillus subtilis* and *Pseudomonas fluorescens* against *R. solanacearum*, applying inhibition zone assay technique. The experiment was planned with CRD and all treatments replicated thrice. Results revealed that the test biocontrol agents evaluated exhibited antibacterial activity against *R. solanacearum* with a wide range of inhibition zone. However, it was significantly highest with *P. fluorescens* (25.11 mm), followed by *T. harzianum* (22.50 mm), *Bacillus subtilis* (19.83 mm), *T. viride* (17.50 mm), *T. koningii* (15.17mm) and *A. niger* (13.83mm); whereas, it was significantly least with T. virens (11.33 mm) and *T. longibrachiatum* (9.17mm).

P (S 13) 04: Management of bacterial wilt of tomato through induced resistance

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Bacterial wilt, caused by *Ralstonia solanacearum*, is one of the vexatious diseases of all the solanaceous vegetables. The disease can cause upto 90 percent yield loss in tomato. In the absence of resistance in commercial cultivars limited available options in chemical control, it is very difficult to manage the disease. In the present investigations, different abiotic resistance-inducers evaluated. Potassium chloride and oxalic acid at 300 and 200 mM concentration were most effective in managing the disease and increasing plant weight and plant height with minimum disease incidence of 24.44 and 35.55 per cent and maximum disease control of 70.27 and 56.76 per cent, respectively. Sodium salicylate was least effective in managing the disease. Study of mechanism of induced resistance revealed that total phenol content progressively increased in all the treatments upto 7th day after the spray of abiotic inducers of resistance and thereafter it declined. Maximum increase was observed in potassium chloride sprayed leaves (94 ìg/g tissue) followed by oxalic acid (92 ìg/g tissue). It was recorded the lowest in sodium salicylate sprayed leaves (72 ìg/g tissue). While, polyphenol oxidase, peroxidase and phenyl alanine lyase activity was found to be at the peak immediately after 24 h of elicitation and was found maximum in potassium chloride treated leaves and minimum in sodium salicylate treated leaves. These abiotic inducers have the potential to be used for the development of environment-friendly disease management strategy for bacterial wilt of tomato.

Session 14

Genomics and bioinformatics

Keynote Papers

KN (S 14) 01: Genomics of fungal plant pathogens: A perspective

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Plant diseases have been a great concern to Indian agriculture, as they are important biotic constraints, which cause significant crop losses. In order to sustain agricultural production, a sound and effective disease mitigation strategy must be in place. With the increasing global connectivity, threat of invasive pathogens and exotic diseases affecting our crop production is quite a reality. Rapid advancement in genomics technology in the recent years has altered the landscape of plant pathology research. Therefore, it is hoped that the modern genomics technologies have the potential to assist the development of new strategies for crop protection. Therefore, in this era of genomics, there is a need to understand pathogen evolution, biology, lifestyle, novel disease management using genome sequence data. Next generation sequencing (NGS) has become indispensable for modern day molecular biology research within biological sciences, mainly in evolutionary biology of fungi. Among the total of 3, 72,055 organisms under sequencing or already sequenced, vast majority of them are microorganisms (https://gold.jgi.doe.gov/). All major plant pathogens are already genome sequenced and the sequence information is publically available in International Nucleotide Sequence Database Collaboration. The genomes of 1090 fungal species are available in the public domain. Plant pathogenic fungi comprised the largest category (35.5 %) i e., 191 genomes of pathogenic fungi are available in which 61.3 % cause diseases on food crops. In India, only few fungal plant pathogens have been sequenced. Concerted efforts on pathogenomics have been made to generate high quality sequence data on nationally important fungal plant pathogens affecting wheat and rice. Full genome sequence of *Puccinia striiformis tritici* race I (38S102) has been generated for the first time and submitted to NCBI database with accession no. MKXH00000000. *Tilletia indica* (causal organism of Karnal bunt of wheat) isolate RAKB_UP_1 genome assembly size of 33.7 MB was generated having GC content of 55.0 per cent (Accession no.-MBSW00000000). *Bipolaris sorokiniana* BS-112 was sequenced using three platforms *viz*. Illumina HiSeq, Ion torrent and Nanopore. The generated whole genome size is 35.64 MB with G+C content of 50.2% having 235 scaffolds. This whole-genome project has been deposited in DDBJ/ENA/GenBank under the accession number RCTM00000000. Whole genome sequence of *Fusarium fujikuroi* isolate F250 (42.47 Mb; Accession No. KM50526) has been generated and published in NCBI database. Comparative genome, transcriptome and secretome analysis of these important pathogens have led to identification of small secreted proteins and other pathogenesis related genes. The functional genomics attempts to illustrate the functions and interactions of these genes and proteins by comparative genome-wide approaches is the application part of genomics. Finally, the most promising application lies in using fungal plant pathogen genomics to reform plant disease management and risk assessment strategies. This will curtail the risks of future disease outbreaks and assist in preparation for emerging pathogens/races. The major impact of fungal genome sequencing is a better understanding of the pathogenicity, life-style and evolution of pathogens. Genomes are also resources where genetic tools can be used to extract information for further studies.

KN (S 14) 02: RhDB: Development of a dedicated, comprehensive, and user-friendly web resource for *Rhizoctonia solani* pan-genomes

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Rhizoctonia solani (teleomorph: *Thanatephorus cucumeris*) is a ubiquitous, soilborne basidiomycetous fungus with a wide host range that causes significant damage to economically important crops. Isolates of *R. solani* are classified into 13 Anastomosis Groups (AGs), some of which are further subdivided into interspecific subgroups with distinctive morphology, physiology, pathogenicity and highly divergent genetic composition. Till now eight draft genome assemblies belonging to four of the 13 AGs have been reported. However, a large number of *R. solani* isolates are still not sequenced and our understanding of genes and other effectors associated with pathogenesis in those AGs is less advanced. Also lacking is a dedicated, comprehensive web portal for hosting and analyzing the available genomic information at the level of gene, transcript, and protein of different *R. solani* AGs. We present a dedicated, comprehensive, and user-friendly web resource, RhDB (http://rsolanidb.kaust.edu.sa/RhDB/) for hosting, visualizing, and analysis of 15 diverse *R solani* whole genome assemblies and their annotated components. We performed genome and transcriptome sequencing, assembly and annotation of 15 *R. solani* isolates belonging to 7 different AGs. The presented web-resource includes detailed information on each *R. solani* isolate, such as the genome properties, predicted gene/ transcript/protein sequences, predicted gene function, protein orthologues among other AG sub-groups, along with tools for Gene Ontology (GO) enrichment analysis, sequence retrieval and IGV visualization of gene structures. Since the genomes of nine isolates belonging to three AGs and two subgroups of previously sequenced AGs are sequenced for the first time, the database stands as a valuable resource for formulating new hypotheses for studying pathosystems of *R. solani* sub-groups. A comparative analysis of these annotated genomes revealed a large set of novel genes in different AGs whose function could be potentially involved in range of pathogenic processes- e.g. synthesis of secondary metabolites, plant pathogenicity, and plant cell wall degradation. We conclude that RhDB will help a broad range of mycologists working on understanding genetic components and biomolecular processes that cause *R. solani* infection.

Invited Papers

I (S 14) 03: Refinement of draft genome assemblies of pigeon pea [*Cajanus cajan* (L.) Millsp.], predction of resistant gene analogues for *Fusarium* wilt.

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We report reconstruction & refinement of draft genomes of Pigeon pea and prediction of *Fusarium* wilt resistant candidate genes. Short read assembly of large plant genomes remains a challenge in computational biology despite major developments in next generation sequencing. Of late multiple draft assemblies are being reported in many organisms. Draft assemblies of Pigeon pea come with different levels of genome completeness; contain large number gaps, repeats and segmental duplications. Draft assemblies with portions of genome missing are shorter than the referenced original genome, have low map accuracy and incomplete gene space. Incomplete assembly hinders annotation and there by prediction of gene component as desired by crop researchers. Present work is aimed at improvement of coverage in reported *de novo* sequenced draft assemblies (GCA_000340665.1 and GCA_000230855.2) of Pigeon pea, a legume widely cultivated in India. We employed assembly reconciliation approach to compare draft assemblies and merge them to a superior near complete assembly with enhanced contiguity. The technique was capable to close more scaffolding gaps, resolve high repeats problem using alignment information and mate-pair read libraries. The finished mate assembly has higher genome coverage i.e. 82.4%, compared with two other misassembled counterparts. Besides, reconciled metassembly has fewer gaps, improved scaffold lengths thus provides a higher gene space. Completeness of assembly was evaluated for presence of specific disease resistance genes. We report successful prediction and isolation of putative host resistance genes against *Fusarium* wilt disease and used them for screening Pigeon pea cultivars both in laboratory (PCR) and field conditions.

I (S 14) 04: Leveraging proteomics to decipher the interactome of disease resistance in sugarcane

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Plant biology *per se* needs to be understood in toto, so as to harness the maximum potential of any crop plant to meet out the future food requirements of the growing world population. There is an unprecedented shift in the pace with which the tool of "*omics*" is carrying forward progressively to address many unresolved issues in agricultural research. Genomics research with the phenomenal upsurge to the next generation sequencing platform has proven to be robust enough to decipher complete genetic information coding for useful traits of interest. Proteomics –a complementary tool to genomics is gaining substantial progress in many crop plants like rice, maize, sorghum, etc., besides having been well established in the model plants. It is quite evident that proteomics is a powerful tool in the post-genomic era and plays a key role in empowering systems biology in plants. Disease resistance mechanism in sugarcane is complex and multigenic, which is yet to be fully elucidated. Despite proteomics of sugarcane is in its infancy, few proteomics-based investigations in sugarcane–pathogen interactions involving the sugarcane smut pathogen – *Sporisorium scitamineum* and the red rot pathogen - *Colletotrichum falcatum* have led to the identification of potential defense-related proteins of sugarcane, few putative orthologous effectors of *S. scitamineum*, and key potential PAMPs and effectors of *C. falcatum*. Considering the developments in sugarcane proteomics in the absence of whole genome information of sugarcane, it is appropriate to state that the potential of proteomics to understand disease resistance is being harnessed in a progressive manner. Integration of the tools of "*omics*" approaches is likely to enable researchers to reconstruct the whole cascade of cellular events leading to rapid responses and adaptation to the various important abiotic/biotic stress stimuli.

I (S 14) 05: Harnessing plant-microbiome interactions for improving crop resilience in a changing climate scenario

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Plants have co-evolved with microbiomes, sharing mutually beneficial functions, which can be engineered using combination of genetics, breeding and management practices to produce sustainable solutions in harsh and unpredictable environments. Nearly all aspects of crop functions, such as nutrient acquisition, growth, development, differentiation and responses to biotic and abiotic stresses, are affected by various members of phytobiomes. Understanding the interactions phytobiomes and crop functions are now providing new targets for manipulation and engineering. We have been studying such phytobiomes-crop interactions using field, laboratory and computational approaches. This talk will provide examples from both experimental models and field crops and will cover the discovery of (i) a novel plant hormone-mimicking system used by the fungal pathogen, *Magnaporthe* during invasion causing rice blast disease [Nature Chem Biol 2017] that provides novel approach for disease control, and (ii) a novel approach to discover phytobiomes-influenced crop functions from more than 200 assembled genomes of leafy *Brassica* vegetables that provide new targets for manipulating plant disease tolerance and nutrition. These findings and framework are useful in developing novel crop production and protection strategies in a changing climate scenario.

Oral Papers

O (S 14) 06: Whole genome and transcriptome analysis reveal adaptive strategies and pathogenesis of *Fusarium fujikuroi* to rice (*Oryza sativa* L.)

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Fusarium fujikuroi causing bakanae disease has emerged as one of the major pathogen of rice across the world. In the present study, *F. fujikuroi* isolate "F250" was sequenced with an assembly size of 42.47 Mb providing coverage of 96.89% on reference IMI58289 genome. A total of 13,603 protein-coding genes were predicted from genome assembly. The average gene density in the *F. fujikuroi* genome was 315.10 genes per Mb with an average gene length of 1.67 kb. Additionally, 134,374 single nucleotide polymorphisms (SNPs) are identified against IMI58289 isolate, with an average SNP density of 3.11 per kb of genome. Repetitive elements represent approximately 270,550 bp, which is 0.63% of the total genome. A total of 1,194 secretory proteins were identified in its genome among which there were 356 genes encoding carbohydrate active enzymes (CAZymes) capable for degradation of complex polysaccharides. Out of them glycoside hydrolase (GH) families were most prevalent (41%) followed by carbohydrate esterase (CE). Besides this, 585 genes essential for the pathogen–host interactions were also identified. Two contrasting genotypes of rice i.e. resistant (C101A51) and susceptible (Rasi) were taken and transcriptome analysis. Transcriptomic analysis was conducted between C101A51 control (CC) vs C101A51 inoculated (CI), Rasi control (RC) vs Rasi inoculated (RI) and C101A51 inoculated (CI) vs Rasi inoculated (RI). When we compared CI vs RI 13,662 (72%) genes were identified to be commonly expressed. Further, 280 (1%) genes were exclusive in CI and 532 (3%) genes were exclusive in CI. Cysteine proteinase inhibitor 10, disease resistance protein TAO1-like, oleosin 16 kDa-like, pathogenesis-related protein (PR1), pathogenesis-related protein (PR4), BTB/POZ and MATH domain-containing protein 5-like, alpha-amylase isozyme 3D-like (LOC4345814), were upregulated in resistant genotype C101A51. Whereas, GDSL esterase/lipase At5g33370, serine-glyoxylate aminotransferase, CASP-like protein 2C1, WAT1-related protein At4g08290, Cytoplasmic linker associated proteins were found to be upregulated in susceptible genotype Rasi. Selected genes were validated through quantitative real-time PCR analyses in resistant and susceptible genotypes of rice at different days of inoculation. The data offers a better understanding of *F. fujikuroi* genome and will help us to enhance our knowledge on *Fusarium fujikuroi*–rice interactions.

O (S 14) 07: Next-generation sequencing reveals the first complete genome sequence of garlic virus D infecting garlic (*Allium sativum*) - G282 from India

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Garlic (*Allium sativum*) Yamuna Safed-(G-282) plant with symptomatic leaves and bulbs were collected from the Horticulture Research Centre, S. V. Patel University of Agriculture and Technology, Meerut in March, 2018 with the aim to detect and identify viruses infecting garlic. The present report communicates the first full genome sequencing of the Garlic virus D from northern India with a genome of 8425 bp ssRNA (GenBank accession no. MK518067). The genome sequence contained a 5'UTR with nucleotides 1 to 97; ORF 1 (98-4786) (1,562 aa) Replicase -RNA dependent RNA polymerase; ORF 2 (4885-5598) (237 aa) TGB1; ORF3 (5612-5923) (103 aa) TGB2; ORF 4 (6034-7128) (364 aa) 40kDa Serine rich protein; ORF 5 (7176-7928) (250 aa) Coat Protein; ORF 6 (7928-8314) (128 aa) Nucleic acid binding protein and a 3' UTR from 8315-8425. BLASTn searches to the NCBI databases revealed that Garlic virus D (GarV-D) shared 85.83% nucleotide sequence identities with other (GarV-D) isolates identified from Australia (KF550407), 84.01% with Australia (KF555653), 83.63% with Argentina (KR819505), 83.15 % with China (MF795136 and MF363012). The full genome sequence based study of Indian Garlic virus D may reveal the geographical relationship of this virus in India and global origin which may assists in development of control strategy for this virus and to reinforce the need of a garlic-seed certification programme to improve the health conditions of the crop.

O (S 14) 08: Quantitative secretomic analysis of haploid and dikaryotic stages of *Sporisorium scitamineum* - novel insights into the pathogenesis of the sugarcane smut fungus

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Sporisorium scitamineum is a teleomorphic, biotrophic fungus causing sugarcane smut. Under conducive conditions, the smut fungus penetrates through meristematic tissue, colonizes the plant meristem and modifies it into a whip-shaped sori, consequently leading to significant yield loss. *S. scitamineum* teliospores germinate into promycelium, which further upon undergoing meiosis leads to the formation of saprophytic yeast-like haploid sporidia that proliferates by budding. Upon perception and fusion of a compatible mating-type, the non-infective haploid sporidia turns into an infective dikaryotic mycelium. Understanding on this transition of infection cycle of *S. scitamineum* is very limited *at* molecular level. Hence, in the present study, we performed a comparative secretomic analyses of different *in vitro* stages of *S. scitamineum viz.*, opposite mating type haploids, the transition stage of haploid sporidia to mycelium and the mycelial stage, in response to culturing in a host mimic medium. Extracted secreted proteins were trypsin digested and the peptides were labelled with iTRAQ (4Plex) and analyzed in the nanoLC-LTQ Orbitrap XL, which allowed the identification of 254 differentially abundant proteins (DAPs). Functional classification indicated that majority of the DAPs were related to energy production and conversion, transport and metabolism of carbohydrates and amino acids, translation, post-translational modifications and protein turnover. Enrichment analysis indicated that biological processes related to primary metabolism, catabolism, biosynthesis, response to stimulus were significantly enriched. Pathways related to carbohydrate and amino acid metabolism, energy production, biosynthesis of secondary metabolites and several signal transduction pathways were highly represented. *In silico* protein-protein interaction analysis indicated that the identified DAPs could interact with other proteins related to protein folding, sulfur metabolism, ATP metabolic and biosynthetic processes. While further analysis and validation is in progress, it is evident from our study that there is a major reprogramming occurring at the proteome level between the haploid sporidial stage and infective dikaryotic mycelium. Furthermore, the proteins specifically associated with this transition could be potential targets for anti-fungal drugs that could aid in smut disease management.

O (S 14) 09: Diversity and full genome based recombination analysis of *Pepper mild mottle virus*, a serious threat to capsicum cultivation in Himachal Pradesh, India

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Pepper mild mottle virus was first time reported by Wetter in 1984 from Sicily, Italy. In India, this virus was first time reported to infect capsicum from Himachal Pradesh (H.P.) by Sharma and Patiyal in 2011 and the complete genome sequence of this virus was first time reported in 2015 from India. In 2016-17, the surveys conducted in 29 locations of 7 districts H.P. followed by virus confirmation through DAS-ELISA and RT-PCR revealed the maximum incidence of this virus in Kullu district (88.89 %) followed by Mandi (78.57%). During these surveys, isolate each from Mandi and Kullu were selected and their full genome were determined. The genome was assembled and submitted at NCBI database vide accession number MN496153 (PMMoV-16.7-Mandi) and MN496154 (PMMoV-16.9-Kullu). Full genome based phylogenetic and recombinant analysis of these two full genome sequences along with PMMoV-HP1 (KJ631123.1) was performed. All the three PMMoV isolates shared more than 99% similarity at nucleotide and amino acid level. The Mandi isolate (PMMoV-16.7-Mandi-MN496153) shared maximum nucleotide similarity with PMMoV-HP1 (KJ631123.1) that was isolated from Hamirpur district of H.P. with more than 99% similarity. Similarly, the Kullu isolate (PMMoV-16.9-Kullu-MN496154) shared maximum similarity of 99.90% with Japanese isolate (AB000709.2). Both the isolates showed least similarity with a Korean isolate (LC082100.1) with 93.95% and 94.19% similarity. A phylogenetic tree was constructed using three full genome sequences of PMMoV isolates from three different districts of H.P. along with other 25 full PMMoV genome sequences available at NCBI database using MEGAX software.

The Mandi and Hamirpur isolates *viz.*, MN496153 and KJ631123.1 clustered along with the isolates from Venezuala, Brazil and China. However the Kullu isolate (MN496154) clustered close to Japanese and Spain isolates. The recombinant analysis was performed using software RDP4 which revealed the Mandi isolate (MN496153) with one recombination event at nucleotide 5600-6326 detected with GENECONV, BOOTSCAN, SISCAN and 3SEQ method to be the recombinant of PMMoV-HP1- KJ631123.1 (major parent) and PMMoV-HN1-China- KP345899.1 (minor parent).

