Indian Phytopathological Society, New Delhi

NATIONAL e-CONFERENCE

Plant Health and Food Security :
Challenges and Opportunities

March 25-27, 2021

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Citation: B.N. Chakraborty, M.S. Saharan, K.B. Pun, S.C. Dubey, Kalyan K. Mondal, Robin Gogoi, Malkhan S. Gurjar,Rashmi Aggarwal and P.K. Chakrabarty (eds.) 2021, IPS NATIONAL e-CONFERENCE on Plant Health and Food Security : Challenges and Opportunities, March 25-27, 2021 New Delhi, India pp.

Published by:
Indian Phytopathological Society
Division of Plant Pathology
Indian Agricultural Research Institute
New Delhi-110012, India

Edited and Compiled by:
B.N. Chakraborty
M.S. Saharan
K.B. Pun
S.C. Dubey
Kalyan K. Mondal
Robin Gogoi
Malkhan S. Gurjar
Rashmi Aggarwal
P.K. Chakrabarty

Acknowledgement

The financial assistance received from Research and Development Fund of National Bank for Agriculture and Rural Development (NABARD) towards publication of journal/printing of proceedings of the Conference is gratefully acknowledged

Printed at :
Alpha Printographics (India), Naraina, New Delhi 110028
M: 9999039940, 9811199620

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National e-Conference on

Plant Health and Food Security : Challenges and Opportunities

March 25-27, 2021

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All correspondence for the National Conference and Annual Meeting related matters may be addressed to:
Dr. Robin Gogoi, Organizing Secretary, Indian Phytopathological Society, Division of Plant Pathology, IARI, New Delhi 110012, India; E-mail : ipsdis@yahoo.com

PREFACE


Robin Gogoi


Kalyan K. Mondal


Malkhan S. Gurjar

The growing global population demands more food production. And more food production necessitates more acreage under crop production, which is not possible due to the global industrialization. Thus, to feed the growing population we need to reduce the crop losses caused by biotic and abiotic threats. Most of the abiotic threats like flood, draught is very uncertain and difficult to manage. However, crop losses caused by biotic threats including plant diseases, pests are manageable with timely adoption of appropriate control measures. Thus, the required food production can only be achieved to a greater extent through minimising the losses due to biotic factors. To address this challenges, the plant protectionists, globally, engage to devise novel low-input management options for biotic threats. Indian Phytopathological Society since time immemorial has addressed several issues and updates on this fronts of plant protection. The present national e-conference is one of that kind that primarily focused to discuss and deliberate on research & development in Plant protection as a whole and to formulate the road map for future towards meeting the food security.

The proceeding of the abstracts to be presented in this e-conference (w.e.f 25-27 March, 2021) is compiled as "e-Proceedings Book". This compilation broadly centred to 10 thematic areas of the e-conference. The total expert deliberations in the e-conference are prioritised as Plenary lectures (2), Keynote lectures (31), Invited lectures (13), Oral (53) and poster (180) presentations. Beside these, abstracts received for Award lectures (7), contests for Prof. MJ Narasimhan Academic Merit Award (16) and APS-IPS Travel Grant sponsorship Award (5) have also been included. We tried our best to bring this compilation errorless and timely. However, we apologise for any inadvertent mistakes/typo errors which was unavoidable considering the volume of the contents. Our heartfelt thanks to the dedicated team comprising of Prof. BN Chakraborty, Dr. SC Dubey and Dr. MS Saharan (Chairs of Publication committee), Dr. KS Hooda and Dr. MS Yadav (Chairs of Poster committee) for this compilation. We are thankful to Dr.Rashmi Aggarwal, Dean & Jt. Director (Ed) for her key advices and supervision as Chairperson, Technical committee during the compilation. Our thanks to the EC members, IPS for their time to time inputs and valuable suggestions. Lastly, but not least our thanks are due to IPS Secretariat for extending tireless service all throughout.

We wish that this compilation would serve as a valuable reference for Scientists working on Plant Protection.

Robin Gogoi (Organizing Secretary, e-conference)
Kalyan K Mondal (Co-Organizing Secretary, e-conference)
Malkhan S. Gurjar (Convener, e-conference)

March 25, 2021, New Delhi

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त्रिलोचन महापात्र, पीएच.डी.
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TRILOCHAN MOHAPATRA, Ph.D.
SECRETARY & DIRECTOR GENERAL

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कृषि एवं किसान कल्याण मंत्रालय, कृषि भवन, नई दिल्ली 110 001
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AND
INDIAN COUNCIL OF AGRICULTURAL RESEARCH
MINISTRY OF AGRICULTURE AND FARMERS WELFARE
KRISHI BHAVAN, NEW DELHI 110 001
Tel.: 23382629; 23386711 Fax: 91-11-23384773
E-mail: dg.icar@nic.in

Message

I am happy to note that the Indian Phytopathological Society (IPS) Society, IARI, New Delhi is organizing the National e-Conference on “Plant Health and Food Security: Challenges and Opportunities” during March 25-27, 2021. The conference is focusing on broad thematic area to deliberate new challenges and opportunities in our country in relation to crop health protection. The Indian Phytopathological Society (IPS), IARI, New Delhi is one of the pioneering professional society engaged in coordination and dissemination of crop diseases management strategies in our country.

I congratulate the organizers for their systematic planning of the virtual conference and covering various areas on molecular breeding, marker assisted selection, molecular biology, host-pathogen interaction studies, pathogen biology, patho-genomics, eco-friendly management of emerging pathogens and exploitation of biomolecules. I hope this e-Conference will bring out valuable suggestions to resolve various issues for agricultural development.

I wish the National e-Conference a great success.

(T. Mohapatra)

Date: 22nd March 2021
Place: New Delhi-110 001

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Indian Council of Agricultural Research
Ministry of Agriculture and Farmers Welfare
Govt. of India, Krishi Bhavan
New Delhi 110001, India

डॉ. तिलक राज शर्मा
उप महानिदेशक (फसल विज्ञान)

Dr. T. R. Sharma, Ph.D
FNA, FASc, FNAAS, FNASc, JC Bose National Fellow
Deputy Director General (Crop Science)

MESSAGE

Plant health has got renewed much attention in all the nations for global food security. FAO estimates that up to 40 percent of food crops are lost to plant pests and diseases annually. Plant health is increasingly under continuous threat. Climate change and human activities have altered ecosystems, reducing biodiversity and creating new niches where pests can thrive. Plant pathogens are the biggest threat to the global food security. The diseases caused by fungal, bacterial, viral and phytoplasma pathogens are great concern in today's agriculture. Food and nutritional security of a nation can be achieved through the production of healthy crops. Healthy food is the most important prerequisite to ensure food and nutritional security and to boost immunity. Though the tools in plant protection arsenal are diverse and developing, crop losses still occur before and after harvest. To address such issues, meeting and conferences involving researchers, academia, entrepreneurs, farmers and policy makers are organized.

I am pleased to know that Indian Phytopathological Society (IPS), New Delhi, the third largest society in the field of plant pathology with active members from fifty plus countries is organizing a National e-Conference 2021 on the very pertinent issue "**Plant Health and Food Security: Challenges and Opportunities**" during **March 25-27, 2021**. I believe that the conference will attempt to cover all important aspects of plant health through its well-designed 10 thematic sessions over three days discussion. The galaxy of learned delegates will deliberate on the challenges and opportunities in plant health and suggest way forward for future course of action. The outcomes of the event will provide a useful document to the stakeholders for future initiatives in protecting plant health.

I wish this event a great success in all the aspects.

(T.R. Sharma)

E-mail: ddgcs.icar@nic.in Phone: 91-11-23382545 Fax: 91-11-23097003

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कृषि एवं किसान कल्याण मंत्रालय, भारत सरकार
कृषि अनुसंधान भवन I, पूसा, नई दिल्ली 110 012
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डॉ. पी.के. चक्रबर्ती
सदस्य (पौध विज्ञान)
Dr. P.K. Chakrabarty ARS, *FNAAS*
Member (Plant sciences)

March 23, 2021

Message

International year of Plant health 2020 dawned upon the worldwith perils on human health due to invasion of SARS corona virus. Notwithstanding the serious challenge ofCovid pandemic, Plant pathologists, besides other crops crop Scientists in the country last year continued to protect crops from losses due to diseases and insect pests. This is evident from the estimated all time highfood grains production of 297million tons (1.33 mtover 2019-20) and horticulture production of326.58 mt (5.81 mt over 2019-20 crop year) during 2020-21. Increase in crop production results from amelioration of biotic stresses besides improvement of crop productivity through genetic gains. Despite incidental increase in food production, it is needless to emphasize that increased globalisation and climate change have mounted greater challenge to sustain food security due to new, emerging and invasive diseases and insect pests.

I am happy that the Indian Phytopathological Society (IPS) is organizing aNational e-Conference on "Plant Health and Food Security:Challenges and Opportunities" in IARI, New Delhifrom March 25-27, 2021 to mark 74 years of service to the science at national and international level. The Conference will benefit from the new normal set by the pandemic to achieve and sustain food production and livelihood security. Besides, deliberating on usual approaches of disease management through exploitation of host resistance, molecular manipulation and eco-friendly and chemical management, conference will devote sessions on next generation pesticides, sensor based diagnosis, plant quarantine and agro-terrorism, etc. An added interest is due to a session on Impact of Covid-19 on Indian agriculture, export-import hindrance, labour crisisand stakeholders meet on plant protection issues and policies.

The conference is aimed to provide an ideal opportunity for the interaction of scientists/policy makers/corporate sectors towards developing a holistically integrated future strategies envisaging plant disease management to ensure higher productivity and sustainability.

I wish the first e-Annual IPS conference on Plant Pathology a grand success.

P. K. Chakrabarty

कृषि अनुसंधान भवन -I, पूसा, नई दिल्ली-110012 | Krishi Anusandhan Bhawan-I, Pusa, New Delhi-110 012
Tel: 011-25840017; Email: member.ps@asrb.org.in

भा.कृ.अ.प. – भारतीय कृषि अनुसंधान संस्थान, नई दिल्ली–110012 (भारत)
ICAR - INDIAN AGRICULTURAL RESEARCH INSTITUTE
(A DEEMED TO BE UNIVERSITY UNDER SECTION 3 OF UGC ACT 1956)
NEW DELHI-110012 (INDIA)

डॉ. अशोक कुमार सिंह
निदेशक
Dr. Ashok Kumar Singh
Director

Phones : 011-2584 2367, 2584 3375
Fax : 011-2584 6420
E-mail : director@iari.res.in
Personal : aks_gene@yahoo.com
Website : www.iari.res.in

MESSAGE

I am delighted that the Indian Phytopathological Society (IPS), Indian Council of Agriculture Research and Indian Agricultural Research Institute, are jointly organizing a National e-Conference on "Plant Health and Food Security: Challenges and Opportunities" during 25-27 March, 2021 venue at ICAR-Indian Agricultural Research Institute, New Delhi-110012.

Despite, the challenges posed by COVID-19 Pandemic, we could get bumper food grain production of 295 million tons, the credit goes to hard work of farmers and technology backup provided by the National Agricultural Research System (NARS). In order to double the farmers' income, our agri-export earning has to double, which requires focus on meeting international quality standards. Quality of produce is directly affected by different biotic stresses, pest and diseases. Although breeding for resistance to biotic and abiotic stresses are economically viable and environmentally safe method for combating major pests and pathogens, frequent breakdown of resistance among the released varieties due to emergence of new races and pathotypes pose major threat on the crop production. Some of the bio-molecules have the economic significance in terms of export, quality parameters and domestic consumption. Therefore, systematic and strategic researches are required to address all these issues.

This National e-Conference has broad thematic area to deliberate the challenges and opportunities pertaining to with Plant Health and Food Security in the country. I congratulate the organizers for meticulous planning with focused discussions on resistance breeding, MAS, virulence analysis of pathogens, Eco-friendly management of the pathogens, biomolecules, molecular basis of host-pathogen interactions, patho-genomics, genetic analysis of pathogens, plant quarantine and the importance of delivery systems, export-import hindrance in addition to deliberation on impact of COVID-19 on Indian Agriculture. The overview of the conference by plenary lectures and in-depth analysis thorough the Keynote and lead papers will benefit the scientists, farmers, industrialists and policy makers in the country.

I wish the organizers for a grand success of the National e-Conference which is organized by the premier agricultural research institute.

(A. K. Singh)

भारतीय कृषि अनुसंधान परिषद
Indian Council of Agricultural Research
Krishi Bhawan, New Delhi 110 001, India

डॉ. सुनील चन्द्र दुबे
Dr. S.C. Dubey
Assistant Director General
(Plant Protection and Biosafety)

☎: 91-11-23384414
Fax No.: 91-11-23384414
E-mail: adgpp.icar@nic.in;
sunil.dubey@icar.gov.in

Message

I am delighted to know that the Indian Phytopathological Society (IPS) is Organizing National e-Conference on Plant Health and Food Security: Challenges and Opportunities from March 25-27, 2021 at ICAR-Indian Agricultural Research Institute, New Delhi, India.

Plant diseases pose a threat to food security as they cause loss to crop yield which ultimately reduces the availability and increases the cost of food. A significant amount of food currently grown worldwide is lost due to diseases despite great advancement in agriculture technologies. A range of variables affect plant health including environment and diseases. At present, changing climate adversely affects plant health and food security including nutritional security. Under the present COVID-19 pandemic situation, all of us realized the importance of quality and healthy food to ensure health and better immunity to fight the disease. This conference has a topic which is in keeping with the current time and can appropriately address the various issues related to plant health and food security.

I am sure the conference would 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 plant health and food sustainability. I hope the Conference would result in useful recommendations and formulation of sound strategies required to improve plant health and in achieving food and nutritional security.

I wish the conference a great success.

S.Dubey

(S.C. Dubey)

Bushan L. Jalali
F.N.A.Sc.,F.N.A.A.S.
Formerly Director of Research-HAU
Hisar, Haryana

Message

I am happy that Indian Phytopathological Society (IPS) is, this time, organizing the National e-Conference on a pivotal thematic area of ***"Plant Health and Food Security: Challenges and Opportunities"*** on March 25-27,2021 atICAR-Indian Agricultural Research Institute, New Delhi.

Theyear 2020 has been the most tumultuous, and the most definingyear of our life time, because of the COVID pandemic. With this scenario in view, challenges before us have become formidable. Therefore, pragmatic and sustainable crop health management strategies warrants a new paradigm shift. With changing cropping systems coupled with impact of climate change on crop disease manifestation needs appropriate course corrections and subsequent refinements for holistic management of crop health. Over the years, appearance of new exotic pathogens, has taken a central stage in several agro-ecological niches. Systematic research efforts, therefore, need to be embarked upon to unravel the genetic structure of pathogen population, which is pivotal for resistance breeding programmes.

The potential of biotechnology and nanotechnology needs to be further harnessed in phytopathological researches. For this, necessary up-scaling of human resource development strategies need to be put in place.

Hopefully, some tangible recommendations should emanate from the deliberations of this national convention, to address major challenges ahead.

I wish the conference all the best.

Stay blessed.

BL Jalali

(B.L. Jalali)

Prof. C. MANOHARACHARY
M.Sc., Ph.D., F.N.A.Sc., F.N.A.A.S., F.B.S., F.P.S.I., F.A.P.S., F.M.SC, FIMS
Hon. NASI Senior Scientist
Coordinator (UGC SAP), Dean, Development & UGC Affairs
Co-ordinator, AICOPTAX (MOEF)
Vice-Chancellor, Oriental University (Indore, MP)
Professor, Emeritus (CSIR, UGC)

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DEPARTMENT OF BOTANY
OSMANIA UNIVERSITY
Hyderabad, Telangana, India-007
Phone : 040-27682244
(M) : 09391164243
E-Mail : cmchary@rediffmail.com
cmchary@gmail.com

MESSAGE

Agriculture is important in India, as the majority of our rural population belong to farmers community. Around 50% of Indian population is dependent on Agriculture. Agriculture continues to play an important role to meet sustained food security to the growing population. Microbial diversity is an unseen national resource that deserves greater attention. The agriculturally important microbes include bacteria, mycoplasma, viruses, phytoplasma, fungi and also mycorrhizal fungi. Most of the microbes and fungi are involved in organic matter decomposition, N_2-fixation, solubilization of several major and minor nutrients. Microbes also play an important role in maintaining soil structure and soil health.

The absence of chlorophyll has enforced bacteria, viruses and fungi to become parasites and have become responsible in the causation of diseases on crop plants and forest plants. Around 30-40% crop losses are incurring every year due to pathogenic microbes and fungi. Products of microbial origin can be integrated to curtail part of the energy intensive supplies like chemical fertilizers and pesticides. 1/3 rd of the global diversity of microbes and fungi occur in India. India possess immense richness of agri-diversity microbes and fungi contribute towards improved plant health and higher crop yield by production of growth stimulators such as plant hormones, vitamins and other bio-stimulants and also serve as biocontrol agents of plant diseases.

I appreciate the Indian Phytopathological Society, IARI, New Delhi for their concerted efforts not only in disseminating knowledge pertaining to plant protection for the sustenance of agriculture and food security but also for their efforts to reach the farmer with innovation besides training extension workers and HRD in plant pathology. I congratulate the IPS for selecting a topic which is of much relevance to our agriculture based country. I wish a grand success and fruitful deliberations.

Thanks

19/02/2021

Prof.C. Manoharachary

PANJAB UNIVERSITY
CHANDIGARH-160014

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

Dated: February15, 2021

Message

Plant pathogens exert considerable strain on agricultural production and threaten global food security. Their effects range from mild symptoms to catastrophes when the food crops planted in vast stretches are attacked and destroyed. Enormous food losses exacerbate the current deficit of food supply because of which at least 800 million people are not being adequately fed world over. Complete eradication of plant pathogens is difficult because their populations are variable in time, space and genotype. Gradually they evolve, often overcoming the resistance. Recent challenges emerged from climate change have further complicated the problems by affecting complex biological interaction between hosts and the pathogens. In order to reduce the yield losses, it is always necessary to define the problem and then seek the solutions. At biological level, it is essential to accurately identify the causal organisms, severity of the disease, virulence mechanism and their effect on the yield. Most of the diseases can be minimised by the reduction of pathogen inoculums, inhibition of virulence mechanisms and application of genetic diversity of crops. Role of transgenic modification with such endeavours can add to making it possible to double our production by 2050 to meet the needs of ever increasing food requirements of our people increasing at the present rate.

It gives me pleasure to send my good wishes for the success of this National e-Conference with the theme, "*Plant Health and Food Security- Challenges and Opportunities*" being organised by the Indian Phytopathological Society, during March 25-27, 2021 at New Delhi.

S.S. Chahal

(S. S. Chahal)

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

भा.कृ.अनु.प.-भारतीय कृषि अनुसंधान संस्थान नई दिल्ली-110012 (भारत)
ICAR-INDIAN AGRICULTURAL RESEARCH INSTITUTE
NEW DELHI-110012 (INDIA)

R.K. Jain, FNAAS
Emeritus Scientist (ICAR) &
Former Dean (IARI)

Division of Plant Pathology
New Delhi-110012

Date: 20.2.2021

Message

I am pleased to learn that the Indian Phytopathological Society (IPS) is organizing National e-Conference on *Plant Health and Food Security: Challenges and Opportunities*. The theme of the Conference aligns completely with the United Nations sustainable development goals (SDGs), especially SDG 1 and 2. Since the year 2021 has been declared as the International Year of Fruits and Vegetables, it would be more meaningful to lay more emphasis on the health of fruits and vegetables. Production of quality (virus free and true to its type) planting material to facilitate diversification should draw more attention.

IPS, which is more than 74 years old now, has been nurtured by several stalwarts in the field of plant protection. I am confident that the Society would continue to serve the stakeholders by developing green options to produce more from less for more (MLM).

(R.K. Jain)

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

Dr.T.S. Thind
Ph.D.,PDF(France),FulbrightFellow
HonoraryAdjunctProfessor

Message

I am pleased to know that the Indian Phytopathological Society is organizing a national e-conference on “Plant Health and Food Security: Challenges and Opportunities” during 25-27 March, 2021 at New Delhi to mark 74 years of its glorious service to the science of plant pathology and related disciplines. Theme of the conference is pertinent to the role of improved plant health in achieving food security goals in the wake of many challenges including the one linked to Covid-19 pandemic. The IPS in the past years has been regularly providing such platforms to address diverse plant health issues facing agriculture.

We need to produce more food per unit area for feeding rapidly increasing human population. The domain of plant pathology can play a significant role in meeting food security needs through development of affordable solutions for debilitating plant diseases. It holds promise to ensure quality produce by containing microbial invasions and toxin contamination in food crops. The present day agriculture is facing many challenges and one among the most serious challenges is the changing climate. We ought to develop technologies to cope with weather fluctuations that could affect the survival, distribution and multiplication of plant pathogens. We need to act ahead of pathogens in our efforts to ensure normal crop yields.

There is a need to develop a holistic approach in managing plant health problems. Crop protection has come a long way from the predominantly chemical-based approaches to more environment friendly technologies. Development of bio-intensive modules needs to be prioritized for managing pests and pathogens. Use of cutting-edge biotechnologies such as CRISPR gene editing systems and RNA interference can be explored to develop crop varieties having resistance to specific new pathogen races. Decision support systems should be developed for important diseases for their timely management. We need to adopt information technology at a larger scale to facilitate quick dissemination of new crop protection solutions.

I am sure that this national virtual conference will provide an ideal platform to plant pathologists to interact on the emerging issues related to crop health in the present day agriculture. I hope that the conference deliberations will come up with novel ideas for future research on plant diseases that would eventually help in the improvement of food production systems.

I wish the organizers and participants a great success and fruitful deliberations.

TSThind

Dated: 13.02.2021

(TS Thind)

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

Mob. 9838932188, 9532230355
E mail - misra_a_k@yahoo.co.in
Res: 4/1081, Vikas Nagar,
Lucknow - 226 022 (U.P.), India

Message

I am happy that Indian Phytopathological Society, a premier society of the world, has planned to bring the national plant pathologists on a common platform by organising National e-Conference (virtual) on March 25-27, 2021, at New Delhi. During the period of 74 years, since its inception of the Indian Phytopathological Society, it has successfully organised national and international conferences. In the history of IPS it will be the first experience at national level to organise e-Annual meeting and National Conference in the Covid-19 period and all the members will be having a unique experience. The conference theme is rightly titled as “Plant Health and Food Security : Challenges and Opportunities”. Plant pathologists have great responsibility and role to play in achieving this goal and fight against hunger and malnutrition and ensure food security and health to our country men. It is also the duty of plant pathologists to boost production by protecting our crops from various diseases caused by various pathogens and minimize losses of pre and post harvest stages. Human population is growing and Honourable Prime Minister has fixed national priority for doubling the food production. This we have to achieve with the same land and resources. If we success in growing crops minimizing diseases and restrict our post harvest losses, the target can be achieved easily. Hence, growing healthy crop with minimum field diseases and reducing post harvest losses is the priority of plant pathologists to keep pace with growing human population and provide them enough calories of food for their healthy life. The society is having nearly 2,000 members in more than 50 countries. It includes research scientists, teachers, extension professionals, students, technicians, agricultural field representatives and pest management 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 ten Thematic Sessions with plenary lectures, keynote & invited lectures, contributory oral papers, contributory posters, invited corporate lectures, scientists-industries-farmers interface, which will be very informative, useful and interesting for the participants/delegates of the conference.

I am sure the conference will focus on important areas and come out with practical implementable suggestions and recommendations.

I wish the mega event of e-conference a grand success.

Lucknow
Dated : 10.02.2021

(A.K. Misra)

Indian Phytopathological Society
(Regn. No. S399 of 1949-50 under Societies Registraion Act XXI of 1860)
Division of Plant Pathology
Indian Agricultural Research Institute
New Delhi-110 012, India
Tele (Off) : 011-25840023
website: www.ipsdis.org

Professor B.N.Chakraborty
FNAAS, FNBS, FRSC (London), FAScT,
FPSI, FISMPP, FISPC,FMSI,FIMS
Former President, IPS

Message

It is a matter of great pleasure to note that Indian Phytopathological Society, one of the oldest professional and prestigious society is organizing National e-conference (virtual) on **"Plant Health and Food Security: Challenges and Opportunities"**during March 25-27, 2021 to mark 74 years of service to the Science at National and International level.

Low crop yields are common in many developing countries and improved productivity is vital for reducing rural poverty and increasing food security. Whilst the causes of low productivity are complex, one major contributory factor is crop losses due to plant health problems associated with pest and pathogen constraints. Often accurate information on the extent of these losses is missing but estimates of 30–40% loss annually from "field to fork" are common. Any future solution regarding improved global food security must address these losses and that means improving plant health.

The global population crosses 7.7 billion with the loss of biodiversity, increasing pressure on food, water, and energy resources. The food sector is increasingly turning toward sustainability issues. A sustainable food system should provide sufficient, nutritious food for all within limited natural resources. Plant-based food and proteins are a recent, growing trend setting out to contribute to this challenge. However, food industry stakeholders need to be aware of the challenges and opportunities. The several changes happening in environmental, social, economic, technological and geopolitical spheres of our society result in countless risks, challenges and opportunities for human development.

I wish the success of this National e-conference in this specific area with deliberation and interaction among scientists, research scholars and students as well as fruitful recommendations for the benefit of farmers.

(B.N.Chakraborty)

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

Professor & Head (Retd.)
Department of Plant Pathology
B.A.College of Agriculture, AAU
Anand 388 110, Gujarat, India
E_mail: pande56@gmail.com
Cell: 09925952458

Message

It is a matter of great pleasure that *Indian Phytopathological Society*, New Delhi is organizing its **National e-Conference** on***Plant Health and Food Security: Challenges and Opportunities***on

March 25-27, 2021in collaboration with ICAR-Indian Agricultural Research Institute, New Delhi;

Indian Council of Agricultural Research, New Delhi,at Division of Plant Pathology, ICAR- IARI, New Delhi, under the COVID-19 pandemic. The conference is being organized with theaimto bring the world Plant Pathologists/Microbiologists/Biotechnologists, etc. on a common platform to discuss the issues ofplant health i.e. biotic and abiotic stresses related to plant pathogens, poor soil health and extreme weatherfactors which pose the threats to global agriculture and to draw a road map to combat the stresses for achieving global food and livelihood security. The Conference is planned to hold the sessions on ten important theme areas encompassing 'Plant disease resistance; Eco-friendly disease management; Next generation pesticides and application; Host-pathogen interaction and genomics of plant pathogens; Genetic variability and diagnostics; Plant quarantine; Microbial biodiversity; Impact of COVID -19 on Indian agriculture and Stakeholders meet on plant protection issues. The scientists all over the globe have worked extensively to develop various Eco-friendly, efficienttechnologies for sustainable management of the plant diseases 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 to combat them.I express greetings and congratulations to the office bearers, the members,etc. of the society for their dedication to achieve the mandate of the society, even under the COVID-19 pandemic.

The planning of the e-conference is quite good to 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 Health management to draw 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. T.R. Sharma, DDG, Crops, ICAR, for their encouragement and support to organize the Conference.

I take this opportunity to thank and congratulate Dr. P.K. Chakrabarty, President, IPS; Dr. Pratibha Sharma, President-elect. IPS; Dr. Robin Gogoi, 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.

March 15, 2021

(R. N. Pandey)

DIRECTORATE OF INSTRUCTIONS
निदेशालय शिक्षण
INDIRA GANDHI KRISHI VISHWAVIDYALAYA
इंदिरा गांधी कृषि विश्वविद्यालय
Krishak Nagar, Raipur, 492012 (C.G.)

डॉ. एम.पी. ठाकुर
निदेशक शिक्षण एवं परीक्षा नियंत्रक
पूर्व संचालक, विस्तार एवं अधिष्ठाता
पूर्व अध्यक्ष, अखिल भारतीय पादप रोग विज्ञान समिति, नई दिल्ली

Dr. M.P. Thakur *(FISMPP, FIMS, FISPRD)*
Director Instructions & Controller of Examinations
Former Director, Extension & Dean
Former President, Indian Phytopathological Society, New Delhi

Phone : (O) 91-771-2444105
(R) : 91-771-4043523
email : diigkv@yahoo.com
mp_thakur@yahoo.com
diigkvthesis@gmail.com
Mob : 98261-91749

Message

I am very happy to learn that Indian Phytopathological Society, New Delhi is organizing a 3-days **National Conference** on **Plant Health and Food Security: Challenges and Opportunities** from 25-27th March, 2021 in a virtual mode. Plant health has been an important and emerging issues now to produce more from less land for more in order to feed the rapidly growing population of the world. In 1960s, a ha of land was to feed 2 peoples but now in 2021, a ha of land will have to feed 5 peoples which is a real challenge for ensuring food and nutritional security for the billions of peoples on this universe. A lot of innovations and developments in the field of agriculture, horticulture and allied fields have been taken place in the recent past to enhance the production and protection of crops. With the use of recent production technologies of crops, the problems of biotic and abiotic stresses are also increasing and it needs to be properly addressed or dealt with in a integrated manner taking care of not only the diseases but insects pests, weeds and nutrient deficiencies also. There are several challenges in the successful management of these biotic and abiotic stresses in view of their restricted use now to save the environment from the excessive use of inorganic fertilisers and chemicals pesticides. The problems also lies on promoting the crop production using minimum use of synthetic fertilisers and chemical pesticides. Now, chemical free farming or zero budget farming or organic farming is promoted widely by the policy makers which further poses severe challenges in crop protection as well as in crop production. In view of these challenges, the present National Conference is proposed on the above topic to discuss all these relevant issues to improve plant health and ensuue food security, nutritional security and boost immunity to the mankind against the dreaded diseases.

I compliment the organisers of this National Conference who are providing the plateform to all the young talents, researchers, extension personnel, farmers, industry peoples and other stakeholders to actively take part and come out with the concrete recommendation to address the issues of plant health and food security. I also thank the organisers for compiling all the presentations in the form of Souvenir cum Abstract. I wish the conference a great success.

With best regards,

(M.P.Thakur)
Former President of IPS & Director Instructions

SKN COLLEGE OF AGRICULTURE
(SRI KARAN NARENDRA AGRICULTURE UNIVERSITY)
JOBNER - 303329 DISTT-JAIPUR (RAJ.) INDIA

PROF. PRATIBHA SHARMA
ICAR EMERITUS SCIENTIST
PRESIDENT- ELECT, INDIAN PHYTOPATHOGICAL SOCIETY - NEW DELHI, INDIA

Message

The Indian Phytopathological Society established on 28th February 1947 after successful journey of developments in Plant Pathology is entering into it's 75th year of existence. It had a great privilege and opportunity to be associated with the stalwarts of Plant Pathology through their research and publications. The zonal and annual meetings had always been the platform for bringing out the best potential of our scientific achievements. After successful completion of Zonal online meetings in 2020-2021 we will witness annual meeting of 2021 e-Conference on *Plant Health and Food Security: Challenges and Opportunities* 25- 27 March 2021 another important theme of the conference wisely matched with the United Nations sustainable development goals. I congratulate our Indian Phytopathology team who cooperated whole year online activities finally culminating to annual meet. This conference will come out with the useful recommendations and proceedings which will further help in formulating plant protection strategies I wish this e conference a great success.

(PRATIBHA SHARMA)

Phone & Fax:01425-254022, **Email**: psharma032003@yahoo.co.in

भारतीय कृषि अनुसंधान संस्थान, नई दिल्ली–110012
INDIAN AGRICULTURAL RESEARCH INSTITUTE
(A Deemed to be University Under Section 3 of UGC Act, 1956)
NEW DELHI-110012

डॉ. (श्रीमति) रश्मि अग्रवाल
अधिष्ठाता एवं संयुक्त निदेशक (शिक्षा) – कार्यकारी
Dr. (Mrs.) Rashmi Aggarwal
Dean and Jt. Director (Education) - Acting

MESSAGE

I am happy to know that the Indian Phytopathological Society (IPS) is organizing a National e-Conference on "Plant Health and Food Security: Challenges and Opportunities" during March 25-27, 2021 at ICAR-Indian Agricultural Research Institute, New Delhi-110012.

Rapid food price rises have highlighted serious concerns about food security globally and have had a huge impact on achieving Millennium Development Goal 1. Low crop yields are common in many developing countries and improved productivity is vital to reduce rural poverty and increasing food security. Whilst the causes of low productivity are complex, one major contributory factor is crop losses due to plant health problems. Often accurate information on the extent of these losses is missing but estimates of 30-40% loss annually from "field to fork" are common.

Quality of produce with respect to nutrition is main concern now, which directly gets affected by different biotic stresses, pests and diseases. Although the genetic improvement in crop plants is economically viable and environmentally safe method for combating major pests and pathogens, but breakdown of resistance and appearance of new pathogen races is a major challenge. Another challenge is addressing the plant health problems of smallholder farmers. Without practical plant health information to keep crops healthy, people in many regions cannot tackle the damage that pests cause on their own. Ultimately, this affects the health of their families and communities, and threatens their livelihoods. Providing knowledge on plant health to farmers quite simply changes their lives. Therefore, to address the challenges, systematic and strategic researches are needed. I am sure during this national e-conference extensive deliberations will be done on the challenges and opportunities pertaining to plant health management.

I congratulate the organizers for meticulous planning and focusing discussions on resistance breeding, MAS, virulence analysis of pathogens, Eco-friendly management of the pathogens, biomolecules, molecular basis of host-pathogen interactions, patho-genomics etc., in addition to deliberations on impact of COVID-19 on Indian Agriculture. This will benefit the scientists, farmers, industrialists and policy makers in the country.

I wish the organizers a grand success of the National e-Conference being organized by Indian Phytopathological Society in the Division of Plant Pathology, of the premier agricultural research Institute.