O (S 14) 10: Genome analysis of strain UTT-25 of *Ralstonia solanacearum* isolated from tomato in India

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Ralstonia solanacearum strain UTT-25 was isolated from wilted tomato plants from foot hill area Chorgaliya (Latitude: 29.216709; Longitude: 79.516691), Nainital, Uttarakhand, India. Using Illumina MiSeq tool, we obtained the nucleotide sequence of the *R. solanacearum* strain UTT-25 from the paired end library with an average insert size 145 to 155 bp. The trimmed reads were assembled into contigs using de novo contigs assemblers. Structural annotation was carried out using CANoPi annotation pipeline with non-redundant protein sequences (NCBI) as thereference proteome.Thechromosome is represented by 3.6 Mbp and the megaplasmid by 1.9 Mbp. The overall G/C content of the UTT-25 genome is 67%. Biological functions were assigned to 99% of the predicted proteins. We found171 contigs for the UTT-25 with the longest contigs length of 166,162 bp.Further we predicted 4,819 cds using Glimmer-MG from all the contigs. The predicted proteins 3,679 were annotated using Uniport database. It contains 69 predicted tRNA genes, UTT-25 are most closely related to Phylotype I. BLASTX analysis revealed significant similarities inthese regions with known proteins by providing E-value distribution. Around 99.3% of the predicted protein found using BLASTX have similarity of more than 60% at protein level with the existing proteins at NCBI.We report the draft genome sequence of this representative strain infecting tomato, chilli, capsicum, brinjal and potato. This whole-genome project has been deposited at GenBank under the Gene Bank Assembly Accession number GCA_002930085.1 of *Ralstonia solanacearum* strain UTT-25 isolated from tomato.

O (S 14) 11: Comparative genomics of *Magnaporthe* species infecting rice and pearl millet

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Being a one of the putative centre of origin for *Magnaporthe*, blast disease is a major threat to the Indian productivity of agriculturally important cereal crops. In order to understand the genetic variability, speciation and host specificity, whole genomes of rice infecting *Magnaporthe oryzae* strain RMg-Dl and pearl millet infecting *M. grisea* strain PMg-Dl was sequenced using the Illumina and PacBio platforms. The high throughput hybrid assembly of short and long reads resulted to 341 and 996 scaffolds with the genome size of 47.89 Mb and 34.81 Mb of PMg-Dl and RMg-Dl strain, respectively. Genome size was larger in pearl millet infecting *M. grisea* than rice infecting *M. oryzae* indicative of genome reduction in rice adapted *M. oryzae.* Comparative genome analysis revealed 83 % average nucleotide identity (ANI) and gene calling confirmed a total of 10451 and 12747 genes in both genomes with common and unique proteins/genes, protein family and superfamily between the genomes. A total of 5589 and 5032 genes were uniquely present in both genomes. Similarly, the InterProScan of predicted protein sequences of both genomes annotation revealed that 148 (4.3%) and 65 (1.9%) protein family (PFAM), 38 (7.7%) and 29 (5.9%) super family (PIRSF) were uniquely present in PMg-Dl and RMg-Dl genome. The prevalence of Virulence Factors (VF) determination revealed that majority (90.9%) of VFs were shared between both the genomes. However, two (2) VFs were unique in PMg-Dl and three (3) VFs were unique in case of RMg-Dl genome. CAZmes and unique pathways in PMg-Dl and RMg-Dl were also found. The information generated will be useful to develop specific marker for diagnosis, pathogen surveillance and monitoring & tracking, molecular taxonomy and species delineation which ultimately leads to device better management strategies for blast disease.

O (S 14) 12: Genomics and functional analysis of virulence genes in *Tilletia indica*, pathogen of Karnal Bunt of wheat

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Fungal diseases are important biotic constraints which cause significant crop losses in term of food security. Fungal pathogens are emerging or/ remerging in climate change scenario. Karnal bunt of wheat is an internationally quarantined disease of wheat and affects the seed trade. The present study carried out that the whole genome of *Tilletiaindica* was sequenced and identified transposable elements, pathogenicity-related genes using a comparative genomics approach. The *T. indica* genome assembly size of 33.7 MB was generated through Illumina and Pac Bio platforms with GC content of 55.0 per cent.The comparative genome analysis suggested 3,751 proteins of *T. indica* had orthologs in five fungi whereas 126 proteins were unique to *T. indica*.Fourteen homologous sequences of putative pathogenicity-related genes *viz*. *TiPmk1*, *TiKss1*, *TiHog1*, *TiHsp70*, *TiKpp2*, *TiCts1*, *TiHos2*, *TiChs1*, *TiPrf1*, *TiSid1*, *TiSsp1*, *TiSte20*, *TiUbc4* and *TiUkc1* were identified in *T. indica* by *in silico* analysis. Most of the pathogenicity-related genes were highly expressed in *T. indica* in response to susceptible host factor as compared to resistant host factor. For functional analysis, the *TiHOG1* gene of 1104 bp length was amplified in 1 M NaCl stressed condition in *T. indica*. It was cloned in pJET2.0 cloning vector and the positive clones were confirmed by colony PCR and plasmid digestion. The *TiHOG1*gene was sub-cloned in expression vector (pRS426GPD plasmid) and sequences were analyzed. The *TiHOG1* in pRS426GPD (pRS426GPD-*TiHOG1*) was expressed functionally in heterologous system. TiHOG1 protein exhibits high amino acid similarity with the homologous protein sequences in *Tilletia caries*, *Ustilagomaydis* and *Pucciniagraminis* f.sp. *tritici*. Functional expression of *TiHOG1* in *S. cerevisiae*™*hog1*mutant showed that *TiHOG1* restored salinity stress tolerance up to 1M NaCl, 1M KCl, 0.25 $CsCl_2$, 0.5M $MgCl_2$ and 0.5M $CaCl_2$ and osmostress tolerance up to 1M sorbitol and 1M sucrose. The expression of *TiHOG1* was elicited up to 19.61-fold in response to susceptible host whereas resistant host factors showed 9.52-folds transcripts. It revealed involvement of *TiHOG1* gene in stress tolerance and may have role in pathogenesis of *T. indica*.This will provide window to understand the pathogenesis mechanism, fungal life cycle, survival of teliospores and novel strategies for management of Karnal bunt disease of wheat.

Poster Papers

P (S 14) 01: Developing an inducible vector system for controlled expression of effector proteins of the filamentous fungi, *Colletotrichum falcatum.*

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Identification and functional validation of the effector repertoire of plant pathogens is crucial in understanding the molecular basis of a plant pathogen interaction and is instrumental in developing pathogen-derived resistance strategies in crop plants. Red rot caused by the hemibiotrophic fungus *Colletotrichum falcatum* is one of the devastating diseases of sugarcane causing significant loss to sugarcane production in India and other Asian countries. An insight into the functions of the two identified putative effectors/PAMPs of the red rot pathogen *viz., CfEPL1* and *CfPDIP1,* can be achieved through ectopic expression analyses of these candidate virulence proteins. However, the constitutive expression of such genes can cause severe growth defects or lethality, which strongly recommends the need for inducible expression at a particular stage/condition. Hence, a Dexamethasone inducible expression vector was developed based on the pCAMBIA1302 vector backbone. The coding sequence of the Dexamethasone-interacting DNA elements were conceived from the pINDEX3 vector, which comprises of the GVG [Yeast Gal 4 DNA binding domain, VP16 transactivation domain and Glucocorticoid receptor] transcription factor placed betweenCaMV35S promoter and RbCs E9 terminator and the GVG response elements, cloned upstream of the modified multiple cloning site. This entire stretch was synthesized with the GVG gene optimized for expression in both sugarcane and tobacco and got cloned into pCAMBIA1302. This novel DEX inducible vector pC1302DEX, comprises of DEX inducible cassette, replication functions of both *E.coli* and *Agrobacterium*, Hygromycin and Kanamycin resistance markers, GFP reporter, flexible linker for the fusion protein, Histidine tag and Thrombin cleavage site for protein purification.*CfEPL1* and *CfPDIP1* constructs cloned into pC1302DEX can be used for controlled gene expression in transformed sugarcane and tobacco. Screening of *E.coli* strain DH5á transformants with pC1302DEX:EPL1 and pC1302DEX:PDIP1is under progress, after which these vectors can be used for particle bombardment or agroinfection of the sugarcane calli. Engineering red rot resistance by over expressing the candidate genes *viz., CfEPL1 and CfPDIP1* after DEX induction in sugarcane would hold promise and potential for enhancing pathogen derived resistance in sugarcane.

P (S 14) 02: RNA-seq reveals dynamic expression of genes in *Chaetomium globosum* antagonistic to *Bipolaris sorokiniana* causing spot blotch of wheat

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Chaetomium globosum Kunze, is a ubiquitous filamentous fungus that commonly colonizes the soil and cellulose-containing substrates. The fungus has been reported to be a potential antagonist of various plant pathogens, most of which are soil borne and seed borne. Improved understanding of microbe- microbe interaction in the rhizosphere would assist in the development of potential bio-formulations. The molecular events and patterns of gene expression are not yet explored in *C. globosum.* In this study, we performed global transcriptome profiling of *C. globosum* strain Cg2 during interaction with phytopathogen *Bipolaris sorokiniana* isolate BS112 using RNA- seq in order to gain insights into the potential mechanism underlying the antagonism. Dual-culture technique was done to study bipartite interaction and was followed by isolation of total RNA from pooled samples of individual treatment at different intervals. The two paired end cDNA sequencing libraries were prepared and sequenced using Illumina HiSeq 2×151 bp Chemistry. Approximately 20 million reads were obtained from three libraries with each in duplicate (Cg2 control, BS112 control and Cg2-BS112). Transcriptome analysis showed significant differential gene expression in *C. globosum* during challenge with *B. sorokiniana.* A total of 14366 (log2FC and pval0.01) differentially expressed genes (DEGs) were detected. Among them 7145 were up-regulated and 7221 were down regulated. Functional classification of DEGs based on gene ontology enrichment analysis and KEGG pathway annotations revealed that, 271 Antibiotic biosynthesis genes, 68 Enzymatic Genes and 249 signaling genes were expressed in interaction. We identified various genes of biological function such as biosynthesis of secondary metabolites, polyketide synthase, antibiotic, hydrolytic enzymes, putative fungistatic metabolites, carbohydrate and protein metabolism related genes and some of signaling genes like protein kinases (PKs).This RNA-seq profiling will generate a novel dataset for further studies and will provide a blueprint for further research in biocontrol mechanism of this fungus.

P (S 14) 03: A bioinformatics approach for analyzing role of *Medicago truncatula* miRNAs in defense against viruses

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Background: microRNAs are non-coding small RNAs. The miRNA mediated antiviral mechanism is a well-known fact in animals, recently plant miRNAs are also emerged to be an essential part of plant antiviral-defense mechanisms. miRNAs regulate plant gene expression generally by translational inhibition but occasionally cleavage of complementary mRNAs is also been reported. In the present study, a bioinformatics approach was taken to test whether plant miRNAs from *Medicago truncatula* could have antiviral activity by targeting the genomes of plant infecting viruses. Methodologies: This study includes 756 mature *M. truncatula* miRNAs and their specific interactions with corresponding targets in approximately 500 viral species (predominantly from the major plant-infecting virus families of geminiviruses and potyviruses). The modified and customized miRanda tool is used to filter out the truest positive miRNA-gene pairs. The following criteria were considered to shortlist the output pairs; no mismatch in seed regions (position 2–8), four or fewer mismatches in over-all alignment, no more than two consecutive mismatches in position 13–21, a maximum interaction energy of”20 (kcal/Mol). Results: Several *M. truncatula* miRNAs showed potential for targeting viral genomes. Validated targets in the plant genomes were taken into consideration during selection of parameters used in this study for prediction of miRNA:target pairings. This precaution ensures that in-vivo behaviour of predicted pairing will be similar to natural miRNA-target pairings. Further miRNAs belonging to animal kingdom, randomly generated miRNAs and genomes of animal-infecting viruses were used for comparison with our screening. It has been found that plant miRNAs target plant viruses more efficiently than any other sequence, but also, miRNAs can either preferentially target plant-infecting viruses or target any virus without preference.

P (S 14) 04: A new insight to vertical and horizontal transmission microbiome: a case study with rice phyllosphere microbiome

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Phyllosphere microbiome of rice genotypes (Pusa 1602 and PRR78) grown in two contrasting environments, namely the Himalayan hill ecosystem (Palampur) and the coastal ecosystems of the islands (Andaman and Nicobar Island) was deciphered by culture-independent metagenomic tools and culture-dependent methods. The culture dependent microbiome analysis showed colonization by bacterial species namely *Pantoea ananatis, Enterobacter cloacae, Microbacterium testaceum* and *Pantoea agglomerans* on rice plant irrespective of locations and season indicating spatio-temporal perpetuation of phyllosphere microbiomes. Similarly the core microbiome analysis by comparative metagenomic tools indicated multi microbiota core consisting of *Pantoea ananatis, P. agglomerans, Pantoea dispersa, Erwinia soli, Methylobacterium organophilum, M. adhaesivum, Enterobacter cloacae* and *Sphingomonas yabuuchiae* on phyllosphere. This shows that the rice phyllosphere microbiome consist of certain set of bacteria which are constantly present on rice phyllosphere comprising core microbiome. The analysis also gives an indication of seed being the career of a part of phyllosphere microbiome. Species belong to *Pantoea, Microbacterium, Sphingomonas, Acinetobacter, Aeromonas, Brevundimonas, Comamonas, Klebsiella, Paenibacillus* and *Pseudomonas* isolated on culture media exhibited cooperative or competitive interaction with rice and associated blast pathogen. Microbial volatile compound mediated inhibition of blast fungus *Magnaporthe oryzae* was also displayed by microbiome.

P (S 14) 05: Refinement of *Tilletia indica* genome and comparative genomic analysis for unraveling the complexity of molecular pathogenesis

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De novo sequencing of different isolates of *Tilletia indica* (Ti), a pathogen of Karnal bunt disease in wheat was reported in 2017. Low genome coverage observed in misassemblies ridden with several gaps, repeats and fragments. Incomplete genomes with missing genetic information posing serious limitations in genome functional annotation and understanding the biology of the pathogen. Understanding variation among different isolates of Ti and analysis of various different developmental stages enables identification of individual candidate genes involved in disease pathogenesis. We developed a computational pipeline employs genome reconciliation algorithm to addresses various deficiencies in misassemblies such as gap filling, repeat reduction, contiguity and scaffold length improvement. The computational approach was employed for improving assembly quality of monoteliosporic cultures of wheat Karnal bunt pathogen of Ti. Resulting near complete improved Ti genome helped us in identification of candidate genes related to mating, virulence and growth related to Karnal bunt pathogenesis in wheat.

P (S 14) 06: Comparative genome analysis of *Tilletia indica* causing Karnal bunt of wheat revealed high genomic variation

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Karnal bunt of wheat is an internationally quarantined disease caused by *Tilletia indica*. The disease is important in North-western plain zone of India. Till date no reference or complete genome of *T. indica* is available and reported genomes are variable in size ranging from 26.7 to 43.7 Mb. Recently whole genome of *Tilletia indica* RAKB_UP_1 (GCA_002220835.1, IARI, New Delhi) has been sequenced. In present study, the genomes of seven isolates of *T. indica viz*. DAOM_236416 (GCA_001645015.1), PSWKBGD_1_3 (GCA_001689965.1), PSWKBGH_1 (GCA_001689995.1), PSWKBGH_2 (GCA_001689945.1), RAKB_UP_1 (GCA_002220835.1), TiK_1 (GCA_002997305.1) and Tik (GCA_003054935.1) were compared. For genome mapping, all the genome assemblies were aligned against RAKB_UP_1 genome using minimap2 wherein 86% to 100% similarity was observed with the reference genome. Tik_1 mapped 100% while PSWKBGD_1_3 and PSWKBGH_1 was only 86.92 % similar with the reference genome. Further, comparative genome analysis was done by identification of SNPs, In-Dels, segmental duplicates, LTR and CNV. It revealed that variable number of SNPs were ranging from 1380 (Tik_1) to 160966 (Tik) and 82 (PSWKBGH_1) to 3309 (PSWKBGD_1_3) In-Dels. The maximum number of segmental duplications (SDs) were identified in TiK_1 isolate (60632 regions) while least in DAOM_236416 isolate (2082 regions). LTR retrotransposon regions were found as 307 (DAOM_236416) – 833 (PSWKBGH_2). Copy number variations including duplications and deletions have also been identified and Tik had shown highest number of duplications count (100) while no duplication was found in Tik_1 which was expected also because of 100% mapping with the reference genome. In case of deletion counts, highest (37) deletion were detected in DAOM_236416 and least (14) in PSWKBGD_1_3. Further, this study will be used for functional genomics and to devise the novel management strategies against *Tilletia indica*.

P (S 14) 07: Genome-wide association mapping for blast resistance in Indian rice varieties

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Rice is the staple diet of more than half of the world population. To sustain the food requirement of ever growing global population, there is a need to double the production over the next four decades. Among major biotic constraint, rice blast is one of the most serious and destructive disease of rice causing 10-30% yield losses annually. The utilisation of resistant cultivars is the most preferred strategy to manage the blast disease owing to its cost effectiveness and eco-friendly nature. However, blast fungus overcomes the resistant varieties, within few year of its release so identification of novel broad spectrum resistance genes is essential. In present study, a set of 81 National Rice Research Institute released varieties (NRVs) grown over eight different ecologies were phenotypes against leaf blast resistance at NRRI, Cuttack for two consecutive years. Among them, twenty varieties showed resistance, twenty one were moderately resistant whereas forty varieties (50%) showed susceptible reaction. The cluster and structure analysis categorized NRVs into three groups. The NRVs showed 96% variation among individuals and 4% variation among population. The principal coordinate analysis categorised the resistant and susceptible NRVs into different groups. The genome wide association studies (GWAS) was performed using 135 SSR markers to identify the blast *R* gene/QTLs conferring resistance to the rice blast. The GWAS identified 16 genomic region showed significant association with the leaf blast resistance. This study would help in identification of the potential function, and validation of the candidate *R* genes/QTLs. The associated gene loci could be used in developing blast resistant cultivar through marker-assisted selection.

Session 15

Transgenics and related approaches for disease management

Keynote Papers

KN (S15) 01: Silencing viral multifunctional proteins: Boosting infringed cellular defense of the host

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The cellular dynamic of an infected cell is a complex flow of events, starting from altered gene expression to dysfunctional cellular organelles and finally cell death in extreme cases. Host-virus interactions lead to the initiation/alteration of various cellular responses like: hypersensitive response, signal transduction pathways, RNA interference (RNAi) and proteosomal pathway. Small viral multifunctional proteins act very precisely to redirect central dogma of biology. Viral proteins interfere in the functioning of key components of pathways operating to maintain cellular homeostasis. Geminiviral AC4 protein redirects epigenetic regulations by binding with Argonaute 4 (AGO4) protein. Tospoviral multifunctional NSs protein interferes in RNAi mechanism and alters signaling mechanism. It's possible targeting to vacuoles may lead to cell death or necrosis during infection. Potyviral HcPro (Helper component protease) not only suppresses RNAi machinery but also alter proteosomal pathway in favor of virus. It's interaction with one of the subunits of 26S proteosome is crucial in regulating RNase activity and it might be influencing protease activity. Since viral proteins modulate different steps of cellular pathway, hence silencing these proteins helped in boosting host defense and in developing resistance for viral infection.

KN (S15) 02: Application of transgenic and genome editing technologies for improving banana with disease resistance

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Banana (*Musa* spp.) is one of the major staple food crops grown in over 140 countries in the subtropics and tropics with annual global production of around 148 million metric, feeding about 500 million people. It is a valuable food security and cash crop as it can be cultivated in diverse environments and produces fruits throughout the year in favourable weather conditions. Its production is largely constrained by diseases and pests in addition to other factors like declining soil fertility, narrow genetic diversity in germplasm, and inadequate availability of clean planting material. There is need to develop banana varieties with multiple and durable resistance to combat biotic stresses. Modern breeding tools, including transgenics and genome editing, can be applied for the improvement of banana bypassing the natural bottlenecks of traditional breeding. Intensive efforts using genetic modification have been made to develop improved banana varieties with resistance to biotic stresses. Genome editing, an emerging powerful tool, can be applied for developing durable resistance to diseases. CRISPR/Cas9-based genome editing has been lately established for banana, paving the way for functional genomics allowing identification of genes associated with disease resistant trait, which could be used for the improvement of banana. Application of genetic engineering for improvement of banana through transgenesis and genome editing will be presented during this conference.