(Rashmi Aggarwal)

Date: March 22, 2021

दूरभाष **Tel.: 91-11-25843382 (O): 91-9999675782 (M)** फैक्स **Fax: 91-11-25846420**
ईमेल **Email: dean@iari.res.in (Official), drrashmi.agg@gmail.com (Personal)**

Indian Phytopathological Society

(Regn. No. S399 of 1949-50 under Societies Registration Act XXI of 1860)
Division of Plant Pathology
Indian Agricultural Research Institute
New Delhi-110 012, India
E-mail: ipsdis@yahoo.com
website: http://ipsdis.org/

Dr. Robin Gogoi
Secretary

Message

The Indian Phtyopathological Society, a leading scientific forum of 74 years old, addresses the issues of crop protection. Like a sentinel, the Society keeps alarming every plant scientist and disseminates information on the new findings of applied and basic research in the field of plant pathology through its two main publications *Indian Phytopathology* and *Indian Phytopath News*. The Society regularly organizes conferences, symposia and webinars to exchange the ideas and views among the crop protection workers. Under the escalating global trade and a changing climatic scenario, risks pest and diseases are increasing than ever before that hits food quality and security, especially in the developing countries like India. Taking this into account, the society is organizing a National e-Conference on "**Plant Health and Food Security: Challenges and Opportunities**" during February 25-27, 2021. The conference to be held virtually will address various aspects of plant pathology in particular and crop protection as a whole under ten important themes. Two important themes – 'Impact of COVID -19 on Indian agriculture' and 'Stakeholders meet on plant protection issues' are being purposefully planned to have tripartite discourse amongst industry, academia and government in presence of progressive farmers. Further the conference will provide one universal and affable platform to come closure all the stakeholders for the common causes. I hope the conference will be able draw out useful and applicable recommendations from the deliberations of the scientists and research scholars of India and abroad.

I on behalf of the Society welcome you all to make the National e-Conference a grand success.

February, 15, 2021

(Robin Gogoi)

CONTENTS

PRESIDENTIAL ADDRESS

Plant Health Management for Food Security needs Advanced Research and Enabling Policies

P.K. Chakrabarty*
Member ASRB and President Indian Phytopathological Society, IARI, New Delhi 110012
**Email: pranjibc@gmail.com*

Plant Protection is critical to food and nutritional security not only in India but in the world too. FAO estimates peg global losses of food crops due to weeds, diseases and insect pests to 20-40%. Plant diseases have its own significant share of losses. OECD-FAO Agricultural Outlook report indicates that, without pesticides more than half of the crops would be lost to pests and diseases. Although no systematic studies have been conducted on potential crop losses from pests and diseases in India, it is imperative that such losses are likely to occur throughout the world, including in India, without the use of plant protection practices.

The responsibility of protecting food crops from diseases and pests in the challenging environment is rising with increase in human population and its needs. Status and importance of various diseases have changed over the years in India. Awareness is needed to know their status and to develop management modules to protect them in eco-friendly manner. IDM with biocontrol of diseases is important, but notwithstanding their known efficacy, share of biocontrol formulations is inadequate in the national pesticide scenario. During last more than 5 decades, area under bio intensive IDM remained below 3 percent in the country. Factors impeding pace of their development need removal with advanced research, development of smart formulations and enabling policies. Bio stimulants market is gowning in the world at an AGR of 14% and needs deployment for growth and eliciting plant defence system.Nanotechnology is a branch which showed enormous potential in disease management. Nano pesticides and formulations have demonstrated to possess greater effectivity with minimum usage but lack guidelines for their use in agriculture. Development and use of molecular techniques for pathogen detection along with sensor based optical detectors and electronic noses for detection are the latest diagnostics world has advanced and embarked upon. Their use in quarantine and epidemiology for modeling of disease forecasting needs to be internalized and intensified as a decision support system for safe and rapid management of diseases.

Building resistance through MAS and MAB isa highly promisingapproachand needs to be practicedproactively to realize the goal of food security. Novel research thrust on gene editing needs intensification for disease management. For this targets negatively regulating resistance,needs to be identified for silencing so as to engineer resilience. Transgenic approach for resistance against difficult diseases, where resistance in wild sources are limiting, needs popularization so as to make them acceptable to public and policy makers through science led biosafety research. There needs to exist a seamless collaboration among all stake holders of plant protection including farmers, Scientists, Industries and policy maker. All above research and strategies indicated need enabling policies for deployment in the farm.

Indian Phytopathological Society should also engage proactively to frame plant protection policies for implementation with policy makers.Designated national authority of the country should engage pro-actively with ICAR and SAUs through the Society for taking critical decisions before banning of pesticides, framing regulatory guidelines for crop biosecurity and related issues on quarantine and invasive pest management, pesticide management bills, etc. Together we can strengthen crop biosecurity more effective and ensure agricultural sustainability.

AWARD LECTURES

Mundkur Memorial Award Lecture

AL(01): Plant Pathology in the Era of New Education Policy: challenges and opportunities

Chirantan Chattopadhyay*
ICAR-Indian Institute of Agricultural Biotechnology (Deemed to be University), Garhkhatanga,
Ranchi - 834003, Jharkhand, India
**Email: C.Chattopadhyay@icar.gov.in*

Government of India has been framing education policy since 1968, whereby the third such guideline has been drafted for implementation in 2020. The policy brings a paradigm shift in the Nation’s education system that is bound to influence teaching, course curriculum, pattern of degrees, departments, etc. both quantitatively and qualitatively. The government plans to have subject-wise committees, whereby there could be a committee for the agricultural sciences for catering to all concerned disciplines including that for Plant Pathology. The paper discusses the challenges of students in present times, which coupled with the demand of employers and stakeholders would determine the nature of human resource that would be relevant for the coming times. Globalisation of education in Plant Pathology may challenge mediocrity through a higher level of competition. The subject of plant pathology even today remains reasonably insignificant to the public at large due to lack of awareness related to its contributions in everyday life. Thus, there lies a case of effective advocacy by the concerned professional societies for the contributions made by the science in the past and present. Though the aim of the new policy is to make education more multi-disciplinary, the Indian National Agricultural Research and Education System is already attuned to meet such target. Further, the science of Plant Pathology has also evolved towards multi-disciplinarity by mingling with several allied subjects in order to cater to the needs of times. Professional societies involved with Plant Pathology need to appreciate the changing scenario and identify factors responsible in deciding the choice of students in favour of Plant Pathology, their aspirations related to career development, varying nature of demands, farmers, employers, sub-disciplines and allied subjects with research and extension within the country and across the globe. In the tide of global dynamism, change we must. The effort should necessarily be a journey of continuous perseverance in tune with the growing global demand for food, nutritional and livelihood security.

M.S. Pavgi Memorial Award Lecture

AL(02): Impact of yellow leaf disease in sugarcane and successful disease management to sustain crop production

R. Viswanathan*
ICAR-Sugarcane Breeding Institute, Coimbatore - 641007, Tamil Nadu, India
*Email: rasaviswanathan@yahoo.co.in

Yellow leaf disease (YLD) caused by *Sugarcane yellow leaf virus* (ScYLV), a *Polerovirus, Luteoviridae* occurs in major sugarcane growing countries across the world. During late 1990s it was recorded in India. Although the disease was initially thought to be a minor disease in the country, by 2005 onwards the disease severity attained epidemic status across the states. Currently, the ruling varieties in India are affected disease epidemics thereby cane productivity is reduced up to 50% and juice yield by 40-50% in severe cases. Systemic accumulation of the virus in high titre reduces vigour of the varieties in the subsequent vegetative generations or ratoons, hence their potential yield of the varieties could not be harnessed. The virus was characterized on complete genome basis and about 10 genotypes were recognized across the countries. The genotype ScYLV-IND predominantly prevails in India. Among the serological and molecular diagnostics, tissue blot and RT-PCR assays are commonly used. Among the disease management strategies, disease resistance and clean seed have the practical feasibility. Hence parental clones and pre-release varieties are screened for disease resistance in India. Virus elimination enabled through tissue (meristem) culture in combination with molecular diagnostics is the most efficient approach to contain the disease in the field and to address varietal degeneration. Such efforts led to varietal rejuvenation and increase in cane yield by 30-35% under field conditions.

Sharda Lele Memorial Award Lecture

AL(03): Status of pomegranate wilt (*Ceratocystis fimbriata*) in Karnataka and its management strategies

Devappa V.*
Department of Plant Pathology, College of Horticulture, UHS Campus, GKVK, Bengaluru – 560065,
Karnataka, India
**Email: devappav@gmail.com*

Pomegranate wilt disease caused by *Ceratocystis fimbriata* Ell. and Halst. is severly affecting cultivation in pomegranate growing regions of Karnataka. The severity of wilt disease in the regions of North Karnataka was assessed during *kharif* 2016 and maximum wilt (42.10%) incidence was observed in Babaleswar village (Shruthi *et al*., 2019); and (45.16%) was noticed in Besigeger village of Bellary district (Sonyal *et al*., 2016); (45.80%) wilt was observed in Govindkoppa village during 2015-16 (Somu *et al*., 2018). Whereas, (Raja *et al*., 2017 reported that, highest incidence (33.34%) was recorded in Sira taluk of Tumkur district and (71.12% incidence was noticed in Neerbudihal village of Bagalkot district (Madhushri *et al*., 2019). The black colored perithecium, which measure 5.13 x 4.27 ìm and endoconidia were hyaline, cylindrical and average size was 23.6 x 4.90 ìm. Aleurioconidia were thick walled ellipsoidal or pyriform with size of 18.5 x 10.10 ìm (Raja *et al*., 2015). The highest reduction per cent of wilt incidence was noticed in *Trichoderma* plus, neem cake and neem cake + *Trichoderma* plus treated pot culture experiment under glass house condition (Tirmali *et al*., 2018). *Ceratocystis fimbriata* grew well in all most all hydrogen ion (pH) concentration from 2.0 to 11.0. (Sonyal *et al*., 2015). Whereas, 11 bio-agents were evaluated under *in vitro* condition, among the bio agents tested, *Trichoderma harzianum*, *Trichoderma* isolate 1 and *Trichoderma* isolate 5 recorded the maximum per cent inhibition of mycelial growth (100%) (Karakalamatti *et al*., 2019). The plant extract *Allium sativum* tested at 10 to 30% concentration and recorded mean of (32.96%) and at found effective in inhibiting mycelial growth (Sonyal *et al*., 2015). The pathogen being soil borne, preventive measures are of prime importance to manage this disease. Among the different systemic fungicides tested, 100 % inhibition of mycelial growth of *C. fimbriata* was recorded in propiconazole at 0.05% concentration. Among the different bio agents tested against *C. fimbriata*, *T. harzianum* was found to be the most effective with the highest inhibition of mycelial growth (88.77 %) followed by *T. viride* (86.60 %) and *P. fluorescens* (66.33 %). *Bacillus subtilis* was found less effective with (54.88 %) inhibition (Khan *et al*., 2017).

J.P. Verma Memorial Award Lecture

AL(04): Problems and prospects of utilization of bacterial endophytes for the management of plant diseases

Dhruva Kumar Jha*
Microbial Ecology Laboratory, Department of Botany, Gauhati University,
Guwahati - 781014, Assam, India
**Email: dkjha_203@yahoo.com*

Pests and diseases cause significant loss in crop productivity and are considered a major threat to food security and the incomes of farmers worldwide. We need to increase food production at least by 50% to meet the demand for the projected world's population by 2050. Meeting this tough challenge has become even more difficult because of climate change that might affect water availability and the intensity of diseases. Though pests and disease management have doubled food production in the last 40 years, pathogens still cause significant loss in crop productivity. These biotic stressors can be controlled by applying physical, biological, and chemical measures. The majority of the chemical control agents are toxic to both beneficial as well as pathogenic organisms. The concentration of pesticides in food and the environment has increased over the years due to their irrational use which not only harms human health and the environment but also results in pesticide resistance and a resurgence of some diseases. In contrast to these the biological control agents are non-toxic to humans, are host specific, and affect only one or few species. So there is a need to develop alternative strategies to overcome these shortcomings of chemical applications in agriculture. The most exciting scientific developments in recent decades include the existence of asymptomatic microbial communities residing within plant tissues that equip plants to tolerate biotic and abiotic stresses. There is evidence that these bacteria improve plant growth through the acquisition of nutrients from the soil and developing resistance in plants. Endophytes induce 'priming' effects which elicit a faster and stronger plant defense once pathogens attack. The endophytic bacteria, therefore, seem to be excellent candidates for use as biological control agents. There are, however, challenges like relatively few candidate microorganisms being tested, selection of microbes based on the results of laboratory tests that do not always replicate in field conditions, exclusion of responsiveness of microbes to commercial development selection criterion, compatibility with pesticides, quality control, regulations, etc. on the way to developing a commercially viable biological agent. Minimum or no emphasis has been given on ecologically relevant traits essential for survival in the field during a target functional period. Improving perceptions into the mechanism of endophytic bacterial colonization and subsequent interactions with plants if we need to use endophytic bacteria/microbiome for viable strategies to improve agricultural production. We still don't know how a plant accepts endophytes, how does it keep them within the internal tissues, and how to use them to fight pathogens. To address these, one needs to understand the interactions of the environment, plants, endophytes, and pathogens. Control of plant diseases using endophytes will be of great help to future agriculture in the prevailing situation where we have environmental pollution and destruction caused by agrochemicals.

J.F. Dastur Memorial Award Lecture

AL(05): Understanding of sleeping giant-virus in citrus and cotton: perspective to economic losses in India and a challenge to battle

Kajal K. Biswas*
Plant Virology Unit, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute,
New Delhi – 110012, India
**Email: drkkbiswas@yahoo.co.in*

Citrus tristeza virus (CTV), an aphid transmitted closterovirus has destroyed millions of citrus trees worldwide. This virus is longest known plant virus, 2000 x 11 nm in size, with 19.3kb ssRNA genome. CTV is a century old problem, kills about 1.5 million citrus trees infecting most of the economic citrus cultivated in India causing citrus decline. Based on extensive survey, overall disease incidence is 26.3- 60% in India. Sequencing and analysis of 5'ORF1a and CP gene of 114 CTV isolates of India determined that Indian CTVs are diverse and falls under seven genotypes. Sequencing and analysis of complete genome (19253nt) of a CTV strain, Kpg3 of the Darjeeling hills of NE India and its biological study determined that this strain is slow decline inducing strain, genetically related to Israel severe isolate VT. Sequencing and analysis of A 8.4 kb genomic region of the 32 half of four Indian CTV isolates of Bangalore, Delhi, Assam and Vidarbha show that the Indian isolates fell into four genogroups. The recombination is the major factor for evolution of CTV variants in India. Codon usage biasness (CUB), negative selection and gene flow also play major role for evolution of CTV variants. The CUB patterns of the CP genes of 122 CTV isolates originating from three important citrus hosts, *C. sinensis*, *C. reticulata*, and *C. aurantifolia* showed that CTV displays higher genomic stability with indication of higher adaptability of CTV originating from *C. reticulata* and low adaptability of CTV originating from *C. aurantifolia* and *C. sinensis*. The combination of codon analysis of CTV with citrus genealogy suggests that CTV evolved in *C. reticulata* or other *Citrus* progenitors. For development of transgenic resistant citrus, several anti-sence (RNAi) and hairpin (ihp-RNAi) constructs targeting CP and suppressor

gene of CTV were made in pBinAR and pRNAi-GG. Agrobacterium-mediated transformation protocol was developed. 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 of CTV available in our laboratory. The MCPS is being evaluated by challenging with severe CTV isolates through biological indexing. Cotton leaf curl disease (CLCuD), caused by whitefly transmitted monopartite begomoviruses with association of betasatellite and alphasatellite, is a serious constraint for cultivation of cotton in Northwest (NW) India. Based on survey for the last eight years, from 2012 to 2019, showed overall incidence 37.5 to 63.6%. Till today, 21 CLCuD associated begomovirus (CABs) isolates were characterized based on complete genome sequencing and analysis. Of them 14 are identified as *Cotton leaf curl Multan virus*-Rajasthan (CLCuMuV-Ra) followed by five *Cotton leaf curl Kokhran virus*-Burewala (CLCuKoV-Bu), one each as -Pakistan (PK) and -Faisalabad (Fai), indicating that CLCuMuV-Ra is the most prevalent begomovirus species. Majorities of the CLCuMuV-Ra sequences are recombinants. Several satellite molecukles associated with CLCuD begomovirus are analyzed and a single betasatellite molecule, *Cotton leaf curl Multan betasatellite* (CLCuMB), which is mostly recombinant, and four different *alphasatellite species are identofied*. Two transgenic constructs, one AV2 hairpin ((pRNAi-GG-AV2_ihp) and another antisense construct âC1 ((pCAMBIA-As-âC1) was developed. Agrobacterium mediated *in planta* cotton transformation protocol with two transgenic constructs are developed for development of transgenic cotton resistant to CLCuD begomovirus.

S. Sinha Memorial Award Lecture

AL(06): Current status of Cercosporoid fungi in India, effective management strategies and future directions

Pramod Kumar Gupta*
Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur - 482004, Madhya Pradesh, India
**Email: pkgtaxo@gmail.com*

The kingdom fungus is considered as an important component of biodiversity. The genus *Cercospora* is one of the largest in Hyphomycetes infecting mostly the aerial parts of host of cereals, pulses and medicinal crop plants. They are widely prevailing and most destructive in all over the country. *Cercospora* species are distributed worldwide and cause Cercospora leaf spot on most of the major plant families. Numerous species described from diverse hosts and locations are morphologically indistinguishable. Grain, legume, carrot, eggplant, pepper, tomato, tobacco, rice, corn, sorghum, oil palm, cotton, coffee, and other secondary host crops including medicinal and aromatic plants and forest flora are also associated with the Cercospora. There are various approaches used to control the diseases caused by Cercospora such as cultural, chemical and biological approaches. Numerous literatures are available on use of these approaches to tackle the diseases caused by Cercospora. At present, a sufficient number of protectant and systemic fungicides are registered and can be used by the growers in various parts of the world for disease control. Depending on environmental conduciveness and resistance level of the variety used, crop protection might require from 1–2 to as many as 6–7 spraying per season. Although a considerable progress has been achieved throughout the years in disease management by integrating chemical treatments with the use of genetically resistant varieties and various preventive cultural practices, there is great necessity that even more effective eco-friendly management strategies are to be developed in the future, so that both viability of crop cultivation and environmental quality are safeguarded. In this review, various topics such as symptomology and histopathology of *Cercospora* species; its identification and new record; distribution and host range; disease effects on crop growth and yield traits; disease development; dispersal and epidemiology; approaches for management; disease prediction models; molecular diagnosis along with genetic diversity and future directions have been covered.

M.J. Narasimhan Academic Merit Award

MJN(NEZ)/01: Antibiotic exuding rhizospheric *Streptomyces* for biological management of *Xanthomonas oryzae* pv. *oryzae* in rice

Kakumoni Saikia[1]* and L.C. Bora[2]
Department of Plant Pathology, Assam Agricultural University, Jorhat - 785013, Assam, India
**Email: kakusaikia05@gmail.com*

Biocontrol agents and plant growth promoting microbes viz. rhizospheric *Streptomyces* 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 few promising rhizospheric *Streptomyces* (*S. fimicarius* and *S. laurentii*) could suppress *Xoo* effectively in dual culture assay. *S. fimicarius* + *S. laurentii* showed the highest (56.22%) inhibition of BB pathogen. The effectiveness of the cell suspension (107 cfu/ml) of *S. fimicarius* and *S. laurentii* in suppressing BB of rice was tested *in planta* by applying as seed treatment, root treatment, soil treatment and spray application. Lowest disease incidence was observed in chemical check (10.29%) followed by plants treated with combination of *S. fimicarius* + *S. laurentii* (25.47%). The BB incidence was significantly reduced (54.16 to 86.27%) when the plants were treated with all the combinations of effective microbes including chemical check. The phenol content (1.21 to 2.52%) of the treated plant leaves was assayed to be at higher concentrations (Control= 1.05%). Decrease in disease severity was observed with the increase in phenol content. Various plant growth promoting characteristics were also estimated for *S. fimicarius* and *S. laurentii*. Moreover, based on LCMS analysis, 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 which might be responsible for the profound antibacterial activity.

MJN(NEZ)/02: Synthesis and characterization of biogenic silver nanoparticles: its assessment as antipathogenic activity against *Rhizoctonia solani* and *Xanthomonas oryzae* pv. *oryzae* and toxicity on beneficial microbes and mammalian cells

Arti Kumari[1]*, Pranab Dutta[1]*, Ankita Das[2], Nagendra N. Barman[3] and Bubul Chandra Das[4]
[1]School of Crop protection, CPGSAS, Central Agricultural University (Imphal), Umiam - 793103, Meghalaya, India
[2]Department of Plant Pathology, Assam Agricultural University, Jorhat - 785013, Assam
[3]Department of Microbiology, College of Veterinary Science, Assam Agricultural University, Khanapara, Guwahati - 781022, Assam, India
[4]Regional Agricultural Research Station – Titabar (AAU), Jorhat - 785013, Assam, India
**Email: artikumari14002@gmail.com; pranabdutta74@gmail.com*

Silver nanoparticles (AgNPs) were biogenically synthesized mediating *Trichoderma asperellum*. Biosynthesized AgNPs were characterized using UV-Vis spectrophotometer, DLS, Zeta Sizer, FTIR and NTA.The results revealed characteristic SPR peak 410 nm. The average size of crystalline, hexagonal and amorphous AgNPs were obtained as 49.20 nm with concentration 2.24 X 107particles/ml and zeta potential value -28.4 mV. FTIR analysis showed characteristic bands at 1638.2 and 3339.7 cm-1 which corresponds to bending vibration of amide I, amide II bands of proteins and primary amines respectively. The toxicity of AgNPs were evaluated at 50, 100 and 200 ppm concentration against two pathogen *viz*., *Rhizoctonia solani* and *Xanthomonas oryzae* pv. *oryzae*, three biological control agents *viz*., *Trichoderma harzianum*, *Beauveria bassiana* and *Bacillus thuringiensis* and mammalian cell line (Vero cells). Results showed that AgNPs could cause significant reduction of sheath blight and BLB of rice. Toxicity study showed that AgNPs poses weak toxic effect against *T. harzianum* and *B. bassiana* with highest mycelial biomass inhibition at 200 ppm i.e. up to 31.54% and 28.40% respectively. AgNPs did not showed any inhibitory

effect to *B. thuringiensis.* The study on uptake of NPs by Vero cells revealed rapid uptake in a concentration and time dependent manner. Cellular fluorescence microscopic study also revealed increase in AgNP content within cells with increase in AgNP concentration. Scanning Electron Microscopy (SEM) showed distortions in cellular structure at 200 ppm AgNP. The study on cytotoxicity of AgNPs on Vero cells showed mild toxicity in a dose dependent manner. The percent viability of Vero cells was found to be highest at 50 ppm (75.27%) and lowest at 200 ppm (72.81%). The highest per cent cytotoxicity (28.22%) on Vero cells was recorded at 200 ppm and lowest (12.15%) at 50 ppm. Thus, green synthesized AgNPs posed mild toxicity on fungal biocontrol agents and Vero cells and no toxicity against *B. thuringiensis*.

MJN(DZ)/03: Transcriptomic analysis of *Chaetomium globosum* Kunze. for bioprospection of antagonistic related gene(s)

Darshan K.*, Rashmi Aggarwal, Bishnu Maya Bashyal, M.S. Saharan, V. Shanmugam, Amolkumar U. Solanke and Aditi kundu
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Present address: ICFRE-Tropical Forest Research Institute (TFRI), Jabalpur – 483001, Madhya Pradesh, India*
**Email: darshuuas@gmail.com*

Biological control is a nature-friendly and ecological approach to overcome the problems caused by standard chemical methods of plant protection. *Chaetomium globosum* Kunze (Family: Chaetomiaceae) has been recognized as an internationally emerging biocontrol fungus. A number of basic research articles have been published related to antagonistic activity however molecular events and identification of biosynthetic pathways are not yet explored in *C. globosum*. Here we integrate metabolome and transcriptomic analyses of *C. globosum* strain Cg2 during interaction with phytopathogen *Bipolaris sorokiniana* to explore gene expression patterns and associated antifungal volatile and non-volatile metabolites. The Illumina HiSeq platform (2×150 bp) yielded an average of 20-22 million reads with 50-58% GC. Heat map and cluster categorization suggested an increase in the expression levels of genes encoding secondary metabolites and other hydrolytic CAZYmes. We first time have reported the development of polymorphic EST-SSR markers in *C. globosum* with perfect repeats using the Illumina RNA-Seq data. Out of 27,957 unigenes investigated, 8,485 EST-SSR loci were mined. Out of these EST-SSRs, a total of 50 primer pairs were designed and validated for polymorphic study in 15 available *C. globosum* isolates. To unravel the antagonism of *C. globosum*, further metabolomic profiling was done to identify associated antifungal volatile and non-volatile metabolites. Our findings showed the global antagonistic mechanisms of *C. globosum* Cg2 at the molecular level, including biocontrol factors related to mycoparasitism and antibiosis using transcriptomic and metabolome analysis.

MJN(DZ)/04: Comparative virome analysis in mosaic infected and asymptomatic apple cultivars using RNA sequencing: development of multiplex RT-PCR and evaluation of rootstocks for sensitivity to mosaic disease

Sajad Un Nabi, Govind P. Rao, Deeba Kamil and **Virendra K. Baranwal***
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: vbaranwal2001@yahoo.com*

Apple (*Malus* × *domestica* Borkh.) is a commercially important and remunerative crop in the temperate regions of world as well as in India. However, its productivity is reduced nearly by 15% in severely mosaic infected apple orchards. To ascertain the viruses associated with apple mosaic disease, RNA-Seq. using Illumina Hiseq 2500 platform was performed for two cultivars viz., Oregon Spur (OS), Golden Delicious (GD) showing symptoms of mosaic/necrosis and one asymptomatic apple cultivar Red Fuji (RF). Total Six viruses and one viroid were identified from all the three cultivars. Four viruses (apple mosaic virus-ApMV, apple necrotic mosaic virus-APNMV, apple

stem grooving virus-ASGV, apple stem pitting virus-ASPV), one viroid (apple hammerhead viroid-AHVd), 3 viruses (ApNMV, ASGV, ASPV) and one viroid(AHVd), three viruses (apple chlorotic leaf spot viru-ACLSV, apple green crinkle associated virus-AGCaV and ASPV) were found associated with GD, OS and RF respectively. The complete or partial genome sequences of six viruses viz., ApMV-9kb, ApNMV-8.5kb, ASGV-7.6kb, ASPV-7kb, ACLSV-9kb, AGCaV-6KB and one viroid (AHVd-434bp) were retrieved from RNA-Seq data. The results obtained via RNA-Seq. provided insights into the etiology of mosaic disease by confirming the association of a novel virus ApNMV either individually or in association with ApMV as other viruses did not produce any symptom in asymptomatic apple cultivar. The phylogenetic analysis showed possible introduction of these viruses from other countries to India via import of planting material. The presence of recombination events and SNVs showed occurrence of evolutionary events and quasispecies nature of viruses. In the evaluation of rootstocks for the sensitivity towards symptom development, two rootstocks (T337 and T339) did not express any symptom when grafted with virus infected cv. GD. The transmission rate was maximum on rootstocks MM106 and minimum on T339 and T337. The virome based multiplex PCR was developed for four viruses (ApMV, ApNMV, ASGV and ASPV) which were maximally present in cv. GD. All the four viruses were simultaneously detected in a single tube, which was further validated with symptomatic or asymptomatic apple cultivars. The results revealed the presence of one to four viruses among the apple cultivars. Our study showed that the RNA-Sequencing is highly useful tool to explore the Virome in apple. Multiplex PCR is a cost effective detection method for mixed infection of viruses and has great potential to help in indexing of elite apple varieties for production of certified and healthy planting material especially in perennial crops like apple.

MJN(EZ)/05: Enzyme kinetics and gene expression analysis reveals differential response of aromatic rice landraces from sub -Himalayan Terai region of India to rice blast disease

Debayan Mondal[1]*, Prudveesh Kantamraju[1], Susmita Jha[2], Pulak Bhowmik[2], Kumaresh Pal[1], Poulami Sil[1], Somnath Mandal[1], Bidhan Roy[3], Apurba K. Chowdhury[2], Prateek M. Bhattacharya[2] and Nandita Sahana[1]

[1]Department of Biochemistry, [2]Department of Plant Pathology, [3]Department of Seed Science and Technology, Uttar Banga Krishi Viswavidyalaya, Coochbehar – 736165, West Bengal, India

**Email: mondal.debayan99@gmail.com*

The hot and humid climatic conditions in sub Himalayan terrain plains result in profuse rice blast infection every year which affects the rice production adversely. The rice blast disease caused by *Magnaporthe oryzae* infects different parts of rice plants like leaves, stem, panicle, etc. Neither the strain of the blast nor the potent source of resistance against region specific blast disease has been investigated for this part of the country in past. The local landraces which has been growing in this region from ancient time. lt may be proven as valuable source of resistance against *Magnaporthe* because of the co-evolution of the fungus and the host plants. After genetic diversity studies and assessment of nutritional superiority thirty five such landraces were selected to screen for blast resistance. After two years of on field screening five most resistant and five susceptible genotypes were chosen for further analysis. *In-vitro* disease progression assay with the purified strain of blast fungus the T4M-3-5 and Chakhao Sampark was found to be the most promising genotype against blast whereas Gobindabhog and Kalonunia were found to be highly susceptible to the disease. Stress response enzymes like peroxidise, PPO, SOD, APX, chitinase, â-1, 3- glucanase, PAL showed early induction in case of resistant genotypes but these enzymes showed slow no induction in case of susceptible ones. The qRT-PCR of different genes of the defensive Phenol Propanoid pathway genes like *lox, chitinase, salT, jamB,* PR protein encoding genes like *PR1, PR3, PR5, PR9* showed similar trend in case of resistant genotypes like T4M-3-5, Chakhao Sampark and Sadanunia and comparative low surge of these genes were found in case of susceptible genotypes like Gobindabhog, Kalonunia. Metabolites like jasmonic acid, salicylic acid and other compounds formed in PP pathway were estimated by HPLC and GC-MS which validates our proposed findings. Taking all the evidences it can be concluded that T4M-3-5 and Chakhao Sampark starts the defense response in the early stage of infection (24 hpi) whereas in case of susceptible genotypes the defence response are not induced even after 72 hours post inoculation. The signalling pathway leading to the early defense response of the resistant genotypes should be investigated in detail to understand the mechanism behind the resistance response.

MJN(EZ)/06: Suppressor activity analysis of *Tomato leaf curl New Delhi virus gene(s)* and development of RNAi construct to evaluate their efficacy in inhibiting the virus

M. Sarkar, B. Joshi, D. Gupta, S. Mukherjee, B. Mandal and **A. Roy***
Advanced Centre for Plant Virology, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: anirbanroy75@yahoo.com*

The mechanism of RNA silencing in plants is the most robust defensesystem against viral pathogens. To overcome such formidable defense system, plant viruses have adopted a counter-defensive strategy through one or more viral encoded suppressors of the RNA silencing proteins, which inhibit the RNA silencing process. In case of ToLCNDV, the most important begomovirus causing leaf curl disease, limited information was available on its VSRs. In this study, three putative suppressor genes (AV2, AC2, AC4) of ToLCNDV were amplified from a pure culture of the virus established in *Nicotiana benthamiana* through agroinoculation. These genes were cloned into a GFP tagged binary vector pEarleygate103 and their suppressor activity was evaluated through a GUS reporter and GUS hairpin assay system. All the proteins were found to show strong silencing suppression with the AV2 protein being the most effective. The sub-cellular localization of the GFP fused suppressor proteins was studied through confocal microscopy. Transient over-expression of these suppressor proteins in *Nicotiana benthamiana* induces typical leaf curl symptom in the systemic leaf implying they are also acting as pathogenicity determinant. Reverse transcriptase PCR analysis showed the RNA transcripts of these suppressor genes moves systemically. To inhibit the activity of these suppressor proteins, hp-RNAi constructs against these genes were developed using a golden gate based binary vector pRNAiGG. The efficiency of hp-RNAi constructs was evaluated through their transient expression in *Nicotiana benthamiana* followed by challenged inoculation of ToLCNDV. A significant reduction of symptom was observed with hp-AC4 followed by hp-AC2 and hp-AV2.

MJN(SZ)/07: Molecular characterization and functional analysis of pathogenicity related genes in *Colletotrichum falcatum* causing red rot in sugarcane

Scindiya M.* and P. Malathi
ICAR-Sugarcane Breeding Institute, Coimbatore - 641007, Tamil Nadu, India
**Email: scindiya89@gmail.com*

Red rot caused by *Colletotrichum falcatum* is a major constraint for sugarcane cultivation. The disease is being managed by the release of new sugarcane varieties. In this study, about 28 gene homologs were referred from other *Colletotrichum* spp. and characterized for their presence in *C. falcatum* isolates. Further, about four sets of Subtraction Subtractive Hybridization (SSH) analysis performed to identify differentially regulated genes in *C. falcatum* isolates varying in virulence in correspondence to varied level of host resistance. In addition, functional analysis by RNAi approach for selected pathogenicity genes *viz.*, polyketide synthase 1 PKS1), glucose transporter (GT) and sucrose non-fermenting1 (SNF1) was performed in *C. falcatum* isolates. Results of the present study indicated that all the characterized pathogenicity gene homologs may have a possible role during pathogenesis as they showed intra-specific variation in response to pathogen virulence. In addition, SSH analysis resulted in 37 unigenes related to *C.*

falcatum virulence and among them 10 unigenes were commonly expressed. Validation of selected unigenes showed differential expression in response to pathogen virulence and host resistance. Besides, the knockdown mutants of the genes displayed loss in the production of spores and also exhibited reduced disease progress compared to the wild type isolate during interaction. Hence, the standardized protocol based on RNAi mediated silencing indicates its applicability for functional validation of *C. falcatum* pathogenicity related genes.

MJN(SZ)/08: Characterization and virulence profiling of *Magnaporthe oryzae* isolates from diverse rice ecosystems of Karnataka

Amoghavarsha Chittaragi*
Department of Plant Pathology, University of Agricultural and Horticultural Sciences, Navile,
Shivamogga – 577204, Karnataka, India
**Email: amoghchittaragi@gmail.com*

The present study was carried out during 2018-2020 to document the rice blast disease status, pathotype groups, genetic diversity and resistant source. The roving survey was conducted in different rice ecosystems. Within the irrigated ecosystems, the highest PDI was observed in the Kavery (50.85) and least in Upper Krishna Project (10.58) command areas. In case of rainfed ecosystem, the highest PDI was observed in the hilly ecosystem (53.38) and least in the coastal ecosystem (3.73). The 52 *M. oryzae* isolates were studied for morphological variability and the majority of the isolates were circular followed by irregular, raised, flat, and crateriform. The isolates were inoculated on fourteen days old seedlings of IRBLs containing 24 R-genes. The high virulence frequency (> 70%) was observed on the IRBLs carrying the genes *Pib, Pia, Pi5(t), Pi11, Pi12(t), Pi20(t), Pii* and *Pik-h*. The moderate virulence frequency (30-70%) was observed with the IRBLs carrying the genes *Pi19(t), Pit, Pik-s, Pik, Pi3, Piz-5, Pi1* and *Pi9*. In contrast, the low virulence frequency was observed on the IRBLs with genes *Pikm, Pik-p, Pita, Pi7(t), Pish, Piz(t), Pita-2* and *Piz*. The 52 isolates were classified into 14 pathotype groups (PGs) based on the reaction pattern against IRBLs. The multilocus sequence analysis was used for the evaluation of evolutionary relationship among the isolates using gene sequences of *actin, β-tubulin, calmodulin, TEF-1α* and ITS region. The isolates were grouped into two clusters based on the average sequence data. The screening of rice entries was carried out to determine the resistant source.

MJN(CZ)/09: Exploring potential *Pseudomonas* for plant growth promoting traits and *in vitro* suppression of charcoal rot in soybean (*Glycine max* (L.) Merrill)

Rathod Parshuram* and Anil S. Kotasthane
[1]*Department of Plant Pathology,* [2]*Department of Plant Molecular Biology and Biotechnology,*
Indira Gandhi Krishi Vishwavidhyalaya, Raipur - 492012, Chhattisgarh, India
**Email: parshunaik25@gmail.com*

In this study, Eight-eight rhizosphere soil samples were derived from different locations of Bastar and Bilaspur districts of Chhattisgarh. Four rhizospheric soil samples were derived from *Brassica* spp. from zhahirabad (Telangana). Ten fluorescent *Pseudomonas* isolates (on UV light 360nm) emitting strong fluorescence were selected for the course of the investigation. Phylogenetic affinities of the 16S rRNA DNA and ITS 27+1492 gene sequences resolved the species identity of our potential isolates. For fundamental research and practical application of PGPR strains on different crops, we require potential isolates. The PGPR was also screened *in vitro* for inhibition of *Macrophomina phaseolina* (*Mp*) causing charcoal rot of soybean by performing bipartite (root x *Mp*) and tripartite (root x *Mp* x bioagent) interactions by a model involving root-soil interface. Pot and field experiments result revealed that beneficial effects of fluorescent *Pseudomonas* can be achieved through seed treatment which is simple and cost-effective.

Three fluorescent *Pseudomonas* 9704, BS-4, and 9829 consistently, over different locations, increased seed germination, reduced seedling mortality, improved plant growth, and yield attributes in soybean, chickpea, wheat, and rice. Plant growth-promoting effects and an increase in grain yield by fluorescent *Pseudomonas* isolates were crop-specific.

MJN(CZ)/10: Development of DNA based screening method for yellow mosaic virus infecting black gram and studies on vector (*Bemisia tabaci*) biotypes in Andhra Pradesh

B.H. Chaithanya[1]*, B.V. Bhaskara Reddy[2], L. Prasanthi[2], R. Sarada Jayalakshmi Devi[3], K. Manjula[3] and G. Mohan Naidu[3]
[1]Regional Agricultural Research Station (ANGRAU), Nandyal - 518502 Andhra Pradesh, India
[2]Regional Agricultural Research Station (ANGRAU), Tirupati – 517502, Andhra Pradesh, India
[3]S.V. Agricultural College, Tirupati – 517502, Andhra Pradesh, Inida
**Email: chaitu453@gmail.com*

In our study rolling circle amplification (RCA) based dimeric clones of DNA-A & DNA-B components of MYMV and DNA-A component of MYMIV were constructed in pCAMBIA-2301 vector and transformed into *Agrobacterium tumefaciens* EHA-105 cells by freez-thaw technique. Infectivity analysis of constructed clones was done on known susceptible varieties. Total forty-five black gram genotypes were screened by the sprouted method of agroinoculation using infectious dimeric clones of MYMV-A and MYMV-B to screen resistance against MYMV. Out of forty-five, 24 genotypes offered resistance against MYMV. Similar screening study was conducted to screen resistance against Mungbean yellow mosaic India virus using infectious dimeric clones of MYMIV-A and MYMV-B.22 genotypes were found resistant against MYMIV infection. Interestingly, 13 genotypes were shown a differential response to MYMV and MYMIV infection. Finally 17 genotypes showed resistance to both species of virus. The attempt was made to determine the genetic group of whitefly (*Bemisia tabaci*) transmitting YMV in Blackgram. For this whitefly population was collected from eight districts of Andhra Pradesh and mitochondrial cytochrome oxidase gene was amplified using gene specific primers. The phylogenic analysis of *mt*COI gene sequences revealed that *B. tabaci* population from three districts *i.e* Guntur, East Godavari and Krishna were grouped under Asia I genetic group. *B. tabaci* population from five districts *i.e* Kurnool, Kadapa, Chittoor, Nellore and Prakasam were clustered under Asia II-1 genetic group. The distribution of six secondary endosymbionts were analysed by amplification of 16S rRNA/ 23S rRNA gene. *Hamiltonella* and *Fritschea* endosymbionts were detected in few whitefly samples. Few studies revealed that the composition of secondary endosymbionts varies with each genetic group of *B. tabaci*. Hence it was concluded that there is a possibility for the presence of MED and MEAM biotypesin Andhra Pradesh.

MJN(MEZ)/11: Effect of elevated levels of CO_2 on the development of powdery mildew in cucumber species

Tanveer Fatima Rizvi* and Mujeebur Rahman Khan
Department of Plant Protection, Faculty of Agricultural Sciences, Aligarh Muslim University,
Aligarh -202002, Uttar Pradesh, India
**Email: tanveer.124000@gmail.com*

The environment is the key factor that influences the host-parasite relationship. Elevated CO_2 levels resulting from various anthropogenic sources may directly affect surroundings around pathogens and plants. It is hypothesized that plants may respond differently to pathogens in the environment containing an elevated concentration of CO_2. To test the hypothesis an experiment was conducted to examine the effects of intermittent exposures of elevated levels of CO_2 *viz.*, 400, 500 and 600 ppm (5 hr/ day on alternate days) on the development of *Sphaerotheca fuliginea* causing powdery mildew disease on cucumber species using open-top chambers. The elevated levels of CO_2 acted as a growth promoter and significantly enhanced the plant growth of cucumber plants. Inoculation with the fungus incited specific mildew symptoms on the leaves and decreased the plant growth and biomass production of the tested cucurbit. The intermittent exposures with elevated levels of CO_2 aggravated the disease development. As a result, severe mildew developed on cucumber plants, which expressed tolerance to the pathogen. Fungus colonization in terms of the number of conidia/cm^2 leaf surface was significantly greater on the plants exposed to 500 or 600 ppm CO_2. The stomata and trichome density and stomatal pore width were increased in the leaves of CO_2 exposed plants. The CO_2 exposures also accelerated the photosynthesis rate, but transpiration, stomatal conductance, salicylic acid and total phenols were decreased; fungus inoculation caused the effects just reverse of CO_2. Interaction between *S. fuliginea* and CO_2 was found synergistic at 500 ppm, whereas with rest of the concentrations it was near to additive.

MJN(MEZ)/12: Secretome analysis reveals effector candidates associated with broad host range necrotrophy in *Fusarium udum*

Ruchi Srivastava*, Alok Kumar Srivastava*, Alok Kumar Singh, Praveen Kumar Tiwari, Jagriti Yadav and Anil Kumar Saxena
ICAR-National Bureau of Agriculturally Important Microorganism, Kushmaur, Mau – 275103, Uttar Pradesh, India
**Email: ruchisrivastava.biotech@gmail.com*

Pigeon-pea (*Cajanus cajan*) is the most important crop in arid and semiarid region. Wilt caused by *Fusarium udum*, is one of the most disastrous disease of pigeon pea known to cause heavy losses every year in India. In this study, genome of *F. udum* strain F 02845 was sequenced. The size of genome was recorded to a 56.38 Mb and a total of 16179 protein coding genes were identified, out of that 11,892 (73.50 %) genes were annotated with 8928 (55.18%) KOG annotation. The micro-satellite mining of genome showed a total of 4921 SSRs, covering 0.008 of whole genome, with relative abundance; 87.28, relative density; 1434.51, and percentages of penta repeats; 2.54, hexa repeats; 1.46, mono repeats; 39.76, di repeats; 31.35, tri repeats; 21.35 and tetra-repeats; 3.51, respectively. In addition, 5134 unique InterPro domain was detected. The genome was further analyzed for key pathogenic genes involved in virulence, the PHI-BASE Database could identify 1060 (6.55 %) genes as virulence gene, whereas, 1439 secretary proteins were also identified in the genome, out of which 506 predicted secretary proteins were annotated with the CAZyme database. Glycosyl hydrolase (GH) family proteins are more abundant 45% followed by auxiliary activity (AA) family proteins. Beside this, 421 genes were annotated against the pathogen-host interaction database (PHI database) and a total 7 effectors genes i.e XEG1 (Xyloglucan-specific endo-beta-1, 4-glucanase 1), MoCDIP4 (Cellulose-growth-specific protein), PaNie(25 kDa protein elicitor-like protein), AVR-Pita (avirulence gene/ subtelomericavirulence effector), MoCDIP3, MoCDIP1, CoMC69 (Secreted virulence factor MC69) were found in the secretome. Virulent Effector gene SIX (for Secreted In Xylem) was validated through PCR.The secretomeof *F. udum* F02845was compared with the secretome of 4 different *Fusarium* spp. *i*.e *F. oxysporum f. sp. lycopersici*, *F graminarum*, *F. proliferatum*, *F. verticilliodes*, the result showed that out of 7 effectors only 5 (XEG1, MoCDIP4, AVR-Pita, CoMC69 and MoCDIP1 were common in all with different copy number. Understanding of the genes, responsible for virulence and secondary metabolites production in fungus, will help to explain the mechanisms for virulence functional in fungus and to develop novel drugs against wilt.

MJN(WZ)/13: Seasonal effects on population dynamics of *Phytophthora* spp. and disease development in mandarin

R.S. Lad* and R.M. Gade
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola - 444104, Maharashtra, India
**Email: ranjitlad88@gmail.com*

This may be the first attempt to correlation of environment and soil ecology which impacting disease situation in Nagpur mandarin due to *Phytophthora* spp. Fixed plot survey was undertaken at fortnightly intervals at six locations to analyse correlation between environmental factors and soil moisture with propagules density of *Phytophthora* as well as disease development by using linear correlation. Rainfall, relative humidity and air temperature probes typically consist of three separate sensors packaged in a single instrument called as ‘SENSTUBE’ and that instrument was used for record data in field. Soil moisture was analyzed in laboratory by using digital moisture meter. Fixed plot study indicated inoculum density of *Phytophthora* in the range of 5.2-29.6 cfu/g soil. Peak period of *Phytophthora* root rot in mandarin was seen from June to September and mean disease intensity recorded in between 3.16 to 34.33%. Root rot in mandarin was gradually increased after heavy rainfall and progressed with faster rate when soil moisture with high humidity and low temperature and vice versa. Gummosis studies with fortnightly interval indicated that, disease intensity was in the range of 4.08-30.17%.Peak period of gummosis disease (August up to November) was observed after one to two months of heavy rainfall when there was optimum temperature (below 30^0C) and high humidity. After heavy rainfall the pathogen population is drastically increased but oozing of gum which is peculiar. *Phytophthora* population and disease progression was directly proportional to environmental and soil parameters like rainfall, relative humidity, soil moisture, but inversely proportional to air temperature. When air temperature increases pathogen population and disease progression decreased drastically and vice versa. Whereas, Soil moisture and rainfall are the key factors which were found positively significant for the pathogen growth and disease progression.

MJN(WZ)/14: Variability among *Rhizoctonia bataticola* isolates, causing dry root rot of soybean and its management

R.C. Agale*, A.P. Suryawanshi and Ashwini G. Patil
Department of Plant Pathology, Vasantrao Naik Marathwada Agricultural University, Parbhani - 431402, Maharashtra, India
**Email: agaleram@gmail.com*

Dry root rot caused by *Rhizoctonia bataticola* (Taub) Butler, is one of the most widely distributed and destructive disease of soybean [*Glycine max* (L.) Merril], causing accountable quantitative and qualitative losses. All of the 16 isolates of *R. bataticola* exhibited a wide range of pathogenic variability by using sick soil method and indicated a very meager variability in respect of their cultural characteristics, except colony growth. After seven days of incubation, the colony growth (mm) of the test isolates arranged from 74.32 to 90.00 mm and the growth rate was slow, medium and fast. The morphological characteristics of *R. bataticola* isolates indicated variability in respect of hyphal width and sclerotial characters like shape, colour and size. Dendrogram generated based on UPGMA analysis of RAPD data grouped the entire 16 test isolates, collected from three zone of Marathwada region and their similarity coefficient. A wide range of variability in respect of virulence, morpho-cultural characteristics and molecular variability of the 16 isolates, a single most virulent isolate Rb-4 (Shengaon, Dist. Hingoli) was selected and promoted for further *in vitro* studies. Among the nine bioagents tested, the most effective with significantly highest mycelial growth were *Trichoderma viride* (87.48%), followed by *T. harzianum* (81.61%), *Aspergillus niger* (77.34%), *T. hamatum* (68.43%), *T. koningii* (66.43%) and *T. longibrachiatum* (61.99%). Among the twelve organic soil amendements tested, Neem seed cake was found most effective with significantly highest mortality reduction (77.57%), followed by Castor cake (74.69%) and Karanj seed cake (71.57%). Among various treatments integrated in polybag culture under screen house to manage soybean dry root rot, the most effective treatment with significantly highest disease reduction was Vitavax power 75% WP (ST) @ 3.0 g/kg + *T. viride* (ST) @ 10 g/kg + NSC (SA) @ 50 g/kg (94.32%), followed by Carbendazim 50% WP (ST) @ 1 g/kg + *T. viride* (ST) @ 10 g/kg + NSC (SA) @ 50 g/kg (92.30%), Carbendazim 50% WP (ST) @ 1 g/kg + *T. harzianum* (ST) @ 10 g/kg + NSC (SA) @ 50 g/kg (86.53%) and Vitavax power 75% WP (ST) @ 3 g/kg (84.69%). Under field conditions, all those treatments integrated to manage soybean dry root rot were found effective in reducing dry root rot incidence/ mortality, over untreated control. However, on the basis of better ICBR, the treatments found most effective and most economical in their order of merit were: Carboxin 37.5 % + Thiram 37.5% WP (ST) @ 3 g/kg Ã Carbendazim 50 % WP (ST) @ 1 g/kg Ã Vitavax power 75% WP (ST) @ 3.0 g/kg + *T. viride* (ST) @ 10 g/kg + NSC (SA) @ 5 q/ha.

MJN(NZ)/15: Optimizing the *Agrobacterium tumefaciens*-mediated transformation conditions in *Colletotrichum lindemuthianum* for uncovering the functionality of pathogenicity arsenals

Aasiya-Nabi* and Bilal A. Padder
Plant Virology and Molecular Plant Pathology Laboratory, Division of Plant Pathology,
Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar - 190 025, Jammu & Kashmir, India
**Email: vaniereenu@gmail.com*

The hemibiotrophic fungal pathogen *Colletotrichum lindemuthianum*, the causal agent of bean anthracnose is rated among the top 10 important diseases infecting beans. Currently our knowledge of pathogenicity arsenals and molecular mechanisms underlying the pathogenesis is limited, thus proving to be a serious impediment for disease management. Among the forward genetics tools, *Agrobacterium tumifaciens* mediated transformation (ATMT) has proved to be a versatile technique in deciphering the multifaceted role of fungal pathogenicity genes. In this study, series of experiments were conducted to optimize the key parameters affecting the *Agrobacterium tumefaciens*- mediated transformation (ATMT) for *C. lindemuthianum*. The transformation efficiency increased with increase in spore concentration and co-cultivation time with optimal being 10^{6}/ml for 72hrs at 25ºC on cellulose membrane type. The protocol resulted in establishment of large mutant library including the melanin deficient and conidiation affected transformants. To screen the transformants for altered pathogenicity, two new approaches such as detached leaf and twig techniques were pursued to investigate their reliability. The new methods proved valid alternatives, requiring least resources to screen the large mutant repositories in the short time. Among the transformants tested for virulence, 90% transformants were pathogenically similar to race 2047, 8% and 2% were reduced and impaired, respectively. The altered avirulent transformants can prove vital for understanding the missing link between growth and developmental stages of pathogen with virulence. This platform will help to develop strategies to determine the potential pathogenicity genes and to decipher molecular mechanisms of host-pathogen interactions in more detail.

MJN(NZ)/16: Characterization and mapping of spot blotch in *Triticum durum -Aegilopes speltoides* introgression lines using genotyping by sequencing

Jashanpreet Kaur[1]*, Jaspal Kaur[2], Guriqbal S. Dhillon[3,4], Ritu Bala[2], Puja Srivastava[2], Satinder Kaur[4], Acha Sharma[2], Harmandeep Kaur[1], Jasveer Singh[1] and Parveen Chhuneja[4]
[1]Department of Plant Pathology, [2]Department of Plant Breeding, [4]School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana - 141004, Punjab, India
[3]Department of Biotechnology, Thapar University, Patiala - 147004, Punjab, India
**Email: jashanpreet-coa@pau.edu*

Leaf blight of wheat (*Bipolaris sorokiniana*) is emerging as a major threat to successful wheat production in warm and humid areas of the world. In India, this disease is responsible for high yield losses in Eastern Gangetic Plains Zone. More recently, this disease is extending gradually towards cooler, traditional wheat growing North-western part of the country which is a major contributor to national cereal basket. Deployment of resistant cultivars is considered as the most economical and ecologically sound measure to avoid losses due to this disease. So in this study, efforts were made to evaluate 89 backcross introgression lines (DS-BILs) derived from *Triticum durum* (PDW274-susceptible) X *Aegilops speltoides* (resistant) developed in our wide hybridisation programme against leaf blight for two consecutive years, 2018-19 and 2019-2020. Phenotypic evaluation of these lines showed a continuous variation in disease severity indicating that the resistance to leaf blight is certainly quantitative in nature. These 89 lines were evaluated under polyhouse conditions and further used for mapping QTLs using SNPs obtained by genotyping by sequencing. Thirteen QTLs across chromosomes 2A, 2B, 3A, 3B, 4B and 5B linked to leaf blight resistance were identified using stepwise regression-based Likelihood Ratio Test (RSTEP-LRT) for additive effect of markers and single marker analysis (SMA). These SNP markers were further validated on BC2F1 population developed from DS13 X HD3086 and one marker S5B_703858864 linked to QSb.pau-5B.3 was found to be polymorphic for the parents and thus, may prove to be a potential diagnostic marker for spot blotch resistance.

APS-IPS Travel Sponsorship Award

APS(DZ)/01: Deciphering the *Chaetomium globosum* induced signaling network in tomato against early bight

Jagmohan Singh[1]*, Rashmi Aggarwal[1], Bishnu Maya Bashyal[1], M.S. Saharan, Zakir Hussian[2] and Amolkumar Solanke[3]

[1]Division of Plant Pathology, [2]Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India

[3]ICAR-National Institute Plant Biotechnology, Pusa Campus, New Delhi – 110012, India

**Email: dhillonjagmohansingh@gmail.com*

Chaetomium, a strictly saprophytic fungus that belongs to *Ascomycota* of the family *Chaetomiaceae*. *C. globosum* is the most frequently isolated and has been reported to be a potential antagonist of various plant pathogens. *C. globosum* has been identified as a potential antagonist of *Bipolaris sorokiniana*. Several reports are available on mycoparastism and antibiosis mechanism of *Chaetomium globosum* against a number of plant pathogenic fungi. Few studies to date report the induced resistance as a mechanism of biocontrol by *Chaetomium globosum* toward phytopathogens. In order to gain insights into the potential induced defense mechanism of by *C. globosum* (Cg2) against early blight of tomato, global RNA sequencing is performed and differentially expressed genes of defense induced hormone signaling pathways are validated by using qRT-PCR. The RNA sequencing was performed for tomato plant samples collected at 3-time points after Cg-2 inoculation (control plant, 12hpi, 24hpi, and 96hpi). The transcriptome data revealed 922 DEGs at 12 hrs post-inoculation with Cg-2, 904 DEGs at 24 hrs and 453 DEGs at 96 hrs respectively. At 12 hrs post-inoculation with Cg-2, KEGG enrichment analysis indicated that the DEGs were enriched mainly in the metabolic pathways, biosynthesis of secondary metabolites, plant hormone signal transduction, MAPK signaling pathway, flavonoid biosynthesis, and phenylpropanoid biosynthesis pathways. GO analysis revealed that these DEGs were enriched mainly in the following terms: ROS metabolic process, H2O2 metabolic process, defense response, superoxide dismutase activity, and antioxidant activity. Moreover, many genes such as MC, PI II, PS, PR1a3, PR1, Le4 and GluB that regulate crucial points in defense-related pathways were identified and their expression pattern was analyzed by qRT-PCR. The results revealed the activation of induced resistance mechanism in tomato against early blight disease through salicylic acid and jasmonic acid signaling networks involved in SAR & ISR, respectively.

APS(NEZ)/02: Post transcriptional gene silencing using coat protein gene specific dsRNA molecules against cucumber mosaic virus (CMV) infecting Bhut jolokia crop of Assam

R. Gowtham Kumar[1]*, Munmi Borah[1], Sundaresha Siddappa[2] and P.D. Nath[1]
[1]Department of Plant Pathology, Assam Agricultural University, Jorhat - 785013, Assam, India
[2]Central Potato Research Institute, Shimla - 171001, Himachal Pradesh, India
**Email: gowthamkumaraarta@gmail.com*

Cucumber mosaic virus is the major virus infecting bhut jolokia crop and cause considerable loss in terms of production and productivity of crop. 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 Cucumber mosaic virus (CMV) 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 CMV could suppress viral titters in Bhut jolokia. The specific objectives of the study was to develop a dsRNA construct for CMV resistance in Bhut jolokia and a proof of concept studies for CMV silencing in Bhut jolokia using dsRNA assay strategy. For performing this experiment CMV infected bhut jolokia leaf tissue samples were collected from some bhut jolokia growing locations of Jorhat district and CMV was successfully detected by two-step Reverse Transcriptase PCR (RT- PCR). The dsRNA was successfully produced by following a two step PCR followed by in vitro transcription method. The expression of CMV 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 bhut jolokia plant along with virus CMV, 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 CMV coat Protein gene, caused considerable reduction in CMV infection and allowed a better vegetative plant growth.

APS(NZ)/03: Status and molecular characterization of potato virus Y strains in Kashmir valley

Sumaih Wani*
Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar - 190025, Jammu & Kashmir, India
**Email: sumiahwani@gmail.com*

Potato virus Y (PVY) is widely distributed virus and ranks fifth among the top ten economically damaging viruses worldwide. Potato isolates are historically divided into three main strain groups and the different strains of PVY develops different symptoms on different parts of the host plant species. Knowledge of the nature of PVY strains is essential for breeding PYV resistant cultivars that are durable against a wide range of strains. The survey was conducted to determine the extent of PVY infection in the potato fields of Kashmir valley in 2018-19. Two hundred potato samples collected from different districts of the valley were tested for PVY infection. Out of 200 samples, 74 were tested positive for PVY infection in Das-ELISA. Forty (10 from each district) positive samples were reconfirmed by Reverse Transcription Polymerase Chain Reaction (RT-PCR) using coat protein specific primers (CP Primers). The disease incidence was found to range from 24 to 52.00%, with the maximum incidence recorded in Srinagar (52.00%) district followed by district Anantnag (40%), Baramullah (34%) and Budgam (24%). The positive PVY samples were further characterized into different strains using strain specific primers with NTN, N and O strains being the most prevalent strains of PVY in Kashmir. Some samples also showed mixture of different strains. Furthermore, Multiplex PCR of available germplasm against different viruses viz. PVY, PLRV, PVX, PVS and PVA

revealed the presence all the viruses with PVY and PVX most prevalent. The study reveals the presence of PVY and its different strains in Kashmir valley. The study also indicates the presence of other potato viruses in the seed chain of the valley which requires proper certification.

APS(MEZ)/04: Efficacy of plant extracts against mungbean yellow mosaic India virus (MYMIV) in urdbean (*Vigna mungo* L.)

Sabiha Saeed[1]*, Shabbir Ashraf[1] and Mohammad Akram[2]
[1]Department of Plant Protection, Faculty of Agricultural Sciences, Aligarh Muslim University,
Aligarh - 202002, Uttar Pradesh, India
[2]ICAR-Division of Crop Protection, ICAR-Indian Institute of Pulses Research, Kanpur - 208024,
Uttar Pradesh, India
**Email: sabihasaeed106@gmail.com*

Yellow mosaic disease (YMD) is one of the most destructive viral disease of many leguminous crop including urdbean. It is caused by whitefly (*Bemisia tabaci*) transmitted geminivirus. It can cause upto 100 percent yield loss depending upon the stage when it occur. Many insecticides are available to suppress the pathogenecity of virus but these chemical based insecticides are very hazardous to our ecosystem causing adverse effect to human health. So, to combat this problem an ecofriendly approach have been made for the management of YMD. Present study were performed during kharif season of 2016, at faculty of agricultural sciences, Aligarh Muslim University, Aligarh. Experiments were laid down in a Randomized Complete Block Design in plots of 3×3 m with three replicates on cv. T9 of urdbean. Five different plant extract i.e., *Zingiber officinale* (rhizome), *Azadirachta indica* (leaf), *Datura stramonium* (leaf), *Allium cepa* (bulb), and *Allium sativum*(bulb) with different doses (10%, 15% and 20%) and water in control were sprayed at 20 and 45 days after sowing. Recorded data showed that all the treatments were found effective in disease suppression but extract of *D. stramonium* 20% were the most effective one. It showed minimum disease incidence as compared to control. Least effective treatment was *Z. officinale* (10%). Treatment *D. stramonium* 20% was not only effective in controlling disease incidence but also in lowering whitefly and improving number of pods(37), root nodule(57) and yield (710kg/hec) of the plant.

APS(MEZ)/05: Effect of temperature and pH on mycelial growth and sporulation of *Alternaria brassicae* (Berk.) Sacc. causing Alternaria blight of rapeseed-mustard

Vaibhav Pratap Singh* and R.U. Khan
Department of Plant Protection, Faculty of Agricultural Sciences, Aligarh Muslim University,
Aligarh – 202002, Uttar Pradesh, India
**Email: vaibhavpratapsingh10392@gmail.com*

The present investigation was carried out *in vitro* to study the effect of six different temperatures (10, 15, 20, 25, 30 and 35!) and eleven different pH levels (3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0 and 8.5) on mycelial growth and sporulation of *Alternaria brassicae* (Berk.) Sacc. causing Alternaria blight in rapeseed-mustard. Among the tested temperatures, highest mycelial growth of the fungus (81.00 mm) was recorded at 25°C with excellent (++++) sporulation, which was followed by 30°C (60.66 mm) and 20°C (57.33 mm). However, lowest mycelial growth was observed at 10°C (20.00 mm) with poor sporulation (+). Of all pH levels, maximum mycelial growth was recorded at pH 6.5 (79.00 mm) followed by pH 7.0 and 6.0 showing 69.66 and 63.00 mm growth, respectively. While as, lowest mycelial growth of pathogen was found at pH 3.5 with poor sporulation (+).

PLENARY LECTURES

PL/01: Asia Pacific Scenario on Plant Health and Food Security Challenges

Dr. Ravi Khetarpal*
Asia-Pacific Association of Agricultural Research Institutions, Bangkok 10100, Thailand
**E-mail: ravi.khetarpal@apaari.org*

PL/02: The state of global plant health and the consequences of global changes: seed-based science for farmers

Serge Savary*
UMR Agir, Centre INRAE Occitanie-Toulouse Chemin Borde Rouge 31320 Auzeville Auzeville 31320 Occitanie, France
**Email: serge.savary@inrae.fr*

Two international initiatives have provided overviews of the state of plant health globally. A first one provided pathogens and pests yield loss estimates for five major food crops (rice, wheat, potato, maize, and soybean) in major world food production hotspots. A second initiative, also under the aegis of the International Society for Plant Pathology, is the Global Plant Health Assessment (GPHA), where the current state of plant health is addressed, its trends, and its consequences on ecosystem services: (1) provisioning of food, feed, and fibre; (2) regulating of resources and climate; and (3) cultural, beauty, re-creation, and spiritual. The GPHA considers the entire diversity of plant systems, from cereal-, or root- and tuber-based systems, peri-urban horticulture and household gardens, forests, and urban vegetation. These initiatives lead to different lines of thoughts. One concerns the different impacts that the nature (chronic, acute, or emerging) of plant disease epidemics may have in the short or long term. Another concerns the processes and factors leading to disease emergence. And another concerns the impacts of plant diseases on the components of food security (production, access, nutritional value). The diversity of threats towards plant health is tremendous; these will become more frequent in an uncertain future, where abiotic stresses (droughts, floods, heat waves) will amplify. This suggests that, while building on our current knowledge, future research might expand to multiple, combined, disease and abiotic stresses. A strategic goal of plant pathology could be seed-based, bringing both disease-resistant and stress-tolerant plants to farmers.

SESSION 1

Plant disease resistance

Resistance breeding, MAS, virulence screening, race profiling

Keynote Lectures

KN(S1)/01: Plant protection by double-stranded RNAs, a novel biofungicide for sustainable crop protection: mechanisms and activities

Maria Ladera-Carmona, Femke Benkow, Sudharshini Kannan, Ena Šeèiæ, Abhay Veer Singh, **Karl-Heinz Kogel*** and Jafargholi Imani

Institute of Phytopathology, Centre for BioSystems, Land Use and Nutrition, Justus Liebig University (iFZ), Giessen, Germany

**Email: Karl-Heinz.Kogel@agrar.uni-giessen.de*

RNA interference (RNAi) is a biological process in which small RNA (sRNA) molecules, such as microRNAs (miRNAs) and small interfering RNAs (siRNAs), sequence-specifically silence gene expression at the transcriptional or post-transcriptional level, either by directing inhibitory chromatin modifications or by decreasing the stability or translation potential of the targeted mRNA. The primary trigger for sRNA formation and gene silencing is double-stranded RNA (dsRNA) generated from an endogenous genomic locus or a foreign source, such as a transgene or virus. Given the high potential of RNAi strategies, their use in agriculture, horticulture, and forestry will likely be extensive in the future. Rapid progress in elucidating RNAi mechanisms has led to the first commercial products on the market. While good activities of dsRNA on plant-colonizing viruses and insects have been shown, control of microbes such as fungi and bacteria is still questionable. Among the pathogenic agents affecting crop yield (including viroids, viruses, bacteria, oomycetes and fungi), higher fungi form a large and diverse group. Due to their broad spectra colonizing the host plant, it is very hard to find a single strategy to tackle them. Here, we present the advantages and disadvantages of RNAi technology to control crop-damaging fungi through the direct application of *in vitro* synthesized dsRNA. We summarize our studies on uptake of different types and lengths of dsRNA, as well as their efficacy across various fungal pathogens. Finally, we will discuss possible key factors for dsRNA transfer into fungi and plant tissues.

KN(S1)/02: A New Playbook in host-pathogen interactions and resistance: R-gene labeling, R-gene rotations and KASP markers as new tools in canola-blackleg management in Canada

Dilantha Fernando*
Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada
**Email: Dilantha.fernando@umanitoba.ca*

*Leptosphaeria maculans*is a hemi-biotroph that causes blackleg disease and remains a significant threat to canola (*Brassica napus*) in Canada, Australia, USA and Europe. Single gene (qualitative) resistance is the primary source in many breeding programs around the world with some adult plant (quantitative) resistance in their background to mitigate this disease. Blackleg has been managed for over 3 decades with good genetics but there's been a steady increase of resistance being eroded due to the presence of new races of the pathogen in grower fields. Rlm3 is the predominant gene found in Canadian canola cultivars. AvrLm3 gene has been disappearing rapidly in many fields, and also have been non-effective due to epistatic suppression, enabling the pathogen to cause moderate to severe disease in grower fields. The identification of R-genes in Canadian canola germplasm, the blackleg-pathogen races across the canola growing regions has helped the industry to introduce a new R-gene rotation strategy as a new tool in management. The development of a diagnostic tool, Kompititive Allele Specific PCR (KASP) markers has helped the producers to identify the predominant races present in their fields. This would help them to select the R-genes in the variety they select to grow in the R-gene rotations. The seed companies are starting to label their varieties with the known R-genes and their combinations so growers can make a good selection of varieties that suits their needs. The adoption of major-gene resistance groups and the *L. maculans* race diagnostics will provide producers with new tools to help manage and mitigate blackleg.