KN (S15) 03: The healthy crops project – combatting bacterial blight disease of rice with the *SWEET* resistance kit

Sarah M Schmidt[1], Boris Szurek[2], Bing Yang[3], Frank White[4], Ricardo Oliva[5] and Wolf Frommer[1]

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Genetic resistance is the most effective solution to combat bacterial blight disease of rice caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). We have uncovered a key resistance mechanism that involves *SWEET* genes as susceptibility factors. During rice infection, *Xoo* secretes small molecules, called Transcription Activator Like (TAL) effectors, into the rice cell. Bacterial TAL effectors bind to effector-binding-elements (EBE) in *SWEET* promoters and induce *SWEET* genes. *SWEET* genes code for sucrose exporters that make sucrose available in the apoplast where the bacteria reside to feed upon it, thus establishing rice infection. EBE variants that cannot be recognized by TAL effectors abrogate induction causing genetic resistance of rice to bacterial blight disease. With the Healthy Crops consortium, we are developing rice varieties that are resistant against Bacterial Blight by genome-editing of the *SWEET* promoters for smallholder farmers in Asia and Africa. Healthy Crops is a humanitarian consortium of scientists from Germany, France, the US, the Philippines and Colombia. We have developed a molecular diagnostic kit to enable analysis and surveillance of bacterial blight in the field and identification of suitable resistant lines. We also developed CRISPR-Cas9 genome-edited rice mega varieties with broad-spectrum resistance to selected bacterial blight isolates that represent a global *Xoo* collection. Currently we are exploring the legal frameworks in Asian and African target countries for releasing genome edited crops. I will discuss our approach to obtain Freedom to Operate, that is to use patented technology, within a humanitarian research project. Furthermore, I will present an overview of the current legal frameworks for genome-editing in the EU, US, Australia, Argentina, Colombia, Japan and other countries and provide insights in the ongoing decision process in several Asian and African countries. Finally, I will discuss the regulatory strategy for the Healthy Crops project to make the SWEET resistance kit available to breeders for dissemination, in particular to smallholder farmers.

Oral Papers

O (S15) 04: Doubled haploid population developed from inter-specific hybrid (*Brassica oleracea* x *B. cretica*) could be used as potential source for effective resistance against black rot in *Brassicas*

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One unique doubled haploid (DH) population developed from an inter-specific hybrid (*Brassica oleracea* x *B. carinata*) through isolated microspore culture. The genotype, JTC-1 (*B. carinata*; BC genome) was highly resistant to race 1 and 4 of bacterium *Xanthomonas campestris* pv. *campestris* (*Xcc*) causing black rot in different brassica species. The *B. oleracea* (C genome) genotype, Pusa Snowball K-1 was highly susceptible to black rot. We adopted a modified method with higher concentration of microspores and heat shock treatment to induce the microspore derived embryos. Among the large population developed 114 plants were doubled haploids revealed through flow cytometer analysis. All DH plants were male sterile because of triploid nature and we recovered only 2 male fertile plants (hexaploid). This population was screened against race 1 and 4 of *Xcc* under controlled environment condition with most congenial condition for disease infestation. Besides, these plants were also characterised for various agronomically important traits. Among 114 DH plants 44 were completely resistant to race 1 and race 4 of the *Xcc* although they had varied agronomic features. This unique population was also analysed using a large set of genomes specific AAFC SSR sets for segregation of B and C genome among them. It was revealed that preferential gametic selection for B genome was frequent among the DH populations and most of the plants had similarity *with B. carinata* genotype. However, few plants were also derived with more closeness to *B. oleracea*. The *B. oleracea* genotypes (C genome) are very susceptible to *Xcc* whereas effective resistance is available in B genome *of B. carinata* (BC genome). The DH population developed from the inter-specific hybrid would be instrumental in introgression of black rot resistance genes into B. oleracea and future resistance breeding. Moreover, this population could be used strategically in studying host plant resistance in different genome of *Brassicas* and revealing the molecular genetic pathways for resistance to black rot.

O (S15) 05: Introgression of *Vf* (Rvi6) scab resistance gene in commercially grown cultivars of Apple (*Malus x domestica* Borkh) using marker assisted selection

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Apple scab is one of the most widespread diseases of apple trees causing huge economic losses both quantitatively and qualitatively. The increased expenses associated with labour and fungicides justify the investigation of an alternative, effective, least expensive resistance approach to deal with this disease. So the present study was devised to introgress, *Vf* (Rvi6) scab resistance gene in two commercially grown cultivars (Gala Redlum and Fuji Aztec) of Apple (*Malus x domestica.* Borkh)" using marker assisted selection. Twenty four parental genotypes were screened for scab disease resistance using phenotypic and molecular approaches to find out the highly resistant parental genotype. Phenotypic screening using leaf detach method showed that, in certain genotypes fungus did not proliferate macroscopically and the leaves remained alive, green and also showed hypersensitive response, which gives indication of resistance against apple scab. To validate the results of phenotypic screening, all twenty four genotypes were again evaluated for the presence of *Vf* gene conferring resistance against apple scab disease using nine *Vf* gene specific primers. Certain gene specific markers amplified single fragment in resistant cultivars and confirmed the presence of *Vf* gene in these cultivars. Among 24 parental genotypes 8 genotypes *viz.*, Firdous, Nova Easygro, Gavin, Priscella, Liberty, Selection 5, Selection 1 and Selection 8 were amplified by almost all the primers used. Gene expression studies using Real time PCR also revealed that same 8 genotypes were having highest expression of *Vf* gene. Before hybridization, studies like pollen viability and pollen germination were also done, which revealed that maximum germination and viability were shown by Priscella (91.31 & 90.60% respectively). For hybridization programme to introgress the resistance in susceptible cultivars Redlum Gala and Fuji Azitec, 8 donor parents were selected as pollen donors based on pheno-molecular screening, gene expression, pollen viability and germination studies. Out of total crosses done, the fruit set percentage was highest in Gala Redlum x Firdous with 91.66%, the seed germination and seedling survival percentage was highest in crosses between Fuji

Aztec X Sel. 8 (79.62%) and Gala Redlum x Liberty (79.82%) respectively. The hybrid seedlings were further evaluated for phenotypic screening using same leaf detach method and only two classes were observed either resistant or susceptible. To validate our phenotypic results hybrids were also evaluated using molecular markers and same results were confirmed as in phenotypic screening. The gene expression studies were done for single resistant hybrid from each cross also showed highest expression as against susceptible hybrid. Present study confirmed the resistance both by phenotypic and molecular screening among certain genotypes which can be further exploited for future molecular breeding programme for other commercially growing scab susceptible apple varieties. Also the resistant hybrid obtained from the study can be top worked on different rootstocks to develop resistant variety.

O (S15) 06: Optimization of different promoters for spatio-temporal regulation of transgene expression in tomato

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The use of accurate promoters is an absolute necessity for expressing the gene of interest in the desired tissue at a crucial juncture. Over the years, a diversity of plant promoters has been developed, which differ in the ability to regulate the temporal and spatial expression patterns of a transgene. Nevertheless, systematic comparative analysis of the promoters for useful transgene expression in tomato is lacking. We have isolated constitutive, tissue-specific and inducible promoters from tomato and *Arabidopsis* sp. for directing transgene expression exclusively in targeted tomato tissues and at certain developmental stages in a deliberately controlled manner. Screening of the promoters was based on the expression levels of the corresponding genes in tomato and bioinformatics analysis of the promoter regions. Isolated promoter regions were subsequently fused to the GUS reporter CDS in a binary vector. The resultant constructs were introduced into tomato seedlings or leaves by agroinfiltration. Promoter strengths and tissue specificity were tested by GUS reporter gene-aided fluorometric and histochemical assays. We have found that GUS expression controlled by the cell division-specific AtYAO promoter in the young leaves and hypocotyl was comparable to that of the CaMV35S promoter. GUS activity was also detected in the young roots. Green tissue-specific SlRbcS2 promoter was predominantly detected in the leaves. Constitutive AtUBQ10 and SlEF1á promoters displayed moderate activity in comparison to that of the PCaMV35S in most of the tissues. Additionally, heat-induced GUS activity by 1.6 kb of SlHsp23.8 promoter was witnessed in the leaves after 24 h heat treatment at 40°C. Our study highlights the potential of these promoters for the spatio-temporal expression of transgenes in tomato.

O (S15) 07: Artificial miRNA-mediated targeting of ToLCV genes for virus resistance in tomato

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In the current global scenario, almost every nation specially the developing nations like India, is challenged by plethora of problems, ranging from population growth to increased demand of food supply. Such problems are burden to the nation as well as to the overall global economy. Crop yield loss due to biotic and abiotic factors further adds fuel to the demanding situation. Viruses contribute significantly to crop yield loss. The tomato leaf curl virus (ToLCV), a member of the begomovirus genus of the Geminiviridae family, is transmitted by whitefly (*Bemisia tabaci*). The disease symptoms are curling and yellowing of leaves, and stunted growth of the plant. Recently, the artificial micro RNA (amiRNA)-based strategy has been used successfully to curb virus infections in different crops. The amiRNA strategy uses a natural precursor miRNA, which is reconstituted with an artificial miRNA sequence, i.e., the natural mature miRNA duplex is replaced with the amiRNA sequence, which can target specific genes utilizing the same processing mechanisms as natural miRNAs. In the present study, the amiRNA strategy has been used to target ToLCV RNAi suppressor genes, *AC4* and *AC2*, and pre-coat protein gene, *AV2*. The amiRNA bicistronic constructs, namely, *AC4+AC2, AV2+AC4* and *AV2+AC2* harboring viral sequences were cloned in the pCAMBIA2300 binary vector for *Agrobacterium*-mediated transformation of tomato (cv. Pusa Early Dwarf) and transformations were carried out as per established lab protocol. The presence of transgenes was confirmed in putative transformants by PCR screening using gene-specific and NPT-II (marker gene) primers. The tomato transgenic lines have exhibited the stable expression of the indented amiRNAs. The transgene integration and copy number as well as viral resistance assays of the tomato transgenic lines are being in progress.

Session 16

Human resource development in plant pathology

Keynote Papers

KN (S16) 01: Human resource development in plant pathology

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World's population will grow to reach 8.1 billion by 2030 and thus global food requirement has to be increased by 50%. India will be No 1 in population by 2050. Registering zero hunger in India depends upon increasing food production, minimizing crop losses due to diseases and pests and doubling the income of farmer. India had a rich agricultural heritage since the time of Rigveda (C.8000 B.C.) Plant and soil health have been recognized by the UN to commemorate 2020 as international year of plant health. Inorder to achieve food security and to reach zero hunger, it has to ensure high food production in various forms. In this regard, there is a necessity to concentrate on HRD for reaching sustainable goals. HRD is a process of developing the most superior work force so that the organization and individuals can accomplish their work goals in service to customer. It can be knowledge acquisition, curriculum based course, imparting practical training, human resource management, bringing out changes in agricultural educational policy, to acquire or sharpen capabilities required to perform various functions and others.

HRD needs to be strengthened with reference to Plant Pathology in the following areas:

1. 1/3rd of global fungal diversity including that of plant pathogens exsists in India, Hence there is necessity to impart training to youngsters on the taxonomy, identification, and conservation of fungal pathogens based on morphotaxonomy and molecular approaches
2. Work force needs to be strengthened in developing disease forecasting models, particularly on epidemiology with reference to long term climate data. Well trained extension workers are necessary in Plant Pathology. Therefore, it is imminent to bring in work force on disease management under field conditions, phytosanitation , seed certification, biological control, judicious usage of fungicides, breeding disease resistant varieties, application of nanotechnology and other measures
3. Emphasis has to laid on communication skills between plant pathologists, farmers, and industries, as the communication gap got widened. Therefore, Plant Pathologists have to be trained positively in this direction.
4. Early detection of fungal pathogens and other pathogens, symptom verification and strategies for their management are essential.
5. Post-harvest losses are large as 1/3rd of food produced is lost due to poor storage conditions and contamination by fungi and microbes. There is a great need to train and develop human resource by imparting specific and proper training.
6. To impart affective training on integrated bio-security facilitating trade and conserving biodiversity along with use of bio informatic tools and in-silico work in plant pathology have to be taken up at the earliest.

KN (S16) 02: Microorganisms in intellectual property landscape: carrier opportunities in plant pathology

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Intellectual property involves inventions, fictional and creative work, industrial designs for article, symbols, etc. utilized as a part of trade. Currently IPRs cover patents, copyrights, trademarks , industrial designs, geographical indications (GI), layout designs, trade secrets and new plant varieties. Today, it is widely accepted that any new result of a man's brain work need to be secured as private property. All patentable inventions must satisfy essential criteria that are, the invention must be novel and not obvious, it must have some industrial use, and the description part of the patent application must enable a person skilled in the relevant area of technology to put the invention into practice.The Indian patent system is governed by the Patents Act, 1970 as amended by the Patents (Amendment) Act, 2005 and the Patents Rules, 2003, as amended by the Patents (Amendment) Rules 2006 effective from 5 May 2006. During the late 1970s with the advancement in recombinant gene technology, patenting microbes came into the existence including the famous genetically engineered superbug which catabolizes petroleum oil. His claim on the superbug was previously rejected by the USPTO but later in a case of Diamond *vs*. Chakrabarty, US Supreme Court gave the verdict in the favor of A.M. Chakrabarty. In 1981, motivated by the decision given by US Supreme Court in Chakrabarty case, Japanese Patent Office and European Patent Office also started issuing patenting microbes. Under Indian Patent Act 1970, Amendment 2002, implemented form May 20, 2003 microbe's development can be patented in India. Several PCT and US Patent have been awarded to our group for novel agriculturally important microorganisms. A *Trichoderma harzianum* strain useful as nematode inhibitor, fungicide and plant growth promoter and a process for the isolation have been patented in 2002 (US Patent No. 6,475,772). In 2004 PCT patent awarded to the synergistic fermented plant growth promoting biocontrol composition (PCT WO 2004-087618A1). Another PCT patent has been awarded in 2005 to synergistic bioinoculant composition comprising bacterial strains of *Bacillus subtilis* or *B. lentimorbus* from cow milk (PCT WO 03/020038A1). In the year 2007, US patent has been awarded to a synergistic fermented plant growth promoting, bio-control composition (US Patent No.7,297,659B2).Likewise, bacterial strains of accession no. NRRL B30486, NRRL B30487 and B30488 and method of producing the composition have been patented in 2006 (U. S. Patent No. 7097830 B2).US patent was awarded to the rapid composting of bovine dung using *Trichoderma* of Accession No. NRRL 30598 having ability to promote plant growth. The biocontrol potential of Agriculturally Important Microorganisms (AIMs) is mostly attributed to their bioactive secondary metabolites. However, low shelf life of many potential AIMs hinders their use in agriculture and is the main reason of low adoption by the farmers. Under the present political, technological and socio-economical situation it is very complicated to build up our national system of IPR in according to those of developed nations. Patenting life forms bring with them imperious issues of pious and ethical values. Thus, it would be a great favor to our nation to file, document, keep and modify new microbes isolated from different parts of the country. During the presentation emphasis will be given on Government agencies involved in promotion, development and funding of patent related matters and carrier opportunities of plant pathology students in intellectual property management.

KN (S16) 03: Perspectives in human resource development in plant pathology

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Sustainable Development Goals 1 and 2 relating to elimination of poverty, ending hunger, achieving food security and improved nutrition are the most important and needing urgent attention for agriculture and farmers' welfare. Plant pathology has been the backbone of agriculture, particularly in enhancing crop production through management of many plant diseases. With increasing human population at global level, the sustained improvement in the production of all categories of food such as cereals, pulses, oilseeds, fruits, vegetables etc. is however, needed which necessitates development of new and environmentally-acceptable methods of disease management and the human resource trained accordingly. Currently, plant pathologists have played important and critical role in detection of pathogens such as fungi, bacteria and viruses; study of epidemiology, loss assessment and management of plant diseases; identification of germplasm of different crops resistant/ tolerant to diseases and improving higher productivity, and crop diseases of importance affecting trade. Bacteriology and virology in majority of educational institutions are not adequately addressed, neither for education nor for research. Hence, this needs to be strengthened with reorientation of up-to-date curriculum at UG and PG level. Similarly, molecular plant pathology has to be re-oriented and re-structured to strengthen the human resource for future in molecular aspects of host-pathogen interaction, developing diagnostic kits and plant disease management etc. However, while introducing new courses/syllabi, emphasis on the taxonomy aspect of important pathogens, *viz.*, fungi, bacteria, virus, nematodes etc. must be there. Addressing multi-etiological problems, developing digitized models of disease cycle/ important resources for education, and establishment of well equipped laboratories to provide workable practical knowledge in addition to sound theoretical knowledge to the students are needed. Simultaneously, capacity of academia in teaching and research institutions will have to be augmented with modern and up-dated knowledge in the subject. Harnessing its flexi-time, space and pace potential, the Open and Distance Learning (ODL) can be used alongside classroom mode of education, in training and retraining of faculty, graduate professionals and para-professionals to keep them abreast with new knowledge and developments in S&T. Farmers are now concerned for specific diagnosis of plant health problems and their management strategies to produce more from lesser resources as well as crop of high quality. Hence, scope of clinical plant pathology will increase manifold in days to come. Although several on-site testing/in-field identification diagnostic kits and mobile apps are available or are under process of manufacturing by various companies, they aren't within the reach of farmers due to several reasons including limitation of diagnostic kits, some of them are expensive and their usage requires expert personnel for handling them. Forecasting and forewarning of plant diseases is another aspect which needs more focus for strengthening the human resource development through training on epidemiological aspects. Workforce available with regards to plant pathology, employability of graduates in terms of skill, and competence and qualification required by employer such as pesticide firms and seed industry etc. will also have to be addressed to maintain a demand and supply balance in the market. Concerted efforts are also needed for improving the quality of crop protection products by encouraging introduction of new, effective and environmentally more sustainable agro-chemicals and bio-products; curbing the menace of spurious pesticides and biological laced agrochemicals and stringent action against those involved in supplying non-genuine pesticides and bio-products; usage of personal protective equipment (PPE) and responsible use of crop protection products should be made mandatory by law in view of the current hazardous waste management practices; post harvest loss management during harvesting, transportation, threshing, processing, storage, market etc.; bio-safety and bio-security and value addition etc. It is suggested that a National Plant Pathology Information System be developed which should be a digitized data base on the institutions involved in research, education, extension/development with details of their projects, diseases of economic significance, management practices for important diseases, and specialists available for specific advice etc. Scientific Societies may share the responsibility to take up such work.

KN (S16) 04: Modernisation of instructions and infrastructure for enhancing professionalism in plant pathology in India

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Systematic teaching in plant pathology started much later than systematic studies in agriculture in India. Earlier restricted to taxonomic studies of fungi pioneered by E.J. Butler, it was commenced in 1930s as Mycology and Plant pathology being a branch of Botany. Though a degree programme in plant pathology was initiated in 1945, it became an integral part of agricultural education as a subject with establishment of agricultural universities in the 1960s. Emergence of new threatening diseases in intensive agriculture after green revolution accelerated the demand for human resources trained in plant pathology. Now all the 75 State, Central and Deemed Agricultural Universities and many private Agricultural Higher Educational Institutions (AHEIs) are offering under- and post graduate programmes in plant pathology. It must be mandatory to strictly adhere to the course curriculum recommended by the Indian Council of Agricultural Research (ICAR) which is periodically and regularly revised and updated. Graduates must have knowledge of fundamentals, diseases of crops and integrated pest and disease management. The courses of post graduate programmes must be designed and updated based on modern research outcome on current issues and its application. Content should be demand driven and skill oriented for inculcating professionalism, employability and global competitiveness. Sound mycological knowledge is necessary incorporating latest development in fungal taxonomy following Melbourne Code of Nomenclature based on teleomorphic stage supplemented by molecular data in instructions. Biotechnology and nanotechnology driven advances should be part of syllabi for making instructions relevant to prevailing requirements. Benefit of technology revolution should be accrued by introducing Massive Open Online Courses (MOOCs). Non credit courses like research ethics, research methodology, disaster management and rural development programmes are helpful to broaden the knowledge base. Research topics for PG students must be contemporary, problem oriented and futuristic. AHEIs must fulfil minimum standards prescribed by the ICAR for quality education. Smart classrooms, state-of-the-art laboratories and instructional farm are the basic necessities to meet teaching/learning process and methodologies to institute effective delivery system for attracting best talent and blooming minds to plant pathology. Faculty shortage and long term temporary arrangement must be avoided. The teachers should be motivated and motivating having in depth knowledge, teaching acumen, magnetic behaviour and competence in frontier and emerging areas of the subject. They should be regularly exposed to faculty development programmes, refresher courses/ trainings and other national and international events for capacity building and acquiring management skill. There should be more emphasis on experiential learning, practical, rural, on field farmer and industrial interactive component for skill development in plant pathology graduates. P.G. students should be assigned research topics contributing solution to the national plant disease problems. Seminars on special topics and interactive sessions are useful to enhance interpersonal and communicative skill, negotiation skill, building leadership qualities, confidence building, presentation competence. Interdepartmental cooperation is required for creating sustainable partnership and suitable twining arrangements for developing learning centric education in plant pathology for producing knowledge intensive, employable and professional plant pathologists.

KN (S16) 05: Human resource development and integrated pest management

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Public's increased awareness of and enhanced protestation against environmental destruction ensured institution of initial safeguards and the beginnings of progress on some environmental fronts on *Integrated Pest Management* (IPM) while ecological movement accelerated and burgeoned across the world. This aroused the Government of India and the Indian Council of Agricultural Research (ICAR) also to have IPM as part of the National Agriculture Policy. Thus, came up the ICAR: National Research Centre for Integrated Pest Management (NCIPM) in 1988, which appreciated the task of spreading the message of IPM across India a tough ask due to poor awareness about the subject among people in line departments as also among the farmers. As a result, IPM for a better crop health is not seeing success in the farmers' fields and adoption of IPM is low. Human resource development for IPM essentially should involve public-private-producer partnerships. There is a need for human resource management for updating the skill and knowledge of scientists, students and farmers in different fields at centres of excellence on varied aspects of research at domestic and international level. Enhanced amount should be invested for research and development of IPM keeping parity with that invested for agro-chemicals. There is need for demonstrations while mass media too could play a crucial role. Trained human resource is also becoming scarce. In SAUs, due to downsizing of the funding and consequently the agricultural faculty, all the three agricultural components thereof i.e. teaching, research and extension have been affected. With only a meagre faculty funding from ICAR, the three components are weakening. The situation would worsen at some of the centres which were established on the basis of higher faculty funding of ICAR that now looks dwindling. There is an urgent need for widening the human resource base in dissemination of the developed technologies to the end user in effective manner. Withdrawing of research human resource from established centres need be avoided. There is need for widening the base of plant protection in human resource with States Department of Agriculture and Horticulture. Policies are required for effective knowledge dissemination for technologies and human resource for ensuring the adoption of the same at grass-root level, to resource-starved and remote areas. Keeping track of changing pest situations through regular and intensive surveillance, monitoring pest situations is needed that require to be adequately supported through funding and employing skilled human resource. Human resource as such face higher competition due to increase in population, which is on the rise as technology is reaching to masses. Quality of teaching has dropped and hence a lack of creativity and innovations is evident. Curriculum is not adequately preparing graduates to address emerging needs and thus, instead of leaders, education system is creating primarily followers (i.e. technical work force), who often fail to create job and becomes dependent on Government resources that is dwindling. Thus, uncertainty will be more common than now. Preparing an adaptable work force to changing needs is critically important need of the hour.

KN (S16) 06: Conducting transformational education at Land Grant Universities leads to successful agriculture in the USA

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The United States has an abundant, safe, reliable and relatively inexpensive supply of food for its 327 million inhabitants. Just 2% of the US population is directly involved in agricultural production on 2.2 million farms. Producers are advised on production and marketing issues by Extension educators who are employed by Land Grant Universities throughout the US and associated territories. In North Dakota and Minnesota, growers produce 60% of the US sugar beet, an industry with a total economic activity exceeding $5 billion. In 1998, growers lost over $100 million because they could not effectively control Cercospora leaf spot caused by the fungus *Cercospora beticola*. Basic and applied research were conducted and research-based recommendations were provided at different fora. Growers adopted recommendations and effectively controlled CLS while reducing the average number of fungicide applications over time, resulting in savings of over $14 million in crop protection costs annually with no adverse impact on yield. Growers' needs meetings were conducted to assess and focus on producers' needs, annual surveys were conducted, and personal response device were used to get direct feedback from producers and allied industry representatives that indicated the rapid adoption by producers of University-based recommendations.

KN (S16) 07: Teaching plant pathology-implementations and constraints

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The science of Plant Pathology has a major role in increasing the crop productivity through management of diseases. Therefore, diseases diagnosis as well as management requires the services of trained Plant Pathologist who are well acquainted both with basic concept as well as allied fields i.e., molecular biology and plant breeding. The Indian Council of Agricultural Research (ICAR) an apex body developed new course curricula for UG and PG students under the umbrella of Fifth Dean's Committee keeping in view the requirement and maintain the pace with industrial needs to increase the farmers income as per programme of Prime Minister of India. The essential key courses in plant pathology are mycology, plant bacteriology, plant virology, molecular aspects of plant pathogenesis, interaction of host and pathogen, and mushroom cultivation etc. There is dire need to have specialists in these areas. The courses on molecular diagnostics, molecular basis of host-pathogen interaction, population biology of pathogens using molecular tools, and genetic engineering for disease resistance have been added to the course curricula in universities but may not have much impact oin the training of agricultural graduates since in most of the agricultural universities, there is paucity of scientists to teach basic fundamental courses as well as advanced courses. The existing teachers lack in-depth knowledge as they have to teach several courses in a semester to meet the mandate of the system. This results in vast variation in the standard of theory, and practical teaching of the various courses. In most of the agricultural universities, mycology and basic bacteriology have taken a back seat. Similarly, knowledge of biotechnological techniques is the need of the hour to develop disease resistant genotypes, and majority of the teachers do not have sufficient exposure to this field. There must be rigorous trainings for teachers at entry level. Most teachers are alumina of the same university without outside exposure and unaware of many national and international perspectives of agriculture. It would be in the interest of the development of agriculture teaching if out of three degrees, two are from different universities. CCS Haryana Agricultural University and

Punjab Agricultural university has taken some steps in improving the teaching standard and reducing the inbreeding effect. International exposure of teachers is also essential and adequate opportunities to participate in international trainings, professional conferences and other events should be provided. In agricultural universities, the gap in term of expert in particular field is more so unable to serve the purpose. The gap presently being felt in terms of human resource availability in agricultural field is mainly due to the fact that most of the students and parents have more attraction towards medical and engineering education. Steps need to be taken up in promoting agriculture education from the level of high school, organizing education fair, encouraging high school student's trips to university and colleges and other means to create general awareness. Number of fellowships at degree level should be increased. These steps will help in bridging gap between demand and supply of quality graduates. Further, to attract students towards higher education in agriculture, adequate number of fellowships must be made available as to relieve the students and parents from financial burden. Specialized diploma in plant protection can cater to the need of the farmers at block level. Farmers can also be saved from the clutches of greedy businessmen in pesticide sale through trained persons. These steps if taken up in right earnest will go in long way in generating the human resource for quality teaching as well as in mitigating the sufferings of the farmers. The course curricula provided by ICAR also needs improvement especially in evaluation system. The new course curricula have introduced mid-term examination which needs to be modified or abolished since not much effect on the teaching. Another important steps need to be taken is to introduced external examination both for the theory as well as for practical at-least in PG courses so that proper training should be imparted for better understanding the subject.

KN (S16) 08: Indian Agricultural sustainability can be ensured by adopting dynamic plant pathology pedagogy for no-poverty & zero-hunger

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Plant diseases cause tremendous economic losses(5-15/ up to 25%) to Agriculture in the tropics and subtropics. They spread fast in India. Farmers are ignorant hence can not identify pathogens and control them. They are also unaware about mode of field spread, variations in symptoms etc. Having knowledge of disease cycle and resistant varieties is essential for effective control. Even reliable products to control plant pests are not widely marketed yet . farmers expect miracles from the pesticides they are advised by the vendors and selling spurious materials. We will discuss aspects for HR development for training Plant Pathology for disease control in field by regional teams of students/ extension workers to progressive - crop wise specialized- farmers in disease recognition, resistant variety, therapeutic molecules and IPM measures. Training farmers is most important to ensure Indian agricultural sustainability by addressing the major crop diseases, development of resistant varieties, simple and effective methods of vector control for long-term check on yield/quality losses by overcoming farmer's ignorance. Host plant resistance and better crop management/ sanitation and vector control make it most effective, help prolong virus resistance. Besides, intensive training in disease recognition, understanding the epidemiological aspects and crop management must be imparted. A limited literature on this topic however suggests that it is not receiving the deserved priority. Upgrading farmers' knowledge on common plant diseases with economic losses, will largely save crop losses.. Different therapeutic chemicals are available to plant disease combat infections in progress. Bioagents are effective against plant diseases involving the organisms occurring naturally—within the host's environment/ purposefully applied to the potential parts of the plants, but their action mechanisms are not fully understood; some produce antibiotics killing pathogens while others compete for food. C ultural practices also help exploiting an antagonist *in vivo*. The recent systemic fungicides, *viz*. oxathiins, benzimidazoles, pyrimidines etc can help treat infected plants after infection has begun. Much has been accomplished in developing desired disease-resistant varieties. Although great flexibility and potential for genetic change exists in economically important plants, pathogens are equally flexible, *viz*. a new plant variety is found highly susceptible to a previously unimportant pathogen(s). Heavy emphasis is needed to train student teams in modern methods of detection so that they can coach the large numbers of farmers' teams to fight against plant diseases *viz*.,blasts, leaf spots, mosaics, rusts, rots, smuts, wilts, etc. More attention has to be paid for effect of Climate change, Varietal patterns in relation to diseases of commercial & field/food crop plants. Rigourus Field & Lab training, Understanding of chemical molecules & mode of action is need of the time. Also only a minority of farmers know the role of insect vectors in their spread, and they try to control them by applying any of the available synthetic pesticides. If farmers know better about plant pathogens, insect vectors, and safer cost-effective chemicals, use of synthetic pesticides cost & yield losses can be reduced substantially.

KN (S16) 09: Human resource requirement in seed health testing

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Seed is an important carrier of pathogens across Geographical boundaries. Seed health certification has become mandatory as part of phytosanitary measure. Realizing the importance of seed health testing, Dr. Paul Neergaard and Dr. S.B. Mathur have established Danish Government Institute of Seed Pathology for Developing Countries (DGISP) at Copenhagen, Denmark in 1967 with the support from Danish International Development Assistance. This institute was renamed as Danish Seed Health Centre in 2004. The major aim of DGISP was to alleviate poverty and improve the nutritional status of resource-poor people by serving the developing countries of Africa, Asia and Latin America in their effort to improve seed health and seed quality. This institute has trained many scientists from India, Africa, Bangladesh, Nepal and Vietnam and helped in standardizing the seed health testing protocols for various crop-pathogen combinations that have been adapted by ISTA. The University of Mysore has created the Department of Applied Botany and started offering M.Phil in Seed Pathology in 1980. Dr. Paul Neergaard offered the first course as Visiting Professor. DANIDA has funded University of Mysore under the ENRECA programme during 1992-93 to strengthen the seed virology and seed bacteriology research by creating the necessary infrastructure and training the staff. DGISP has established a formal collaboration in teaching seed pathology courses with Department of Studies in Applied Botany & Seed Pathology (DAB), University of Mysore. DGISP has transferred the Diploma and Modular Courses in Seed Pathology offered by the Institute to DAB to act as a satellite centre for Asian region in the name of Asian Seed Health Centre. DAB has established network with China, Bangladesh, Vietnam, Nepal as well with African Seed Health Centre, SUA, Morogoro, Tanzania for research and training. The collaboration was further extended with European Union support with emphasis on locally available technologies to improve the seed quality. Seed health testing for designated pathogens has become a mandatory phytosanitary requirement for shipment of seeds either for research purpose or for commercial trade. The existing quarantine stations and germplasm testing facilities are finding it difficult to test the seed samples because of trained staff. Hence, it has become very essential to train the personnel at different levels to cope up the great demand for seed health testing. Seed health shall be the essential subject at B.Sc. and M.Sc. levels. All the trained human resources could be pooled and laboratories could be accredited to support the seed industry for research and trade. It is very essential to sensitize the academia, industry personnel and policy makers about the importance of seed health. The personnel should be aware of the country-wise requirements for certification, standard seed health testing procedures as accepted by ISTA and ISHI, including DNA-based methods. It is high time that more number of accredited labs for routine seed health testing and national/ regional reference labs established.

Session 17

International trade and biosecurity

Keynote Papers

KN (S17) 01: Plant quarantine for biosecurity during transboundary movement of plant genetic resources

S.C. Dubey, Kavita Gupta, Jameel Akhtar, V. Celia Chalam, M.C. Singh, Z. Khan, S.P. Singh, Pardeep Kumar, B.H. Gawade, Raj Kiran, Meena Shekhar and T. Boopathi

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Biosecurity is a strategic and integrated approach that encompasses the policy and regulatory framework to analyse and manage risks in the sectors of food safety, animal life and health, and plant life and health, including associated environmental risk. International exchange of plants/ planting material carries an inadvertent risk of introduction of exotic pests or their more virulent races into new areas. History has evidenced several examples of dangerous pests introduced along with plants/ planting material/ plant products that have led to serious socio-economic consequences. Plant quarantine is a legislative measure to regulate the introduction of planting material, plant products, soil and living organisms, etc. in order to prevent inadvertent introduction of pests. International exchange of plant genetic resources (PGR) is important to broaden the genetic base of crops in order to develop better crop varieties. The Government of India has legislated the Plant Quarantine (Regulation of Import into India) Order in 2003 in order to regulate the import of plant material. Under this Order, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) has been authorised to issue Import Permit and to undertake quarantine processing of all imported PGR including transgenics and for issue of Phytosanitary Certificate for material meant for export. The Division of Plant Quarantine at ICAR-NBPGR has developed procedures for systematic and step-wise quarantine processing for pest diagnostics, salvaging and containment to ensure biosecurity during exchange of PGR and transparency in international exchange. Critical quarantine examination of PGR have resulted in interception of several seed-borne fungi, bacteria, viruses, insect pests, nematodes and weeds. Some of these are not yet reported from India, if reported have a limited distribution; have a wide host range and/or cause great economic losses or have more virulent/ large number of physiological races, etc. Presently, since exchange of germplasm has become more difficult under the Convention on Biological Diversity, all attempts are made to salvage the germplasm. All infested/ infected/ contaminated samples are either salvaged prior to release or incinerated depending on the category of pest intercepted. During the past forty three years from 1976-2019, a total of 74 exotic pests including fungi (5), viruses (19), insects/ mites (25), nematodes (9) and weeds (16) of great quarantine significance to the country have been intercepted at ICAR-NBPGR. Had any of these pests were not intercepted and escaped, they could have been introduced into the country and established, as favourable environmental conditions are available in India and subsequently caused havoc to our agriculture. Although, ICAR-NBPGR has *state-of-art* facilities to take up this task properly, more comprehensive efforts are needed to develop adapt and adopt modern detection and eco-friendly salvaging techniques to minimize the risk of pest escape in quarantine. Additionally, the legislation on quarantine needs to be upgraded to the Agricultural Biosecurity Bill being drafted by the Ministry of Agriculture is an attempt at a holistic approach towards biosecurity in India.

Invited Papers

I (S17) 02: Ensuring biosecurity in South Asia through effective regional cooperation

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Regional collaborative efforts need to be more effective to deal with all known or perceived agricultural biosecurity threats mainly due to the commonality among South Asian countries. This would also ensure the optimal utilization of the available resources of the region both in terms of infrastructure and expertise. The main areas for collaboration include harmonizing regulations, streamlining quarantine procedures, risk analyses, research and human resource development (HRD). The regulatory cooperation would be for jointly deliberate on policy issues related to Sanitary and Phytosanitary (SPS) Agreement of WTO, Biosafety Protocol and Invasive Alien Species under Convention on Biological Diversity; harmonization of related regulations to facilitate trade within and also outside the region. Further, harmonized quarantine regulations as per International Plant Protection Convention wherein listing of common pests present in all countries would facilitate import. The quarantine procedural collaboration includes identification of expertise/ accredited labs/ post-entry quarantine/ containment facilities for testing special crops/ pests in a network mode and countries with contiguous borders could also initiate programmes for eradication/ declaration of pest free areas to facilitate exports from the entire region. Documentation and information sharing on pest status, surveillance programmes is essential to develop common pest risk analyses for crops/ pests of quarantine significance. The areas of collaborative research need to be identified based on gap analysis and programmes developed especially to look for alternatives to methyl bromide fumigation, developing standards/ protocols on SPS issues in trade, biosafety risk evaluation etc. Finally, HRD to strengthen research capabilities also needs to be conducted. India has considerable expertise to contribute significantly in ensuring regional biosecurity.

I (S17) 03: Ampeloviruses complex infecting pineapple in Ghana

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Mealybug wilt of pineapple (MWP) is the most destructive viral disease of pineapple worldwide, which causes up to 100% yield losses. The disease is caused by pineapple mealybug wilt-associated virus (PMWaV), a member of the family *Closteroviridae* and the genus *Ampelovirus*, and transmitted by mealybugs. A virus survey was conducted in 2019 to detect and characterize viruses associated with MWP in the Central region of Ghana. Twenty-four symptomatic pineapple leaf samples were collected from three districts in the Central region of Ghana. The districts were Abura-Asebu-Kwamankese (AAK), Ekumfi, and Komenda-Edina-Eguafo-Abirem (KEEA), leading pineapple growing centres in Ghana. Three quantitative real-time polymerase chain reaction (qRT-PCR) assays with PMWaV species specific primers were conducted for amplification of heatshock protein 70 gene (HSP70) of PMWaVs in the diseased samples. Three different viral species namely PMWaV-1, PMWaV-2, and PMWaV-3 were detected from the plant samples, with abundance of mixed infections. Sixteen out of the 24 samples (66.7%) were infected with at least one of the three species of PMWaVs identified. PMWaV-2 had the highest infection rate of 62.5% across the districts, indicating it is the most prevalent virus species; this was followed by PMWaV-1 and PMWaV-3 with infection rates of 33.3% and 8.3% respectively. Purified reverse transcription (RT)-qPCR products of fifteen isolates from AAK, which consist of

PMWaV-1 (5 isolates), PMWaV-2 (8 isolates) and PMWaV-3 (2 isolates) were sequenced in both directions. The heat shock protein 70 gene sequences of our field isolates shared 95.2 to 100% nucleotide identities for PMWaV-1, 98.2 to 100% for PMWaV-2 and 97.5 to 99.3% for PMWaV-3 with corresponding published isolates from GenBank**.** Phylogenetic analyses of both nucleotide and deduced amino acid sequences of the HSP70 genes of our field isolates and 24 published sequences from GenBank, confirmed the presence of PMWaV-1, -2 and -3 in the Central region. This is the first report of detection of PMWaV-1, -2 and -3 infecting pineapple in Ghana and the whole of Africa.

I (S17) 04: Impact of phytosanitary regulations and diagnostics in crop biosecurity against regulated viruses

V. Celia Chalam, A.K. Maurya, Ruchi Sharma, Vaishali Dutt Sharma and S.C. Dubey

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The global trade of agricultural commodities and exchange of plant genetic resources has the potential to introduce new pests including viruses which may pose potential risk to the agriculture of importing country. The combination of regulatory and technical approaches would ensure biosecurity of crops against pests including viruses for a region. In India, the Directorate of Plant Protection, Quarantine and Storage under the Ministry of Agriculture and Farmers' Welfare is responsible for enforcing quarantine regulations and for quarantine inspection and disinfestation of agricultural commodities meant for commercial purpose. The imported germplasm material including transgenics are subjected to quarantine processing at the ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi. The Plant Quarantine (Regulation of Import into India) Order, 2003 requires *Additional Declarations* to be included in Phytosanitary Certificate for seeds and other planting material as free from pests. As per the PQ Order, 264 viruses are regulated pests which are of quarantine significance for India. Early, sensitive and accurate diagnosis is necessary for detection of viruses in quarantine. Biological techniques for virus detection are usually accurate but slow and not amenable to large-scale application. DNA-based technologies improve the speed and accuracy of detection of viruses. Combination of ELISA and PCR technologies are used to improve sensitivity of detection and to avoid problems during PCR with inhibitors. Attention is now given to techniques like Multiplex-PCR, Real-time PCR, LAMP, HDA, etc. LAMP and HDA are isothermal DNA methods which do not require a thermal cycler and has potential applications in quarantine, biosecurity and microbial forensics. Adopting a strategy of post-entry quarantine growing/inspection followed by use of combination of conventional, serological and molecular detection techniques several viruses of great economic and quarantine importance were intercepted in imported germplasm including transgenics in the last two decades. The interceptions include 19 viruses not yet reported from India and not known to occur on particular host(s) in India. As an example, Maize chlorotic mottle virus (MCMV), a seed-transmitted virus, not reported from India, was detected and intercepted in exotic maize germplasm including transgenics from Puerto Rico, Thailand and USA. If not intercepted, MCMV could have been introduced into the country and established as favourable environmental conditions are available in India. If introduced, MCMV would have caused an annual yield loss of Rs.3166.3million, with the incidence of 1%. India need to establish a network of interconnected diagnostic laboratories and strong surveillance programme to identify new viruses. Adopting the reliable techniques with an appropriate strategy for virus detection would go a long way in ensuring biosecured agriculture against transboundary viruses through quarantine, virus-free trade and exchange of germplasm.