KN(S1)/03: Integration of resistance in wheat to counter fast evolving rust pathogens

S.C. Bhardwaj*
ICAR-Indian Institute of Wheat and Barley Research, Regional Station, Flowerdale, Shimla – 171002, Himachal Pradesh, India
**Email: scbfdl09@gmail.com*

Wheat rusts are highly dynamic pathogens and evolve very fast rendering a resistant variety susceptible. In absence of alternate hosts variability in wheat rusts mainly occurs through mutation. Avirulence is usually dominant over virulence, and the loci heterozygous for avirulence mutate more to phenotypic virulence than homozygous loci. Two types of rust resistance genes are generally used for breeding resistant wheat. First one is called R genes which are race specific to the pathogen in their action. These are effective at all growth stages and mostly encode immune receptors of the nucleotide binding leucine rich repeat type. The second category is of adult plant resistance genes (APR) which is mostly expressed after third leaf stage. The levels of resistance imparted by single APR genes are again of two types. First one is only partial and allows substantial rust development without any significant yield loss. Another category is APR genes that provide resistance to some or all isolates of a rust pathogen species and a subclass of these may provide resistance to other rusts also. It is a well known fact that mutation frequency for gaining virulence on one gene is of the order of 10^{-7}. Likewise frequency for two genes would be 10^{-14} and that for three rust resistance genes would be 10^{-21}. Therefore, combining more than two or preferably three resistance gene would add to the durability of a wheat variety as it would be difficult to mutate for three resistance genes. A combination of seedling, adult plant and slow rusting resistance would not only add to the durability but also diversity for rust resistance. Another strategy is to combine known slow ruster with a major gene. In breeding for rust resistance, selection of parents with desirable traits and good agronomic characters are very important. Backcrossing method to pyramid resistance to rusts is a widely adopted procedure for rust resistance breeding. Modified bulk method is widely used for selecting the desirable traits. Proper screening at seedling and multi-location evaluation at adult plant stage is another aspect of resistance breeding. Deployment of different varieties with diverse resistance by using pathotype distribution data had been the key strategy for the management of wheat rusts in India. Our claim is testified with the fact that we had no rust epidemic for the last about five decades and now crossed 107 million tonne mark of wheat production.

Invited Lectures (Lead Lectures)

IP(S1)/01: Unfurling maydis blight resistance in maize germplasm of India

Robin Gogoi*
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: r.gogoiiari@gmail.com*

Maize (*Zea mays* L.) is affected by various fungal diseases and maydis leaf blight (MLB) caused by *Bipolaris maydis* is the prime one. Initially, the race of *B. maydis* prevailing in India was confirmed as ‘race O’ through phenotyping of normal and cytoplasmic male sterile (CMS) lines. Histopathological, physiological and molecular characterization of two germplasm SC-7-2-1-2-6-1 (INGR 07025) and SC 24 (92)-2-3-2-1-1 (INGR 08117) registered in ICAR-NBPGR as highly resistant lines and one highly susceptible line CM 119 were differentiated by histopathological, physiological and molecular characters. Light and scanning electron microscopy (SEM) revealed dense trichomes, less stomata number, wax deposition around stomata, thin mycelia colonization in mesophyll cells of the resistant lines. Stomatal conductance, photosynthetic and transpiration rates were very contrast between resistant and susceptible lines. The simple sequence repeats (SSR) primer umc1590 located on chromosome 1 showed polymorphism which resolved a band (153bp) in the resistant lines. Six genetic populations P1, P2, F1, F2, BC1P1 and BC1P2 were derived from CM 119 and SC-7-2-1-2-6-1 and evaluated artificially for MLB resistance. Segregation analysis revealed at least two major genes associated with MLB tolerance. Expression of PR proteins and PAL enzyme associated genes was studied by qPCR at different time intervals post inoculation of CM 119 and SC-7-2-1-2-6-1. The enhanced expression indicated their association with infection stages of *B. maydis* and response of the resistant line during disease establishment.

IP(S1)/02: Innacte immunity in plants and systemic acquired resistance for plant health – Challenges and opportunities to ensure food security

H. Shekar Shetty*
Department of Studies in Applied Botany & Biotechnology, University of Mysore, Manasagangotri,
Mysore - 570006, Karnataka, India
**Email: hss_uom@hotmail.com*

Green revolution based agriculture crop protection is managed by applying a range of synthetic agrochemicals. Growing public awareness to both the environment and human health has created a growing demand for environment friendly crop protection techniques. Plant innate immunity and resistance inducer (PRI) is one of the recent approaches for crop protection by the researchers and commercial interested organizations. Systemic immunity triggered by local plant-microbe interactions studied as systemic acquired resistance (SAR) or induced systemic resistance (ISR) depending on the site of induction and the life style of the inducing microorganism. SAR is induced by pathogen interacting with leaves, whereas, ISR is induced by beneficial microbes interacting with roots. Salicylic acid (SA) is a central component of SAR, with additional signals promoting systemic and root local immunity. The non-SA SAR pathway is driven by pipecolic acid or its bioactive derivative; N-hydroxy pipecolic acid. In addition, these pathways further regulates inter plant defence propagation through volatile organic compounds (VOC) that are emitted by SAR induced plants and reorganized as defence signals by neighbouring plants. Knowledge gain on SAR has yielded to develop new strategies to induce resistance in crop plants and protect against pest and diseases on the sustainable basis. However, there are many areas where our knowledge is not enough to make the SAR a successful technology for plant disease management. Mainly the issues of initial triggering molecule for SAR inducer is yet to be understood and also the signal molecules required for inducing resistance and understanding the mobile signals involved in the process of SAR are important.

IP(S1)/03: Studies on occurrence, variability and sources of resistance for head scab of wheat in India

M.S. Saharan*, M.S. Gurjar and Rashmi Aggarwal
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: mssaharan7@yahoo.co.in*

Wheat (*Triticum aestivum* L.), is the second most important staple food crop of the world accounts nearly 30 per cent global cereal production covering an area of 220 million hectares. Wheat production in India has increased many folds from 6.4 mt in 1950 to 107.2 mt during 2019-20. *Fusarium* head blight or head scab of wheat caused by *Fusarium* spp. is a devastating disease that cause significant yield and quality losses in humid and sub humid regions of the world. Currently head scab is of minor importance to India but the disease is likely to increase due to global climate change and the preference of farmers for reduced tillage practices in the northern plains of India. Extensive disease surveys undertaken in different wheat growing zones of the country during 2010-21 revealed the association of six *Fusarium* species *viz*., *F. graminearum*, *F. verticillioides*, *F. oxysporum*, *F. equiseti*, *F. solani* and *F. semitectum* with head scab disease. *Fusarium graminearum* was found in most of the samples collected from Lahaul valley, Punjab as well as from Wellington. During 2021, disease has also been observed at farmers' fields in Maharashtra and Madhya Pradesh. Pathogenic variation among *Fusarium* spp./isolates have been studied by inoculating on a set of wheat varieties under artificially inoculated conditions. *Fusarium graminearum* was found most pathogenic as compared to other *Fusarium* species. Genetic variation among *F. graminearum* isolates have been detected with RAPD, microsatellite and SSR markers. Evaluation of more than 5000 wheat lines (indigenous germplasm, released varieties and exotic lines) during last two decades led to the identification of resistant sources. Since disease is emerging in more wheat growing areas, there is need to characterize the *Fusarium* spp./isolates causing head scab and more wheat germplasm needs to be evaluated for sources of resistance.

Oral Presentations

OP(S1)/01: Enhancing genetic gain for wheat blast resistance in bread wheat using genomics

Philomin Juliana[1]*, Xinyao He[1], Arun Joshi[2], Gyanendra Singh[3], Muhammad Kabir[4], Krishna Roy[4], Md. Babul Anwar[4], Felix Marza[5], Jesse Poland[6], Sandesh Shrestha[6], Ravi Singh[1] and Pawan Singh[1]

[1]*International Maize and Wheat Improvement Center (CIMMYT), Mexico*
[2]*Borlaug Institute for South Asia (BISA)/International Maize and Wheat Improvement Center (CIMMYT), India*
[3]*ICAR-Indian Institute of Wheat and Barley Research, Karnal – 132001, Haryana, India*
[4]*Bangladesh Wheat and Maize Research Institute, Bangladesh*
[5]*Instituto Nacional de Innovación Agropecuaria y Forestal, Bolivia, South America*
[6]*Kansas State University, Manhattan, USA*
**Email: p.juliana@cgiar.org*

Wheat blast caused by the fungus *Magnaporthe oryzae* pathotype *Triticum* (MoT) is an emerging threat to bread wheat production in South Asia. To enhance the rate of genetic gain for blast resistance, we first identified genomic regions associated with blast resistance using a large genome-wide association study (GWAS) with 1,106 lines from the International Maize and Wheat Improvement Centre's (CIMMYT) international nurseries evaluated in Bolivia and Bangladesh. We identified 36 significant markers with consistent effects across different site-years, which included 20 markers that were significant in all the 49 datasets and tagged the 2NS translocation from *Aegilops ventricosa*. The mean blast index of lines with and without the 2NS translocation was 2.7 ±4.5 and 53.3 ±15.9, respectively, substantiating its strong effect on blast resistance. We then fingerprinted a large panel of 4,143 lines for the 2NS translocation that indicated its presence in about 94% of lines in the international nurseries distributed by CIMMYT in 2019. We also evaluated the potential integration of genomic selection (GS) in blast resistance breeding for increasing the selection accuracy. While our results demonstrate the effectiveness of using genomics to enhance the genetic gain for 2NS-based blast resistance, they also emphasize the urgent need to identify novel non-2NS sources of blast resistance.

OP(S1)/02: Parental polymorphic survey and screening of F$_2$ mapping population derived from a cross between Bhut Jolokia (CC0164) X IVPBC-535 against anthracnose (fruit rot) in chilli

Neeraj Dwivedi[1]*, Dipti S. Tirkey[1], Shabnam Katoch[2] and Lakshman Prasad[2]

[1]*TERI–Deakin Nanobiotechnology Centre, TERI Gram, The Energy and Resources Institute (TERI), Gwal Pahari, Gurugram - 122002, Haryana, India*
[2]*Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
**Email: neeraj.dwivedi@teri.res.in; ndbiotech@gmail.com*

In India, anthracnose or fruit rot caused by *Colletotrichum* spp. is a serious disease of chilli which may result in losses of upto 50 percent of the marketable yield through pre and post-harvest fruit rot. An effort has been made to develop an interspecific F2 mapping population derived from the cross between Bhut Jolokia (CC0164) X IVPBC 535. The parental polymorphic survey has been conducted using microsatellite markers. A Total of 380 earlier reported microsatellite (SSR) primers pair distributed across the chilli genome were synthesized and applied for parental polymorphic survey of selected parents. Standard PCR conditions were followed for SSR amplification. PCR products were separated on 3.4 % agarose gel and visualized in the presence of ethidium bromide (5ìg in 100 ml) using a gel documentation system. Out of them 72 (18.94%) SSR markers were found polymorphic among parents. All microsatellite markers amplified in a range of 150bp to 350bp. Moreover, Fruits and leaves of thirty-seven F2 individuals were screened against *Colletotrichum capsici* (ITCC 6078) and *Colletotrichum gloeosporioides* (ITCC 6270). Thirteen F2 lines were found symptom less, 6 showed highly resistant reaction, two F2 lines were

found moderately resistant, six showed moderately susceptible and 10 F2 individuals displayed highly susceptible reactions. However these are preliminary results and more F2 lines are being generated for the mapping as well as phenotyping for anthracnose resistance. The polymorphic microsatellite markers and initial screening results will be utilized for the identification of QTLs for anthracnose resistance in chilli.

OP(S1)/03: Identification and characterization of Indian mustard accessions with novel resistance against multiple isolates of *Albugo candida* occurring at Wellington

J. Nanjundan[1]*, Naveen Singh[3], Navinder Saini[3], J. Radhamani[2] and Reshmi Yadav[2]
[1]*ICAR-Indian Agricultural Research Institute, Regional Station, Wellington - 643231, The Nilgiris, Tamil Nadu, India*
[2]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi – 110012, India*
[3]*ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
**Email: agrinanju@gmail.com*

The ICAR-Indian Agricultural Research Institute, Regional Station, Wellington, located at the Nilgiri hills is a hot spot for several *Brassica* pests and diseases due its unique geographical location and climatic conditions. Among the diseases, the white rust caused by *Albugo candida* is a major problem in most of the mustard growing regions of India under the favorable climatic conditions. Most of Indian mustard cultivars widely grown in India are highly susceptible the white rust and so far only few resistant varieties and genetic stocks have been developed by employing the exotic (East European) donors. The ever evolving pathotypes of *A. candida* is also a cause for concern, the status of which is not systematically studied in India. Thus, continuous efforts are necessary to search for new sources of resistance to all the existing pathotypes of *A. candida* in India. In this study, 10,267 Indian mustard accessions were first evaluated at Bharatpur, Rajasthan under natural epiphytotic conditions and 2,183 resistant accessions were identified, which were further evaluated at Wellington, under hot spot conditions which resulted in identification of 86 accessions with complete resistance. Continuous screening of these 86 accessions over the past ten years at Wellington resulted in identification of 86 accessions with resistance against the “few isolate(s)” of *A. candida* present prior to *kharif* 2019 and 31 accessions with resistance against “all the isolates” of *A. candida* occurring at Wellington, presently. Further studies to confirm this type of differential reaction, molecular characterization of 86 resistant accessions with publicly available markers linked to three white rust resistant loci viz. AcB1.4.1, AcB1.5.1 (BjuWRR1) and BjuWRR2 to test the homology, allelic test to identify “new” white rust resistance genes other than the earlier reported ones and to transfer these “novel” resistance gene(s) to popular Indian mustard cultivars are underway at Wellington.

OP(S1)/04: Marker assisted pyramiding of stem rust, leaf rust and powdery mildew resistance genes for durable resistance in wheat (*Triticum aestivum* L.)

Vikas V.K.[1]*, Sivasamy M.[1], Jayaprakash P.[1], Prasad P.[2], Kumar S.[2], Bhardwaj S.C.[2], Geetha M.[1], Nisha R.[1], Shajitha P.[1] and John Peter[1]
[1]*ICAR-Indian Agricultural Research Institute, Regional Station, Wellington - 643231, The Nilgiris, Tamil Nadu, India*
[2]*ICAR-Indian Institute of Wheat and Barley Research, Regional Station, Flowerdale, Shimla - 171002, Himachal Pradesh, India*
**Email: physiovikas@gmail.com*

Wheat production is essential for food security. Stem and leaf rust diseases of wheat continually pose a threat to wheat production at national and international level. In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential yield threat to wheat. Resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew diseases of wheat. Resistance based on single gene has short life span. Same time, selection of two or more genes in a single genotype can be difficult using conventional selection system. In such a scenario, phenotype neutral selection based on marker-trait association backed by host pathogen interaction becomes inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr24/Lr24*, *Sr26* and *Sr36/Pm6* were pyramided in the background of Indian wheat cultivars through marker assisted backcross approach. The presence of the rust and powdery mildew resistance genes were confirmed using microsatellite markers such as *Sr24#12*(*Sr24/Lr24*), *Sr26#43*(*Sr26*) and *stm773-2*(*Sr36/Pm6*) in the backcross derivatives. Stable lines were selected at BC3F4 generation. Seedling reaction of pyramided lines showed resistance to most of the stem and leaf rust pathotypes prevailing in India, while the adult plant reaction at Wellington exhibited resistance reaction to stem and leaf rust and powdery mildew. The use of gene pyramids (*Sr24/Lr24*, *Sr26* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability and sustainability to the cultivars than single gene deployment.

OP(S1)/05: Molecular characterization of tobacco etch virus (TEV) infecting hot peppers (*Capsicum chinense*) in Trinidad and Tobago

Mounika Kollam*, Chinnadurai Chinnaraja, Adesh Ramsubhag, Jayaraj Jayaraman
The University of the West Indies, Department of Life Sciences, Faculty of Science and Technology, St Augustine, Trinidad and Tobago, WI
**Email: mounikollam@gmail.com*

The tobacco etch virus (TEV) belongs to the genus *Potyvirus*, which is becoming a serious pathogen of hot peppers (*Capsicum chinense*) in Trinidad and Tobago, causing significant economic losses. The three isolates of TEV from three different landraces, viz, Scotch Bonnet, CARDI Green, and Scorpion pepper were characterized and designated as a new genotype, TEV-TRINI based on genomic variations from other described strains. Phylogenetic analyses revealed that TEV-TRINI isolates had 6.4-7.0% variation with the closest related isolates, including HAT (USA), SD1 (China), and Shannxi (China). In the polyprotein region, 256 variable amino acids were recorded with their closest relative TEV isolates. The extent of recorded variation throughout the genome with other isolates proved this to be a new TEV genotype. This study revealed a high level of up to 21.7% aa variation in P1 protein with other reported isolates. Through recombination analysis, detected eight recombination events in TEV-TRINI isolates revealed the contribution of other TEV recombinant sequences as major and minor parents of the genome of the new genotypes. Based on greenhouse experiments, the possible modes of TEV-TRINI spread were identified through mechanical, seed, and aphid vector (*M. persicae*) transmission. The TEV virion levels in leaves, aphids, seeds, and fruit carp were quantified in different growth stages of the plant by relative and absolute RT-qPCR quantification methods.

OP(S1)/06: Black pepper endophytic *Pseudomonas putida* BP25 modulates defense elicitation in rice against blast disease

Mushineni Ashajyothi[1]*, Aundy Kumar[1], Neelam Sheoran[1], Prakash Ganeshan[1], Robin Gogoi[1], Gopalakrishnan Subbaiyan[2] and Ramcharan Bhattacharya[3]
[1]Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
[2]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
[3]National Institute for Plant Biotechnology, Pusa Campus, New Delhi - 110012, India
**Email: aashjyo18@gmail.com*

Rice blast disease induced by *Magnaporthe oryzae* is the major production constraint in rice farming worldwide despite tedious resistance breeding programmes and application of chemical pesticides. Eco-friendly novel biocontrol strategies are the current need of the hour to combat this globally important plant pathogen. In this study we found black pepper associated *Pseudomonas putida* BP25 endogenously colonized rice -a monocot, in a density-dependent

manner with altered root phenotype and induced defense activation, also showed biocontrol activity against rice blast disease. Fluorescence imaging of *P. putida* BP25 primed rice seedlings based on confocal laser scanning microscopy, revealed an extensive bacterial colonization in roots that was further confirmed in plate count assay and qPCR studies. The initial bacterial counts could be correlated with bacterial dose used for seed priming, however the population stabilized 14-days post priming suggesting internal population regulation of *P. putida* BP25 colonization. Endophytism of rice triggered alteration in root morphology, possibly, due trade-off between growth and defense. *P. putida* BP25 significantly inhibited the mycelium of *M. oryzae* by both volatile and non-volatile metabolites and also seed priming protected the rice from blast. Activities of defense related peroxidase and phenols were found increased in primed plants. qPCR assay of rice defense and developmental genes indicated increased expression of Systemic Acquired Resistance (SAR) related Os*PR1-1* (Pathogenesis Related protein 1-1) and down-regulation of Os*PR3*. In addition, rice seedlings emerged from endophyte priming showed down-regulation of stress responsive Os*ACO4* and Os*ACS6* involved in inter-nodal elongation which plays an important role in growth and development. Our study explains how endophyte *P. putida* BP25 induced root phenotypic alteration in rice along with its potential to exploit as an alternate for rice blast management.

Poster Presentations

PP(S1)/01: Antibacterial activity and their GC–MS analysis of bioactive compounds of plant extracts against inciting bacterial stalk rot (*Dickeya dadantii*)

Sujata Singh Yadav* and Y. Singh
Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakhand, India
**Email: sujatasingh62@gmail.com*

Dickeya dadantii, the causal organism of bacterial stalk rot of sorghum is a widely spread and destructive disease in India. The use of previously reported various chemicals and antibiotics has been against this disease with variable degrees of success, besides, excessive use of antibiotics and chemicals causes detrimental consequences to health hazards and development of resistance to various other human pathogenic bacteria. Hence, it is important to look for alternative strategies for disease control that can be used as an integrated disease management approach. It was delineated that methanolic extract of twenty plant extracts evaluated against the *D. dadantii. In-vitro* the antibacterial activity was carried out by disc diffusion method, minimum inhibitory concentration (MIC50) at different concentration (5, 10, 15, and 20%) of the twenty tested plants, only eucalyptus (*Eucalyptus globulus*) and bael (*Aegle marmelos*) depicted the highest zone of inhibition in the range (2.0-2.1cm) at 20% concentration. MIC50 values (5%) concentration revealed that the extract of *Eucalyptus globulus* (0.224 mg ml-1) and *Aegle marmelos* (0.218 mg ml-1) having high antibacterial activity against *D. dadantii*. The present study also focused on the evaluation of phytochemical compounds from *Eucalyptus globulus* and *Aegle marmelos* by Gas chromatography-mass spectrometry (GC-MS). To investigate the antibacterial, the physiological and morphological changes in *D. dadantii* were observed by scanning electron microscope (SEM) after treatment with *Eucalyptus globulus* and *Aegle marmelos* extract.

PP(S1)/02: Plant disease management by new generation fungicides

Vishal Gandhi[1]* and Rakesh Mehra[2]
[1]*Department of Plant Pathology, CCS Haryana Agricultural University, Hisar - 125004, Haryana, India*
[2]*Regional Research Station, CCS Haryana Agricultural University, Karnal - 132001, Haryana, India*
**Email: vishalgandhi1991@gmail.com*

In the modern intensified agriculture, the efficient management of plant diseases is essential. At present the most reliable means of managing disease is by the use of fungicides. Fungicides are the toxic substances which either kill or check the growth of the fungi. During the last two decades, fungicide research has produced a diverse range of fungicidal products with novel modes of action which had a significant impact on plant disease control. The need for new and innovative fungicides is driven by resistance management, regulatory hurdles, and increasing customer expectations. Compounds having a novel mode of action with enhanced characteristics such as systemicity, curativity, and longevity of disease control are of special interest. The technical feature of new generation fungicides are target specific action and safer to non target sites. Over the past few years, however, several truly novel compounds have been launched commercially and have reached an advanced stage of development, which include phenylpyrroles, anilinopyrimidines, strobilurins, oxazolidinediones, anilinopyrimidines, diarylamines etc. with effects on respiration, cell membrane components, protein synthesis, signal transduction and cell mitosis. In India, 52 fungicides are registered for use on agricultural crops. Some of the recently developed fungicides have also been registered for use against different diseases and a good number of the novel action fungicides are currently under evaluation. Two novel fungicides namely azoxystrobin and pencycuron have been registered for use against powdery and downy mildews in grape vine and rice sheath blight, respectively. Many of the important plant diseases, which were not controlled satisfactorily by the previous traditional fungicides, can now be well managed by the new compounds which are mostly systemic in nature. In view the risk of resistance development with most of the systemic, site specific compounds, there is a need to develop more classes of fungicide with novel target sites.

PP(S1)/03: Pathogenicity and molecular characterization of *Burkholderia glumae* causing bacterial panicle blight of rice

Sanjeev Kumar*
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: sanjv007@gmail.com*

Bacterial panicle blight (BPB) of rice is a severe disease caused by *Burkholderia glumae*. It has been emerging as a major constraint in rice productivity in rice growing areas of the northern part of India including Uttar Pradesh, Haryana, Delhi, and national capital regions. In this study, we isolated seven strains of the bacteria from the diseased samples collected from different states of Northern India. The bacterial colony grew at 42°C but not at 4°C and produced a diffusible light yellow pigment on King's B agar, which is characteristic of *B. glumae*. The bacteria utilized sorbitol, inositol, manitol, acetate, succinate, gluconate, and citrate but not maltose nor sucrose. The bacteria did not produce indole, H2S, nor cyanide but produced catalase and gelatinase. The pathogenicity was confirmed at the panicle initiation or boot leaf stage by infiltrating bacterial suspensions (1 × 108 cfu ml”1) using a sterile syringe into the sheath, leaf, and flag leaf (boot leaf) of susceptible basmati rice (cv. Pusa basmati 1) under nethouse conditions. Plants infiltrated with sterile distilled water (1 plant per part) served as control. The plants were kept under high humidity (>80%) and warm conditions (28 to 30°C) and monitored for disease development. After 7 to 10 days, the artificially inoculated rice leaves and sheaths produced lesions similar to that observed during natural rice infection in the field. At 10 to 15 days post-inoculation, the panicle appeared from the inoculated boot leaf with light brown discoloration similar to that of bacterial panicle blight symptoms. Bacteria were reisolated from the infected rice plants and their identity was confirmed to be identical to the original strain by 16S rRNA sequence analysis. This study confirms the dominance of BPB in the rice growing belts of north India. We have been analyzing these strains for different virulent traits including toxin, toxoflavin production and T3SS effectors. The detailed insights on virulence factors would be useful in exploring the management strategy for this disease.

PP(S1)/04: Genetic analysis and identification of molecular marker linked to downy mildew resistance gene Ppa207 in cauliflower (*Brassica oleracea* var. *botrytis*)

Partha Saha[1]*, Chandrika Ghoshal[1], Soham Ray[2], Namita Das Saha[3], Mohita Shrivastava[1], Pritam Kalia[1] and B.S. Tomar[1]
[1]Division of Vegetable Science, [3]Centre for Environmental Sciences and Climate Resilient Agriculture,
ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
[2]ICAR-Central Research Institute for Jute and Allied Fibres, Barackpore, Kolkata - 700120,
West Bengal, India
**Email: hortparth@gmail.com*

The present study was undertaken to identify molecular markers linked to downy mildew resistance gene. The resistant and susceptible lines in 84 RILs from cross of 'Pusa Sharad' and 'DMR-2-0-7' segregated in 1 (R):1 (S) ratio indicating monogenic resistance and named the gene as *Ppa207*. Two markers viz. BoGMS0486 and BoGMS0900 showed polymorphism in BSA and could distinguished resistant and susceptible bulk and segregated in 1 (R):1 (S) ratio. The recombination frequencies between BoGMS0486 and BoGMS0900, BoGMS0486 and *Ppa207*, BoGMS0900 and *Ppa207* were 4.8%, 3.6% and 1.2%, respectively. We mapped the resistance gene *Ppa207* in 4.8 cM linkage interval on linkage group 2 (C02) of cauliflower, flanked by the markers BoGMS0486 and BoGMS0900 at 3.6 cM and 1.2 cM apart from the said gene, respectively. The marker BoGMS0486 is located 2.9 Mb position of chromosome C02 and BoGMS0900 at 23.2 Mb position of same chromosome, this 4.8 cM marker interval actually correspond to 20.3 Mb physical distance. The identified SSR markers linked to the new resistant gene *Ppa207* will be very useful in marker assisted selection in cauliflower.

PP(S1)/05: Artificial screening of Brassica accessions for two isolates of *Sclerotinia sclerotiorum*

Shabnam Katoch, Sonia, S. and **Lakshman Prasad***
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: laxmanprasad25@yahoo.com*

Brassica juncea (L.) Czern adds a huge contribution in terms of area and production of oilseeds. Crop production is adversely affected by various biotic and abiotic factors among them white rot caused by *Sclerotinia sclerotiorum*. Stem rot is one of the major constraint known to cause upto 60 per cent yield losses. White rot results in the formation of brown water soaked lesions on leaves and stem with whitish soft lumps which later on turns to hard black colored structures (sclerotia). The sclerotial bodies clog the stem which ultimately leads to wilting of infected plants. Fungicides being use to protect plant are ineffective alongside increasing awareness for pesticide free food. Though, disease resistance cultivars are not available against this disease. Therefore, identification of resistance sources has taken important place in disease management. In this study, 263 *Brassica* accessions were evaluated against two isolates of *S. sclerotiorum* using artificial stem inoculation technique under field conditions. Five-six plants of each genotype were inoculated at flowering stage and after 7 days of inoculation, the inoculated plants were observed for disease severity based on lesion length, stem girdling and wilting. Out of 263 accessions, some of them were resistant and moderately resistant to *Sclerotinia* isolates collected from Punjab and Rajasthan. Five accessions viz. RT-57, RLM-198, 4.3.1.8.4 P1, Vulcan, IM-46 and IM-85 showed resistance to both of the isolates. The resistant accessions identified in the present study could be screened for other *Brassica* diseases to develop multi-disease resistance cultivars.*Brassica juncea* (L.) Czern adds a huge contribution in terms of area and production

of oilseeds. Crop production is adversely affected by various biotic and abiotic factors among them white rot caused by *Sclerotinia sclerotiorum*. Stem rot is one of the major constraint known to cause upto 60 per cent yield losses. White rot results in the formation of brown water soaked lesions on leaves and stem with whitish soft lumps which later on turns to hard black colored structures (sclerotia). The sclerotial bodies clog the stem which ultimately leads to wilting of infected plants. Fungicides being use to protect plant are ineffective alongside increasing awareness for pesticide free food. Though, disease resistance cultivars are not available against this disease. Therefore, identification of resistance sources has taken important place in disease management. In this study, 263 *Brassica* accessions were evaluated against two isolates of *S. sclerotiorum* using artificial stem inoculation technique under field conditions. Five-six plants of each genotype were inoculated at flowering stage and after 7 days of inoculation, the inoculated plants were observed for disease severity based on lesion length, stem girdling and wilting. Out of 263 accessions, some of them were resistant and moderately resistant to *Sclerotinia* isolates collected from Punjab and Rajasthan. Five accessions viz. RT-57, RLM-198, 4.3.1.8.4 P1, Vulcan, IM-46 and IM-85 showed resistance to both of the isolates. The resistant accessions identified in the present study could be screened for other *Brassica* diseases to develop multi-disease resistance cultivars.

PP(S1)/06: Functional validation of rice proteins that associate with *Xanthomonas oryzae* pv. *oryzae* XopF effector in the development of bacterial blight disease in rice

Aditya Kulshreshtha* and Kalyan K. Mondal
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: aditya.ihbt@gmail.com*

Xanthomonas oryzae pv. *oryzae* (Xoo) causes a most destructive bacterial blight disease in rice. It secretes many type three secretion system (T3SS) effectors for bacterial growth and efficient invasion in rice tissues. In our previous work, we demonstrated the role of XopF effector in Xoo growth and suppression of PAMP-triggered immunity (PTI). Further, we also identified two XopF interacting rice proteins; photosystem I (PSI) reaction centre subunit V (PSI-G) and cyclophilin II through Y2H system. In this study, we validated the functional role of PSI-G in rice::Xoo interactions using virus-induced gene silencing (VIGS). The PSI-G sequence was analysed using computational tools and a small fragment for efficient gene silencing was identified. The cDNA was prepared from extracted rice RNA and PSI-G fragment was PCR amplified. The amplified fragment was cloned into rice tungro bacilliform virus (RTBV) VIGS vector at *Pac*I and *Mlu*I restriction sites. The empty vector (RTBV), VIGS construct (RTBV-PSI-G) and positive control (RTBV-PDS) were separately transformed into competent *Agrobacterium tumefaciens* (strain EHA 105) cells. The positive colonies were grown in LB medium and suspended into infiltration buffer. The suspended cultures were infiltrated into rice leaves (cv. PB1) in the following combination: (i) RTBV, (ii) RTBV-PDS and (iii) RTBV-PSIG. The validation of gene silencing and disease related events in rice::Xoo interactions in both mock (only RTBV) and silenced rice (RTBV-PSIG) plants are in progress. This insight will be useful for development of durable disease resistance strategies by targeting the host proteins.

PP(S1)/07: Management of Cercospora leaf spot of mungbean [*Vigna radiata* (L.) Wilczek] through fungicides and host resistance

Durga Prasad*
Department of Plant Pathology, College of Agriculture, Banda University of Agriculture & Technology, Banda – 210001, Uttar Pradesh, India
**Email: dp.shubh@gmail.com*

The pulses, mainly mungbean [*Vigna radiata* (L.) Wilczek] is an important crop grown extensively in Bundelkhand region of Uttar Pradesh. Despite the multifaceted importance of this crop, its production could not be stabilized in the Uttar Pradesh as well as in the country. There are several biotic constraints like diseases and insect-pests hampering the production of mungbean crop. Among the diseases, Cercospora leaf spot is the most important fungal disease occurring regularly in the mungbean growing areas. The disease is caused by *Cercospora canescens* Ellis and Martin. Cercospora leaf spot disease appears during warm and humid weather leading to Chlorosis, defoliation and low yield. Keeping in view of importance of disease, experiments were conducted to to find out the efficient management strategies for this disease. During both of the crop seasons i.e. *Kharif* 2019 and 2020, twice sprays of Carbendazim at 1st appearance of symptoms and 15 days' interval gave the maximum reduction in incidence and severity i.e. 45.57% and 58.45%, respectively; of Cercospora leaf spot disease along with significant enhancement (53.39%) in seed yield (quintal/ha) as well as in yield components (except number of primary branches per plant and number of seed per pod) over the unprotected crop. It was followed by the twice sprays of Carbendazim + Mancozeb with respective parameters. Sprays of Captan + Hexaconazole were found to be least effective to reduce the disease incidence/ severity as well as to increase the yield and its components. Out of 190 mungbean genotypes evaluated against Cercospora leaf spot during two consecutive crop seasons, four genotypes viz., PDM 04-123, PDM 54, EC520034-1 and EC 520022 were found to be resistant against Cercospora leaf spot.