Oral Papers

O (S17) 05: Integrated approach for identification of *Ralstonia solanacearum* free areas in major potato growing districts to boost export from West Bengal

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Potato is one of the main commercial crops grown in the country. It is cultivated in 23 states in India. Uttar Pradesh, West Bengal, Bihar, Punjab and Gujarat account a lion's share in total production. Further it has been reported by the International Food Policy Research Institute **(IFPRI)** and International Potato Centre **(CIP)**, India is likely to have highest growth rate of potato production and productivity during 1993 to 2020.Although India was the world's second largest potato producer at 48 million tons in 2014-15, its exports were less than one per cent of the output. India exported 1.80 lakh tons of potatoes in 2014-15 fiscal, which was lower than 3.05 lakh tons in the previous year, as per the government data. Due to the bumper crop and glut situations developed in the market for the surplus yield every year which ultimately results in declining the prices drastically. Potato can be exported to many countries in the world, if pest related issues are addressed and standard operating procedures are rightly followed. Bacterial wilt or brown rot has a worldwide distribution (Elphinstone, 2005). *R. solanacearum* (Smith, 1896) race 3 biovar 2 Yabuuchi *et al.* (1995) is among the most serious quarantine pathogens of potato worldwide, which is responsible for estimated $950 million losses in each year. (Swanson *et al.,* 2005). In India, the disease is endemic in Karnataka, Western Maharashtra, Madhya Pradesh, eastern plains of Assam, Orissa and West Bengal and North eastern states (Shekhawat *et al*., 2000). In India, the bacterial wilt of potato is known to be caused by Gram (-) Bacterium strains and phylotype I, IIB and IV of *R. solanacearum* (Sagar *et al*., 2014).Monitoring of the pathogen in terms of pre cropping, cropping and post harvest survey have been conducted in 2018-19 & 2019-20. The collected soil sample, water samples, stem segments and tuber samples are tested in lab through culture based detection using SMSA/ TZC medium followed by colony PCR, serology based detection through ELISA and Molecular detection through PCR using *Ralstonia solanacearum specific primer* Y2: and OL1: (Seal et al.,1993). During 2018-19, out of 83 mouzas under 5 districts (Hooghly, Purba Bardhaman, Paschim Medinipur, Bankura and Birbhum), 24 mouzas (28.9%) were infested by *R. solanacearum.* Rest areas were free from this pathogen as per culture dependent analysis. In the year 2019-20, under molecular based detection, the result shows that in Hooghly and Paschim Medinipur, out of 45mouzas, in 11 mouzas *R. solanacearum* was detected .Rest mouzas exhibited pathogen free area. During 2019-20 the survey work has been continuing in these above mentioned 5 districts along with laboratory analysis and data have been generating for compilation and further reaching to a final conclusion.

O (S17) 06: Conventional techniques of seed health testing: pivotal in disease-free import and safe conservation of plant genetic resources in National Genebank India

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Seed health testing (SHT) is carried out involving conventional techniques such as dry seed examination, stereo-cum-microscopic observation, incubation test in addition to advanced molecular techniques. During last one decade, testing for quarantine clearance of imported plant genetic resources (PGR) ensured the interception of quarantine pathogens in seeds of different crops. In addition, several other pathogens of economic significance have also been intercepted from non-host crops such as *Bipolaris oryzae* in chilli from The Netherlands, *Bipolaris sorokiniana* in bitter gourd, *Phomopsis phaseoli* in Jatropha from Germany, *Phomopsis eres* in black locust from Hungary, *Phoma leveillei* in tree lucerne from Australia, *Fusarium equiseti* in wild onion from Japan etc. Similarly, SHT for conservation of indigenously collected/ multiplied PGR ensured detection and identification of fungal pathogens of economic/ quarantine concern from host as well as non-host crops such as *Bipolaris sorokiniana* in eggplant and tomato, *Phomopsis helianthi* in safflower, *Phomopsis longicolla* in chilli, *Alternaria brassicicola* in opium, *Bipolaris oryzae* in wild mustard, *Dinemasporium americana* in goat grass (*Aegilops*) etc. Interception of many pathogens of quarantine or economic significance on a wide range of crops from different countries emphasizes the importance of SHT involving conventional techniques and need for utmost care during quarantine examination leading to safe introduction of PGR required for crop improvement programmes in the country. On the other hand, associations of several fungal pathogens were not only detected in indigenous non-host crops seed but also recorded with reduced seed germination as well as seedlings mortality. Detection of these pathogens signifies the role of critical microscopy and taxonomic identification in safe conservation of plant genetic resources in the National Genebank, India. Otherwise, these infected seeds could have been a source of inoculum and spread of the pathogens across the country and could have posed a serious threat to the crops.

O (S17) 07: Detection and identification of plant parasitic nematodes during international exchange of vegetative propagules and rooted germplasm

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Plant parasitic nematodes are serious threat to agriculture and causing significant yield losses worldwide. Plant nematodes spread with vegetative propagules and once establishes it is very difficult to manage them. During past ten years, a total of 662 samples of imported vegetative and rooted germplasm samples observed for detection and identification of plant nematodes. Both roots and growth media were observed for association of detection purpose. Out of 662 samples, 279 samples found infected with nematodes which share 42% of observed samples. Nematode species were identified using microscopy and taxonomic keys. Major nematode species identified were, *Helicotylenchus dihystera* on *Annona squamosa* from Taiwan*, Pratylenchus penetrans* on *Prunus armeniaca* from USA and *Malus domestica* from The Netherlands*, Rotylenchus minutus* on *Hypoxis hemerocallidea* from South Africa*, Tylenchulus semipenetrans* on *Citrus sinensis* from Israel, *Meloidogyne incognita* on *Artocarpus heterophyllus* from Nepal. Besides, stem cuttings and rooted plants with media other than soil were also observed and were found free from nematodes. It was found that, in vegetative propagules, bare rooted plants were most infected with nematodes. The genus *Pratylenchus* was most intercepted nematode as it was identified in 156 samples (46%). Interestingly, roots of *Artocarpus heterophyllus, Citrus sinensis, Hippophae rhamnoides, Robinia pseudoacacia* were found infected with three distinct genera. Intercepted exotic root endoparasitic nematodes, *Pratylenchus penetrans* and *Meloidogyne incognita* are difficult to control therefore, post entry quarantine treatment and inspection was done for 327 samples of *Artocarpus heterophyllus* (75) *Malus domestica* (150) and *Phoenix dactylifera* (102) at indenters site. The root and soil samples were collected, processed and observed. All soil and root samples were found free from nematode. In conclusion, bare rooted plants poses high risk of introduction of nematodes and stringent quarantine measures required for endoparasitic nematodes.

Session 18

Extension plant pathology: challenges in implementation

Keynote Papers

KN (S18) 01: *Trichoderma* spp. in plant health management and their commercialization for sustainable agriculture and rural prosperity

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Bio-agents *viz. Trichoderma viride,T. harzianum,T. asperellum,* etc. have been found quite beneficial for sustainable and eco-friendly management of biotic stresses viz. seed and soil borne diseases of crops particularly wilt (*Fusarium* spp.), root rot (*M. phaseolina*, *R. solani*), collar rot (*A. niger*), stem rot (*S. rolfsii*), etc. which may cause huge quantitative and qualitative yield losses in crops, avoid development of resistance in plant pathogens and chemical pollution in nature, etc. Bio-agents are successful colonizers of their habitats, promote plant growth and root development, induce systemic resistance (ISR), manage the abiotic stresses *viz*. extreme temperatures, drought, salinity, allelopathic effects, oxidative stress, etc. Besides, *Trichoderma* spp. are capable of managing farm and urban organic wastes by mineralizing them with their powerful cell wall degrading enzymes *viz*. chitinase, cellulase, protease, chitinase, xylanase, ß-1,3- glucanasesendoglucanase, etc., to make available of the nutrients for plant growth. *Trichoderma* spp. can improve seed germination and restore plant'svigor. The use of bio- agents to manage soil and plant health is the present day need for eco-friendly management of plant diseases and for sustainable crop productivity, reduction of cost of cultivation and remunerative return of agricultural produce,generation of employment for their production, etc, and thus it is one of the best sector for improving socio-economic conditions of farmers of developing nations and help the nations to become prosperous and self-reliance. Mass productiontechnologies of the bio-agents i.e. fermentation, formulations, delivery systems, etc. have been developed. Commercial production of the efficient strains of bio-agents has now emerged as a potential sector for employment generation, where millions of skilled persons will be required at different levels by the year 2030 particularly in developing world, where unemployment among the youths are the emerging problem. Besides, ICAR and SAU's have introduced ELP's for UG students to become entrepreneurs. The KVK's, NIPHM, etc. impart training to farmers for establishing bio-agents production. Being a sun rise sector, the funding agencies viz. RKVY, DBT, DST, NHM, Banks, NFSM, State Govt., etc. need to support SAU's, NGO's financially in the form of projects to train the farmers, entrepreneurs, NGO's, SHGs, extension agencies, etc. The farmers will gain hands on training in the production process & develop need based commercial products of the bio-agents. However, there is a need to identify the efficient local isolates of *Trichoderma* preferably the endophytes, for management of biotic and abiotic stresses and registered them with CIB & RC, New Delhi. The students should establish the 'Bio-agent Production Unit' with the help of funding agencies through novel schemes launched by GOI and Cooperative systems, Creation of bio-resource complex for production, training and guidance of needy human resource; Establishment of societies for awareness and use of bioagents &*Trichoderma*; Establishment of collaborative research groups nationwide as well as globally for innovative outcomes.The detailed account on these will be discussed in the conference.I (S18) 02: Transformative technologies in strengthening extension plant pathology

KN (S 18) 02: Biocontrol formulations as strategy towards SDGs-Key issues

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Interest in biocontrol research is increasing. Growing emphasis on technological innovations in this context is relevant also, in context of SDGs. Overemphasis of partial results and exaggerated claims have overshadowed prime challenges to be identified and solved at laboratory scale, if biocontrol agents have to be potentially used as a strategy of pest control. Research priorities most often reflect an academic perspective than a clear action plan on industry-oriented product development. The usual approach of loading the BCAs in a carrier/ medium without comprehensive control on the interactions among loaded BCAs and other components, leads to inconsistent and variable results and is thus, a key issue in development of biocontrol formulations of industry and practical relevance. Regulatory requirements for quality of bioformulations are very well described and should make basis of research strategy for development of practically feasible technologies. There is a need to consider biological control not only as a scientific and academic subject of research but like another potential pest control strategy which requires integrated and multidisciplinary vertical research oriented toward product development, as in case of chemical pesticides.

Invited Papers

I (S18) 03: Transformative technologies in strengthening extension plant pathology

M.B. Patil[1], B.M.Chittapur [2], K.N.Kattimani[2] and Kenganal Mallikarjun[3]

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Adoption of precision plant protection practices is critical and use of transformative technologies and digital communication is necessary to bridge the technology gap in Extension Plant Pathology. However, the present extension systems needs to strengthened to address the challenges faced by the farmers in the context of the changing agricultural scenario. Data-driven technologies such as artificial intelligence (AI) and intelligent automation (IA) are already revealing their power to transform organizations and are reshaping business models and workforces while enhancing decision-making. The Digital Advisory Services (DAS) are either part of the offering of input providers or stand-alone for profit, typically start-up platforms. DAS adoption is limited because of digital infrastructure and illiteracy, areas where India has significant advantages. Transformative technologies like Geo-Spatial tools, IoT, AI, VR, AR, Sensors, Spectral Imaging, Big data, robotic process automation (RPA), machine learning, cognitive computing, advanced analytics and 5G are disruptive ones and will strengthen the extension and advisory services further under collaborative platforms that enhance agricultural service delivery and bring both private and public extension stakeholders together in order to address prioritized farmer demands in a bottom-up and coordinated way and require influence from both public and private sectors. An information and technology-based farm management system leads to precision plant protection with optimum profitability, sustainability and protection of the land resource. Further, creation of multi/trans disciplinary teams involving agricultural scientists in various fields, engineers, manufacturers and economists to study the overall scope of precision plant protection. Some have been proposed as leapfrog technologies that can help achieve Sustainable Development Goals (SDG). The visibility of viable decentralised, democratic, farmer-centric, demand-driven, vibrant and participatory institutional mechanisms has to be ensured

at the lowest cutting-edge administrative level (panchayat-level institutions) to cater to the needs of the farming community and rural youth and sensitise them on technology management.

I (S18) 04: Role of plant clinic in decision making of farmers for pest management

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Due to intensive cropping and indiscriminate use of pesticides incidence of diseases, insect pest and weeds are increasing day by day resulting in considerable yield losses. In spite of much emphasis on IPM farmers still heavily rely on chemical control measures. A questioner survey of 200 farmers was conducted during All India Farmer's fair & Industrial Exhibition organized by the University in September 2019 to understand how farmers get their field problems diagnosed particularly with respect to pest management, the decision making process for selection of control measures they choose to apply and their pesticide use behaviour. Farmers regarded any pest problem as "*kida*" irrespective of whether it is due to insects or diseases. Majority of the farmers (46%) either visit local pesticide dealer for getting the solution or diagnose it themselves (25%) or in consultation with fellow farmers (7%). Since most of the shopkeepers are not sure about the exact cause of the problem they recommend use of cocktail of pesticides. Most of the farmers (92%) used cocktail of pesticide, out of which 45 per cent farmers found to be using combination of >3 pesticides at a time without having any knowledge of their compatibility(88%). Only 22 per cent farmers consult KVK, helpline numbers or research institutions for getting their problems diagnosed. Majority of farmers did not have proper knowledge about safe use of pesticides. Even those farmers had some knowledge do not follow it completely. In such situation plant clinics have to play pivotal role for capacity building of all the stakeholders involved in diagnostic process so that indiscriminate use of pesticides can be minimize. Diagnostic and advisory services have to be made at the door step of the farmers through mobile plant clinic and use of various ICT tools.

I (S18) 05: Biological control of rice viruses transmitted by the brown planthopper (BPH), *Nilaparvata lugens*(Stål) using endophytic fungi

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Rice (*Oryza sativa* L.) is an important food crop, constitutes the main nutrient resource for more than 60%of world's population including most developing countries. Rice has been severely affected by several pests and diseases, of which the brown planthopper (BPH), *Nilaparvata lugens* (Stål) (Homoptera: Delphacidae),is a serious concern in tropical Asia, where rice crops arecontinuously cultivated.Rice BPH causes direct damage to the plant by sucking the phloem sap and transmits viral diseases such as grassy stunt virus (RGSV) and ragged stunt virus (RRSV). In the past, rice viruses have caused devastating damages in China, India, Japan, Korea and Vietnam. In 1980s and 1990s, India reported a combined yield loss of 1.9 million tons of rice due to direct damage by BPH, while a yield loss of 0.4 million tons in Vietnam was mainly due to two virus diseases, RGSV and RRSV transmitted by BPH. The virus infectioncycle involves host-finding, vector encountering virus infected plants,acquisition of virus by sucking plant sap, transmission and delivery of virus to a new host plant. Epidemics of rice viruses were reported to limit plant development and reduce production of quality rice grains. Existing control measures involving monitoring of virus vectors, cultivation of virus-resistant varieties, eradication of virus sources and use of insecticides against vectors are not provided satisfactory control of rice viruses and its vector. Exploring novel microbial strains capable of inducing systemic resistance in plants against BPH and rice virusesis long-term innovative approach.Microorganisms that colonize internal plant tissues without causing damages to the host are called endophytes.Endophytic strains of *Beauveria bassiana*, *Metarhizium anisopliae* and *Verticillium lecanii* can induce such resistance in plantsby producing numerous metabolites. Co-application of promisingstrains of fungal endophyteswith selective concentration of insecticides has been suggestedfor concurrent control of plant viruses and their vectors.This paperattempts to summarize about plant-endophyte-insect vector interactions and exploitation of entomopathogenic fungal endophytes for long-term control of BPH transmitting rice viruses.

I (S18) 06:Citrus diseases and theirmanagement: A Review

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The *Citrus*is one of the most important, nutritive and popular fruit crops in India and Vidarbha region of Maharashtra. The genus *Citrus*is native to Southeast Asia and world famous NagpuriSantra, Acid Lime cultivating in Vidarbharegion of Maharashtra. The disease complex are associated with these citrus cultivation since from nursery to old age and decline in production and quality, hence therefore area under cultivation is not increased. Production and productivity is directly dependent on health status related to disease complex, their management and nutritional input. Citrus cultivars in Vidarbha region are mostly affected by fungal, bacterial, virus and virus like diseases. As a result of many years roving survey in Vidarbha region of Maharashtra revealed that fungal diseases viz., *Phytophthora*, *Colletotrichum,* bacterial especially *Xanthomonas* and virus and virus like diseases viz., CTV and Greening (haunglongbing) diseases are major factors which responsible for citrus decline in Vidarbha region. Two applications of Bordeaux paste (1:1:10) at pre monsoon (May) & after monsoon (October) on trunk along with the spraying of 30 g copper oxychloride + 1 g streptocycline in 10 litre of water in the month of June, July and August followed by soil application of *Trichodermaharzianum* +*Trichodermaviride*+ *Pseudomonas fluorescens*(100g/plant each mixed with 1kg FYM) at the initiation of disease followed by Fosetyl-Al (0.2%) spray was recommended for management of fungal and bacterial plant pathogen. Study was also carried out to know the population dynamics of micro-flora in rhizosphere soil ecosystem and its correlation with physico-chemicals parameters of that healthy and diseased soil rhizopsphere of citrus. A forecasting model was developed for the twig blight and citrus canker in Nagpur mandarin and Acid lime, respectively to forecast the occurrence of the disease before 15 days. For early diagnosis of virus and virus like diseases by the molecular indexing the addition of sodium sulphite (ss) to Tris – EDTA was followed for extraction of DNA.

I (S18) 07:Chickpea wilt: History and management approaches

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Chickpea wilt is one of the major disease as per as it is responsible for causing 20-30% losses in India. It has the eight races world wide of which four existing in India. The race 1, 2, 3, 4, are most common in India. As per the resistance is concerned no variety except Warangal 315 showing resistance to all four races. The molecular approaches for distinguishing for various races, the work is being carried out in India. As the pathogen is monophyletic the existence of different races is being questioned. The molecular approach and differential host shows that being monophyletic the pathogen as different races. The one of the question is that the pathogen is symptomless carrier in linseed which helps the pathogen to survive without showing the symptoms on linseed also saprophytically by developing resistance chlamydospores which exist in soil for 4-5 years. The various approaches like conventional breeding, maker assisted selection, the gene pyramiding, gene tagging and gene replacement are various approaches are being practiced in India.

I (S18) 08: Extension practices in plant disease management for doubling farm income

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Farming has not been profitable over past two decades. Rural family incomes are far behind than their urban counterparts. Salaries of both government and private sector have witnessed average of 8 to 20 percent annual hike. However, the farming incomes which mainly sourced from cultivation and wages have not seen expected raise, instead have declined and cost of inputs have surged. These have worried farmers and increased their distress as a result migration in search of livelihood in metro cities is increasing. There is need to ensure agriculture is more profitable than other service sectors. In this regard cost reduction profit maximization is key for extension plant pathologists who can play key role in contributing towards doubling farm income. Although government has initiated various strategies & schemes intervening crop production, protection, processing and allied enterprises. The strategies and extension plant pathology methods by KVK, Yadgir especially in dealing with crop disease management is the subject of this study, which has been very much promising in ensuring more returns for every rupee invested. Method demonstrations, front line demonstrations, follow-up visits, field days, personnel communications, Kissan Melas, what sup messages, radio and TV talks, printed materials played crucial in adoption of low cost and effective integrated management practices. F Availability of organic inputs demonstrated at institutes helped many farmers for their quick adoption in many commercial and food crops. Irrespective of education level, method demonstration results convinced many farmers about importance of seed treatment and soil application of bio-control agents in disease management. Their confidence level increased when disease management measures proved low cost and effective. Follow-up visits were found building trust between extension personnel and farmers. The study over the past three years concludes that preventive measures recommended were more profitable than management or control measures recommended options because of their low cost. Designing tailored recommendations based on farmers resources and size and age of the crop were found accepted by farmers. The extension plant pathologists certainly have very important role in cost reduction and income maximization in disease management practices to ensure doubling farm income.