PP(S1)/08: Identification of tolerant landrace genotypes against rice false smut through artificial screening

Preeti[1], **D. Ladhalakshmi[1]*,** R. Lokesha[2], M. Bhaskar[1], P. Koteshwar[1], C. Gireesh[1], M.S. Anantha,
L.V. Subba Rao and C.N. Neeraja[1]
[1]*ICAR-Indian Institute of Rice Research, Hyderabad - 500030, Telangana, India*
[2]*University of Agricultural Sciences, Raichur - 584104, Karnataka, India*
**Email: ladhasavitha@gmail.com*

Rice false smut caused by *Ustilaginoidea virens* (teleomorph: *Villosiclava virens*) has become most devastating grain disease of rice. The pathogen infects during flowering stage and affects both grain yield and grain quality. It's essential to identify resistant genotype using standardized artificial screening technique. During, *Kharif* 2020, 207 landrace genotypes were screened through artificial inoculation under field conditions. Booting stage plants were inoculated with 2 ml of *U. virens* conidial suspension (2 x 105 conidia/ml) using a sterile hypodermic syringe during evening hours. For each genotype, 5-8 panicles were inoculated. Data were recorded 15 days after inoculation. Percentage of panicle infection ranged from 20 -100% with the number of smut balls varied from 1-20 and percentage of spikelet infection was ranged between 0.15- 69.69%. Three genotypes (IC126295, IC379047 and IC134486) were identified as tolerant with score of 3. Eight genotypes were found highly susceptible with maximum number of smut balls ranging from 11-20 and remaining genotypes showed varied level of susceptibility (with maximum number of smut balls/panicle ranging from 5-9). The identified tolerant genotypes will be re-evaluated during *Rabi* and *Kharif* 2021. The screening technique developed and standardized at ICAR-IIRR can be adopted under field conditions to identify the resistant sources against false smut disease of rice.

PP(S1)/09: Introgression of rust resistance gene *Lr37* and soft grain *pinaD1a* gene in wheat through marker assisted backcross breeding

Tej Pratap Jitendra Kumar[1], Anjali Rai[2], Arvind K. Ahlawat[2], Namita Bedi[3], Malkhan Singh Gurjar[1] and **Anju Mahendru Singh[2]***
[1]*Division of Plant Pathology,* [2]*Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India*
[3]*Department of Biotechnology, Amity Institute of Biotechnology, Amity University, Noida - 201313, Uttar Pradesh, India*
**Email: anju.singh@icar.gov.in*

A marker-assisted backcross breeding (MABB) based gene introgression approach in wheat (*Triticum aestivum L.*) was improved, where 96% or more of a recurrent parent genome (RPG) can be recovered just two backcross generations. The present study aimed that MABB was successfully used to improve rust resistance in Near Isogenic Lines (NILs) of DBW14 wheat variety. Barham which is an Australian wheat variety was used as the donor parent for introgression of the *Lr37* and Puroindoline gene *Pina-D1a*. In a segregating population, *Lr37* and *Pina-D1a* (positive selection) and *Pina-D1b* (negative selection) was used for foreground selection to select plant carrying *Lr37* and *Pina-D1a* gene. Background selection, involving 55 polymorphic SSR markers dispersed throughout the genome, was exercised to recover the genome of DBW14. Improved NILs had significantly lower rust infection and displayed 96.3-96.5 percent of the recurrent parent genome (RPG). For grain yield, selected NILs were at par with Indian wheat variety HD2967, suggesting that there was no yield penalty. The whole exercise of transfer of *Lr37* gene, *PinaD1a* and reconstitution of the genome of DBW14 was completed with a period of three and half years demonstrating particular utility of MABB for developing rust resistance NILs with soft grain in the background of any elite and popular wheat cultivar with relatively higher speed and precision.

PP(S1)/10: Area under disease progress curve and apparent rate of infection: A measure of slow mildewing in mulberry varieties

Vijaykumar K.N.*, S.A. Ashtaputre and Yuvaraja S.
Department of Plant Pathology, College of Agriculture, Dharwad - 580005, Karnataka, India
**Email: vijaykn549@gmail.com*

Mulberry (*Morus indica* L.) is perennial woody plant belongs to the family *Moraceae*. The powdery mildew caused by *Phyllactinia corylea* (Pers.) Karst causing the leaf yield loss of about 5-10 per cent by defoliation and an additional loss of 20-25 per cent by destruction of leaf area. Nine mulberry varieties *viz.*, M-5, DD, S-36, S-41, V-1, MR-2, Mysore local, S-13 and S-34 were screened against *Phyllactinia corylea* under natural epiphytotic conditions in the field during late *kharif* 2019. The disease severity was recorded at an interval of seven days starting from 40 to 82 days after pruning (DAP) using 0-9 scale. The results revealed that out of nine varieties screened, none was found to be immune or resistant. Only V-1 and Mysore Local were found to be highly susceptible and the remaining seven varieties were found to be susceptible. Apparent rate of infection (r) of the disease on mulberry varieties at different stages showed a wide variation. The highest 'r' value was observed in the variety S-41 (0.1954) between 47-54 DAP, followed by Mysore Local (0.1868) between 41-47 DAP and the least 'r' value was observed in the variety DD (0.0103) between 75-82 DAP. The AUDPC values have also differed considerably for different varieties. The highest AUDPC value was observed in Mysore Local (1442.63) followed by V1 (1351.21), S-36 (1326.78). The least AUDPC value was observed in M-5 (584.04).

PP(S1)/11: SWEETs and their targets by the bacterial blight of rice pathogen

Rashmi E.R.* and K.K. Mondal
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: rashmier.6666@gmail.com*

Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is one of the major diseases that impact rice production globally. The bacterium uses transcription activator-like effectors (TALEs) to hijack the host susceptibility(*S*) genes, specifically members of the SWEET sucrose uniporters. Xoo TALEs specifically recognises the effector-binding element (EBEs) in the promoter regions of rice *SWEET* genes and takes the control of its expression. In this study, we performed genotype screening of 20 rice cultivars varying their resistance to bacterial blight collected from IARI, New Delhi. Specific primers for EBE sites (that constitutes the targets of four TALEs, namely, PthXo1 PthXo2, PthXo3 and AvrXa7) of major *SWEET* genes are designed to screen the *SWEET* genes in those cultivars. Our screening revealed that 6 cultivars are positive for *SWEET11*, 10 cultivars are positive for *SWEET13* while 14 cultivars are positive for *SWEET14*. This depicts variation in the promoter region of the SWEETs. Out of 20 cultivars, the promoter region of 3 cultivars (two susceptible and one resistant) were sequenced to know the variations in EBE. There is no variation found in the sequence of SWEETs EBE even though cultivars are resistant to the pathogen, depicting that, the resistance of host is governed by many other factors. However, our study unravels the rice EBEs that are being targeted by Indian Xoo strain during pathogenesis, particularly in susceptible rice cultivar. This would be helpful in altering the promoter sequence of the susceptibility gene by genome editing tools for developing resistant lines. In this direction, we designed guide RNA for three important *SWEET* genes (*SWEET11*, *SWEET13*, and *SWEET14*) using CRISPR Cas9 mediated genome editing of rice and cloned in p2XSgRSpCas9-Os vector for further editing in rice. Our study would lead to provide improved resistance in rice for bacterial blight.

PP(S1)/12: Systemic acquired resistance: An alternative approach to manage the mango anthracnose

Adikshita Sharma*, I.M. Sharma, Monica Sharma and Kishor Sharma
Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India
**Email: sharmaadikshita89@gmail.com*

Colletotrichum gloeosporioides (Penz.) Penz. & Sacc. (Telomorph: *Glomerella cingulata*) (Stonem.) Spauld & Schrenk) causing mango anthracnose is highly devastating disease in pre and post harvest stages. Presently, the fungicide has been used to control the disease thereby posing threat to environment and human health. New alternative strategies should be developed which exploits the plant defence system to control the disease by using abiotic and biotic agents. Field study was done to examine the efficacy of chemical agents, which induces systemic acquired resistance in plants prior to pathogen infection. Six systemic acquired resistance chemicals were evaluated against mango anthracnose by giving two consecutive sprays starting from the mid of august at an interval of 20 days under natural epiphytotic conditions at Regional Horticultural Research & Training Station Dhaulakuan, among which salicylic acid sprayed @ 0.075 per cent was highly effective and provided maximum 77.18 per cent disease control. It was followed by dipotassium hydrogen orthophosphate sprayed @ 0.075 per cent with 73.57 per cent disease control whereas potassium metabisulphite was least effective with 53.37 per cent disease control. Highest level of total phenols, activity of peroxidase, polyphenol oxidase and phenylalanine ammonia lyase enzymes was observed in salicylic acid sprayed plants followed by dipotassium hydrogen orthophosphate and it was minimum in potassium metabisulphite sprayed plants. Thus, substantiated their role in inducing resistance against anthracnose through increasing the level of phenols and activation of their oxidising and synthesizing enzymes.

PP(S1)/13: Indexing of *Ty*-resistance gene containing donor lines of tomato against different begomoviruses occurring in India

Firoz Mondal[1], Shipra Saxena[1], Zakir Hussain[2], Bikash Mandal[1] and **Anirban Roy[1]***
[1]Advanced Centre for Plant Virology, Division of Plant Pathology, [2]Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: anirbanroy75@yahoo.com*

Tomato leaf curl disease (ToLCD) is a major threat in cultivation of tomato throughout the world. In India at least 14 species of begomoviruses are reported to be associated with the disease thus posing challenge to resistance breeding programme. Six resistance genes (*Ty*-1 to *Ty*-6) are identified from different wild *Solanum* species against tomato yellow leaf curl virus, however, little information was available on their behavior against the begomoviruses occurring in tomato in India. We indexed 18 donor lines of tomato, containing different combinations of *Ty*-genes, against seven different begomoviruses with species specific primers along with a begomovirus universal primer. Out of 18 lines, 17 showed positive result in begomovirus universal primer. Among those 17 lines, tomato leaf curl New Delhi

virus, Tomato leaf curl Palampur virus, Tomato leaf curl Gujarat virus, Tomato leaf curl Bangalore virus, Tomato leaf curl Joydebpur virus, Croton yellow vein mosaic virus and Chilli leaf curl virus were detected in 6, 11, 8, 7, 2, 13 and 4 samples respectively, indicating presence of multiple begomoviruses in them. Maximum 7 number of begomoviruses were detected from the donor line EC814911 with Ty-5 gene. Detection of croton yellow vein mosaic virus in majority of the lines indicated probable adaptation of this virus in the *Ty*-gene containing lines, thus imposing further challenges towards the resistance breeding programme.

PP(S1)/14: Validating interactions between XopF-TTSS effector of *Xanthomonas oryzae* pv. *oryzae* race 4 and two putative rice interactor(s) during bacterial blight pathogenesis

Aarzoo Qamar*, Aditya Kulshreshtra and Kalyan K. Mondal
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: aarzooqamar@gmail.com*

Bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) is a devastating disease of rice. Xoo infects by releasing effector proteins directly into the rice cytosol through a specialized tubular proteinaceous structure called type three secretion system (T3SS). XopF is one of the Xop T3SS effectors which plays key role during BB development, Xoo growth and suppression of PTI. Previously, we identified XopF interacting rice proteins using yeast two-hybrid system. Two interactors, namely PSI-G (Photosystem I reaction centre subunit V) and Cyc II (Cyclophilin II) were found to interact with XopF. This study aims to validate the interactions between rice proteins and bacterial XopF using biofluorescence complementation (BiFC) assay as well as using Y2H system. We cloned the interactors gene as well as *xopF* gene into BiFC vectors [pSPYCE(M) (C-terminal eYFP) and pSPYNE173 (N-terminal eYFP)] and Y2H vectors (bait and prey vectors). We verified the constructs for the respective inserts through PCR using insert specific primers. For BiFC assay, we transfer the developed constructs into *Agrobacterium* cells. The tobacco plants (*Nicotiana benthamiana*) infiltrated with transformed *Agrobacterium* are being observed for epifluorescence using confocal microscopy. Our study, thus would confirm the underlying interactions between rice proteins and Xoo XopF during bacterial blight development. This insight would help in devising novel strategy for BB resistance through silencing the interactors in rice.

PP(S1)/15: Screening of potato genotypes against early blight disease of potato

Abhishek Kumar*, S.K. Singh and S.P. Singh
Department of Plant Pathology, Acharya Narendra Dev University of Agriculture and Technology, Kumarganj, Ayodhya - 224229, Uttar Pradesh, India
**Email: abhishekpathology9511@gmail.com*

Potato (*Solanum tuberosum* L.) is one of the most important vegetable cash crop growing in the world, belongs to family Solanaceae. Potato remains prone to several diseases caused by bacteria, fungi, plant parasitic nematodes and virus. Alternaria blight caused by *Alternaria solani* is one of the major diseases of potato. It causes yield losses upto 80% under favourable conditions, disease symptoms are characteristic dark brown to black lesions with concentric rings. To find out the host resistance against early blight, disease incidence under field condition at vegetable section, Acharya Narendra Dev University of Agriculture and Technology in *rabi* 2017-18 was recorded on 38 potato genotypes. Amongst them, none of the genotypes showed immune and resistant reaction. Whereas, six genotypes *viz*. Kufri Pukhraj, Kufri Lalima, AICRP-C-17, AICRP-P- 6, Kufri Ganga and Kufri Anand were found moderately resistant. Eight genotypes *viz*. AICRP-C-4, Kufri Ashok, Kufri Jyothi, Kufri Pushkar, Kufri Chipsona-1, Kufri Garima, AICRP-P-7 and Kufri Sinduri were moderately susceptible. nineteen genotypes showed susceptible reaction and five were found highly susceptible in genotypes Kufri Lalit, Kufri Bahar, Kufri Surya, Kufri Chandramukhi and AICRP-C-18. The moderately resistant source will be exploited for further breeding purpose and cultivation of potato in future.

PP(S1)/16: Reassessment of host specificity of different *Phomopsis* spp. in *in-vitro* and green house condition

Nishmitha K.[1]*****, S.C. Dubey[2], Jameel Akthar[2] and Deeba Kamil[1]
[1]Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
[2]Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus,
New Delhi - 110012, India
**Email: nishmitha3005@gmail.com*

The genus *Diaporthe* (*Phomopsis*) is a well-known pathogen infecting a wide range of agricultural important crops. They cause important diseases such as damping off, blight, fruit rot and canker resulting in yield loss up to 15-30%. Host specificity of twelve morphologically and molecularly characterized *Phomopsis* isolates were determined *in-vitro* and in greenhouse condition. Cross pathogenicity of all twelve isolates belonging to five *Phomopsis* species were carried out on three agriculturally important crop, brinjal, soybean and chilli in *in-vitro* and in greenhouse condition. The isolates belonging to *P. vexans*, *P. phaseolorum*, P. *longicolla* and *P. helianthi* were able to successfully infect and cause lesion on brinjal in both *in-vitro* and pot experiment in greenhouse. On chilli, isolates belonging to *P. phaseolorum*, *P. helianthi, D. eres* and *P. vexans* produced lesion under both assays. On soybean, *P. phaseolorum*, *P. longicolla, D. eres* and *P. helianthi* could successfully infect and cause lesion. Comparing result of detached leaf assay and under pot condition, brinjal showed highest degree of incompatibility to different isolates of *Phomopsis*, while soybean was susceptible to all the isolates except *P. vexans.* The present study disapproves the earlier finding that *P. vexans*, *P helianthi* and *P. phaseolorum* are specific to brinjal, sunflower and members of fabaceae, respectively. This clarifies that species of *Phomopsis* are host non-specific and naming only based on host association leads to confusion and is not justified.

PP(S1)/17: Evaluation of sugarcane clones for resistance to red rot disease caused by *Colletotrichum falcatum*

T.M. Hemalatha*, M. Hemanth Kumar, K.R. Tagore, B. Vajantha and N.V. Sarala
Agricultural Research Station (ANGRAU), Perumallapalle, Tirupati – 517505, Andhra Pradesh, India
**Email: hema.agri@gmail.com*

Red rot is one of the most dreaded disease of sugarcane and generally referred to as the ‘Cancer of sugarcane’. The losses due to red rot may range from 10-50 % depending upon the cultivars, environment and pathogen strain. It has become a major constraint in the profitable cultivation of sugarcane. The pathogen is a facultative saprophyte and due to continuous mutations, heterokaryosis and adaptation results in development of new pathogenic race in nature and henve it has became very challenging task for sugarcane breeder to develop a resistant variety against red rot pathogen. Effective management of the disease has been advocated mainly through the usage of resistant varieties and to a lesser extent by agronomic practices. Hence the newly developed sugarcane clones has to be evaluated for their resistance towards the red rot disease before their release. In this context, a field experiment was conducted to study the reaction of 40 sugarcane genotypes for red rot disease by nodal and plug methods of inoculation against three prevalent pathotypes in Andhra Pradesh viz., Cf 419, Cf671 and Cf997. The experiment was conducted during 2018-19 and 2019-20 at Agricultural Research Station, Perumallapalle. Among the forty clones tested, only four entries ie., 2017T17, 2017T108, 2017T154 and 2017T237 showed resistant to moderately resistant reaction to all the three pathotypes in both the methods while most of the entries showed moderately susceptible to susceptible reaction to Cf 671 and Cf 997 pathotypes. Four entries viz. 2017T2, 2017T42, 2017T203 and 2017T256 showed susceptibility reaction to all the three pathotypes in plug method. The clones showing moderately susceptible to one

or all the pathotypes by plug method and resistant reaction in cotton swab method can be released for cultivation in areas where the disease has not been recorded so far. Sugarcane clones possessing red rot resistance with good agronomic attributes can be released for general cultivation in the red rot endemic areas.

PP(S1)/18: Qualitative and quantitative analysis of lignin degradative enzymes in *Ganoderma* strains to decipher the basal stem rot in *Prosopis cineraria*

Mahesh Kumar and **Ritu Mawar***
Division of Plant Improvement and Pest Management, ICAR-Central Arid Zone Research Institute,
Jodhpur - 342003, Rajasthan, India
**Email: ritumawar1976@gmail.com*

Ganoderma lucidum is well known to causes extensive heart rots of standing trees by growing in the central, non-living woody tissue decomposing lignin and cellulose. Recently we have reported new strain *Ganoderma tsugae* which is more prone to cause wood decay by their higher enzyme activity. Lignin, the second most abundant renewable organic polymer on earth, is a major component of wood. Because of the importance of wood and other lignocellulosic as a renewable resource for the production of paper products, White rot fungi produce various extra cellular enzymes. These enzymes can oxidize phenolic compounds creating phenoxy radicals, while non phenolic compounds are oxidized via cation radicals. Lignin resists attack by most microorganisms; anaerobic processes tend not to attack the aromatic rings at all, and aerobic breakdown of lignin is slow. Fungi are more efficient in the breakdown of lignin than bacteria, in which delignification is slower and more limited. In nature, only basidiomyceteous white-rot fungi are able to degrade lignin efficiently. Few white rot fungi contain all lignin degradative enzymes though most white rot fungus are not able to produce all enzymes but still they can decay the woody substance, this indicate that all enzymes are not essential for degradation. Laccase, lignin peroxidase and manganese peroxidase are the most common enzymes for lignin degradation. Microbial degradation of lignin has not been intensively studied in organisms other than few fungi. Recently, some studies have identified Lacc1 gene present in some white rot fungi is mainly responsible for laccase enzyme activity but the information is very limited regarding the other genes involved in lignin degradation. Our preliminary study showed significant difference in the laccase and other enzyme activity in two different *Ganoderma* strains. In this paper we have identified the species of *Ganoderma* which is producing more degradative enzymes.

PP(S1)/19: Evaluation of chickpea (*Cicer arietinum* L.) genotypes against collar rot disease caused by *Sclerotium rolfsii* Sacc.

Babariya Vishruta D.[1] and **Kedar Nath[2]***
[1]*Department of Plant Pathology, N.M. College of Agriculture, Navsari Agricultural University, Navsari - 396450, Gujarat, India*
[2]*Regional Rice Research Station, Navsari, Agricultural University, Vyara, Gujarat, India*
**Email: drkdkushwaha@nau.in*

Chickpea (*Cicer arietinum* L.), is the world’s third most important food legume crop after dry bean and dry pea. Collar rot disease caused by fungus *Sclerotium rolfsii* Sacc. is one of the most prevalent fungal disease of chickpea under rice based cropping system and significantly reduced the yield. It caused up to 68 per cent plant mortality in susceptible cultivar under natural field condition in rice based sequence system. In the present climate change scenario chickpea crop is facing the tough competition of minor disease became a major disease now. Keeping in view of devastating nature of collar rot disease under rice based cropping system need to develop good management practices through host plant resistant is cheapest method to minimized yield loss of chickpea. Collar rot chick pea pathogen was isolated from infected collar region of chick pea plant on potato dextrose agar media and exhibited initialy white fluffy mycelium appearance and microscopic view of mycelium was hyaline, branching, compact with septate and had a clamp connection. White sclerotia were formed after 4th days of incubation and later within 10 days after incubation it become mature and colour change brown to dark brown. Sclerotia appeared shiny due to presence of gummy material. Pathogeneciry was proved on chick pea genotype GG-5 by active mycelium bits incorporated in sterilizes soil. Thirty nine chickpea genotypes were evaluated against collar rot disease caused by *S. rolfsii* under field conditions to identified source of resistant for further used in breeding program. The inoculum was thoroughly broadcasted in soil @ 10g/row. Thirty chickpea seeds were sown for each genotype at 30 x 10 cm distance in 3 m row length in field after inoculating with pathogen which was multiplied on sorghum grain. Germination percent and disease incidence was recorded as per cent plant mortality before the harvesting. The experiment was conducted during *Rabi* 2019-20 at Regional Rice Research Station, NAU, Vyara. Seed germination and plant mortality was recorded in range from 42.86-90.00 and 13.03- 68.15 per cent, respectively. Among all the genotypes, highest seed germination (90.00%) was recorded in PKV-2 genotype while it was lowest in GJGK-1616 genotype (42.86%). Highest plant mortality (68.15%) was observed in genotype PKV-2. The lowest plant mortality (13.03%) was recorded in genotype GJG-1713 which was at par with 5 genotypes *viz.*, GG-6, GJG-1509, Phule Vikram, JGK-1 and GJG-1607 with 13.33, 15.53, 17.41, 18.33 and 20.20 per cent plant mortality, respectively. Out of 39 genotypes only five *viz.*, GJG-1713, GG-6, GJG-1509, Phule Vikram and JGK-1 were identified as moderate resistant against *S. rolfsii*. Whereas, 15 genotypes were showed moderate susceptible reaction, 13 genotypes showed susceptible reaction and 6 genotypes showed highly susceptible reaction. None of the genotypes were found resistant against collar rot disease under inoculums inoculated rice fellow cropping system. Moreover, genotypes GJG-1713, GG-6, GJG-1509, Phule Vikram and JGK-1 may be used under breeding program to development of resistant variety for management of collar rot disease.

PP(S1)/20: Screening of pigeonpea genotypes against *Fusarium udum* butler under the artificial epiphytotic condition in Bihar state

B. Deepak Reddy* and Birendra Kumar
Department of Plant pathology, Tirhut College of Agriculture, Dr. Rajendra Prasad Central Agricultural University, Pusa - 843121, Bihar, India
All India Co-ordinated Research Project on Pigeon Pea (2019-2020)
**Email: deepakreddyagrico.108@gmail.com*

Wilt of Pigeon pea is a very destructive disease caused by the fungus *Fusarium udum* Butler. In India, Pigeonpea crop suffers a great loss due to this disease. The use of resistant varieties is one of the best methods of disease management. Therefore, studies were planned to search the resistant genotypes against Fusarium wilt through the sick plot technique. Out of 127 AICRP genotypes screened, twenty-eight (ICPL17116, BDN716, IBTDRG-8, IBTDRG10, IPA13-1, IPA14-4A, IPA18-33, MAL52, KRG33, WRGE122, BDN2013-1, PT0723-1-2-3, TDRG59, IPA16-18, MAL50, BSMR79, BSMR553, BSMR153, BSMR254, IPA203, KPL44, BDN1, ICP7035, ICP8858, ICP8859, ICP8863, ICP9174, and GJP1606) were found resistant, thirty-one were moderately resistant and sixty-eight were susceptible to wilt disease.

PP(S1)/21: Marker assisted selection for mapping population against chickpea wilt

Renuka Tatte[1], S.S. Mane[1], S.T. Ingle[1], E.D. Bagde[2] and P.V. Jadhav[3]
[1]*Department of Plant Pathology,* [3]*Biotechnology Center, Post Graduate Institute,*
Dr. Panjabrao Deshmukh KrishiVidyapeeth, Akola – 444104, Maharashtra, India
[2]*RFRC Katol*

The chickpea wilt caused by *Fusarium oxysporum* f. sp. *ciceri* is one of the major limiting factors in production. Being soil born it is difficult to control the disease. The only means by which of the disease can be managed is use of disease resistant varieties hence the present investigation aimed at screening of the mapping population of the crosses to obtain the resistant genotype. Marker assisted characterization of The 30 chickpea genotypes of chickpea F4 generation were selected for screening from three mapping population of different crosses (JG 62(Susceptible) X ICCV 08113, PG 04154 (resistant) X JG 62 (susceptible) and PG 07101 (resistant) X JG 62 (susceptible). 10 genotypes from each population were selected for Fusarium wilt reaction was carried out using two molecular markers reported by earlier workers linked to disease resistant/susceptibility. In the present study, Allele Specific Associated Primer (ASAP) marker (namely, CS-27F/R700) linked to susceptibility and three Sequence Tagged Microsatellite site (STMS) marker (TA-59258, TA-96275, TR-19227) linked to resistance allele were validated. The results indicates that ASAP (CS 27F/CS 27R) marker linked to susceptibility alleles and susceptibility is dominant over resistance. ASAP marker, (CS27F/R) screened on the 30 genotypes and gave no amplified product of 700 bp. in all 30 genotypes STMS marker, TA-59, TA-96 and TR-19 linked to resistance and produce amplification in resistant genotypes. The amplification sizes of TA-59, TA-96 and TR-19 as characterized in Cicer sp. were 258, 275 and 227 bp, respectively. Amplification was observed in all 30 genotype.

PP(S1)/22: The use of silicon in integrated disease management

Vijay Shree Gahlot[1]*, Bhushan Berari[2] and S. Dilip Kumar Reddy[3]
[1]ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
[2]Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola - 444104, Maharashtra, India
[3]Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut – 250110, Uttar Pradesh, India
**Email: vijayshree1789@gmail.com*

Silicon, considered to be the second-most abundant mineral element in soil, plays an important role in the mineral nutrition of plants. A wide variety of monocot and dicot species have benefited from silicon nutrition, whether direct or indirect, when they are exposed to different types of abiotic and/or biotic stresses. Besides the many agronomic and horticultural benefits gained by maintaining adequate levels of this element in the soil and also in the plant tissue, the most notable effect of silicon is the reduction in the intensities of a number of plant diseases caused by biotrophic, hemibiotrophic and necrotrophic plant pathogens in many crops of great economic importance. Silicon can reduce levels of several important diseases of rice, including blast brown spot, sheath blight, leaf scald and grain discoloration. Levels of control are equal to that achieved by fungicides for disease such as blast and brown spot. Hence, the number of fungicide applications and rates can be reduced significantly. Residual activity of silicon was effective for disease control in the second year crop and was comparable to a first year silicon application or a full rate of a fungicide. Silicon enhanced performance of partially-resistant cultivars so that they were comparable to highly resistant cultivars for both blasts and sheath blight.

PP(S1)/23: The effect of pleiotropic leaf rust resistance gene *Lr68* on wheat rusts in Indian conditions

T.L. Prakasha[1]*, Suresh Chand[2], A.N. Mishra[1], J.B. Singh[1], S.V. Sai Prasad[1], Divya Ambati[1], V.K. Singh[3], D.P. Walia[4], O.P. Gangawar[5] and M. Sivasamy[6]
[1]*ICAR-Indian Agricultural Research Institute, Regional Station, Indore - 452001, Madhya Pradesh, India*
[2]*Department of Life Sciences, Devi Ahilya Vishwa Vidyalaya, Indore - 452001, Madhya Pradesh, India*
[3]*ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India*
[4]*ICAR-Indian Agricultural Research Institute, Regional Station, Shimla - 171004, Himachal Pradesh, India*
[5]*ICAR-Indian Institute of Wheat and Barley Research, Regional Station, Flowerdale, Shimla - 171002, Himachal Pradesh, India*
[6]*ICAR-Indian Agricultural Research Institute, Regional Station, Wellington - 643231, Tamil Nadu, India*
**Email: prakash7385@gmail.com*

Wheat rusts are the major diseases responsible for yield losses across the globe. Due to continued evolution of new pathotypes, major genes deployed in varieties are being rendered ineffective in few years after their deployment. Pleiotropic adult plant resistance (PAPR) genes gained lot of global interest due to their greater durability to wheat rusts. *Lr68*, a PAPR gene which confer non-hypersensitive slow rusting resistance was recently reported. Nearly 1500 bread wheat germplasm were evaluated for the presence of 'leaf tip necrosis' (*ltn*) trait which is closely linked with *Lr68* gene. Using molecular marker, 20 genotypes were identified to be carrying *Lr68* gene either singly or in different combinations. These lines were screened in field and glasshouse against stem, leaf and stripe rusts pathogen. The lines carrying the gene either singly or in combinations along with all stage resistance gene/s (ASR) had shown very high levels of field resistance. The effectiveness of the gene was very low without a seedling genes. The rust resistance offered by *Lr68* alone was not adequate and the genotypes showed susceptibility under heavy disease pressure. However, rust resistance was improved when it was present in combination with other pleiotropic adult plant resistance genes. Therefore, a combination of *Lr68* along with other pleiotropic genes and ASR genes will offer better and durable field resistance to wheat rust diseases.

PP(S1)/24: Exploration of resistance response of soybean cultivars against aerial blight

Kumari Surbhi* and K.P. Singh
Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakhand, India
**Email: surbhi.gbpuat2018@gmail.com*

Soybean is one of the most important oilseed crop grown throughout the world for its health and nutritional benefits. Aerial blight caused by *Rhizoctonia solani* Kuhn, causes severe damage to the crop and may lead to around 80 per cent yield losses under favourable environmental conditions. Use of resistant varieties is an important strategy for management which could help in lowering the incidence of disease in the field and also reduce the frequency of chemical sprays required. To evaluate the resistance response of twenty soybean cultivars against aerial blight, an experiment was conducted at soybean pathology block, Crop Research Center, GBPUA&T, Pantnagar during 2016-17. The per cent disease index of aerial blight on the twenty cultivars under study was recorded using 0-9 scale of severity. Molecular studies on the resistance response of the cultivars were performed using three SSR markers, viz., Satt 119, Satt 281 and Satt 245. The results revealed that PS -1556, PS -1518, PS-1572, PS-1546 and PK-416 exhibited resistant response to aerial blight both in the field and molecular screening. The cultivars identified as source of resistance in the study could be further utilized in breeding programs for development of new improved resistant varieties against soybean diseases.

PP(S1)/25: Evaluation of brinjal entries against little leaf of brinjal

Rakesh Kumar Chugh[1]*, Kushal Raj[1] and S.K. Dhankhar[2]

[1]*Department of Plant Pathology,* [2]*Department of Vegetable Science, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India*

**Email: drrakeshchugh@rediffmail.com*

Brinjals referred to as eggplants, belong to the Solanaceae family. The plant grows in hot climates, but cannot tolerate drought. Brinjals are sensitive to cold weather and are damaged easily by frost. Brinjal is one of the most common tropical vegetables and large number of cultivars differing in size, shape and colour of fruits are grown in India. Immature fruits are used in curries and a variety of dishes are prepared out of brinjal. Fruits are moderate sources of vitamins and minerals like phosphorous, calcium and iron and nutritive value varies from variety to variety. This is prone to massive attacks by several species of fungi and bacteria that causes bacterial wilt (*Pseudomonas solanacearum*), Cercospora Leaf Spot (*Cercospora solani -melongenae, C. solani*), Alternaria leaf Spot (*Alternaria melongenae, A. solani*), Little Leaf of Brinjal (Phytoplasma), Fruit rot (*Phomopsis vexans*) and Collar rot etc. Amongst different diseases little leaf of brinjal is one of serious disease to cause losses upto 90%. Resistance source is one of the most economical method for prevention of the diseases. In order to find out resistance source amongst different cultivars, screening of thirteen entries during 2018-2019 was carried out against little leaf of brinjal and found three entries as moderately resistant, five as susceptible and five as highly susceptible. Losses in yield ranged from 11.37 to 58.65 per cent. Maximum loss was observed in entry HE-36-2 whereas minimum loss exhibited in entry HE-119. During 2019-20, twenty entries were screened against little leaf of brinjal and found that twelve entries as resistant, three moderately resistant, four susceptible and one as highly susceptible against little leaf of brinjal. The resistance source identified during 2019-2020 will be further utilized in improvement of cultivars.

PP(S1)/26: Developing a robust nursery of tomato by amending a multifaceted cyanobacterium to soil-less potting mixes

Jyoti Shukla[1]*, Udita Gulia[1], Himani Gupta[1], Krati Gupta[1], Rishi Buddhaddeo[1], Robin Gogoi[2] and Radha Prasanna[1]

[1]*Division of Microbiology,* [2]*Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*

**Email: jyotishukla.del@gmail.com*

The interplay of cyanobacteria with phytopathogenic fungi is a less explored aspect, although cyanobacteria are widely used as biofertilizers. A novel approach of employing cyanobacteria as amendments to phytopathogenic fungi challenged soil-less potting mixes was developed to obtain healthy nursery of tomato. Our present study focused on evaluating the biocontrol potential of cyanobacterium *Anabaena laxa* (*A. laxa*),when used as amendment to three types of soil-less substrate mixes [P: C, perlite: cocopeat (1: 1); C: V, cocopeat: vermiculite (1: 1); P: C: V, perlite: cocopeat: vermiculite: (1: 1: 1)]. *A. laxa* amended mixes showed enhanced activity of hydrolytic enzymes (Chitosanase and CM Case), phenols and other metabolites. Preliminary analyses were undertaken to evaluate the inhibitory dose of inoculum of the available *Fusarium solani* and *Rhizoctonia solani* isolates, using tomato as the target crop, which showed that 2% inoculum was most optimal. Percent inhibition of seed germination to an extent of 27.97 % and 75 % was shown by *R. solani* and *F. solani* in tomato. The nursery of tomato raised using *A. laxa* amended potting mix was transplanted into mesocosms which were challenged with /without *F. solani* or *R. solani.* Significant increases were recorded in the total polysaccharides and dehydrogenase activity, besides chlorophyll accumulation in P: C: V amended mixes with *A. laxa* primed plants, challenged with *F. solani* compared to control. Stimulatory interactions of cyanobacterium-*F. solani* led to better growth of tomato plants and can be a promising strategy for raising a healthy nursery of vegetable crops.