Oral Papers

O (S18) 09: Performance of on farm trails on management of rhizome rot disease of ginger in Bundelkhand region of Madhya Pradesh

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Ginger (*Zingiber officinale* Rose) is widely cultivated and has ready market at village level in Bundelkhand region of Madhya Pradesh. To assess the impact of rhizome rot disease management on growth and yield of ginger, the present study was carried out in Chhatarpur and Sagar districts of Bundelkhand region (central India) at 75 farmer's fields selected in 08 villages during *Kharif* season from 2011 to 2017. To find out the constraints in ginger production, Participatory Rural Appraisal (PRA) technique was used. Each trial was conducted on an area of 0.20 ha with a local check (farmer's practice) in same plot size adjacent to the demonstration plots. In most of the surveyed plots, the pathogen *Fusarium* and / or *Pythium* associated with infected plants and the disease noticed as yellowing of leaves; they ultimately wither and die out. Seed treatment with copper hydroxide (T_1) increased ginger germination significantly (86 per cent) which was at par with *Trichoderma viride* (81 per cent) over T_3-local check (72 per cent). The data of the trials showed that rhizome rot of ginger effectively controlled (67 per cent) with reduced disease incidence (from 14.2 to 4.2 per cent) by copper hydroxide application as seed treatment and soil drenching in rainy season. An additional net return of Rs 61500 and 5600 per ha obtained in T_1 and T_2 treatments, respectively in comparison to that of local check (T_3). An extension gap of 2.5 t/ha and technology gap 3.2 t/ha was estimated between demonstrated technology and farmers' practice. Farmer-to-farmer technology transfer was the major source of advice, farmers may have received the information from the input dealer, possibility of this trend was agreed to by several farmers. The adoption of raised bed planting of ginger found in 53.3 per cent farmers, use of bioagents *Trichoderma viride (*26.6 per cent), disease free seed (29.3 per cent) and seed treatment was found in 24 per cent by the farmers. The respondents revealed that all of them were using chemical sprays but the number of sprays reduced with adoption of the integrated disease management techniques.

O (S18) 10: Plant health clinics in biotic and abiotic stress diagnostics and technology dissemination

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Biotic and abiotic causes lead to regular losses in crop or timber yield and its quality. Diagnosis is made difficult by a diversity of causes and symptoms with multiple possible origins. Field to field variations are bound to be most common in perennials. Technology transfer by extension workers in plant health management has limitations. Plant health Clinics (PHC's) have high versatility and is a part of integrated support system delivering services with demand driven advices. Practically PHC's enable plant health specialists to work closely with extension workers. Uttara Kannada in the central western Ghats part has uniqueness of Ghat, plains and coastal ecosystem with Agri-Horti-Silvi components. PHC catering farm service is being rendered through multidisciplinary and multi-departmental tie-ups. PHC proved potential in ascertaining the cause and providing solution for existing and invasive plant health problems in horticultural, agricultural and forest species. New plant health problems *viz*., nut fall, nut crack, blossom blight, root rot, shot hole in live trees, leaf yellowing and choking in arecanut. Other problems as bract mosaic, nematodes complex and choking in banana; reddening of Pineapple, kokkaine in Cardamum, veinal fleck in ginger, mosaic in pepper, sclerotial rots in fruit and vegetable crops, leaf and root rot in Vanilla, stone rot of mango, unnatural death of cashew were also diagnosed with management suggestions. In forest tree species also PHC helped to characterise new and most serious problems *viz*., Root rot in plantations of *Melia dubea* and red sanders, pongamia diseases, mass mortality of *Azadirachta indica*, heart rot of *T. alata,* Phytoplama diseases of *Ficus* sp., *Dendrocalamus* sp., leaf blight of *Vateria indica* and many others. Even it has helped in promoting on cheap technology on-farm bioinoculants, developing crop disease calenders. PHS's and extension wing with multidisciplinary specialists will have a strong impact in successful diagnostics and management technology dissemination.

Poster Papers

P (S18) 01: Standardization of cultivation technology of King Oyster (*Pleurotus eryngii*) mushroom in Rajasthan

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The present investigation was carried out to explore the cultivation technology of king oyster mushroom since this being newly introduced to Rajasthan. The key aspects under study were the spawn production, cultivation methodology, the cultural requirements and the suitability of various factors affecting the production and yield attributes of *Pleurotus eryngii*. Paddy straw was found to be the best substrate giving the highest B.E.% and producing maximum number of fruiting bodies. Whereas, maize straw showed fastest spawn run and pin head emergence out of 6 substrates and supplements tested. But, due to the unavailability of Paddy straw in this region, the other straws resulting in optimum yields are to be recommended. Chemical steeping of substrate with Formalin @4% + Carbendazim@2%+ Dichlorovos @ 0.1% of the water used for soaking showed best results in terms of B.E.% whereas, hot water treatment of substrate at 85-90°C for about 60-90 minutes supported the fastest mycelial run out of four sterilization methods tested. The Hot Water Treatment results in leaching of nutrients and thus, B.E. gets lower. Out of four spawn rates used, spawn rate of 5% was found significantly best resulting in maximum B.E.%, fastest mycelial run, primordial initiation and the highest average fruit body weight. All the experiments were found statistically significant except the experiment for evaluating the optimum quantity of substrate for bag preparation. There was not much difference in the obtained yields with respect to increase in amounts of substrate. Out of four different months tested for spawning, the fastest mycelial run and pinhead initiation occurred in December and January months whereas, maximum B.E.% was observed in the month of December followed by November. Hence, it clearly indicates that the best suited time for cultivating King Oyster (*Pleurotus eryngii*) Mushroom is during winter months of the year. The quality parameters of *Pleurotus eryngii* including moisture, protein, carbohydrate, crude fiber and phenol contents were studied. Moisture contents of fruit bodies of mushroom grown on 6 different substrates and supplements, range from 82-90%. The fruit bodies harvested from Wheat straw and Wheat straw + 5% wheat bran had the highest (90%) and the lowest (82%) moisture content, respectively. The percentage of total protein on dry weight of mushrooms were found to be the highest (33%) on Maize straw and the lowest (15%) being recorded on Wheat straw + 5% wheat bran, respectively. The highest (67%) and the lowest (44%) total carbohydrate contents were obtained with the Wheat straw + 5% wheat bran and Sorghum straw, respectively. The crude fiber content was the highest (31%) and the lowest (11%) with Wheat straw and Wheat straw + 5% wheat bran, respectively. The total phenol contents of *Pleurotus eryngii* grown on all experimental substrates and supplements were found to be in the range of 5.3-7 mg/g of dry weight. The total phenol content was the highest on Wheat straw + 5% wheat bran, followed by Sorghum straw and Wheat straw + 5% rice bran and the lowest found on Maize straw.

P (S18) 02: Implementation of ecto-mycorrhizal inoculums and nutrients on growth of *Shorea robuta. Gaertn* to overcome plantation challenges

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The present investigation deals with the suitability of different mycorrhizal inoculums and fertilizer application on mycorrhiza formation and initial growth of *Shorea* seedling. The study revealed soil inoculums are more effective than the other inoculums which gave higher shoot length value (41.34 cm),followed by root inoculums and spore inoculums (32.70cm and 27.11 cm) respectively over control. Root length value was also higher in soil based inoculums over control (19.21 cm), followed by root inoculums (14.45 cm) and spore inoculums (12.09cm).The same trends were found in case of live and total mycorrhizal count because soil inoculums become highly in infective and its viability as well as suitability are more. The interaction effects of fertilizers and compost was noticed in *Shorea robusta*. In soil, the increase in root length was directly proportional to the fertilizer dosages. Significantly better root lengths were obtained in soil and compost (2:1) without fertilizer (33.6cm). In soil and compost (1:1) root length were poor and showed no significant differences at different fertilizer dosages though the tendency for increases in root length was observed at higher fertilizer dosages. Addition of compost to soil (1:1) was not significant in *Shorea robusta*, addition of two part of soil and one part of composed soil (2:1) significantly improved shoot height (12.9cm) in *Shorea robusta*. Addition of fertilizer at dosages 1N and above increased shoot height though such increase was significant only at 1N (14.6cm) and 4N levels (14.5cm) in *Shorea robusta.* The result shows that mycorrhizal development and dry weight of seedling was best in 1/2 normal NPK (63.75%) and moderate (26.60%) in 1/4 normal NPK and in treatment without P (22.5%).

P (S18) 03: Biochemical characterization and antimicrobial activity of *Pleurotus* spp.

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Biochemical analysis of five different *Pleurotus* spp. revealed that highest phenol content (903.11 mgGAEs/100 g dry wt.), tannin content (35.42 mgCAEs/100 g dry wt.), alkaloid content (675.42 mgBOEs/100g dry wt.) and saponin content (36.32 mg/100g dry wt.) was reported in *Pleurotus sapidus*. Consequently, extracts of these species was also evaluated for its antimicrobial activity against prevelant plant pathogens like *Fusarium oxysporum*, *Alternaria alternata*, *Rhizoctonia solani,* and *Bipolaris maydis*. Correlation among biochemical constituents and antimicrobial activity of mushrooms revealed highly positive correlation among antimicrobial activity and phenol as well as tannin while moderately positive correlation was observed among antimicrobial activity and alkaloid as well as saponin. Regression equation showing the role of biochemical components in antimicrobial activity was also recorded.

P (S18) 04: Performance of different species of oyster mushroom (*Pleurotus spp*.) under sub tropical climate of South Western Rajasthan

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Mushroom come under higher Basidiomycetes barring few which are in Ascomycetes. This is a wonder food having higher protein dietary fiber, vitamins, anti cancer value and minerals suitable for all the people irrespective of all age group. Mushrooms are fiber rich, low calorie food with some of them having hallucinogenic properties through enhanced immune system of consumer. This mushroom has species suitable for both temperate and sub-tropical regions. For temperate region *Pleurotus ostreatus, P. florida* (winter strain) and *P. fossulatus* (Kabul dhingri), *P. eryngii* (King oyster) are ideal. At present, in Rajasthan, mushroom cultivation is increasing and two mushrooms *viz., Agaricus bisporus* (78%) and *Pleurotus* (16%) species have occupied a noble place among progressive growers. Large volumes of wheat straw are produced as agricultural by-products in this region so wheat straw is used for mushroom cultivation. In this present investigation a total of eight different species of oyster mushroom are cultivated under sub tropical climatic condition of south western Rajasthan. On the basis of this experiment observed that two strains have better performance in these harsh climatic conditions. On an average 600gm and 550gm fresh oyster mushroom harvested from 3 Kg wet substrate bag of PL-19-05 and PL-19-06, respectively. It is grow at 24-28^{o}C temperatures and 80-90% relative humidity in rainy season. The rate of spawn is usually 3% of wet weight of substrate**,** but when early spawn run is required 4% may be taken. Ideal wet weight of substrate is 3 Kg and spawning done in three layers. In this experiment observed that minimum spawn run period (14-19 days), minimum period of pin head formation (17-21 days), minimum period for fruit bodies formation (20-25 days), recorded at 27-28^{0}C.

P (S18) 05: Paddy straw decomposition through *Trichoderma*: improve soil quality of farmer’s field at Raipur district in Chhattisgarh

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Trichoderma is boon for agriculture to promote organic farming and also use for improving soil quality of farmers field of Chhattisgarh. Rice is the main crop and staple food of the people of Chhattisgarh and it is grown extensively from low lying traditional paddy fields. In rice-based cropping systems it is a common practice that after harvest the rice stubble is left in the field and becomes exposed to microbial degradation. Decomposition of rice straw depends on those microbes that can colonize and degrade its various constituents, especially cellulose, hemicellulose and lignin. Decomposition is a complex process made up of a number of sub processes and involves a multitude of organisms, where fungi play an important role. Soluble components such as simple sugars and storage materials are utilized first and relatively quickly, followed by structural. Fungi like *Trichoderma viride and T. herzianum* were found associated with rice stubble in different stages of decomposition. These fungi were then inoculated separately onto rice stubble in order to study their efficiency in biodegradation. The present investigation showed that trichoderma based vermicompost, when used in the farmer’s feild trichoderma decomposed paddy straw and convert it into compost and also control soil borne diseases namely wilt of chick pea, coller rot, *Sclerotium* fungi also control damping off in vegetables. Farmers adopting the technology of trichoderma mass production through broken rice. It is very cheap and easy method for preparation of trichoderma powder and very much helpful for farmers. Farmers prepared trichoderma by own and mass multiply by using carrier as vermicompost/ FYM. Farmers use 1 kg pure *Trichoderma* powder with 10 Kg Vermicompost/Gobar Khad and 1 Kg Jaggery mixed all these homogeneously and store it in cool place in shade cover with moist gunny bag from both sides for 7 days. *Trichoderma* multiply very faslty within 7 days and ready for use. Simultaneously *Trichoderma* multiply from prepared above trichoderma based vermicompost/FYM. This technology adopted by Chhattisgarh farmers very rapidly for improving the soil quality. The results of the present study showed the usefulness of biomass degrading microorganisms. Incorporation of rice straw to the soil treated with decomposing microbial agents *Trichoderma* along with vermicompost/Gobar Khad had enhanced the organic carbon and nutrients content of the soil, which resulted in increased grain yield of chick pea. Till now it is big challenges in implementation of this technology towards the farmers of Chhattisgarh state.

P (S18) 06: Constraints and problems in plant pathology extension

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Agricultural in India is marching towards commercialization unlike in past. There is dual pressure of food security and food safety. Later has become more serious concern for every plant protection experts. The current plant pathology extension has many challenges in making agricultural more profitable. Although massive transformations have taken place in mass communication, from radio and news papers to smart phones with internet have brought the world at finger tip. However, in India, still educating farmers about plant protection has entirely different challenges. The current study identifies suitable extension strategy for educating farmers of plant protection measures. Among the various extension practices, technology demonstrations & method demonstrations followed by frequent field visits had very high rate of adoption (93%) of disease management practices. Effective communication with farmer was found second most important strategy (88%) in disseminating required information to end users. It was followed by cost effectiveness of plant protection measure (81%) recommended played important in making the plant pathology services more effective. With over six years of farmer's perceptiveness study, it was found essential that inculcation of extension skills is equally essential as research methodologies while training agricultural faculty especially plant pathology extension scientists. An interesting observation noted was there is growing awareness among farmers about importance of bio-pesticides and their need in organic farming, however, ensuirng their availability locally is only making their reccomendations useful otherwise often many good technologies in this regard end-up finding no place in farming practices. It was noted that farmers reach with scientists without time limit was key behind the successful plant pathologist. Ultimately, plant pathology with human touch had more practical application for successful extension of technologies from lab to land in producing enough and safe food, feed, fodder, fuel and fiber.

Session 19

Plant pathogists entrepreneurship and policy perspectives for food security

Keynote Papers

KN (S19) 01: Onion: cultivation, production and disease problems

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Onion is an important vegetable crop and is next only to tomato. In India yearly two or three onion crops are grown as: *Kharif* crop - from June to August, Late *Kharif* crop (also known as Rangda) – from September to November and Rabi crop – from December to February. Onion bulbs of *Rabi* crops are suitable for export and are storable for four to six months whereas, the bulbs of *Kharif* and late *Kharif* crops do not withstand storage under ambient conditions and perish within a month.

Oral Papers

O (S19) 02: Mushrooms and fungal revolution: possibilities and perspective in Chhattisgarh

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Mushroom cultivation is a potential biotechnological process wherein the waste plant materials or negative value crop residues can be converted into valuable food. Protein conversion efficiency and productivity of mushrooms per unit land area and time is far superior than plant and animal sources. In recent years mushroom cultivation in Chhattisgarh has witnessed a tremendous growth with respect to the type of mushrooms and their productivity. Mushroom cultivation is recognized as an eco-friendly alternative for agro-waste recycling with tremendous capabilities to provide better nutrition for the vast vegetarian population, employment generation and a good income source. At present, four mushroom varieties namely, *Volvariella* spp, *Calocybe indica*, *Pleurotus* spp. and *Agaricus bisporus* have been recommended for round the year cultivation in the country. Chhattisgarh is an ecological hub of many natural wild edible species of macro-fungi which has been extensively surveyed, documented, characterized and preserved as dry and wet specimens from different agro- ecological zones. The dominant forest mushrooms identified as food is *Termitomyces microcarpus*, *Termitomyces eurhyzus*, *Termitomyces clypeatus*, *Rassula* spp, *Canthrellus* spp, *Rhizopogon*, edible *Amanita*, *Lentinus* spp*, Pleurotus* spp*, Macrocybe* spp*, Tricholoma* spp*, and Volvariellavolvaceae*. The production technology of different species of Oyster mushroom like *Pleurotus eous, Pleurotus djamor, Pleurotus florida, Pleurotus, flabellatus, Pleurotus sajor-caju, Hypsizygous, Volvariella volvacea, Lentinula edodes, Lentinus sajor-caju, Heriecium* and *Calocybe indica* has been standardized with reference to their production temperature, suitable agro-wastes and supplements. Similarly, different production systems have been identified for *Volvariella volvaceae* cultivation. Open cultivation of *Volvariella* in mango orchards, bamboo plantations, border rows of green houses in protected cultivation sheds and indoor cultivation in growing rooms have been popularized across Chhattisgarh**.** A low-cost viable button mushroom production model has been developed for farmers using long method of composting. Similarly button mushroom production in solar panel enabled growing rooms have also been initiated at pilot scale and has been demonstrated for year-round cultivation in tropical areas like Raipur**.** The Mushroom Research Laboratory of IGKV is instrumental in capacity building of >15,000 students, entrepreneurs, women self-help groups, landless farmers, farmer producer companies and unemployed youth with various on- campus and off campus National/State/District Level Trainings on spawn production, mushroom crop production and processing technologies. Awareness has also been created by organizing All India Mushroom Workshops/Seminars National Exhibitions. Trainings have also been organized for specially- abled people, surrendered naxalites and inmates of jail to empower them on social platforms. Seven such trainings have been organized. The training of mushroom cultivation techniques have also been given to more than 2000 NSS youth across state, many of them have been successfully growing mushrooms as well as giving trainings to people in their areas. Every working Saturday, a free hand on training on different aspects of mushroom cultivation is imparted at the university campus. For promoting mushrooms as food and livelihood enterprise, substantial policy level intervention is required in regulating the marketing, pricing and food label claims.

O (S19) 03: Plant pathologists entrepreneurship from idea to business

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Tomato (*Lycopersicon esculentum* Mill) “Super food” is adversely affected by Early Blight caused by *Alterneria solani*. Management of the disease through agrochemicals had resulted in increase of toxicity in food chain and several health hazards. There is a great need to develop bioformulations that can enhance crop yields and additionally protect them from pests as well, to promote confidence among end users. One of the common hurdles is the diffusion of innovation in agriculture because of poor communication of science to farmers. This is the reason that farmers adopt certain technologies but leave out others. So, the main objective of the project was to develop a low-cost remedy in the form of bioformulation for bull’s eye pathogen in tomato plants and taking the product from lab to land communicating with the farmers. Different in vitro and in vivo studies necessary for product development were undertaken Keeping in view an eco-friendly approach for sustainable agriculture understanding the nature of market, farmer’s aspirations and providing appropriate solution to them through organic farming a bioformulation **‘Bioelexir’** is developed. Farmers will be highly benefitedas it is very effective against those *Alternaria* isolates which has developed resistance against fungicides. It is a non-chemical based formulation to reduce disease of tomato plant combining with features for enhancing soil structure and fertility, maintaining soil biological activities and promoting plant growth & biomass. Additional Features include protection of environment and human health and increased income of farmers. So, to overcome the challenges in food security with organic methods bridging the gap between farmers & scientists is necessary for which several demonstrations, interactive training programs and awareness camps sharing the scientific research were organized. Finally to convert it into a successful business, TrichoAgronicaPvt Ltd, supported by IOCL Start-up scheme has been set up and is an example of a plant pathologists entrepreneurship.

O (S19) 04: Biofortification of *Pleurotus Sajor-caju* using zinc sulphate nanoparticle

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Since the stone age, mushrooms served humans as food, medicine, psychoactive drugs, religious symbols and helpful tools. *Pleurotus* spp. commonly known as oyster mushroom has not only medicinal but huge nutritional value also with vitamin C, B complex and trace minerals. Zinc, a necessary mineral for human health and also called as "essential trace element" is next to iron in its concentration in the human body. Since the human body does not store excess zinc, it must be consumed regularly as part of the diet. Zinc deficiency is characterized by growth retardation, loss of appetite, and impaired immune function. Biofortification of food crops for increasing the zinc content and its bio-availability is one of the potential alternatives for combating zinc deficiency. Hence, the present study pertains to the development of zinc bio-fortified *Pleurotus sajor-caju*, using zinc sulphate nanoparticles. ZnSo4 nanoparticles (NPs) were studied as a potential solution to alleviate Zn deficiency in human diet due to their special physicochemical properties. *Pleurotus sajor-caju* was grown on wheat straw and treated with zinc sulphate nanoparticle after complete spawn run at different concentrations (0, 10, 20, 30, 40ppm). The effect of nanoparticle treatment was analyzed by measuring the morphological growth parameters viz., number of fruiting bodies, pileus width, stalk length, stalk diameter and biological efficiency. The Atomic Absorption Spectrophotometer (AAS) was used to estimate zinc content of each treated sample. The use of zinc sulphate nanoparticle enhances the economic yield as well as zinc content significantly. The study concludes that nanoparticle treatment can improve the nutritional value of *Pleurotus sajor-caju* by increasing its zinc content.

Session 20

Farmers-Scientists-Industries interface

Invited Papers

I (S20) 01: Commercial production of microbial pesticides for livelihood security of rural population involving self help groups and farmers following principles and practices of lab to land programmes

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Sustainable rural livelihood is a multifaceted concept and refers to maintenance or enhancement of access of rural families to food and income-generating activities on a long-term basis. In the Indian context, where average farm-size is very small, and poverty and food-security continue to be preponderant among small landholders, the notion of sustainable agriculture ought to be viewed in the context of need for enhancement of productivity, production and profitability of agriculture and above all, for improvement in the economic conditions of rural population. The biopesticides are the sunrise sectors for developing Agri- entrepreneurship due to scopes of supply and demand with the continuous use of these inputs in agricultural production systems and can be help in employment generation and uplift of socio-economic conditions of the resource poor farmers for nation's prosperity. Despite the promising impacts of biopesticides, the Indian biopesticide industry is growing at a very slow pace. Poor quality of microbial pesticides commercially available at higher cost and adverse effect on viability due to long travel as well as poor transportation facilities are major concerns. Therefore, a major goal has been to develop for local sourcing of biopesticides as a means of ensuring availability at a low cost to benefit poorer farmers, and as a base for expanding an Indian biotechnology industry. To take-up the commercial production of bio pesticides and to encourage the entrepreneurship in rural areas, large number of pilot plants should be established at village and block level using technologies and efficient indigenous strains of bio pesticides developed by state agricultural universities located in different parts of country. Commercial production of microbial pesticides can be taken up by self help groups (SHGs) as source of their livelihood and income generating activities. On above said model, nine production units were established in different parts of Chhattisgarh state involving tribal women in nine self help groups and started production of *Trichoderma harzianum*. In three years, Rs 8.927 lakhs of *Trichoderma* were sold by different self help groups through department of Agriculture and other private firms to farmers of Chhattisgarh (Ann., 2014). There was increase on the monthly income of beneficiaries involved in the production of *Trichoderma* from 10.25 to 39.61 per cent. Self help groups (SHGs) can also be trained in bio control laboratories as mentioned earlier. Further, financial assistance can be provided by the Department of Agriculture under ATMA scheme or under RKVY or by NABARD or by Jila Panchayat through schemes launched by central and state governments i. e. Atal incubation scheme, Skill development programme etc. for establishment of biocontrol laboratory at their respective places. Responsibility to get registration at CIB and obtain manufacturing license from respective states and development of market net work is to be also taken up by the same institute. Under the second proposed model, commercial production of biocontrol agents can also be taken up by self help groups (SHGs) of farmers or individual farmer for their own use. Farmers should be provided extensive training through audio- visual aids and thereafter farmers should be assign to produce biocontrol agents in large scale under the supervision of scientists. During 2015-2017, total quantities of 77.21 q of biofertilizers and biopesticides were produced by the group of farmers from their respective production units. There was additional saving of Rs 926520/- has been estimated considering production cost and market price of biofertilizers and biopesticides. Installing production units of biofertilizers and biopesticides with minimum amount of investment (Rs 5000/-) can be a very good model for the group of farmers to produce biofertilizers and biopesticides for their own use and make their produce chemically free as an organic produce. This model can also be developed as lively hood source of income for rural population which do not have other sources for their livelihood. A part of *Trichoderma*, *Pseudomonas* and *Rhizobium*, many more biofertilizers and biopesticides can be taken for their production and use in different crops. The scientist involved in the programme should provide help in technology transfer, consultancy, training and quality control to rural population. In view of labour intensive nature of the biopesticides production programme, rural population should be involved and received adequate financial support as well as encouragement by state and central governments to set up bio pesticides production units.

I (S20) 02: Empowerment of small-holder farmers through filling information, input and investment gaps – Greenlife model

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According to the FAO, four-fifths of the developing world's food is a product of small-sized farms, and yet small-holder farmers make up the majority of people living in absolute poverty, and half of the world's undernourished people. This link between farming and poverty that those feed the world are likely to face hunger themselves. Farmers in India are no exception to this harsh reality. Lack of knowledge of scientific cultivation of crops is one of the several known reasons for this dismal situation. Although tremendous advancement has been achieved in agricultural sciences, the knowledge level of small-holder farmers still remains very low and as a consequence, the agriculture as such has remained less or non-remunerative to small-holder farmers. In addition to this, non-availability of critical inputs and credit facility has also added to the misery of these farmers. Realizing these gaps, by its own survey in its command area, Green Lifescience Technologies (Greenlife) aimed at filling the three critical gaps – information gap, input gap and investment gap. Greenlife was started with an aim to solve some of these problems in Mysore district, Karnataka, 18 years ago. It started giving the most needed scientific knowledge, critical inputs on interest-free credit (without any collateral) and also stayed with the farmers, throughout the crop season, giving moral, knowledge and input support. Greenlife believes that the farmer is not a borrower, but the partner. This philosophy of "Partnering with the Farmer" has been working successfully, for the last 18 years, and more than 12,000 farmers are being benefitted by this scheme. Recently this service has been extended to a bunch of 20 villages in dry belt of Mandya district as well. The farmers in these villages are small, resource poor, choiceless and voiceless Chrysanthemum growers. Despite their best efforts and good price for flowers their income had remained at minimal. After the introduction of Greenlife model, in the last three years, there has been tremendous increase in their net income. Introduction of integrated nutrition, water and pest & disease management has led to reduction in chemical pesticides and fertilizers and there by reduction in cost of production, reduction in loss due to pests and diseases and increase in yield and quality. More than 1000 farmers have been the beneficiaries at this point of time and by next six months a target of 2000 farmers will be reached. This has given these farmers four 'E's'; Economic benefit, Environmental/Ecological benefit, Employment benefit and Emotional benefit. This can result in higher and quality production at lower cost and make the farmer debt-free and lead an independent, respectful and happy life. Greenlife is also confident that this project can help not only in retaining rural youths in farming but also can lead to reverse migration of youths who have been doing menial jobs in cities.

I (S20) 03: Developments in mushroom industry: production, consumption and marketing patterns

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Mushrooms are probably the only macro fungi consumed for the purpose of food and nutrition. Low in calories and fats with no cholesterol, mushrooms are rich in proteins, fibre, minerals (copper, potassium, magnesium, zinc) and vitamins (B complex, vitamin C and probably the only vegan source of vitamin D). Mushrooms are the richest dietary source like selenium, glutathione (GSH), ergothioneine (ERGO), substances believed to protect cells from damage and reduce chronic disease and inflammation. Mushrooms are reported being consumed as food and medicine in olden treatise of different civilizations in of the world, but their cultivation at larger scale started only after World War II. Recent estimates predicted 5.1 million species of fungi existing on earth. Out of which, 1,60,000 species are macro-fungi and 16,000 (15%) species are mushrooms. About 3,000 species from 231 genera are prime edible, 200 experimentally grown, 100 are economically cultivated and around 60 are exploited at commercial scale while only 10 mushrooms are produced on an industrial level. Button (*Agaricus bisporus*), Shiitake (*Lentinula edodes*), Black ear (*Auricularia* spp.), Oyster (*Pleurotus spp*), Enokitake (*Flammulina velutipes*), Paddy straw (*Volvariella volvacea*) mushroom contribute about 90% of the world mushroom production. Mushroom industry has seen a Cumulative Annual Growth Rate (CAGR) of 10.56% during 1961 to 2018. Recently, rapid increase in production of wood rot fungi like *Lentinula edodes*, *Auricularia, Pleurotus* species, etc cultivated in east Asian countries in general and China in particular, relative contribution of button mushroom has declined from 73% in 1975 to 15% in 2013. These species have started making inroads in western countries but even today *Agaricus bisporus* is prime contributor to European and American mushroom industry (contributing 80 to 100%). The global mushroom industry has expanded rapidly in the last two decades by the addition of newer types of mushrooms for commercial cultivation. However, mushroom is yet to find regular place among the Indian diet. Despite of favourable agro-climate, abundance of agro wastes, relatively low-cost labour and a rich fungal biodiversity, India has witnessed a lukewarm response in its growth. At present, the total mushroom production in India is approximately 0.18 million tons. Mainly, five mushroom species *viz*; *Agaricus, Pleurotus, Volvariella, Calocybe* and *Lentinula* are cultivated in India. From 2010-2018, the mushroom industry in India has registered an average growth rate of 4.3% per annum. Out of the total mushroom produced, white button mushroom share is 73% followed by oyster (16%), paddy straw (7%) and milky mushroom (3%). Compared to other vegetables; per capita consumption of mushrooms in India is meagre and data indicates it is less than 100 grams per year. In the year 2018, Indian mushroom industry generated revenue of Rs. 7282.26 lacs by exporting 1054 quintals of white button mushroom in canned and frozen form. Major bottleneck in the growth of mushroom industry is the availability of spawn, uniform farm design, mechanization & automation in mushroom industry, availability of mushroom strains suitable for Indian condition and the awareness amongst the masses about the nutritional and medicinal benefits of mushrooms.

I (S20) 04: Biopesticides and biofertilizers: Green technology for sustainable agriculture

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Indiscriminate use of chemical pesticides in agriculture leads to cause various hazardous effects in humans and animals. Various chemical pesticides have been banned in world as well as in India by adopting legislative actions. Bio pesticides and Bio fertilizers have ability to overcome these problems due to its potential of environmental safety, target-specificity, biodegradability, suitability in the IPM programs, alternative source of plant nutrition, ability to increase resistance to pests & pathogens, growth promotion activity etc. The consortium of various beneficial microorganism's like *T. viride*, *T. harzianum, N. relayi, B. basisiana, M. anisopliae* may help in solving the majority of these problems. Consortium of beneficial microorganisms was prepared by the department on farmers demand. This microbial consortium product was used by the farmers for the disease and pest management of various crops in the Maharashtra state. This was used by farmers on large scale in turmeric. Its sale during the year 2018-19 and 2019 till the date was 90 MT and 100 MT respectively; worth's near about RS 1.75 crores for the running year only. Use of this microbial consortium and its beneficial effects were studied in turmeric growing belts in this area. Observations were recorded on per cent disease incidence, pest incidence and its yield and quality parameters. It was observed that average number of fingers Increased by 17.46 per cent and 17.73 per cent increase in total yield was recorded. Impact of microbial consortium applications on Incidence of rhizome rot and Intensity of foliar diseases of turmeric on farmer's fields were also studied and results obtained that, per cent disease incidence of Leaf spot, Leaf blotch and rhizome rot was decreased by 51.02, 69.48 and 84.14 per cent respectively. Major turmeric pests *i.e.* Rhizome fly and White grub infestation also found to be decreased by 55.19 and 95.05 per cent over control.

I (S20) 05: Citrus decline: A major threat to citrus industry

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India ranks sixth among top citrus producing countries contributing 4.80% to the world's total citrus production. Still, the production per ha is much lower than other countries like USA, Brazil and Spain. In 2016-17 total area of citrus in India was 10.55 Lakhs ha and the production was 127.46 Lakhs metric tons. The major reason for low productivity and short productive life of citrus plants is the problem of Citrus decline. The abrupt and adamant event like uneven rainfall patterns, severe heat-wave periods and uncertainty in local agro-meteorological weather conditions during the past few decades, these uncertainties have resulted in increased crop failure. Over the last few years these conditions have worsened due to inadequate understanding of plant-soil-water-weather-disease continuum that largely influences the crop production and judicial utilization of water resources. In order to address the pest / disease management, there is a need for multi-modal information dissemination about disease management system. Citrus decline has been a widespread problem in central India and *Phytophthora* disease has been identified as the major cause of decline. Citrus succumbs with many diseases which results in to decline in citrus. However a few diseases cause significant damage and require due attention for their effective management. *Phytophthora* reduces around 45% yield of citrus plants. The losses to Citrus industries are about $12.9 million annually due to this disease. Nearly $5 million annual loss cause, because of root rot. *Phytophthora* species are widely distributed in almost all the citrus growing belts of India and are the major cause of citrus decline. Faulty cultural practices such as flood irrigation to induce flowering disturb the balance of water uptake of plant with decayed feeder roots and water demand for excessive bearing which results in sudden decline of such plants. In most of the citrus orchards the population ranged from 1 to 20 propagules/cc soil but occasionally it may be 100 to 200 propagules /cc soil. Greening disease is also one of the causes of citrus decline. The symptoms are displayed on different parts of the plant. In general, the greening- affected trees show the open growth, stunting, twig dieback, sparse yellow foliage, or severe fruit drop. In some cases, green colour develops on fruit at the peduncle rather than the styler end, as in normal case. Although the Asian form of greening causes extensive dieback. Citrus Tristeza is an important viral pathogen which has killed about 100 million citrus trees worldwide over last 70 years . The virus contains a long flexuous particle of 2000 × 10-12 nm size, transmitted by brown citrus aphid (Toxoptera citricida) predominantly in a semi-persistent manner. CTV genome contains a single-stranded positive strand RNA molecule of 20 kb length, comprising 12 open reading frames. CTV causes various disease symptoms like mild symptoms to seedling yellows, stem pitting, severe stunting and ultimately decline of the plant depending on citrus species, virus strains, scion/rootstock combinations and environmental factors .

I (S 20) 06: Importance of weather based Agromet advisories in crop and pest management

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Agricultural production depends upon many factors, of which weather is the most important factors determining success or failure of agricultural production. It effects on every phase of growth and development of plant. Any variability in the weather during the crop season, such as delay in the monsoon, excessive rains, flood, droughts, spells of too-high or too-low temperatures would affect the crop growth and finally the quality and quantity of the yield. Weather varies with space and time, hence, its forecast can help to minimize the farm losses through proper management of agricultural operations. The complete avoidance of all farm losses due to weather factor is not possible but it can be minimized to some extent by making adjustments through timely and accurate information of weather forecast. Weather forecast also provides guidelines for selection of crops best suited to the anticipated climatic conditions. Occurrence of pest in any crop depends upon temperature and humidity. Based upon past weather and weather forecast, forewarning for pest incidence can be given in advance to the farmer so they can do proper management in time based upon the weather condition. weather forecast based agromet advisory bulletin contains, summary of previous week's weather, value added medium range weather forecast information for the next 5 days, crop management which is based on weather forecast and giving warning to farmers much in advance regarding rainfall variation its amount and other weather variables including pest/disease problems etc. so that farmers can decide about his choice on crop management such as time for sowing, wedding, harvesting, fertilizer application, irrigation scheduling, time and dose of pesticides spray, contingent plan against weather at critical crop stages. Weather forecast and weather based agromet advisories play essential role in agricultural production. Economic gain can be due to the crop management done by the farmers such as optimum time for land preparation and sowing, seed rate and suitable varieties, proper time for weeding, proper time of harvesting, amount and time of irrigation, agricultural operations and management of pest and diseases of crops according to the weather conditions. Increased yield and reduced cost of production, led to increased net returns. Thus, application of agromet advisory bulletin based on current and forecasted weather is useful for enhancing the production and income by reducing the farm input cost by doing crop and pest management in appropriate time.

Oral Papers

O (S20) 07: Pranic agriculture – An ancient technique for enhanced crop production

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Pranic agriculture is an ancient science which uses Prana to enhance plant growth. Prana is the vital energy mentioned in Yogic texts and Ayurveda. It involves projection of prana to plants to promote faster development. The present study aimed to understand application of pranic agriculture protocol on tomatoes, pole beans, cucumber, European cucumber and brinjal. Physical parameters including plant length, stem diameter, flower initiation, time taken for fruit development, fruit yield and shelf life during storage were studied of pranic treated plants against the control. Increase in plant length of 18.5% and 49% was noticed in tomato and European cucumber as compared to control groups. Also, pranic group plants had 12-24% more stem diameter than control. Additionally, pranic tomato plants had 31.7% more flowers per plant when compared to control. When group-wise yield was verified, Pranic group yielded significantly more in tomato (31%), cucumber (18%) and in European cucumber (17%) than control group. During storage period, pranic treated brinjal and tomato had significant improvement in firmness, decay, color, gloss and shrivelling against the control. This clearly shows that pranic agriculture could play a significant role in improving the quality and quantity of vegetables and also extending the shelf life. Further studies are needed to study the mechanism and the difference in their nutritional compositions.

Session 21

Workshop on rust diseases of cereals

Keynote Papers

KN (S21) 01: Immunity to rusts in wheat- theory, fact and practice

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Wheat rusts are very devastating and historic pathogens. Natural selection for rust resistance in wheat is going on at the centre of origins for wheat. A resistant mutant of wheat gets an advantage over susceptible. Likewise a virulent and fit pathotype overtakes the pathogen population of rusts. Therefore, there is a continuous race for supremacy in wheat breeders and rust pathogens. Wheat-rust interaction works totally on gene for gene theory and is very mathematical unlike other biological systems. Resistance forms a vital tool in the management of wheat rusts. Continuous efforts for breeding rust resistant varieties are going on for long time. However, systematic breeding of wheat against rusts is around 115 year old. Immunity is non host resistance. Practically immunity for rust pathogens does not exist in wheat. Any wheat may be immune to rust till it become susceptible. When 1BL-1RS translocation/ substitution (*Lr26/Sr31/Yr9*) were made into wheat from immune rye, we thought to have attained immunity to wheat rusts. Since rye was known non host to wheat rusts, therefore, the efforts of Mettin and co-workers as well as Zeller in 1973 were widely lauded. However, myth was short lived as within 11 years virulent isolates of *Puccinia triticina*, then *P. striformis* and in 1998 of *P. graminis tritici* were identified. Two things became clear, immunity to rusts may not exist/short lived and rust pathogens can outsmart human efforts. We made similar observations for other alien introgressions or other tertiary relatives of wheat. Since mutation/sexual recombination go independently , therefore, there is every chance that a virulent isolate gets selected on immune/ resistant host. In some cases new virulences emerged even before a resistant variety having alien blood went to the farmers' fields. New virulences emerge on alternate host. However, in absence of alternate hosts, mutation is the major cause of evolution of new virulences. In 1980s, came the concept of durability of rust resistance. While durability is contributed by few genes with minor effects, some vertical resistance genes have also remained durable for long. Resistance of Eagle (*Sr26*) to stem rust in Australia, Cappelle Desprez to stripe rust in Europe remained effective for long time. Over the years concept has changed. Therefore, we have to learn to live with wheat rusts. Wheat rusts cannot be eradicated but managed. It also warrants the need for a pro active, sensitive and vibrant wheat breeding programme in place. It is now well realized that for effective management of wheat rusts, diversity is key word. Diversity of cultivated wheat varieties and types of resistance are the effective tools for rust management. At present we harness all time rust resistance, adult plant resistance of low infection and slow rusting to have durability for rust resistance, a number of genes with minor effect are also being used in breeding programmes. Since virulence for one gene emerges easily than for two or three, therefore, gene pyramiding for more than one effective rust resistance gene would be more useful. In past many neighbouring countries, European and North America had epidemic of one or other wheat rusts but we had none in India. Our strategy to combat wheat rusts through pathotype distribution based deployment of varieties/resistance, combined with diversity for rust resistance have been very fruitful as we had no rust epidemics on wheat for the last about five decades.