PP(S1)/27: Effect of agro-organic waste formulations on germination of *Triticum aestivum* and *Brassica nigra*

Smita Jadhav, Sunita Singh and **Arpita Gupte***

School of Biotechnology and Bioinformatics, D.Y. Patil Deemed to be University, Sector 15, Plot No. 50, CBD Belapur, Navi Mumbai - 400614, Maharashtra, India
**Email: smitajadhav20@gmail.com*

In virtue of environmental concerns, there is a need to reduce the usage of chemical fertilizers and pesticides in agriculture. Organic fertilizers as an alternative sought to improve crop establishment and health. It has been reported that organic fertilizers have a positive effect on growth attributing to high microbial load, macronutrients, micronutrients and growth hormones. The current study highlights the use seed priming on *Triticum aestivum* (wheat) and *Brassica nigra* (mustard) with four organic formulations (OF1 to OF4). The seeds priming was carried out at different concentrations viz., 1:50, 1:100, 1:150 and 1:200 respectively. The control seeds were treated with sterile distilled water. The seed quality parameters like germination, seedling length, seed vigour were evaluated after eight days. The wheat seeds primed with 1:150 dilution showed increased germination percentage (95%) for OF3 and OF4 respectively; while OF1 at 1:200 dilution gave 100% germination. Mustard seeds primed with 1:150 dilution gave higher germination percentage (96% and 98%) for OF4 and OF3 respectively. Maximum vigour index and seedling length was observed in OF4 (1:150) for both wheat and mustard seeds. Statistical analysis indicates a positive correlation in utilization of diluted agro-organic waste on germination of seeds.

PP(S1)/28: Identification of resistant genotypes against *Phomopsis vexans* causing fruit rot of brinjal

Niranjan Prasad H.P.[1]*, Atul Kumar[1], Jameel Akhtar[2], Partha Saha[3] and Shailendra Kumar Jha[4]

[1]Division of Seed Science and Technology, [3]Division of Vegetable Science, [4]Division of Genetics, ICAR-Indian Agricultural Resaerch Institute, New Delhi – 110012, India
[2]Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi - 110012, India
**Email: atulpathiari@gmail.com*

Brinjal (*Solanum melongena* L.) is an important solanaceous crop of sub-tropics and tropics. Brinjal is known to be invaded by many phytopathogens, among them fruit rot caused by *Phomopsis vexans* is considered to be the most destructive disease of brinjal which reduces yield and marketable value of the crop in different proportion. As far as resistant genotypes are concerned, the variety which is resistant today will become susceptible after few years due to evolution of new virulent races of the pathogen. Therefore, present study was conducted to screen thirty-four genotypes against fruit rot of brinjal. Out of thirty-four genotypes studied nine genotypes namely Bhangar Local, G-204, G-175, G-131, G-9, DB-7, Arka Nidhi , Pant Samrat and G-43 showed highly resistant, five genotypes G-203, G-31, Pusa Upkar , Arka Kusumarkar and Kashi sandesh showed resistant, one genotype Pusa uttam showed moderately resistant, nineteen genotypes namely G-160, G-145, G-65, G-10, G-5, G-22, Pant Rituraj, Pusa Shymla, Pusa Kaushal, Pusa Safed, G-23, DB-9, G-17, G-109, G-60, G-181, G-164, Pusa Kranti and Pusa Purple Round were found to be highly susceptible against *Phomopsis vexans*. In our studies an extensive screening of thirty-four genotypes which includes few elite lines, few local genotypes, few hybrids and many released varieties has been done. Screening of wide spectrum genotypes and then classifying them into four different categories of highly resistant, resistant, moderately resistant and highly susceptible gives complete information to breeders to utilize them in development of resistant genotypes.

PP(S1)/29: Identification and phenotyping of resistant sources against Fusarium wilt of chickpea in semiarid region of Haryana

Promil Kapoor* and A.K. Chhabra

Pulses Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar - 125004, Haryana, India

**Email: kapoorpromil@gmail.com*

Chickpea is one of the most important pulse crops of Haryana. The major constraint in Chickpea production and productivity is prevalence of diseases like Wilt, Root rot, Blight, Botrytis grey mould and chickpea stunt etc. To develop high yielding disease resistant chickpea varieties, proper phenotyping of genotypes or cultivars is pre-requisite to identify resistance sources before taking into a commercial level for the farmer's field. A total of 300 genotypes were screened & evaluated against Fusarium wilt in sick plot for three years consecutively. Out of these 50 genotypes were found to be resistant to wilt disease. The disease incidence ranged between 2%-100%. The mean wilt disease incidence is 65% for three years. Since, the chickpea genotypes were screened since their inception as elite genotypes in the preliminary yield trials; this generated very useful material in chickpea leading to long lasting genotypes/ cultivars for identifying resistant material that can be used in Plant Breeding programmes to introgress resistance in high yielding varieties. Some of these genotypes were even resistant to heat and drought. These genotypes form a unique pool for hybridization programme. The detailed data will be presented in the conference.

SESSION 2

Eco-friendly management

Biocontrol, organic farming, conservation agriculture, biopesticide, IPM/IDM

Keynote Lectures

KN(S2)/01: Eco-friendly management of plant parasitic nematodes

Becky B. Westerdahl*
Department of Entomology and Nematology, University of California, Davis, CA 95616, USA
**Email: bbwesterdahl@ucdavis.edu*

Plant parasitic nematodes are plant stressors that cause significant yield reductions worldwide. Nematode management is in a transition phase from the use of fumigant nematicides to products less acutely toxic to non-target organisms. Building on research begun more than 60 years ago in India, the United States and other locations, eco-friendly nematode management products have become a reality in recent years. Field trials comparing these new products with fumigants have demonstrated the efficacy of a variety of new modes of action. These include biopesticides such as DiTera (*Myrothecium verrucaria*) and Melocon/BioAct (*Paecilomyces lilacinus*); plant extracts such as Nema-Q (*Quillaja*) and essential oils (Duogard, Cinnamite); self-defense inducers such as Nemat-X; and more environmentally benign chemicals such as Nimitz (fluensulfone), Salibro (fluazaindolizine), and Velum One (fluopyram).

KN(S2)/02: Precision agriculture and geo spatial techniques for sustainable disease control

Dan Roberts[1]*, Nick Short[2], James Sill[2], Lain Graham[2], Dilip Lakshman[1], Xiaojia Hu[3] and Michael Buser[4]
[1]*USDA-Agricultural Research Service, Sustainable Agricultural Systems Laboratory, Beltsville, MD, USA*
[2]*Environmental Science Research Institute, Redlands, CA, USA*
[3]*Oil Crops Research Institute, Key Laboratory of Biology and Genetic Improvement of Oil Crops, Wuhan, China*
[4]*USDA-Agricultural Research Service, Office of National Programs, Beltsville, MD, USA*
**Email: dan.roberts@usda.gov*

The agricultural community is confronted with dual challenges; increasing production of nutritionally dense food and decreasing the impacts of these crop production systems on the environment. New approaches to enhance sustainability of crop production systems and, importantly, plant disease control need to be developed and adopted. By leveraging advanced geoinformatic techniques, advances in computing and sensing infrastructure will aid in the monitoring and management of pesticides and biologicals, such as cover crops and beneficial microbes, to reduce the impact of plant disease control and cropping systems on the environment. This includes geospatial tools being developed to aid the farmer in managing cropping system and disease management strategies that are more sustainable but increasingly complex. Geoinformatics is also being enlisted to speed development of crop germplasm that has enhanced tolerance to pathogens and abiotic stress and is in tune with different cropping systems and environmental conditions. Finally, advanced geoinformatic techniques and advances in computing infrastructure allow a more collaborative framework amongst scientists, policymakers, and the agricultural community to speed the development, transfer, and adoption of these sustainable technologies.

KN(S2)/03: *Trichoderma* spp. in the management of stresses in plants, their commercialization for sustainable agriculture and rural prosperity

R.N. Pandey*
Department of Plant Pathology, B.A. College of Agriculture, Anand Agricultural University, Anand - 388110, Gujarat, India
**Email: pande56@gmail.com*

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*), etc. which may cause huge quantitative and qualitative yield losses in crops, 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 decomposing them with their efficient cell wall degrading enzymes *viz*. chitinase, cellulase, protease, xylanase, ß-1,3- glucanases endoglucanase, etc., to make available of the nutrients for plant growth. 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 through their commercialization, etc. Thus, it is one of the best sectors for improving socio-economic conditions of farmers of developing nations and helps the nations to become prosperous and self-reliant. Mass production technologies 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. 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 collaborative research groups nationwide as well as globally for innovative outcomes. The detailed account on these will be discussed in the conference.

KN(S2)/04: Integrated nano-based microbiome and smart agriculture for plant health management

M.S. Reddy[1]*, R.Z. Sayyed[2], Hesham El Enshasy[3], Hameeda Bee[4], Naveen K. Arora[5], Ni L. Suriani[6] and S. Lalitha[7]
[1]*Asian PGPR Society for Sustainable Agriculture, Department of Entomology & Plant Pathology, Auburn University, AL, USA*
[2]*Department of Microbiology, PSGVP Mandal's Arts, Science and Commerce College, Dist - Nandurbar – 425409, Maharashtra, India*
[3]*Institute of Bioproduct Development, Universiti Teknologi Malaysia, Johor Bahru, Malaysia*
[4]*Depart of Microbiology, Osmania University, Hyderabad - 500007, Telangana, India*
[5]*Department of Environmental Science, Babasaheb Bhimrao Ambedkar University, Lucknow - 226025, Uttar Pradesh, India*
[6]*Biology Study Program, Udayana University, Bali, Indonesia*
[7]*Department of Botany, School of Life Sciences, Periyar University, Salem – 636011, Tamil Nadu, India*
**Email: prof.m.s.reddy@gmail.com*

Food demand measured by population growth nearly doubled from 1966 to the present. It is projected to increase another 39 percent by 2050. The current global population is 7.6 billion. It is expected to be around 10 billion in 2050. Plant health management is the science and practice of understanding and overcoming the succession of biotic and abiotic factors that limit plants from achieving their full genetic potential as crops, ornamentals, timber trees, or other uses. Managing healthy plants using an integrated approach enhances the chances of growing healthy plants. Genetic host resistance, cultural practices, chemical applications, biological control, and regulatory measures are the categories of integrated plant health management. Agriculture is influenced by an array of biotic and abiotic stresses, which must be managed through multipronged strategies. A strategic science-based approach is needed to address the plant health risks and issues that affect productivity. Intensive use of ecosystems to enhance productivity can affect agro-ecosystems through soil erosion, water depletion / contamination, biodiversity loss and disruption in flow of ecosystem services, which will have a bearing on plant health and biosecurity. The indiscriminate use of chemical pesticides has been causing widespread environmental pollution, resistance, resurgence of insect pests and is impacting food safety. Our research showed to date, it is evident that crop yields and fitness are linked to the nano-based plant microbiome coupled with smart agriculture. Harnessing the plant microbiome therefore can potentially revolutionize agriculture and food industries by integrating crop health with better smart management practices for specific climatic conditions to improve productivity and quality. The global microbial or nano based soil inoculants market size was around USD 452.07 million in 2020. It is expected to grow at a CAGR of 9.5% to reach USD 751.51 million by 2025. The use of microbial agricultural inoculants enhances the plant growth, suppresses the diseases, and increases the yield and protects the environment. The global key participants to expand their market share in the nano-based microbial inoculants market engage upon strategic acquisitions and joint venture techniques to ensure long term sustenance of these inoculants market around the globe. These technologies will become an integral part of the sustainable increase in agricultural productivity via smart agriculture ensuring food and nutrient security for future global populations.

KN(S2)/05: Research to commercialization pathway of a public biocontrol innovation: The case of aflatoxin biocontrol in Africa

R. Bandyopadhyay[1]*, A. Ortega-Beltran[1], A. Akande[1] and M. Konlambigue[2]
[1]International Institute of Tropical Agriculture (IITA), Ibadan 200001, Nigeria
[2]IITA, Accra, Ghana
**Email: r.bandyopadhyay@cgiar.org*

Aflatoxins pose a significant public health risk, decrease productivity and profitability of animal industries, and hamper trade. To minimize aflatoxin contamination in several crops, a biocontrol technology based on atoxigenic strains of *Aspergillus flavus* that do not produce aflatoxin is used widely in the US. The technology has been improved and adapted for use in Africa by the International Institute of Tropical Agriculture (IITA) in partnership with several national institutions under the tradename Aflasafe. Country-specific Aflasafe products have been developed or are currently being developed in 20 African nations. The four atoxigenic *A. flavus* genotypes used as active ingredient fungi in the biocontrol formulations competitively displace aflatoxin producers during crop development and this results in less aflatoxin content. Using incentivization mechanisms (AgResults: https://agresults.org/projects/nigeria) and commercialization approaches (www.aflasafe.com), Aflasafe is being scaled up through a mix of public, private, and public-private partnership interventions. The use of biocontrol, accompanied by pre- and post-harvest technologies, awareness and sensitization campaigns, testing, market development, policy interventions, is implemented in coordination with relevant stakeholders across value chains of each target nation. Crops produced using the tailored interventions typically accumulate over 80%, sometimes 100%, less aflatoxins than untreated crops grown, processed, and stored using traditional practices. Several African nations have commercially treated more than 360,000 ha of maize and groundnut crops achieving >90% less aflatoxins. This presentation will provide information on the long road from development to large-scale deployment of biological control for improving food security, promoting trade, contributing to healthier farm families, and creating wealth.

KN(S2)/06: Developing integrated disease management systems for sustainable vegetable production in the tropics

Jayaraj Jayaraman*, Adesh Ramsubhag, Omar Ali, Chinnaraja Chinnadurai and Antonio Ramkissoon
Department of Life Sciences, Faculty of Science and Technology, The University of the West Indies (UWI), St. Augustine, Trinidad and Tobago
**Email: jayauwi@gmail.com*

Enhancing the production of vegetables is very essential for the food and nutritional security of the Caribbean. Vegetable production in the Caribbean has not achieved self-sufficiency, despite this region having a conducive climate, soils and favourable environment for growing a variety of tropical and sub-tropical vegetable crops. Vegetable production is being less efficient in the Caribbean due to increased disease and pest pressures on crops and global climate change. Several attempts were recently initiated under various projects to develop integrated disease management systems for vegetable crops. This included the following actions: development of molecular diagnostic facilities in the Caribbean; development and use of PGPR consortia for seed and seedling applications; development of community nurseries for disease-free seedling production; recommendation for use of organic manures and judicious levels of fertilizers; recommendation regarding minimum use of safe-chemical pesticides and maximal use of biopesticides. The research findings on the optimised methods/inputs were demonstrated in the field in three Caribbean countries. Several farmers' groups and agricultural officials of member countries were trained with the assistance of member states. The developed integrated disease management models are adoptable for any vegetable crop production system in the tropical environment. Implementation of the developed systems by farmers has demonstrated overall improved productivity of vegetables in an environmentally sustainable manner.

KN(S2)/07: The impact of biocontrol of plant diseases on increasing food crops in Nigeria; Sub-Saharan Africa

D.B. Olufolaji[1]* and S. Fakoya[2]
[1]*Department of Crop, Soil and Pest Mgt., Federal University of Technology, Akure, Nigeria*
[2]*Department of Biological Sciences, Olusegun Agagu University of Science and Tech. Okitipupa, Nigeria*
**Email: tundefolaji022@gmail.com*

Biocontrol is a method of controlling pests and plant diseases using other biologically active entities (microorganisms and botanicals) In sub-Saharan Africa, crises caused by plant diseases has been very overwhelming, causing huge loss to the agrarian community and negatively affecting the standard of living in their domain. Due to their mode of life, usage of more advanced diseases control methods have been too cumbersome for them. Two afore mentioned methods that are commonly used in biocontrol of plant diseases are (i) the use of antagonistic fungi and (ii) the use of plant extracts from botanicals. Very prominent antagonistic fungi that are commonly used in Nigeria are *Trichoderma* spp. For instance, *Trichoderma harzianum* as biocontrol agent against *Macrophomina phaseolina* the cowpea charcoal rot pathogen, control of black rot disease of okra with *Trichoderma harzianum*, control of *Sclerotium rolfsii* the rot fungus of tomato using *Trichoderma asperellum*. They possess some attributes which empower them in carrying out mycoparasitism on the fungi which prevent them from causing crops diseases. Furthermore, biocontrol aspects which involves the use of botanicals dwells on the extraction of active principles (i) essential oils and (ii) extracts in the botanicals and applying them accordingly to confer prophylactic and curative means of controlling the plants diseases. An example of this is the use of plant extracts from *Azadirachta indica* in controlling *Choanephora* wet rot of *Amaranthus* sp., control of brown blotch disease of cowpea with essential oils of *Gmelina arborea* and *Zingiber officinale.* These biocontrol methods have enhanced increase in food productivity and improved both food and cash crops which has enhanced Nigeria's economy and solved hunger to a great extent. On the contrary, the negative effects of biocontrol are; impact of the methods on non-target and beneficial organisms in the agro-ecosystem. The slow speed at which they confer control actions when compared with the chemicals and other methods.

KN(S2)/08: *Trichoderma harzianum*, a multipotential organism for biological control of plant pathogens

Gomathinayagam Subramanian[1]* and Rekha Gomathinayagam[2]
[1]Faculty of Agriculture & Forestry, University of Guyana, Berbice Campus, Guyana
[2]Department of Microbial Technology, School of Science, Madurai Kamaraj University, Madurai - 625021, Tamil Nadu, India
**Email: directorugbc@uog.edu.gy*

In agriculture, about 30000 plant diseases were recorded all over the world affecting the crop plants and in India alone 5000 plant disease are known to be prevalent (Rangaswamy, 1996) in Guyana have more prevalent disease in rice and sugarcane such as blast brown spot, sheath blight, bacterial blight and smut, rust, brown rust respectively. Protection of agricultural crops against diseases and insects is managed by different methods viz. cultural, chemical and biological. The cultural method of crop protection includes crop rotation, alteration of sowing time etc. By this method, there is reduction in the proliferation and attack of pathogens, but it cannot give guarantee of complete protection. Chemical pesticides and diverse antibiotics were widely used to achieve high levels of crop protection. However, the indiscriminate use of chemicals posses serious problems such as development of resistance to pesticides, resurgence of target pests, secondary pest outbreak, killing of non-target organisms, residual toxicity and environmental pollution (Brent, 1995; Sharma *et al.*, 1998; Urech *et al.*, 2000). Biological control of plant diseases is gaining momentum in recent years since use of chemical pesticides lead to various healths hazardous to human beings (Brent, 1995; Sharma *et al.*, 1998). In the last two decades, numerous biological disease control agents are being examined and the use of microorganism based bio pesticides is being increased for the management of various crop diseases. *Trichoderma harzianum* is a potential fungus, showing antagonistic activity against plant pathogenic fungi (Peng and Sutton, 1991; Kumar and Jha, 2002). *T. harzianum* is a soil fungus and also exist in dead matter and living tissues as saprophyte and parasite, respectively, *T. harzianum* is a weak pathogen and upon infection, induces host plant resistance and also plays a major role in growth promotion of plants. In this study, *T. harzianum* was thoroughly investigated for its growth kinetics in different culture conditions, antagonistic activity towards various plant pathogens and tolerance to fungicides in order to develop an effective bio control agent for the management of crops diseases in agriculture.

KN(S2)/09: Platform technology for large scale production of biological control agents for fungal oil palm diseases

Hesham Ali El Enshasy*
[1]Institute of Bioproduct Development (IBD), Universiti Teknologi Malaysia (UTM), Skudai, Johor, Malaysia
[2]City of Scientific Research and Technology Applications, New Burg Al Arab, Alexandria, Egypt
**Email: henshasy@ibd.utm.my*

Oil plam (*Elaeis guineensis* Jacq.) is one the main economic oil crops in the world. This based on its high oil yield per Hectare compared to other oil crops. Therefore, nowadays, palm oil is widely used in food, cosmetics and pharmaceutical industries. As vegetable oil derived from tropical crop. Malaysia and Indonesia account for almost 80% of world palm oil production. During the recent years, the plant productivity per hectar showed significant losses due to many biotic and abiotic stresses. According to many agroeconomic studies, fungal and insect diseases account for big losses in plant yield and over all oil production. Among different pathogens studied, Basal Stem Rot (BSR) disease caused by the soil born pathogen *Ganoderma boninense* is considered as main fungal disease in oil palm plantation in Malaysia and Indonesia and account for huge losses in overall oil production yield. Therefore, development of sustainable strategy to control ganodermal disease is considered as important topic for both scientific and industrial societies in South East Asia. This lecture will present a complete integrated industrial platform for the development of biological control product to reduce the harmful impact of this type of fungal disease. Complete information will be provided starting from the scientific approaches used for the isolation of suitable biological control agent from soil. Furthermore, we will present a complete techno-industrial platform for the development of sustainable biological control product for oil palm plantation market.

Invited Lectures (Lead Lectures)

IP(S2)/01: Management of common scab and root-knot diseases of potato in field through bio agents

S.K. Patel, H.C. Prajapati, **D.J. Patel*,** Karan Virji and Kartik Laijawala
Nico Orgo Manures, Dakor, Dist. Kheda - 388225, Gujarat, India
**Email: davabhai@yahoo.com*

Field experiment was conducted to control common scab (*Streptomyces scabis*) and root- knot nematodes(*Meloidogyne incognita*) on potato roots and tubers on farmer's field at village Bhudasan in Dist. Gandhinagar,Gujarat during 2017-18 and 2018-19. The treatments consisted of seed treatments with Boric acid @ 3% (w/w), Niconeem @ 1500 ppm,@ 3 % (v/w), NicodermaI (*Trichoderma viride* 2x 106 cfu)+Power All(*Pseudomonas fluorescens* 2x106cfu),Bioniconema(*Purpuriocillium lilacinum* 2x 106 cfu)+ Power All each @ 3 % (w/w) and control coupled with soil application of Nicoderma+Bioniconema, Nicoderma + PowerAll, Bioniconema + PowerAll, Nicoderma + Bioniconema + Power All each @ 4 kg/ha applied as soil application a week prior to potato seeding and control tried in factorial RBD design replicated three times. Plot size was 1.8 m x 2.5 m. Disease susceptible potato variety Pokharaj was seeded at 30cm x 15 cm @ 2500 kg /ha. Recommended POP were followed . Two years pooled data of the study indicated that potato seed treatment with Boric acid + Nicoderma + PowerAll each @ 3 %(w/w) coupled with soil application of Nicoderma+ Bioniconema + PowerAll each @ 4 kg/ha applied under the crop row a week prior to potato tuber seeding proved to be effective to control both common scab and root- knots on potato tuber to the extent of 32.5 % and thereby enhanced healthy potato tuber yield by21.3 % over other treatments including control.

IP(S2)/02: SIX-STEP management practices: An effective, economical and eco-friendly technology to control bacterial blight in Pomegranate

Jyotsana Sharma*, Manjunatha N., Somnath S. Pokhare, Ramakant Gharte and Vijay Lokhande
ICAR-National Research Centre on Pomegranate, Solapur – 413255, Maharashtra, India
**Email: jyotisharma128@yahoo.com*

With the intensification of pomegranate cultivation, bacterial blight caused by *Xanthomonas axonopodis* pv. *punicae* recorded huge yield losses (40 to 100 %) during past years. Presently the disease is managed using IDIPM schedules and avoiding rainy season crop. However, since pomegranate is arid/semi-arid region crop, hence, farmers prefer to take rainy season crop. The present technology of 'Six-Step management practices' is eco-friendly, economical and effective strategy for blight management. These practices were evaluated at NRC pomegranate orchards with 100 % bacterial blight free yield of 11.45 kg/plant from earlier orchard infected with 40 % bacterial blight. The same practices were demonstrated in one of the blight infected orchards of farmer in Akkalkot, Maharashtra. Results were100 % blight control and yield increase by 305 % with saving of 25 % (Rs.60000) on cost of cultivation. The schedule was also demonstrated in an organic block where in previous season 85-90% fruit yield loss was there, but after following six steps 100% disease free produce with quality fruits was harvested. The major components of modified six step management practices are: (i) taking main pruning soon after harvest of rainy season crop in December/January (ii) applying rest period fertilizer dose and plant protection according to the age of the plant (iii) stopping irrigation from mid/end March to put crop on stress till 100% natural defoliation occurs (iv) exposing defoliated stems to solar radiation for 15-20 days before crop initiation that kills bacteria in the nodes (MOST

IMPORTANT STEP) (v) light pruning of top 8-10 inches of branches, also remove any stem canker if observed (vi) follow crop season fertilizer, irrigation and IDIPM spray schedule (without antibiotics) to harvest a blight free quality pomegranate production.

IP(S2)/03: Important nematode problems in cereal crops and their management

Mujeebur Rahman Khan*
Department of Plant Protection, Aligarh Muslim University, Aligarh – 202002, Uttar Pradesh, India
**Email: mrkhan777in@yahoo.co.in; mrkhan.amu@gmail.com*

Nematodes constitute the most predominant community among the multicellular organisms present in the soil. However, only a fraction of nematode species have ability to parasitize plants. Among various groups of plant pathogens, phytonematodes cause 5-20% yield decline in cereal crops, which may account to a net loss of 2-7% in crop-based food. Rice, wheat, and maize are most important cereal and are frequently attacked by plant nematodes. Generally, the crop damage caused by nematodes remains hidden to farmers because of the nonappearance of discernable symptoms recognizable by necked eye. In addition to direct damage, nematodes aggravate the infection of soil-borne pathogens or act as vector leading to development of disease complexes. To prevent yield losses and to improve crop productivity and yield quality, it is essential to make realize the growers about the economic significance of plant nematodes. Adequate extension programs are needed to advise the growers about the effectiveness of nematode management methods. With regard to cereals, primary emphasis may be given to some of the most important nematode genera such as *Meloidogyne*, *Pratylenchus*, *Ditylenchus*, *Heterodera*, and *Anguina*, etc. as these nematodes are widely distributed in agricultural fields and cause considerable crop damage. Common cultural practices, viz., deep ploughing, flooding, fallowing during summer, removal, and burning of weeds and remnants of previous crops, use of certified and disinfested planting materials and cultivation of non-host, resistant or tolerant crops may substantially prevent crop losses in cereals caused by nematodes. Further, seed priming with bio-pesticides of *Trichoderma* spp. or *Pseudomonas fluorescence* as a general treatment may prove quite effective in improving plant healthy crops with a considerably higher yield.

IP(S2)/04: Prospects of plant growth promoting microorganisms for the management of plant diseases under changing scenario

Gururaj Sunkad*
Department of Plant Pathology, University of Agricultural Sciences, Raichur - 584104, Karnataka, India
**Email: sunkadgururaj@gmail.com*

Plant diseases are responsible for the loss of at least 10% of global food production, representing a threat to food security. The prevention of diseases mainly dependent on agro chemicals especially from the past few decades. Despite the great effectiveness and ease of utilization of chemicals products, their use or misuse has led to hazardous effects to environment. Some microorganisms, the bio-control agents are able to colonize the soil surrounding plant roots, the rhizosphere, making them come under the influence of plant roots. Plant growth promoting rhizobacteria (PGPR) generally refers to a group of soil and rhizosphere free living bacteria and fungi colonizing roots in a competitive environment and exerting a beneficial effect on plant growth as well as disease management. PGPR play key role not only in transforming nutrients in the soil but also giving protection against plant diseases. The beneficial effect of PGPR on plant growth involves the ability to act as phyto stimulators or biofertilizers. PGPR could enhance crop yield through nutrient uptake and plant growth regulators. PGPR could also act as bio-control agents by the production of antibiotics and triggering induced local or systemic resistance. The exact mechanism by which PGPR stimulate plant growth is not clearly established, although several hypothesis such as production of phytohormones, suppression of deleterious organisms, HCN and siderophore production, activation of phosphate solubilization, volatile compound production and promotion of the mineral nutrient uptake and plant growth promotion are usually believed to be involved. The studies conducted on groundnut, chickpea, pigeon pea diseases at our department indicated that PGMs can be used for plant growth promotion and management of diseases in these crops. Hence, there is a lot of scope for PGPMs in agriculture in general and plant disease management in particular. Sustainable agriculture based on environmentally friendly methods, tends to use PGPR as tool that could as a by product reduce the use of chemicals. There is a great need for eco-friendly management of plant diseases through bio-agents such as PGPR in worldwide.

IP(S2)/05: Mitigating environmental pollution and improving soil health using fungal resources

Lata*
Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: latambio@yahoo.com; latarajat@gmail.com*

Microbes can be a valuable bioresource for valorization of biomass. Most of the industrial processes involve harsh chemicals and energy intensive processes; with this as background, efforts were made to identify promising microbes with the ability to breakdown agri-biomass into useful products or enrich soil with nutrients. A biological delignification process was developed to minimise the use of chemicals for the pretreatment of lignocellulosic biomass to generate second generation biofuel. Two potent fungi, namely *Myrothecium roridum* LG7 and *Trametes hirsuta* were found to be efficient for delignification of paddy straw, within 5 days of solid-state fermentation, leading to substantial removal of lignin.Since 40 % of biofuel cost is accounted for the purchase of deconstruction enzymes, several potent mesophilic and psychrophilic fungi (*Aspergillus niger* SH3, *A. terreus* CM20, *Phoma exigua*) were explored and conditions were optimized to produce a cocktail of hydrolytic enzymes. The secretome analysis revealed the presence of an array of glycosyl hydrolases, involved in depolymerisation of cellulose and hemicellulose of LC biomass, resulting in high titre of reducing sugars.Crude laccase from white-rot fungus *Pseudolagarobasidium acaciicola* LA 1 produced by SSF of *Parthenium* biomass, decolorized Remazol Brilliant Blue R (RBBR) and Reactive Black 5 (RB5) dyes within 4h without a mediator. Disposal of paddy straw is a major problem in the North-West part of India, which leads to its burning and accounts for 0.05% to the total greenhouse gas (GHG's) emissions in India; additional effects include losses of soil organic carbon and nutrients, with adverse effects on soil properties, soil flora, and fauna. Our earlier efforts led o the development of an efficient microbial consortium for composting paddy straw, comprising four hypercellulolytic fungal cultures (*Aspergillus nidulans*, *A. awamori Trichoderma viride* and *Phanerochaete chrysosporium*). This was most efficient for bioconversion of paddy straw, pearl millet & maize stover into humus rich compost within 60 days. Its application (5 t/ha) along with half the dose of recommended fertilizers, resulted in 25% increase in crop yield and better soil fertility. Building on our earlier success story, for *in situ* degradation of paddy straw and stubbles in the field, systematic screening led to *Coprinopsis cinerea* LA2 and *Cyathus stercoreus* ITCC3745 as promising option. This consortium brought about significantly higher activities of soil hydrolytic enzymes, modulation of microbial community profiles, better soil health and 20% increase in the yield of succeeding wheat crop.These studies highlight the immense potential of fungal bioresources in reducing the environmental pollution and beneficial industrial applications.

IP(S2)/06: Disease dynamics and associated soil health parameters in rice wheat cropping systems under conservation agriculture

Apurba Kumar Chowdhury* and Prateek Madhab Bhattacharya
Department of Plant Pathology, Uttar Banga Krishi Viswavidyalaya, Coochbehar - 736165, West Bengal, India
**Email: akc_ubkv@rediffmail.com*

Conservation agriculture (CA) comprises the practical application of three interlinked principles i.e. no or minimal tillage, biomass soil mulch and crop specific diversification. Globally, conservation agriculture covers 180 million hectares (2018) and mostly adopted by large farmers having heavy types of machinery. The adoption of CA by the small farmers is very less and it is practiced by the farmers of Asia and Africa. West Bengal, India has been developing the elements of conservation agriculture for small farms for 15 years, but the adoption of full conservation agriculture on farms is just beginning to take off. From pathological point of view, no or minimum tillage of soil and retaining residues in the field principally increases the soil borne pathogens, and poses challenges to pathologists to grow a crop in healthy state. The disease incidence and severity under CA conditions depend on the host specificity, pathogen's biology along with its mechanisms for dispersal and survival, crop rotation, weather and microclimate effects as well as regional and temporal factors. Reports show many conflicting results under different agro-climatic situations. However, this agriculture practices having the presence of crop residues in the soil surface provide the residue- and soil-borne microorganisms including plant pathogens with a favourable habitat as observed by several researchers. On the contrary, several diseases were reduced under conservation agriculture practices mainly due to increase in population of soil antagonistic microflora and improved soil health. The increase in disease severity due to residue borne pathogens may be tackled with additional control efforts like disease control chemicals; biological control and host plant resistance so that more growers adopt CA practices for the interest of the farmer's income and sustainability of agriculture production system.