KN (S21) 02: Insights into the rust resistance base of common wheat in India

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A total of 270 lines showing leaf tip necrosis (*ltn*) phenotype including released varieties, advanced generation lines and genetic stocks representing a cross section of the recently developed / used common wheat (*Triticum aestivum* L.) genotypes in India were studied for rust resistance during 2016-2019. They were characterized for the presence of *ltn*-associated race-non specific pleiotropic adult plant resistance (PAPR) genes viz., *Lr34*/*Yr18*/*Sr57*, *Lr46*/*Yr29*/*Sr58*, and *Lr67*/*Yr46*/*Sr55* using closely linked molecular markers, *cslv34*, *wmc44*, and *cfd71*, respectively. These lines were seedling tested with prevalent and virulent rust pathotypes viz., 11 (79G31), 40A (62G29), and 40-3 (127G29) of *Puccinia graminis tritici*; 77-5 (121R63-1), 77-9 (121R60-1), and 104-2 (21R55) of *P. triticina*; and 46S119, 110S119, 238S119, 110S84, and 'T' of *P. striiformis tritici*. The test genotypes were evaluated for field resistance to the three rust diseases under heavy disease pressure at six hot spot locations viz., Indore, Delhi, Wellington, Dhaulakuan, Mahabaleshwar, and Dalang Maidan. None of the test genotypes was found to carry all the three PAPR genes. The genes *Lr67*/*Yr46*/*Sr55* and *Lr34*/*Yr18*/*Sr57* occurred more frequently, compared to *Lr46*/*Yr29*/*Sr58*. About one-fourth of the genotypes each carried these genes singly, whereas about one-fifth of the genotypes carried them in combination. Only about 9% of the genotypes carried *Lr46*/*Yr29*/*Sr58*, either singly or in combinations with the other two PAPR genes. None of the PAPR genes could be validated in about 20% of the genotypes. Nearly two-third of the lines each showed field resistance (Average Coefficient of Infection up to 10.0, and Coefficient of Infection up to 20.0) to leaf rust or stem rust, but only less than one-fourth of the lines were resistant to stripe rust. While high levels of resistance to leaf rust or stem rust were generally associated with seedling resistance to the test pathotypes, field resistance to stripe rust was observed to be based more on the adult-plant resistance. Levels of resistance manifested individually by the three PAPR genes appeared to be similar, and no significant additive effects were apparent among various combinations of these genes in imparting rust resistance in the genotypes studied. The genes *Sr31* and *Lr24/Sr24* are the only widely effective ones among the *Sr* and *Lr* genes commonly postulated in the Indian common wheat germplasm. Stripe rust resistance genes *Yr5*, *Yr10*, and *Yr15* are the only known ones imparting adequate levels of resistance to Indian stripe rust pathogen populations, and have been used to a limited extent in recent years. The present study indicates that additional undesignated genes for seedling or all-stage resistance as well as adult-plant resistance are functional in the recently developed / used common wheat genotypes in India which need to be characterized. Meanwhile, the genotypes identified with multiple rust resistance could be immediately utilized in breeding for rust resistance and other desired traits as most of them have proven agronomic superiority also.

KN (S21) 03: Surveillance for wheat diseases–an analysis

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Wheat crop health was monitored thoroughly during the crop season as well during the off season during 2000-2016. Special teams of scientists were constituted every year during the All India Wheat Workers' Meets. Major focus was on the occurrence of stripe rust in north western and northern hill zone. In 2001, a new pathotype 78S84 of *Puccinia striiformis* with virulence on PBW 343 was detected whose inoculum got built up steadily due to the cultivation of PBW 343 over a large area. The variety was high yielding and occupied 6-9 million hectares area in different years. It became popular amongst farmers in the hilly regions and eastern India as well. Since 2006-07, the stripe rust is occurring in high intensity in one or the other parts of North Hill Zone (NHZ) and NWPZ. Emphasis was laid for growing rust resistant wheat varieties such as PBW 550, DPW 621-50, WH1021, HD3043, WH 542 of bread wheat in disease prone areas of NWPZ whereas HS375, H490, HS507, VL892 and VL907 in NHZ. Due to congenial weather for stripe rust, two pathotypes, 78S84 (*Yr* 27 virulence on PBW 343) and 46S119 (*Yr* 9 virulence) were most prevalent during 2010-11 crop season and many of the varieties grown in North Western Plain Zone became susceptible. During 2010-11 due to congenial weather, stripe rust appeared in severe form in the plains of J & K , foot hills of Punjab and Himachal Pradesh, parts of Haryana and *tarai* region of Uttarakhand wherever susceptible varieties were grown. In Punjab, especially in the districts of Ropar, Nawan Shahar and Hoshiarpur, the disease was well spread over a large area on most of the varieties being grown by the farmers. In Haryana, the disease was severe in Yamunanagar district. Stripe rust was noticed in mid December in 2010, 1st week of January in 2012, 2nd week of January in 2013, 19th December in 2014 and on 18th December in 2015. Frequent surveys are being taken during the off season in the high hills of Himachal Pradesh (Lahaul, Spiti and Kinnaur) and J & K (Ladakh). Information on wheat crop health was disseminated through the "Wheat Crop Health Newsletter" and Mehtaensis which was issued on monthly basis during the crop season. Advisories for varietal deployment and protection technologies are issued to the farmers for stripe rust management as and when required. Extensive surveillance, release of mega varieties like HD 2967 and HD 3086 and coordinated efforts by ICAR-IIWBR, SAUs', DAC and State Agriculture Departments during this period helped in in averting the stripe rust epidemic. In addition to stripe rust monitoring, strict vigil was also kept on leaf and stem rust as well as other important wheat diseases in all wheat growing zones of the country. Analysis of a large number of grain samples was also done for monitoring the status of Karnal bunt disease and to identify the disease free areas for facilitating wheat trade. Concerted efforts of wheat surveillance has contributed significantly in keeping vigil on new pathogens, pathotypes and devising strategy for developing new resistant varieties ahead the pathogen can cause loss to the crop.

Keynote Papers

I (S21) 04: Discovery and integration of wheat stem rust resistance

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Epidemics of wheat stem rust, caused by *Puccinia gramins* f. sp. *tritici*, historically devastated regional wheat production. Since the Green Revolution of the late 1960's, significant stem rust epidemics have been averted through the deployment of genetic resistance. But, *Puccinia graminis* f. sp. *tritici* races detected in Africa and the Middle East, including Ug99, are virulent to the majority of wheat varieties currently grown globally. Because of this threat, researchers have doubled the number of described stem rust resistance genes effective to Ug99 to a total of 42, including 10 cloned resistance genes. However, the dynamic population of *Puccinia graminis* f. sp. *tritici* continues to adapt to deployed resistance genes rendering the majority of current varieties as susceptible. To address emerging races of *Puccinia graminis* f. sp. *tritici*, single-race field evaluation nurseries identified wheat lines with adult plant resistance effective to multiple virulent races. In order to utilize multiple major-effect resistance genes, linkage blocks were assembled and backcrossed into elite cultivars. Integration of pathogen surveillance, resistance monitoring of breeding populations, targeted pre-breeding for stem rust resistance, and international collaboration can improve stem rust resistance durability in future wheat cultivars.

I (S21) 05: Current status of maize rust diseases in India

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In India, Maize (*Zea mays* L.) is the third important crop after rice and wheat that provides food, feed and fodder and serves as source of basic raw material for the industrial products. Maize has attained an important position as industrial crop because 83 per cent of its produce are used in starch and feed industries. Maize is being cultivated in an area of 8.69 million ha in India with the production of 21.81 million tones and productivity of 2509 kg/ha. Maize productivity in peninsular India is severely limited on account of foliar diseases. Among the foliar diseases, two rust diseases of maize occur in India. Common rust is caused by the fungus *Puccinia sorghi* occurs more frequently. The polysora rust is caused by *Puccinia polysora* which occurs less frequently. Both diseases can increase in severity rapidly particularly if infection occurs early in the growing season and favourable environmental conditions persists for extended periods of time. Severe infections can impact yield by causing leaf damage leading to defoliation and premature senescence. Further predisposes plants to infection by post flowering stalk rot pathogens. Common rust appears mostly during the *rabi* season only in the states of Bihar and Andhra Pradesh whereas in northern Karnataka and Maharashtra states it appears during *Kharif* in moderate to severe form. In India presence of polysora rust was first confirmed from Tibetan refugees colonies in Mysore district in Karnataka state in 1999. Polysora rust has noticed in southern districts of Karnataka. Cool, moist weather, relative humidity of more than 90 per cent and leaf wetness for long periods favour development of these diseases. The disease development was very much favoured by maximum temperature (27-30°C), minimum temperature (18-20°C), relative humidity (>90 %) and excessive rainfall during August. Relative humidity showed positive correlation while maximum and minimum temperature showed negative correlation with disease severity. Rust incidence increased on crop sown later than first week of August. Peak rust incidence noticed in October. The most susceptible stage of the crop by rust is 55-60 days that coincides with flowering stage. Yield losses in tolerant and susceptible cultivars were 16.5 and 33.7 per cent. Tebuconozole 250EC @ 0.1 per cent sprayed twice at 35 and 50 days after sowing found very effective in controlling both common rust and polysora rust diseases and increased grain yield followed by Propiconazole 25EC, Azoxystrobin 18.23% + Difenconazole 11.4%, Trifloxystrobin 25% + Tebuconazole 50%, Difenconazole 25EC and Hexaconazole 5EC. Among the Indigenous Technology Knowledges tested, Jeevamruta @ 20 per cent concentration caused significantly less per cent uredospore germination followed by Panchyagavya @ 20 per cent. Host resistance offers the best control measure. The non-specific or quantitative type of resistance is effective and is relatively easy to incorporate into cultivars through recurrent selection. New plantings should not be made adjacent to older infected maize fields. Foliar sprays with fungicides provide an effective control and can be applied when economically feasible.

I (S21) 06: Rust Resistance-Role of wild wheat and its impact

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To combat food supply of burgeoning world population with fixed land and water resources, food production will have to be met by increasing productivity. Wheat productivity is constantly challenged by ever evolving biotic and abiotic stresses and consistent effort is required to combat these stresses. Among the biotic stresses' rusts with its three major types: leaf rust caused by *Puccinia triticina* Eriks, stripe rust caused by *Puccinia striiformis* Pers. f. sp. *tritici* and stem rust caused by *Puccinia graminis* Westend f. sp. *tritici* are major culprit in wheat yield reduction worldwide. Low diversity of cultivated wheat gene pool cannot withstand ever evolving pressure of these rust pathogens. So, there is need to sneak into wheat's close and distant relatives to identify new sources of resistance in order to compete with rust pathogens. Genetic diversity for rust resistance can be augmented by exploiting the primary, secondary and tertiary gene pools of wheat. Primary gene pool with progenitors of cultivated wheat can be readily hybridized with wheat due to common genome with wheat and is more easily available resource for rust resistance. The secondary gene pool consists of *Tritcum* and *Aegilops* species with at least one genome in common or partially common with wheat. These species can be intercrossed but only recombination between homologous chromosomes is possible while transfer from non-homologous genome require special cytogenetic manipulations. *Aegilops* in this pool is one of the largest and most widely exploited species for resistance genes with six different genomes as C, D, M, N, S and U and 22 species of which 10 are diploid, 10 tetraploid and 2 are hexaploid. Tertiary gene pool includes more distantly related species whose chromosomes will not recombine with those of wheat and special chromosomal manipulation are required to transfer resistance genes. In this pool there are 325 species, of which 250 are perennials and rest are annuals. Ease of hybridization and reduced linkage drag make introgression from species in the primary gene pool preferred by wheat breeders to incorporate new alleles in their breeding programs. Of the designated rust resistance genes more than 30 were derived from progenitor species alongwith large number of undesignated genes. Species in the secondary and tertiary gene pools also constitute an important reservoir of genetic variability as more distant from wheat the relative is, the more likely it is to have genes new unique gene to enrich gene pool of wheat. More than 50 designated rust resistance were from non-progenitor species. With such a huge contribution towards rust resistance the wild relatives of wheat had great role in subsiding the rust pathogens thus having a major role in sustaining productivity. With the development of next-generation sequencing technologies and sequencing of wild species, mapping and cloning of these genes has become feasible and relatively cost-effective. Though a large genetic resource has already been exploited but still lot remain unexploited and will continue to provide a support system to wheat productivity.

I (S21) 07: Stripe rust of wheat: Threat and preparedness in North Western India

P.P.S. Pannu and Parminder Singh Tak

Wheat is an important crop in India, mainly concentrated in indo-gangetic plains. Its yield is influenced by biotic and abiotic factors. Among biotic constraints stripe rust also known as yellow rust caused by a biotrophic fungus *Puccinia striiformis* f.sp. *tritici* (*Pst*) is a major constraint in wheat cultivation world over. The pathogen has been found to be highly variable, capable to adapt to wide range of habitats and possess the ability to spread across continents through wind currents. Himalayas have been considered to be the cradle for emergence and spread of new races of the fungus due to genetic recombinations on alternate host *Berberis* spp. However, in the absence of alternate host under Indian conditions, mutagenesis and somatic hybridization have been found to play an important role in the development of new races and frequent breakdown of resiatances especially in NWPZ. Since, the inception of dwarf wheat germplasm in India during 1966, the pathogen has been kept at bay through deployment of resistant *R* genes like *Yr2* and *Yr9* before their knockdown by *Pst* pathotype 47S102 in 1982 and 46S119 in 1996, respectively. PBW 343 released in 1995 carried resistance to *Yr9 and Yr27* virulence, is the most successful example of use of genetics to control stripe rust in time and space. At a single point of time, cultivars carrying these two *R* genes were resistant to predominant pathotype 46S119 and occupied more than 70 per cent area in NWPZ. As expected under 'boom and bust cycle' the single point mutation in *Avr* gene of the *Pst* resulted in emergence of new race 78S84 (virulent on *Yr9* and *Yr27)* in 2001. It possessed ability to withstand warm temperatures and thus prolonged infectious period i.e. till March, resulted in wide spread occurrence of stripe rust in severe forms in Punjab, Jammu and Kashmir, Himachal Pradesh and Uttar Pradesh during 2008 to 2011 causing losses of more than 39 million US dollar. Co-evolution of *Puccinia striiformis* fsp. *tritici* with resistant wheat cultivars released from time to time is a cause of concern for breeders and a threat perception not to be taken lightly. Continuous monitoring of new virulences like recently detected 238S119, mining of resistance genes against new races, robust screening of germplasm, exploring cultural and phytochemical based management practices can keep the country's food security intact. Out of more than 70 *R* genes identified so far, *Yr5, Yr10, Yr11, Yr12, Yr13, Yr14, Yr15, Yr16,Yr26, Yr36, Yr46, Yrsk* are still effective and can be introgressed into high yielding cultivars to genetically tackle the disease threat. Recently released wheat varieties like HD 2967, HD 3086, UP 2338, *Unnat* PBW550, PBW752, PBW725, DBW88, WH1105, PBW660 etc. carry such resistance to known *Pst* pathotypes, is the most economical, effective and environment-friendly method to reduce the disease development. Deployment of this varietal diversity especially in disease prone sub-mountainous areas of NWPZ and in NWHZ and avoiding sowing of susceptible and un-recommended varieties can help to check initial foci of stripe rust during December - January despite weather remaining favourable for its development and spread. The pathogen survives in adjoining Himalayan ranges at different altitudes on off-season crop and volunteer plants and serve as source of primary inoculum for wheat crop in plains. Off-season surveys in lesser Himalayas from April to October are being done to predict the time of onset and frequency of initial infection foci in main season wheat crop in NWPZ. Early (October) sowing in sub-mountainous regions can also be avoided to decreases stripe rust as uredospore bunches falling early in the season will miss the crop or small crop canopy will have low probability of inoculum materialising to successful infection. Intensive monitoring of off-season crop in hilly areas and main season crop in NWPZ December-January to detect initial foci and their timely management by spot application of fungicides and issuing advisories based on weather forecasting and prevalent genotypes is a way forward to alleviate the threat of yellow rust.

Oral Papers

O (S21) 08: Exploring and harnessing rust pathogen effectors for rust resistance in cereals

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Rust diseases are major constraints to wheat (*Triticum* spp.) production worldwide. The pathogens causing black (stem) rust (*Puccinia graminis* Pers. f. sp. *tritici*), brown (leaf) rust (*P. triticina* Erikss. & Henn.) and stripe (yellow) rust (*P. striiformis* Westend f. sp. *tritici*) are obligate biotrophic, macrocyclic and heteroecious fungi. During their interactions with plants, rust and other filamentous fungi secrete thousands of secreted proteins, probably containing effectors, in to the plant cell. Effectors are generally small, cysteine rich, secretory proteins (<300 amino acids) harboring a canonical N terminal signal peptide. Effectors manipulate host physiology or suppress host immunity to help pathogen in establishing a successful infection. Studies to interpret the molecular basis of host-pathogen interaction has augmented during the last decade as a consequence of ever-increasing number of available fungal and plant genomes data. Moreover, advances in high-throughput sequencing technology, transcriptome analysis and integrated bioinformatics tools have offered new opportunities for identification and characterization of effector genes involved in pathogenicity. Certain effector molecules also called avirulence effector (Avr-effector) activate cognate cytosolic R-proteins of the NBS–LRR class. The interaction of Avr-effectors and R-proteins leads to disease resistance through effector triggered immunity in resistant hosts. The understanding of such mechanisms of interactions between R-proteins and Avr-effectors, and functional profiling of Avr-effector genes have been employed by breeders for identification, functional characterization and cloning of *R-genes*. Effectors are now being considered as the functional markers to be used in marker assisted selections for resistance breeding. They could also be used as molecular probes to identify *S*-genes and to decipher the molecular basis of plant processes other than defense responses. These developments in effector biology promise to expand the mechanistic detail of interaction of pathogen effectors with plant R-proteins and to apprise future research strategies for effective and sustainable rust management.

O (S21) 09: Current status of stripe rust of wheat in Haryana and assessment of avoidable yield loss

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Wheat offers more calories and protein in the diet than any other crop. Among biotic and abiotic stresses, stripe rust (yellow rust) incited by *Puccinia striiformis* f. sp. *tritici* proves major bottleneck than brown and black rust. It can infect at any stage from two-leaf (seedling) to milk development. Maximum stripe rust severity was recorded in Yamunanagar (28.57%) followed by Ambala (23.33%) and least was observed in Fatehabad (5%).Maximum terminal disease severity was expressed in WH 147 (100%) and HD 2967(100%) in seedling and tillering stage disease appearance followed by stem elongation (96.66% and 93.33%) and least disease severity was observed on milk development i.e. 43.33 and 36.66 per cent, respectively.Whereas, it varied 30 to 3.33 per cent in WH 1105. Maximum yield loss was exhibited by WH 147 (73.46%) followed by HS2967 (68.4%) and least was recorded in WH1105 (23.56%) when disease appeared at seedling stage. With the increase in plant age there was decrease in disease severity and minimum yield loss was recorded at milk development stage (4.34%, 3.84% and 2.14%), respectively. Most widely grown and maximum area occupying variety HD2967, yield loss was 3.84 to 68.4 per cent.

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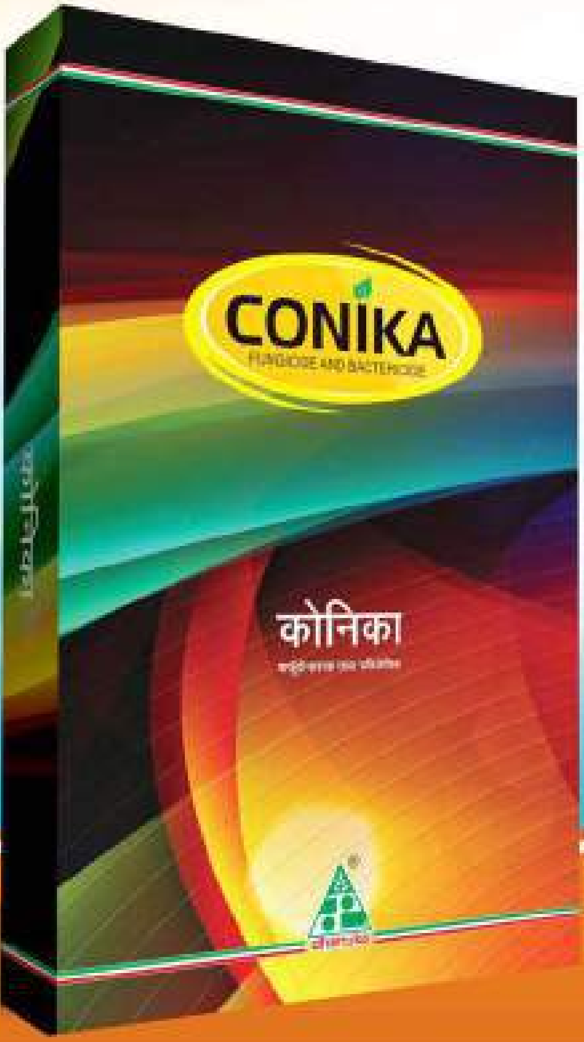
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