IP(S2)/07: Viral disease scenario in solanaceous vegetable crops in western Maharashtra and developing effective management strategies

Savarni Tripathi*, Raj Verma and G.K. Mahapatro
ICAR-Indian Agricultural Research Institute, Regional Station, Aundh, Pune – 411007, Maharashtra, India
**Email: savarni@yahoo.com; savarni.tripathi@icar.gov.in*

Solanaceous vegetables are important components of overall vegetable cultivation in western Maharashtra. Among them tomato and chilli/ capsicum are important and widely grown in large area. Tomato and chilli/ capsicum are prone to several viruses mainly due to favourable climatic conditions for viruses and their vectors throughout growing periods. 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 remerging viruses. Therefore, the study was undertaken to understand the present status of viruses infecting tomato, chilli/ capsicum in western Maharashtra and to develop effective and affordable solution for farmers for minimizing losses and maximizing profit. Surveys and surveillance were conducted over several years in various districts of western Maharashtra. Serological and molecular characterization indicated that occurrence of viruses belonging to Potyvirus, Geminivirus, Cucumovirus, Tospovirus, and Tobamovirus groups are common and in most of the cases complex mix infection resulted into severe symptoms and substantial crop loss. Thus, the field management trials were conducted using various combinations of mulching, crop cover and reduced application of biopesticides and insecticides in order to develop the integrated management practices for managing viral diseases in solanaceous vegetables with more emphasis on eco-friendly practices. The integrated management practices were found promising in delaying and reducing the viral diseases significantly and enhancing the marketable yield. The optimized management practices are also validated at farmers' field. These practices could help to enhance famers' profitability.

Oral Presentations

OP(S2)/01: Exploring biocontrol potential for management of alternaria leaf spot of aloe vera

Kushal Raj[1]*, Rakesh Kumar Chugh[1] and Rakesh Kumar Sehrawat[2]
*[1]Department of Plant Pathology, [2]Department of Microbiology, CCS Haryana Agricultural University,
Hisar – 125004, Haryana, India
Email: kushalraj@hau.ac.in

Aloe vera belonging to family Liliaceae is highly important, extensively cultivated medicinal plant and also extensively used in the cosmetic industry. *Aloe vera* is a rich source of antioxidants and vitamins that may help to protect our skin. *Aloe vera* plant has a short, stout stem and a rosette of fleshy, lanceolate leaves which have a serrated margin of small white teeth. Many fungal pathogens are responsible for the production of mycotoxins that alter the potentiality of this highly important medicinal plant. It has been frequently reported that *Aloe vera* suffers from *Alternaria* leaf spot disease in various parts of the world. Various fungicides used to combat this disease, have deleterious effects on the environment and on pharmacologically important constituents of *Aloe vera*. To avoid the harmful effects of fungicides an eco-friendly approach was adopted for management of *Alternaria* leaf spot. Different bioagents *viz*., *Trichoderma harzianum*, *Trichoderma viride*, *Pseudomonas fluorescence*, *Bacillus subtilis*, *Azotobacter chroococcum* HT-54 were evaluated under *in vivo* conditions. Amongst the tested bioagents, *Trichoderma harzianum* and *Trichoderm viride* were found promising in controlling the *Alternaria* leaf spot disease up to 44.56 and 43.97 per cent respectively as compared to control and were at par with copper oxychloride.

OP(S2)/02: Bio-intensive strategy for sustainable management of disease in *Brassica juncea*

M.S. Yadav[1]* and N.S. Yadav[2]
*[1]ICAR-National Research Centre for Integrated Pest Management, LBS Building, Pusa Campus,
New Delhi – 110012, India
[2]Krishi Vigyan Kendra (CCSHAU), Mahindergarh - 123029, Haryana, India
Email: dr.msyadav65@gmail.com

India is a leading producer of rapeseed-mustard, contributing about 23% of country’s total oilseed production. *Brassica juncea* (L.) Czern & Coss} is the major oilseed crop, occupying more than 80% of total rapeseed-mustard cultivated area in India. *B. juncea* is withered by various fungal diseases viz., Sclerotinia rot {*Sclerotinia sclerotiorum* (Lib) de Bary}, white rust {*Albugo candida* (Pers. Ex. Lev.) Kuntze} and Alternaria blight {*Alternaria brassicae* (Berk. Sacc.} causing losses up to 50 % of seed yield in mustard in India. The success of bio-intensive strategy could reduce the excessive use of chemical and favour the adoption of integrated disease management modules as well as agricultural practices that help to restore the natural conditions for survival of beneficial microbiota. Keeping in view, the hazards related to use of chemical fungicides, an experiment was planned and carried out at CCSHAU, regional research station, Bawal (Rewari), Haryana during *Rabi* crop season 2018-19 in randomized block design with four replications. Experiment comprises three module (treatments) viz., T1= soil application of *Trichoderma viride* (NCIPM strain), seed treatment with *T. viride* @ 10 g /kg and two foliar spray of freshly prepared aqueous garlic bulb extract @ 2% w/v at 45 and 60 days after sowing (DAS); T2= seed treatment with carbendazim 50 WP @ 1g a.i. / kg followed by two foliar spray of carbendazim 50 WP @ 0.5 g a.i./l of water at 45 and 60DAS and T3= control (untreated). The results showed that soil application and seed with *T. viride* followed by two foliar spray of freshly prepared garlic clove extract was best over other treatments in significantly reducing the major diseases and increasing the seed yield. Minimum disease incidence of Sclerotinia rot (11.9%), disease severity of white rust (34.3%), Alternaria blight (29.1%) and maximum seed yield of 2404 kg/ha was found in bio-intensive strategy in comparison to corresponding values of 20.5%, 49.7%, 44.0% and 1967 kg /ha in untreated control. Bio-intensive strategy was found best as compared to other treatment besides being eco-friendly management of diseases.

OP(S2)/03: Molecular programming of drought challenged *Trichoderma harzianum* bioprimed rice (*Oryza sativa* L.)

B.M. Bashyal[1]*, Pooja Parmar[1], Kirti Rawat[1], Najam Waris Zaidi[2] and Rashmi Aggarwal[1]
[1]Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
[2]International Rice Research Institute, New Delhi – 110008, India
**Email: bishnumayabashyal@gmail.com*

Present investigation was undertaken to evaluate the different biocontrol agents i.e. *Trichoderma harzinum* 1, *Trichoderma harzianum* 2, *Chaetomium globosum* and *Talaromyces flavus* against the drought in resistant (DRR 42 and Sahbhagi Dhan) and susceptible (IR 64) varieties of rice. Biocontrol agent *Trichoderma harzianum* was observed most effective for drought tolerance and after 13 days of drought treatment minimum wilting (20%) was observed in Sahbhagi Dhan treated with *Trichoderma harzianum* 2. Significantly positive correlation (r = 0.91) was observed between wilting and Malondialdehyde (MDA) content. While negative correlation (r = -0.67) was observed between wilting and average plant weight. Cell viability test was conducted with fluorescein diacetate (FDA) and propidium iodide (PI) staining showed clear differences after 10 days of drought stress in rice variety IR 64 and Sahbhagi Dhan. Study on nuclear DNA content after 10 days of drought stress indicated more nuclei in treatment T1 compared to control Transcriptomic analysis of rice cultivar IR64 bioprimed with *Trichoderma harzianum* under drought stress was carried out in comparison to drought stressed samples using next gen sequencing techniques. Out of the 2506 significant (p<0.05) differentially expressed genes (DEGs), 337 (15%) were exclusively expressed in drought stressed plants, 382 (15%) in *Trichoderma harzianum* treated drought stressed plants and 1787 (70%) were commonly expressed. The genes exclusively expressed in *T. harzianum* treated drought stressed plants were mostly photosynthetic and antioxidative such as plastocyanin, small chain of Rubisco, PSI subunit Q, PSII subunit PSBY, osmoproteins, proline-rich protein, aquaporins, stress enhanced proteins and chaperonins. The KEGG enrichment analysis states that the most enriched pathways were of metabolic (38%) followed by pathways involved in synthesis of secondary metabolites (25%), carbon metabolism (6%), phenyl propanoid (7%) and glutathione metabolism (3%). Some of the genes were selected for the validation using real time PCR which showed consistent expression as RNA-seq data. Overall, it can be concluded that *T. harzianum* biopriming delays drought stress in rice cultivars by multitude of molecular programming.

OP(S2)/04: Eco-conscious approaches to manage fungal diseases of aroids

S.S. Veena*, M.L. Jeeva and A. Asha Devi
ICAR-Central Tuber Crops Research Institute, Sreekariyam, Thiruvananthapuram - 695017, Kerala, India
**Email: veena.ss@icar.gov.in*

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. Leaf blight in taro (*Phytophthora colocasiae),* collar rot (*Sclerotium rolfsii*) and corm rot in elephant foot yam are the most destructive and prevalent diseases in aroids. Organic cultivation of these crops is given high importance and effective management of pest and disease is an area of research which warrants more attention. At ICAR-CTCRI, attempts were made to locate resistant genes in taro and elephant foot yam accessions; 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. Identified 10 accessions of taro and 3 of elephant foot yam with disease resistance; incorporation of *Trichoderma asperellum*, *Bacillus amyloliquefaciens*, *B. subtilis* and *P.indica* resulted

in disease reduction as well as yield increase; organic amendments, vermicompost and vermitea promoted plant growth; increased yield and reduced the disease incidence and treating EFY corms in *T. asperellum* amended cowdung slurry protected the corm from postharvest rot and mealy bug infestation. Later attempts were made to integrate various eco-smart approaches and adoption of these approaches can ensure healthy and pesticide free aroids for consumption.

OP(S2)/05: Antagonistic and phosphorus solubilizing activities of native *Pseudomonas* spp. against soil and tuber-borne diseases of potato (*Solanum tuberosum* L.)

Mehi Lal[1]*, Ashwani Kumar[1], Sorabh Chaudhary[1], R.K. Singh[3], Sanjeev Sharma[2] and Manoj Kumar[1]
[1]ICAR-Central Potato Research Institute, Regional Station, Modipuram, Meerut - 250110, Uttar Pradesh, India
[2]ICAR-Central Potato Research Institute, Shimla - 170001, Himachal Pradesh, India
[3]ICAR-Central Potato Research Station, Regional Station, Patna - 801 506, Bihar, India
**Email: mehilalonline@gmail.com*

Soil and tuber-borne diseases are serious threat for potato cultivation worldwide, which causes severe losses in the yield and quality of potato and extremely difficult to control. Biological control offers an environmental friendly alternative approach to conventional control methods for sustainable disease management. In this regard, native bacterial isolates collected from different crop rhizosphere soil, were evaluated for antagonistic activities against major potato pathogens. Based on the morphological and phenotypic characters, most of the isolates were identified as *Pseudomonas* spp. A total of twenty-two bacterial isolates were screened for bio-control activity in dual culture assay and isolate Pf14 showed the highest mycelial inhibitory potential (ranged from 62.2 to 59.3%) against all the tested pathogens. The strain Pf14 produced antifungal volatile compounds that significantly inhibited mycelia growth (ranged from >80 to >50%) in sealed plate assay. Maximum reduction in fungal biomass (ranged from >80%) was observed in King's broth in shake liquid culture in all the pathogens. Cell-free culture filtrate of the selected isolate inhibited mycelial growth ranged from 68.9 to 42.6% of the tested pathogens with 48-hr culture filtrate. Additionally, the isolate exhibited excellent phosphorus solubilizing efficiency on PVK media. Due to the novel antifungal and phosphorus solubilization potentials, the strain Pf14 can be used as a promising bio-agent against the soil- and tuber-borne pathogens of potato.

OP(S2)/06: Controlling the transmission of chilli leaf curl virus by exogenous application of dsRNA targeting hsp70 gene of its vector, *Bemisia tabaci*

Amalendu Ghosh* and Prosenjit Chakrabarty
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: amal4ento@gmail.com*

Silverleaf whitefly (*Bemisia tabaci* Gennadius) is recognized as one of the important invasive pests worldwide. It transmits begomoviruses in a persistent-circulative manner and causes severe yield losses. Leaf curl disease in chilli caused by *B. tabaci*-transmitted *Chilli leaf curl virus* (ChiLCV, genus: *Begomovirus*) is a major constrain in chilli production in India. Based on the transcriptomic response of *B. tabaci* to ChiLCV infection, double-stranded RNA (dsRNA) targeting heat shock protein 70 (hsp70) of *B. tabaci* was synthesized by cloning into L4440 expression vector and transforming into *E. coli* HT115 strain. Oral delivery of *hsp70*dsRNA at 1, 2, and 3 µg/mL showed 67.78, 70.00, and 82.22% mortality of *B. tabaci*, respectively after 24 h of ingestion. Quantitative RT-PCR (qRT-PCR) analysis showed that dsRNA treatment at 1, 2, and 3 µg/mL reduced the *hsp70* mRNA expression level by around 5.4, 10.4, and 12.4-fold, respectively. Although the virus copy number was decreased 35.1-fold in *hsp70*dsRNA-treated (at 1 µg/mL) *B. tabaci* compared to untreated control, there was no significant reduction in

virus transmission in test plants. *Hsp70*dsRNA treatment at 2 µg/mL reduced virus copies in *B. tabaci* by 3.61E+04-fold and transmission efficiency by 40%. No virus copies were detected in *B. tabaci* fed with *hsp70*dsRNA at 3 µg/mL resulting in no transmission of ChiLCV in test plants under controlled conditions. Topical application of *hsp70*dsRNA on ChiLCV-infected chilli plants at 10 µg/mL under glasshouse conditions recorded 68.33% knockdown of *B. tabaci* post 24 h exposure to treated plants and further restricted the transmission by surviving *B. tabaci* population.

OP(S2)/07: Impact of IPM intervention on inoculum density and disease development relationship between pathogen and antagonistic microbials in transplanted and direct seeded rice

M.K Khokhar*, Manoj Choudhary, R.K. Tanwar, Rekha Balodi, P.N. Meena, Sonali Singhal, Satyendra Singh, Rakesh Kumar, Anoop Kumar, S.P Singh and C. Chattopadhyay
ICAR-National Centre for Integrated Pest Management, Pusa Campus, New Delhi – 110012, India
**Email: khokharmk3@gmail.com*

The study was carried out to monitor inoculum density in terms of colony forming units (cfu) of pathogen and to assess disease development relationship of antagonistic microbials with pathogen in IPM and Non IPM fields under direct seeded (DSR) and transplanted (TR) rice. Density of *Trichoderma harzianum* and *Pseudomonas fluorescence* was higher in soils of IPM plots but not that of *Fusarium verticillioides* compared to Non IPM. Higher population density of *Trichoderma, Pseudomonas* and *Fusarium* were recorded in TR in comparison to DSR. In TR density of *Pseudomonas* was initially high in IPM as compared to Non IPM fields but during the mid-crop season the trend changed, i.e. cfu count of *Pseudomonas* remained higher in Non IPM while in DSR inoculum density of *Pseudomonas* was initially high in Non IPM. The significant difference (P£0.05) were recorded in density of *Trichoderma, Pseudomonas* and *Fusarium* in soils of IPM plots and Non IPM plots. A significant change over the years and change over Non IPM was also observed in IPM fields. Disease dynamics study shows that bacterial leaf blight (BLB), bakanae and sheath blight were major diseases in TR while BLB and brown spot were predominant in DSR. A significant positive correlation was found between (i) *Fusarium* density each against bakanae and brown spot in TR; (ii) *Trichoderma* density against Bakanae in DSR while negative correlation observed for (i) *Trichoderma* against each of BLB and Brown spot in DSR (ii) *Pseudomonas* density against bakanae, BLB and sheath blight in TR and (iii) *Fusarium* density against bakanae in DSR. Soil sample analysis revealed a significant improvement in soil physico-chemical properties in IPM fields. Socio-economic studies indicated higher yield as well as benefit-cost ratio in IPM as compared to Non IPM. The information obtained in this study could provide a basis for development of bio control strategies for sustainable management of rice diseases in TR and DSR.

OP(S2)/08: Identification of an effective isolate of *Trichoderma asperellum* AT172 for the management of arecanut basal stem rot disease

R.T.P. Pandian[1]*, S.H. Thube[1], Bhavishya[1], N.R. Nagaraja[1], V.H. Pratibha[2], Merinbabu[3], M. Chaithra[1], P. Santhoshkumar[1], B.J. Nirmalkumar[1] and V. Hegde[2]
[1]*Regional Station (ICAR-CPCRI), Vittal - 574243, Karnataka, India*
[2]*ICAR-Central Plantation Crops Research Institute, Kasaragod - 671124, Kerala, India*
[3]*Regional Station (ICAR-CPCRI), Kayamkulam - 690533, Kerala, India*
**Email: R.Pandian@icar.gov.in; r.thavaprakash@gmail.com*

The basal stem rot (BSR) disease of arecanut caused by *Ganoderma lucidum*, also known as *Ganoderma* wilt or foot rot is one of the major diseases of arecanut (*Areca catechu* L.). The disease has been reported from almost all arecanut growing areas of India including north-eastern states (especially in Assam) and Andaman and Nicobar Islands. The disease is mainly soil-borne and mortality of 94% has been reported in neglected gardens. The BSR being a soil-borne disease, biocontrol is the most suitable option for disease management since deploying fungicides to manage the diseases may result in high production costs and health risks to terrestrial and aquatic habitats. Application of *Trichoderma asperellum* enriched neem cake has been found to be effective in the management of basal stem rot of coconut caused by *Ganoderma*. It is known that the efficacy of biocontrol depends upon the strains of the biocontrol agent and the performance of native isolates of Trichoderma is always better in suppressing the disease incidence. Hence, the aim of the present study was to identify an effective strain of *Trichoderma* suitable for the management of BSR in arecanut. A total of 69 *Trichoderma* isolates were obtained from the soil samples collected from the rhizosphere of arecanut in major arecanut growing areas of Assam. Based on growth characteristics and spore morphology, 42 isolates were selected for evaluating antagonistic activity against the arecanut BSR pathogen, *Ganoderma lucidum*. Antagonistic assay resulted in the identification of three effective *Trichoderma* isolates *i.e*., AT172, AT166 and AT121 with 82.2%, 70.0% and 68.9% inhibition of pathogen respectively. All the isolates showed rapid growth with a mean colony growth rate of 2.3 cm day-1. Growth promotion activity of seven isolates studied under net house condition recorded significantly higher total biomass in arecanut seedlings treated with *T. asperellum* AT172 (49.1 g) as compared to control (45.5 g). Holistically, *T. asperellum* strain AT172 was found to be promising with respect to antagonistic activity, mean growth rate and total biomass production. Since this *Trichoderma* isolate is obtained from soil collected from arecanut orchards, the rhizosphere competence of this isolate will certainly be more in arecanut gardens. Therefore the *T. asperellum* isolate AT172 identified under the present investigation will help to formulate a biocontrol based eco-friendly integrated disease management for basal stem rot of arecanut under Assam conditions.

OP(S2)/09: Monitoring of native *Trichoderma* species population in tomato field

Rekha Balodi*, Raghavendra K.V., Babita Singh, H.R. Sardana and Surendra Kumar Singh
ICAR-National Research Centre for Integrated Pest Management, Pusa Campus, New Delhi – 110012, India
**Email: rekha.balodi@icar.gov.in*

Trichoderma species are important biocontrol agents for management of plant diseases having plant growth promotion activities. Though these fungi are found very effective biocontrol agents under laboratory conditions, their efficacy reduces under field conditions due to a multitude of factors like the viability of the strain in the formulation as well as colonization of the fungus in the crop rhizosphere. In this study four native strains of *Trichoderma* spp were isolated from the rhizosphere of the tomato field, Padhana village, Karnal, Haryana and tested for their efficacy against soil-borne pathogens *Rhizoctonia solani* and. *Fusarium* spp. *Trichoderma* isolate with 88% against *Rhizoctonia solani* and 84% against *Fusarium* spp. was grown in the sorghum grains. From sorghum grains, talc formulation of the isolate was prepared with a CFU count of 2×106/ gm talc. This talc formulation was applied to the 1×1 m2 area soil in the rhizosphere of tomato at five spots in open field conditions at Padhana village, Karnal, Haryana. The CFU count of *Trichoderma* spp. at these spots was monitored for three months following inoculation. It was observed that CFU count of *Trichoderma* spp. increased by 5 times and 3.7 times in the second month and third-month following spot inoculation respectively. The average CFU count in the field was 15 × 105 / gm dry soil at the end of third month. In addition, it was observed that the colonies were more homogenous in appearance than before inoculation of *Trichoderma* spp. The study demonstrates that native strains which are better adapted to agroecology can have better establishment under field conditions.

OP(S2)/10: Adoption of modules for management of banded leaf and sheath blight of maize in India

S.K. Aggarwal[1]*, K.S. Hooda[2], P.K. Bagaria[1], Harleen Kaur[3], Robin Gogoi[4], Prashant Chauhan[5] and R.P. Singh[6]

[1]ICAR-Indian Institute of Maize Research, PAU Campus Ludhiana - 141004, Punjab, India
[2]ICAR-National Bureau of Plant Genetic Resource, Pusa Campus, New Delhi – 110012, India
[3]Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana - 141004, Punjab, India
[4]Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
[5]CCS Haryana Agricultural University, Regional Research Station, Karnal – 132001, Haryana, India
[6]Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakhand, India
**Email: sumit.aggarwal009@gmail.com*

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 approaches (chemical, organic-I, organic-II and Integrated disease management (IDM)) in the fields of Ludhiana, Karnal, Delhi and Pantnagar during kharif 2018 and 2019. In the first approach, seed treatment with salicyclic acid (100 ppm) was done followed by foliar spray with Azoxystrobin 18.2%w/w + Difenoconazole 11.4% w/w SC @0.1% twice at 3 and 15 days after inoculation. In the second approach, soil amendment with Trichoderma formulation @6t/acre Farm yard manure, seed treatment with Trichoderma @20g/kg seed followed by foliar spray with neem leaf extract @ 1% twice at 3 and 15 days after inoculation was carried out. In the third approach was slightly different from the first one where Trichoderma @1% was sprayed on foliage twice at 3 and 15 days after inoculation instead of the neem leaf extract while reaming treatment were same as alone. In last fourth approach, soil amended with Trichoderma (@6t/acre Farm yard manure), seed treatment with salicylic acid (100 ppm) followed by foliar spray with Azoxystrobin 18.2%w/w + Difenoconazole 11.4% w/w SC @0.1% at 3 days after inoculation (DAI) and neem leaf extract @1% at 15 days after inoculation. 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. The overall results varied with the location due to environmental and soil conditions. Cost-benefit ratio of different treatments revealed that the specific approach will be useful to manage BLSB for local farmers. In case of Ludhiana and Karnal apart chemical, IDM and organic approach-I will also be beneficial. In case of Delhi and Pantnagar chemical and IDM approach can be utilized effectively to manage the disease.

OP(S2)/11: Status of Cercospora (*Cercospora tageticola* Fresen.) leaf spot of marigold in Himachal Pradesh and its novel management strategies

Shivani Gupta* and Sunita Chandel

Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India
**Email: Sivani849@gmail.com*

Cercospora Fresen. is a universally destructive plant pathogen occurring on a wide range of hosts in almost all major families of monocotyledonous families which consequently implicit higher risk of diseases. Cercospora leaf spot disease incited by *Cercospora tageticola* Fresen. is adversely affecting cultivation in all major marigold growing regions of Himachal Pradesh. Hence, incidence and severity of Cercospora in the regions of Solan and Sirmour district was assessed during active growing season 2017-2018 and maximum incidence and severity was observed at Nauni (62.4% and 70.4%) and Rajgarh (46.7% and 52.6%). Moreover, Morphological studies revealed that pathogen was fast growing on Carrot decoction agar medium with colony diameter 90 mm having mycelial diameter (8.54-11.34mm) whereas pathogen produced geniculate, conidiophores (3.5-6 x 50-300 mm) on which hyaline

conidia (2.7-5 × 70-200 mm) were formed. Among different systemic and non-systemic fungicides tested, 83.70% inhibition of mycelial growth of *Cercospora tageticola* Fresen. was recorded in Folicure 25% EC (tebuconazole) at 250ppm concentration. Among different botanicals and bioresources, darak leaves extract was found to be most effective with highest mycelial growth inhibition (79.79 %) followed by beejamrit and jeevamrit (63.38 and 57.19 %). Since *Cercospora tageticola* Fresen. is a seed borne pathogen, seed health testing studies were conducted prescribed by ISTA with desired amount of best fungicides, botanicals and bioresources, three treatments, Folicure 25% EC, Score 25% EC 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.

Poster Presentations

PP(S2)/01: Rice phyllosphere associated *Chryseobacterium* species: an untapped bacterial antagonist displays volatile organic compound mediated protection against blast disease incited by *Magnaporthe oryzae*

M. Kumar[1], K. Charishma[1], K.P. Sahu[1], A. Patel[1], N. Sheoran[1], A. Kundu[1] and **A. Kumar[1]***
[1]Division of Plant Pathology, [2]Division of Agricultural Chemicals, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: kumar@iari.res.in*

Pigmented flavobacterial *Chryseobacterium* species displays functional diversity and comprises species that are both pathogenic and non-pathogenic. Nine-endophytic bacterial isolates obtained from the leaf of rice seedlings planted in Almora, India, were identified as belonging to diverse species of bacterial genera *Chryseobacterium* based on16S rRNA gene sequence similarities. Molecular phylogenetic analysis by maximum likelihood method clustered the nine isolates with plant or soil-inhabiting species such as *Chryseobacterium taklimakanense* (*Os*Ep-PSA33); and *Chryseobacterium camaliae* (*Os*Enb-ALM-D20 and *Os*Enb-ALM-D11) with a high confidence level of above 50.0 % bootstrap support. However, isolates *Os*Enb-ALM-C23, *Os*Ep-PPA23, *Os*Ep-PPA6, *Os*Enb-ALM-D3, and *Os*Enb-ALM-A6, *Os*Enb-ALM-A22 were found clustered with *Chryseobacterium culicis* and *Chryseobacterium endophyticum*, respectively, with low bootstrap support (<50.0 %). Activity testing of *Chryseobacterium* isolates showed excellent antifungal activity with over 80.0 % mycelial growth inhibition of rice blast fungus. Among the three isolates tested, *Os*Enb-ALM-A6 and *Os*Enb-ALM-A22 showed over 90 % inhibition of fungal growth only by volatile compounds. *In planta* seed and seedling treatments showed significant blast disease reduction over 40.0 % with bacterial isolates belong to *Chryseobacterium endophyticum* cluster. qPCR based expression analysis of *Os*CEBiP, *Os*CERK, *Os*PAD4, *Os*NPR1.3, *Os*PDF2.2, and *Os*FMO1 indicated their enhanced transcription of *Os*CEBiP, *Os*CERK, *Os*PAD4, *Os*NPR1.3, and *Os*FMO1 in rice seedlings exposed to volatiles emitted by *Chryseobacterium* isolate *Os*Enb-ALM-A6. The seedlings exposed to volatiles or live cells showed altered growth pattern suggestive of activated innate immunity. Elevated expression of the defense genes appeared to have impacted the growth in bacterized seedlings as a trade-off between plant growth and defense. Rice phyllosphere adapted flavobacterial *Chryseobacterium* species showed potential for exploitation as an effective biocontrol agent for combating rice foliar blast disease. Our data on blast suppression by volatile mediated pathogen inhibition, and host defense activation will be a potential alternative to tricyclazole based, current, blast management.

PP(S2)/02: Eco-friendly management of urdbean leaf crinkle virus

J. Raja*
Department of Plant Pathology, Faculty of Agriculture, Annamalai University, Annamalainagar - 608002, Tamil Nadu, India
**Email: rajajeyaraman71@gmail.com*

Urdbean leaf crinkle, a disease of pulses that threatens blackgram production in India. It is a monopartite, positive-sense, single-stranded DNA virus and the type member of the genus Begomovirus in the family Geminiviridae. The virus spreads from seeds and through aphids, whitefly and also leaf eating beetle. The disease causes stunting of plants, enlargement and crinkling of leaves. Temperature, relative humidity and plant growth period have direct relationship with the development and spread of disease. The antiviral principles from various plant sources were found to induce resistance in host plants against viral diseases. Cow urine application on crop plants to prevent the development of pests and increased level of immunity. The aim of this study was to evaluate the antiviral activity of cow urine extract of *Datura metel* seeds against urdbean leaf crinkle virus infection blackgram plants. Foliar spray with cow urine (20%), water extract of *D. metel* seeds (20%) and cow urine extract of *D. metel* seeds (20%) on blackgram plants reduced disease incidence under glasshouse and field conditions. It was observed that cow urine extract of *D. metel* seeds showed maximum inhibition of disease incidence in blackgram crop. In the present study significantly increase in the plant height, number of pods per plant, number of seeds per pod was observed in plants sprayed with cow urine extract of *D. metel* seeds at 10 and 20 days after sowing. Pre-treatment of blackgram plants with cow urine extract of *D. metel* seeds significantly increased photosynthesis pigments, soluble intracellular protein, phenol and peroxidase activities. *D. metel* contains tropane alkaloids may be act as antimicrobial agent. The majority of the nitrogen in cow urine is in the form of urea, ammonia and uric acid. Urea denatures the protein of virus due to which the plants treated with cow urine managed the leaf crinkle disease effectively.

PP(S2)/03: Bioremediation of textile waste dye effluent by bacterial isolates

R.M. Shinde[1,3]*, Toshi Agrawal[3], A.S. Kotasthane[2] and S.B. Verulkar[3]
[1]Vasantrao Naik College of Agricultural Biotechnology, Yavatmal – 445001, Maharashtra, India
[2]Department of Plant Pathology, [3]Department of Plant Molecular Biology and Biotechnology, Indira Gandhi Krishi Vishwavidyalaya, Raipur – 492012, Chhattisgarh, India
**Email: roshan.agricos@gmail.com; roshanshinde@pdkv.ac.in*

Among the various types of environment pollution, water pollution is a major concern. Discharged synthetic dye effluents from industries can be damaging to the receiving water bodies. The dyes are harmful to life forms as they are recalcitrant, carcinogenic and mutagenic in nature. Such polluted water generate adverse effects on crops. To overcome this problem in this study bacterial isolates from different soil and sludge samples were collected and the potential isolates was screened for treatment of industrial waste dye. Their degradation efficiency was assessed and the molecular study of the potential was done using 16s RNA sequencing. The cultures were inoculated in to the medium supplemented with dyes (RBBR, Aniline blue) and incubated. It was found that 18 isolates were found able to decolorize aniline blue dye above 50% in 10 days, with highest dye decolorizing ability 84.53% by isolate (SH2A) *Stenotrophomonas sp*. and 32.72 to the lowest by (RDC) *Klebsiella pneumoniae* strain NJ8. Eight isolates were able to degrade RBBR dye above 50% with the highest 68% by (GS 5A) *Enterobacter asburiae* strain PW2a and lowest 34 % by (S9) *Vibrio cyclitrophicus* strain HS8. Only 6 isolates were found to decolorize Azure B dye with the highest 77.77 by *Vibrio cyclitrophicus* strain HS8(S9).

PP(S2)/04: Phyto-chemicals mediated induced resistance in tomato plants against *Alternaria solani*

Rashmi Tewari*, Ruchi Tripathi and Divya Bhatt

Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakhand, India

**Email: rashmipnt@gmail.com*

Botanicals or plants extracts are effective bio-pesticides being environmentally safe, easily biodegradable suitable for plant disease management and also be fitting in organic farming. Phytochemicals from plant origin may be used as alternatives to agrochemicals for managing plant diseases. Early blight caused by *Alternaria solani* is one of the destructive seed borne disease of tomato. The physiological and biochemical effects of methanolic extracts of *Eucalyptus globules* and *Azadirechta indica* on infected tomato plants was investigated using the whole plant bioassay through ROS modelling and seedling vigor study method. All the tested compounds positively enhanced the physiological traits (Root length, Shoot length and leaf area index) of treated plants and the enzymatic activities of phenyl ammonia lyase (PAL), peroxidase (PO), and polyphenol oxidase (PPO), super oxy dismutase (SOD), total phenolic content (TPC) and Secondary metabolites (alkaloids, flvonoids, tannins, saponins, terpenoids, reducing sugar and steroids). Moreover, the treatment with the plant extracts significantly increased the vigor of the plant. Considering the fungitoxicity of plant extracts against *A. solani* with no phytotoxicity on treated plants, we believe that the plant extracts might be a sustainable eco-friendly control strategy to reduce the usage of chemical fungicides partially or entirely against *A. solani* particularly and fungal diseases in general.

PP(S2)/05: Application of entomopathogenic fungi as natural regulator of agricultural pests

Dilip Kumar Chaurasiya[1]*, Siddharth Singh[2] and Sangita Sahni[1]

[1]*Department of Plant Pathology, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur -848125, Bihar, India*

[2]*Department of Plant Pathology, Faculty of Agriculture, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia - 741252, West Bengal, India*

**Email: dilipkchaurasiya39@gmail.com*

Insect pests cause about 42% of crop losses worldwide and the mainstay use of synthetic chemical pesticides over the last 50 years causes severe damage to human and environmental health. Entomopathogenic fungi are a diverse group of insect pathogenic fungi, playing a vital role as a biological control agent of insect pests. These fungi have the ability to infect insects with sap-sucking as well as chewing and biting mouthparts. The mode of action of these fungi is mostly through contact and penetration. The infection cycle of entomopathogenic fungi involves several steps like adhesion and germination of spore, development of infection structure, penetration of the cuticle and production of toxins. In an agriculture system, these fungi or biopesticides can be used to control insect pest population directly in the field as well as in storage houses. Thus the demand for IPM strategies influencing the use of biocontrol agents. The use of microorganisms as biological control agents is the most attractive and non-hazardous alternative method for insect pest management. These agents cause devastation to pest population without any health hazards to the human population. Also, the complex mode of action of these pathogens reduces the chances of resistance development.

PP(S2)/06: Evaluation of osmotic stress tolerance of the antagonistic yeast formulation

Jasmin Thomas* and J. Saha

Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur - 741252, West Bengal, India

**Email: jasminthomas64@gmail.com*

The application of yeast based biocontrol formulation is safe and economic alternative for reducing post harvest fungal decay of fruits. When the yeast is in an environment with high osmolarity, water flows from the cell into the extracellular medium. This results in a decrease in the cellular volume and turgor pressure and may result in cell death. Tolerance to environmental stresses is a prerequisite for development of biocontrol yeast formulation. The viability of antagonistic yeast Y-27 (*Meyerozyma caribbica*) in molasses urea based liquid formulation was evaluated after exposing them to osmotic stress with molasses urea media containing salt (NaCl) at different concentration and also with changing the concentration of molasses *viz* 5%, 15%, 20%, 25%, 30%, 35%, 40%, and 45% .The cell number of Sc YZ-7 in molasses urea media containing salt (NaCl) at different concentration *viz* 1%, 1.5%, 2%, 2.5% was improved by varying degrees in all the concentrations compared to the population in molasses urea formulation without NaCl which kept as control at 28±1 °C. The formulation containing upto 25% molasses maintained the cell population even after 4 months of storage whereas, in control with 5% concentration of molasses the population drastically reduced. The population was highest in the formulation with 15% molasses concentration. The formulation prepared with yeast isolate had highest viability in 1% NaCl and 15% molasses added separately upto 120 days of storage.

PP(S2)/07: Studies on inoculum potential of *Meloidogyne incognita* (kofoid and white, 1919) Chitwood, 1949, on cucumber (*Cucumis sativus* L.) and efficacy of biocontrol agents in its management

Poojashree, Satya Kumar, **Shilpi Rawat*** and Manisha Dev

Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar – 263145, Uttarakhand, India

**Email: rawatshilpi19@gmail.com*

Cucumber (*Cucumis sativus* L.) belongs to Cucurbitaceae family and is an important vegetable that is cultivated globally. It is the eighth most grown vegetable crop across the world (Edom, 2017). In Asia it ranks fourth after tomatoes, cabbage and onion (Tatlioglu, 1993; Eifediyi and Remison, 2010). Cucumber is a good source of vitamins, fibers, minerals and roughage (Mukhtar *et al*., 2013b). Cucumber is threatened by tremendous yield losses from *Meloidogyne incognita*, which attacks on roots of the plant (Wehner *et al*., 1991; Walters *et al*., 1993; Mukhtar *et al*., 2013b) and cause yield loss of 6-69.2 per cent in India (Krishnaveni and Subramanian, 2003; Khan *et al*., 2014; Walia *et al*., 2016). For the non chemical management, biocontrol agents against nematode are very effective. Efficacy of biocontrol agents were evaluated at three different doses in the management of *M. incognita* infesting on cucumber susceptibility hybrid variety Malini under glass house condition. The biocontrol agents viz. *P. lilacinum*, *P. chlamydosporia*, *T. harzianum*, *Trichoderma* spp. (native isolate) and *P. fuorescens* tested on malini cucumber hybrid was tested with respect to various growth parameters, number of gall formation and final nematode population in the soil as compared to untreated control. Experimental results showed that, all the 3 different doses i.e. 5g, 7.5g and 10 g of biocontrol agent formulations showed significant increase in plant growth parameters (shoot length, root length, fresh shoot weight, dry shoot weight, fresh root weight and dry root weight) and thereby reduced the number of gall formation in roots and final population of nematode in soil, over inoculated check. Amendment of pot soil with *P. lilacinum*, *P. chlamydosporia*, *T. harzianum*, *Trichoderma* spp. (native isolate) and *P. fluorescens* recorded significant reduction in total nematode population. *P. lilacinum* @ 10 g per kg of soil was found to be most effective among other biocontrol agents followed by *T. harzianum*, *Trichoderma* spp. (native isolate), *P. fluorescens* and *P. chlamydosporia*, respectively. All treatments showed better performance at the dose of 10 g per kg of soil followed by 7.5 and 5 g per kg of soil i.e increased dosage of biocontrol agents reduce the total population of nematode in the soil. Among the different biocontrol agents *P. lilacinum* applied @ 10 g/kg of soil showed best results followed by *T. harzianum*, *Trichoderma* spp. (native isolate), *P. fluoresecens* and *P. chlamydosporia*, respectively over the inoculated check. So, the results confirms the use of bio control agents for management of *M. incognita* in susceptible cucumber variety and also a eco friendly approach for the farmers.

PP(S2)/08: Transcriptome reprogramming of tomato by *Chaetomium globosum* to induce systemic defense mechanism against early blight

Jagmohan Singh[1]*, Rashmi Aggarwal[1], Bishnu Maya Bashyal[1], M.S. Saharan[1], Zakir Hussian[2] and Amolkumar Solanke[3]

[1]Division of Plant Pathology, [2]Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India

[3]ICAR-National Institute Plant Biotechnology, Pusa Campus, New Delhi – 110012, India

**Email: dhillonjagmohansingh@gmail.com*

Chaetomium, a strictly saprophytic fungus that belongs to *Ascomycota* of the family *Chaetomiaceae*. *C. globosum* is the most frequently isolated and has been reported to be a potential antagonist of various plant pathogens. *C. globosum* has been identified as a potential antagonist of *Bipolaris sorokiniana*. Several reports are available on mycoparastism and antibiosis mechanism of *Chaetomium globosum* against a number of plant pathogenic fungi. Few studies to date report the induced resistance as a mechanism of biocontrol by *Chaetomium globosum* toward phytopathogens. In order to gain insights into the potential induced defense mechanism of by *C. globosum* (Cg2) against early blight of tomato, global RNA sequencing is performed and differentially expressed genes of defense induced hormone signaling pathways are validated by using qRT-PCR. The RNA of tomato plants treated with *C. globosum* isolate Cg-2 and control plants (mock-inoculated with water) was sequenced. The transcriptome data revealed that 22473 DEGs were expressed in tomato on Cg-2 inoculation as compared to control plants and among these 922 DEGS had fold change -2 to +2 and $p<0.05$ The KEGG pathway analysis reveals that most of the DEGs belong to metabolic pathways, biosynthesis of secondary metabolites, ribosome, carbon metabolism and plant hormone signal transduction. GO analysis revealed that these DEGs were enriched mainly in the following terms: ROS metabolic process, H2O2 metabolic process, defense response, superoxide dismutase activity, and antioxidant activity. Moreover, the marker genes of hormone signaling pathways such as PR1, PiII, PS, PAL, Le4 and GluB were validated by qRT-PCR. These results provide the basis for understanding the molecular mechanism by which the biocontrol fungus Cg-2 induces the resistance in tomato against early blight.

PP(S2)/09: Biocontrol of fungus-nematode disease complex in mungbean

Irfan Ahmad* and Mujeebur Rahman Khan

Department of Plant Protection, Faculty of Agricultural Sciences, Aligarh Muslim University, Aligarh - 202002, Uttar Pradesh, India

**Email: ahmadirfan8923@gmail.com*

The impact of biocontrol agents viz., *Trichoderma harzianum*, *Trichoderma viride*, *Pseudomonas fluorescence*, and *Bacillus subtilis* o the root-rot, root-knot, and fungus-nematode disease complex caused by *Meloidogyne incognita*, *Macrophomina phaseolina*, jointly in green gram was evaluated under pot condition. The inoculation with *M. incognita* (2000J2/plant) and *M. phaseolina* (4g fungus/kg soil) caused oval and fleshy galls and rotting on the roots of green gram. The concomitant inoculation with fungus and nematode caused significantly greater root-rot, but galling was decreased. Soil application of *T. harzianum*, *T. viride*, *P. fluorescence*, and *B. subtilis* at the rate of 4g or ml/ pot suppressed the diseases and improved the growth of mung bean. Treatments with *T. harzianum* decrease the galling and root-rot by 22.2 & 52.3% and 27.3 & 54% in plants singly or concomitantly inoculated with *M. incognita* and *M. phaseolina* over inoculated control, respectively. The plant growth and yield were increased by 5-9.4 and 7-10%, respectively, over uninoculated control. The overall order of effectiveness of biocontrol agents was: *T. harzianum* Ã *T. viride* Ã *P. fluorescence* Ã *B. subtilis*. Physiological and biochemical parameters *viz*., photosynthesis rate (PR), stomatal conductance (SC), transpiration rate (TR), total chlorophyll (TC), total phenol (TP), and salicylic acid (SA) contents were studied in response to the single or concomitant inoculation with the root-rot fungus and root-knot nematode. The physiological parameters viz., PR significantly decreased, whereas the TR and SC increased with time in the infected plant. The biochemical parameters viz., TC, TP, and SA were reduced in mung bean leaves with single or concomitant inoculation over control. Whereas PR, SC, TR, TC, TP, and SA further enhancement after applying BCAs with the progress of time in the treated or untreated of the mung bean plant.

PP(S2)/10: Management of common scab in potato

G. Biswal*, A. Mishra, A. Sasmal, D. Ghosal and A.K. Mohanty
College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar – 751003, Odisha, India
**Email: gayatribiswal1965@gmail.com*

The common scab (*Streptomyces scabies)* is an important disease of potato not only in Odisha but also in India. The disease usually damage the tubers by disfiguring it, reduces the yield and also market value. The present study was undertaken to identify most promising management strategy for common scab of potato. The trials were conducted with four treatments and six replications in the variety Kufri Jyoti at All India Co-ordinated Potato Research Project on Potato in Central Farm Odisha University of Agriculture & Technology, Bhubaneswar during 2018-19 and 2019-20. The four treatments included in the trials were, i.e. T1- Untreated diseased tubers (Control); T2- Tuber dip treatment with 3% boric acid for 20 minutes before storage; T3- Tuber treatment with *Trichoderma* formulation (8g/kg seed) at the time of planting; T4- Tuber dip treatment with 3% boric acid for 20 minutes before storage and tuber treatment with *Trichoderma* formulation (8g/kg seed) at the time of planting. After harvest it was observed tha all treatments significantly reduced common scab incidence compared to control. Minimum incidence of common scab (5.0%) with maximum tuber yield (19.86 t/ha) was realized due to tuber dip treatment with 3% Boric acid for 20 minutes before storage followed by tuber treatment with *Trichoderma viride* formulation (7.6%) where the yield was 18.16t/ha. The minimm tuber yield 16.6 t/ha was recorded in control where scab incidence was maximum (18.6%) among these treatment.

PP(S2)/11: Eco-friendly management of damping-off in chilli nursery

K. Manikandan*, P. Renganathan and P. Balabaskar and J. Raja
Department of Plant Pathology, Annamalai University, Annamalainagar - 608002, Tamil Nadu, India
**Email: manipatho23194@gmail.com*

The aim of this study was to evaluate plant extracts and oilcake extracts were tested alone and together *in vitro* and *in vivo* experiments for the management of damping-off disease is caused by *Pythium aphanidermatum* (Edson) Fitz. in chilli nursery. Among the plant and oilcake extracts tested, rhizome extract of *Acorus calamus* L. (Sweet flag) and *Madhuca longifolia* (Konig) Macbr. (Mahua) oilcake extract at 20% concentration showed the complete inhibition of mycelial growth of *P. aphanidermatum*. The *in vitro* studies revealed that Sweet flag rhizome extract combination of Mahua oilcake extract @ 1:1 at 20% concentration showed the complete inhibition of mycelial growth of *P. aphanidermatum*. The *in vivo* studies revealed that seed treatment with combined application of Sweet flag rhizome and Mahua oilcake extracts was superior in reducing the pre- and post-emergence damping-off incidence and increased the plant growth and fruit yield of chilli when compared to control. Seed treatment with sweet flag rhizome extract combination of mahua oilcake extract induce accumulation of high levels of phenols and activities of peroxidase, polyphenol oxidase, phenylalanine ammonia lyase, â-1,3-glucanase and chitinase in chilli plant compared to other treatments and control. The antifungal activity of plant and oilcake extracts suppressed *P. aphanidermatum* or increased oxidative enzymes in plants that can play an important role in the resistance to infection with diseases and consequently, increasing growth parameters and fruit yield. Our study demonstrated that plant products can be used for management of damping-off disease in chilli. Thus, this method can contribute to minimizing the risk and hazard of toxic fungicides.

PP(S2)/12: Probiotic as biocontrol agent in management of post harvest diseases of papaya

K. Greeshma*, C.D. Deokar, K.S. Raghuwanshi and V.K. Bhalerao
Department of Plant Pathology and Agricultural Microbiology, Post Graduate Institute, Mahatma Phule Krishi Vidyapeet, Ahmednagar, Rahuri - 413722, Maharashtra, India
**Email: kgreeshmareddy9296@gmail.com*

Probiotics are defined as the microorganisms which are beneficial in the human health. These are orally administered or given in food supplements and are present in the gastrointestinal tract of human being. The fruit crops like papaya (*Carica papaya*) are the most important horticultural crops in Maharashtra as well as in India. Post harvest losses caused by micro organisms are reported up to 30 to 35% losses of which anthracanose showed highest incidence of 46% with reduction in quality and quantity of marketable fruits. Over the years, the plant protection was achieved by use of synthetic chemicals. However, use of probiotics for control of post harvest diseases has taken momentum in recent years in management of post harvest plant pathogens. The post harvest pathogens like *Colletotrichum gloeosporoides, Alternaria alternata*, can be checked by post harvest probiotic spray which includes the Commercial probiotics (Prowel, Flora and Vbact) and Probiotic isolates, which were isolated and cultured from curd, fermented dosa material, fermented jowar and bajra flour. The studies on use of probiotics in the management of post-harvest diseases of papaya suggest that the post-harvest pathogens particularly *Colletotrichum gloeosporoides, Alternaria alternate* can be checked up to 71.8 % and 73.3 % respectively under *in vitro* conditions and the probiotic sparyed fruits showed a reduced disease development under *in-vitro* conditions and resulted in increase in the TSS brix (1.0 over control) in the fruits and also showed an increased shelf life over the control. The efficacy of probiotics against post-harvested pathogens indicates that probiotics can be used in management of post harvest diseases and they can form an integral part of organic farming system.

PP(S2)/13: Biological management of linseed wilt (*Fusarium oxysporum* f. sp. *lini*)

Shamsher Alam* and Gopal Krishna Awadhiya
Department of Plant Pathology, Indira Gandhi Agricultural University, Raipur – 492012, Chhattisgarh, India
**Email: alamshamsher1992@gmail.com*

Linseed (*Linum usitatissimum* L.), also known as flax is a member of genus *Linum* in the family Linaceae. It is commonly known as Alashi or Alsi. Every part of the linseed plant is utilized commercially, either directly or after processing. In India, it is grown mainly for seed, used for extracting oil. Seeds of linseed contain about 33 to 45 per cent oil, which is one of the oldest commercial oils used for various purposes. Linseed wilt incited by *Fusarium oxysporum* f.sp. *lini* (Bolly) Snyder and Hansen was first reported by Luggar (1890) from Minnesota, USA. In India, disease was first reported by Pearl (1923) in Madhya Pardesh. *Fol* is the most important disease among all diseases of this crop. *Trichoderma* and *Pseudomonas* have been successfully and extensively employed by showed antagonistic effect against *Fol*. In present investigation we tried to select best *Trichoderma* and *Pseudomonas* isolates to manage the Fusarium wilt of linseed. Among 30 isolates of the *Trichoderma* tested, strain Tr-20 was found most effective with significantly least mycelial growth (15 mm) and highest mycelial growth inhibition

(83.33%) of the test pathogen, followed by Tr-28, Tr-29 and Tr-25. In *Pseudomonas* isolates *Pseudo*-2 are best among the all. In pot condition Tr-20 and *Pseudo*-3 is also best compare to all others.

PP(S2)/14: Effect of resistance inducers in management of yellow vein mosaic virus disease of okra (*Abelmoschus esculentus* L. Moench)

Pankaj*, V.K. Malik and L. Yadav
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: raopankaj000@gmail.com*

Okra (*Abelmoschus esculentus* L. Moench) is an important vegetable crop of family *Malvaceae*, and grown extensively throughout the world. The crop is prone to damage by various diseases but okra yellow vein mosaic virus (OYVMV) disease transmitted by whitefly is a devastating viral disease which has a wide occurrence and causes considerable yield losses quantitatively and qualitatively. In case of heavy infection, up to 80-94 per cent yield losses are reported. The OYVMV disease can appear at all stages of crop growth depending upon favorable conditions. For the investigation susceptible cultivar of okra 'Pusa Sawani' was grown in randomized block design during *kharif* 2018. At the time of sowing the seeds were soaked in salicylic acid with concentrations 50, 100 and 150 mg/litre water and *Trichoderma viride* @ 5 g/litre water and later sprayed with the same doses at 15 days interval from 30 days after sowing i.e. 30, 45 and 60 days. Amongst different treatments, salicylic acid @ 150 mg/litre as seed priming and spray @ 150 mg/litre water recorded significantly less terminal PDI (28.89%) as compared to other treatments and untreated check plot (73.33%). The fruit yield was also recorded highest in treatment with salicylic acid @ 150 mg/litre as seed priming and spray @ 150 mg/litre water as compared to control and all other treatments. The treatment with bio agent *Trichoderma viride* @ 5 g/litre as seed priming and spray @ 5 g/litre water also enhanced fruit yield significantly as compared to control.

PP(S2)/15: Botanical and bioagent induced defense response and management of grey blight of tea (*Camellia sinensis*)

Popy Bora*
Department of Plant Pathology, Assam Agricultural University, Jorhat - 785013, Assam, India
**Email: popy_aau@yahoo.com*

Microbial bioagents are well known in triggering host defense response besides their antagonism against many phytopathogens. Botanicals, known as green pesticides are also reported to enhance plant defense, however, the studies on these lines are limited. An experiment was conducted using some microbial bioformulations and botanicals for their efficacy against grey blight disease and to study host response in triggering plant defense. We evaluated two talc- based bioformulations viz., Biogreen at 2% (composition: *T. viride*, *Pseudomonas fluorescens*, *M. anisopliae*, *Beuvaria bassiana* and *B. thuringiensis*); Biometa 2% (*Metarhizium anisopleae*); Biogreen plus Biometa at 2% each ; two botanicals viz., *Pongamia pinnata at* 10%*; Xanthium strumarium* at 10% and their combination (*Pongamia pinnata* plus *Xanthium strumarium* at 5% each) through foliar sprays at 10-days interval during May-September (2018-20) with a total seven treatments and four replications in a rendomsied block design against naturally infected grey blight susceptible clone TV-23 incited by *Pestalotiopsis theae* in a organic tea (12-year old bushes) production system. The PDI was significantly reduced with treatments involving bioformulations (33.56 to 12.16) than treatments involving botanicals (30.25 to 23.14), displaying the superiority of bioformulations over botanicals at 150 days after spray (DAS). The combination of either botanicals (23.62 PDI) or bioformulations (12.16 PDI) proved significantly better over their individual response of botanicals (30.25-27.14 PDI). PDI reduced gradually in all the treatments except control where PDI increased to 87.28 %. All the botanicals and bioformulations not only controlled grey blight incidence through direct action, but also induced defense related enzymes viz., Phenyl alanine ammonia lyase (PAL), Polyphenol oxidase (PPO), peroxidase (PO) and Beta 1,3 glucanase. However, activity of all the enzymes were observed highest in case of combination application of Biogreen + Biometa followed by Biogreen alone and combined application of *P. pinnata* + *X. strumarium*. Our study hence, shows that botanicals and bioagents trigger same defense respone in tea, although with varied magnitude and thereby establish role of botanicals and bioagent for organic tea production.

PP(S2)/16: Enhancing the antioxidant capacity of tomato plant with a fungal root endosymbiont against fusarium wilt

Anupriya Chatterjee, Ayushi Kataria, Ikneet Kaur, Ajit Varma and **Swati Tripathi***
Amity Institute of Microbial Technology, Amity University, Nodia – 201313, Uttar Pradesh, India
**Email: swatitri@gmail.com*

Tomato (*Lycopersicon esculentum*) is one of the widely cultivated vegetable worldwide. Tomato vascular wilt is a highly devastating disease caused by *Fusarium oxysporum* f. sp. *Lycopersici* leading to 20% to 60% yield loss globally. The disease is characterized by wilting and browning of the leaves, yellowing, stunted growth, and eventual death of the plant. Use of microbes as bio-control against the phytopathogens has been proved to an efficient, cheap and eco-friendly measure of disease management. In the present study, we have tried to explore the biocontrol quality of *Piriformospora indica* against fusarium wilt of tomatoes. The variation in total activity of peroxidase (POD), a pathogenesis related (PR) enzyme was studied in the tomato plants in presence of the fungal root endosymbiont *P. indica* and *F. oxysporum* f. sp. *lycopersici*. POD is a member of the plant enzymatic antioxidant system which is responsible for scavenging the excessive reactive oxygen species (ROS), which are produced during stress to limit its deleterious effects. Total POD activity was determined spectrophotometrically at 470 nm. Compared with the control plant, total activity of POD was increased in *P. indica* (7.5±0.0007 vs 12.1±0.0009 nmol min”1 mg protein”1) and decreased in *F. oxysporum* (7.5±0.0007 vs 2.5±0.0001nmol min”1 mg protein”1) colonized 1 month old tomato roots. In comparison to *F. oxysporum* colonized roots, the total POD activity was witnessed to rise in the *P. indica and F. oxysporum* (2.5±0.0001 vs 8.5±0.0005 nmol min”1 mg protein”1) colonized roots. In overall the total activity of POD was found to be lesser in the leaves of the *P. indica* and *F. oxysporum* colonized and non-colonized plants but the variation pattern of the total POD activity was found similar to that in the roots. These results showed that *P. indica* significantly increased the total POD activity and lowered oxidative damage in biotic stress. This study highlights the role of *P. indica* as an effective bio-control against *F. oxysporum.*

PP(S2)/17: Integrated disease management against ginger rhizome rot complex

A.C. Patil*, N.D. Kawathe and K.T. Apet
Department of Plant Pathology, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani – 431402, Maharashtra, India
**Email: aashutoshppatil2254@gmail.com*

Ginger (*Zingiber officinale* Rosc) is one of the most important spice crops belongs to the family Zingiberaceae and order Zingiberales. Suffering from several diseases, among which rhizome rot complex is one of the serious diseases in major ginger growing areas. Integrated disease management (pot culture) study was conducted against *P. aphanidermatum* by employing CRD method, eight treatments and three replications *Viz.*, T1: Carbendazim 50 % WP, T2: Metalaxyl 75 WP, T3: *Trichoderma asperellum*, T4: *Trichoderma harzianum*, T5: Carbendazim 50 % WP + Metalaxyl 75 WP, T6: *Trichoderma asperellum* + *Trichoderma harzianum*, T7: Carbendazim 50 % WP + Metalaxyl 75 WP + *Trichoderma asperellum*, T8: Control. Revealed that the average per cent reduction in pre and post emergence rhizome rot with all the treatments ranged from (88.32 %) to (11.86 %). The maximum per cent reduction in pre and post emergence rhizome rot was recorded with *Trichoderma asperellum* +*Trichoderma harzianum* (88.32%) followed by the treatment *Trichoderma asperellum* (70.79%), Carbendazim 50 % WP (59.27%), Carbendazim 50 %

WP + Metalaxyl 75 WP + *Trichoderma asperellum* (50.09%), *Trichoderma harzianum* (35.39%) and T5 Carbendazim 50 % WP + Metalaxyl 75 WP (23.71%). Comparatively minimum per cent reduction in pre and post emergence rhizome rot was recorded with Metalaxyl 75 WP (11.86%).

PP(S2)/18: Integrated management of yellow mosaic disease of blackgram under wheat - blackgram cropping system in Kymore Plateau and Satpura Hills agro climatic zone of Madhya Pradesh

Jai Singh[1]*, K.K. Mishra[2] and A.K. Chaubey[1]
[1]*Krishi Vigyan Kendra (JNKVV), Singrauli – 486886, Madhya Pradesh, India*
[2]*ACRIP Wheat (JNKVV), Zonal Agricultural Research Station, Pawarkheda, Hoshangabad – 461110, Madhya Pradesh, India*
**Email: sidhi_jai01@rediffmail.com*

Backgram is an important kharif legume crop in India just after Pigeonpea in terms of area and production. It is most affordable source of vegetarian protein (25%). In India Blackgram grown in 321.46 lakh hectare with 19.56 lakh tonnes production with productivity of 604 kg/ha. It is mostly grown in Andhra Pradesh, Bihar, Karnataka, Maharashtra, Madhya Pradesh, Odisha, Rajasthan, Uttar Pradesh and West Bengal. Blackgram Production is severely affected by number of biotic factors, among them yellow mosaic disease caused by Mungbean Yellow Mosaic Virus is one of the most destructive, causes up to 100 percent yield loss. The present study is mainly adhered to know the current status of Yellow Mosaic Disease of Blackgram in Sidhi, Rewa, Singarauli and adjoining areas in the Zone. Here our aim is to evaluate prevailing integrated management modules elsewhere with required and suitable adjustments so as to get efficacious management of viral disease complex. The results revealed that all treatments were significantly superior over the farmers practice (T1). The forth treatment (T4: Tolerant variety (Shakher-2 + Seed treatment (Carboxin- 37.5% @ 3g/kg of seed and Thiomethaxam-75WP @ 2.5g/kg of seed + weed control in and around field and spray of Imidachlopriod @ 0.3ml/lit. at 20 DAS on bunds + foliar spray of NSKE @ 5% at 45 followed by Need based spray of Imidachloprid @ 125 ml ai/ha at 60 DAS) was found most effective in reducing YMD disease incidence (77.92%), increasing yield (39.42%), net return (Rs. 10356.60) and cost –benefit ratio(0.49). second best treatment was T3 (Tolerant variety (Shakher-2) + seed treatment (Carboxin- 37.5% +Thirum-37.5%) @ 3 g/kg of seed + Thiomethaxam-75WP @2.5g/kg of Seed +early removal of infected plant + spray of Imidachloprid - 17.8 SL @ 125 ml/ha at 30 DAS and NSKE @ 5% at 45 DAS. Hence T4 may be recommended for sustainable management of Yellow Mosaic complex in Blackgram.

PP(S2)/19: A simplified technique to evaluate biocontrol activity of volatile organic compound released by putative mutants of *Trichoderma atroviridae* (T-14)

Sandhya Sahu* and Anil S. Kotasthane
Department of Plant Pathology, College of Agriculture, Indira Gandhi Agricultural University, Raipur – 492012, Chhattisgarh, India
**Email: sandhyasahuagri@gmail.com*

Trichoderma spp. release a high diversity of volatile organic compounds (VOCs) which can inhibit growth of some plant pathogens also beneficially acts on plants by enhancing growth and inducing systemic resistance in plants. *Trichoderma atroviridae* (T-14) emits coconut like flavour which is due to the production of volatile organic compound, 6PP and it speculated to be the VOC responsible to inhibit the growth of *Sclerotium rolfsii*. Progenies derived after Gamma radiation treatment of *T. atroviridae* (T-14) resulted in putative mutants with a difference in 6PP production ability (evaluated after sensory test). Using a simplified technique we were able to demonstrate the effect of 6PP

(VOC) on the inhibition of *Sclerotium rolfsii in vitro.* Forty eight putative mutants were identified which expressed strong inhibitory activity against *Sclerotium rolfsii* without any physical interaction.

PP(S2)/20: Recent trends in bioformulations of antagonistic microbes

Divya Mishra[1]*, B. Rajeswari[1] and C. Kannan[2]
[1]*Department of Plant Pathology, Professor Jayashankar Telangana State Agricultural University, Hyderabad - 500030, Telangana, India*
[2]*Department of Plant Pathology, ICAR- Indian Institute of Rice Research, Hyderabad - 500030, Telangana, India*
**Email: mishradivya04@gmail.com*

A formulated microbial product is composed of biomass of a biocontrol agent and ingredients to improve the survival and effectiveness of the product. The development of formulations and delivery systems for biocontrol by using antagonistic microorganisms to suppress the incidence of diseases is a great importance. In recent era of formulations, encapsulation procedure has gained enormous importance in the field of agriculture. Encapsulation is a process in which active agents are capped or coated by carrier material in order to form particles or capsules in micrometer or nanometer scale. Encapsulation technology is applied to encapsulate microbes/ bioactive compounds (polyphenols, micronutrients, enzymes, and antioxidants) by forming protective barriers against the light, oxygen, pH, moisture, heat, shear, or other extreme conditions. Two things are generally required for successful encapsulation, one is selection of encapsulating materials for the preparation of suitable encapsulate system and another is encapsulation technique. It is also important to consider the functionality, encapsulate concentration, target release, and stability requirement. Several encapsulation techniques are quite popular to encapsulate bioactive compounds such as emulsification, spray drying, freeze drying, extrusion, electrospinning, and coacervation. In the finished application, encapsulation enhances bioavailability, controlled release, and targeting precision of microbes/bioactive compounds. For a successful future of encapsulated bioformulations, it is necessary to improve the existing methods, formulations and encapsulate systems, as well as meet the commercial demands for their industrial-scale production.

PP(S2)/21: Potential of endophytes from *Gossypium spp* as biocontrol agents against diseases

Neelakanth S. Hiremani[1]*, Shailesh P. Gawande[1], Pooja Verma[1], Satish K. Sain[2], Dipak T. Nagrale[1] and Nandini G. Narkhedkar[1]
[1]*ICAR-Central Institute for Cotton Research, Nagpur – 440010, Maharashtra, India*
[2]*ICAR-Central Institute for Cotton Research, Regional Station, Sirsa – 125055, Haryana, India*
**Email: nhneelmani@gmail.com*

Fungal endophytes from two cultivated cotton species namely *Gossypium hirsutum* and *G. arboreum* were isolated by standard tissue isolation procedure for endophytes. Six endophytes were selected based on preliminary *in vitro* study against *Corynespora cassiicola* for further evaluation. Among these isolates CEL-41 was inhibiting up to 58.33% of colony growth which was followed by M1-4 (53.42%), CEL-48 (52.16%) and CEL-19 (46.30). Interestingly, when these endophytes were tested against *Macrophomina phaseolina*, there was a peculiar zone of inhibition in isolates CEL-19, M1-6 and M1-8 whereas, remaining isolates found to be overgrowing on the colony of *M. phaseolina*. To test if any volatile organic compounds (VOCs) are being released from endophytes forming inhibition zone, endophytes were subjected to GC/MS analysis. The total ion chromatogram revealed a list of different VOCs wherein, four major compounds viz 1, 3 diethyl benzene, 1, 4 diethyl benzene, p-Cymen-7-ol and m-Ethylacetophenone identified were found to be antimicrobial. Further, pathogenicity and cross-pathogenicity tests of endophytes were performed on Suraj and Phule Dhanwantary and none of the endophytes showed any disease symptoms. Cross-pathogenicity of M1-4 was tested on wheat, cowpea, sorghum and red gram and no

symptoms were seen on any of the tested plants. Therefore, endophytes can play a potential role in inhibiting major plant pathogens and become promising biocontrol agents in future.

PP(S2)/22: Role of biotechnological tools in Plant Pathology

Abhishek Kumar[1]*, Kushal Raj[1] and Manish Kumar Maurya[2]
[1]CCS Haryana Agricultural University, Hisar - 125004, Haryana, India
[2]Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya – 224229, Uttar Pradesh, India
**Email: abhishekthakur2153@gmail.com*

Biotechnology is defined as the manipulation, genetic modification and multiplication of living organisms through novel technologies, such as tissue culture and genetic engineering, resulting in the production of improved or new organisms and products that can be used in many ways. Anthers of a plant are plated on a nutrient medium and produces unrestricted amounts of insulin that can be further manipulated to produce homozygous diploid plants and through tissue culture, millions of identical plants can be obtained in just a few months. Plant biotechnology helps plant pathology to obtain pathogen-free mother plants through rapid clonal propagation. New plants to which genes have been incorporated through genetic engineering are likely to show instability towards environmental conditions and towards the pathogenic microflora of their habitats. Here, pathology plays its part. The main vehicle for transferring genes from donor to recipient, in plant pathogens, particularly the bacterium *Agrobacterium tumefaciens* and the cauliflower mosaic virus. Study of plants genes for resistance to disease and of pathogen genes for virulence to pathogen has already added considerably by genetic engineering techniques. CRISPR/Cas9 is a new technique in genome editing that has enabled manipulation of plants allowing study of resistance genes, and has been used in mutational breeding in rice, tomato and tobacco. CRISPR/cas9 was also used to modify elF4E gene in cucumber thereby creating resistance to a number of viral diseases including cucumber yellowing virus and papaya ring spot virus. The technique has also been used against fungal diseases. Currently, gene transfer is being widely incorporated in crop improvement techniques to pioneer resistance mechanisms to plants. Plant biotechnology users in a new era working to maintain healthy plants, optimize crop yields, and minimize pesticide usage for the better way to control plant disease. The other aims of agricultural biotechnology are to feed an ever increasing world population.

PP(S2)/23: Bioformulation of organophosphate degrading bacteria and plant growth promoting microbes for pesticide degradation *vis-à-vis* management of bacterial wilt pathogen *R. solanacearum*

Shenaz Sultana Ahmed*
Assam Agricultural University, Jorhat – 785013, Assam, India
**Email: shenazcm113@gmail.com*

The introduction and extensive application of xenobiotics, more precisely, the chemical pesticides have left diversified hazards on both, environment and human health via accumulation of pesticides residues. The most widely used group of pesticides belonging to the organophos phosphorous, accounting to 38% of the global pesticide market. Continuous and excessive use of OP contaminated the agroecosystem due to accumulation of their residues. An attempt was made to identify some bacterial isolates for biodegradation of OP pesticides which is considered as an environmentally benign and economically preferred option. A total of 10 bacterial isolates were isolated from pesticide contaminated agricultural soils having OP pesticide (chlorpyrifos) degrading potential. The most efficient ones displaying the potential growth up to 1000ppm of chlorpyrifos were studied for their growth analysis spectrophotometrically and establishing their degrading potential via HPLC. The selected isolates were subjected to morphological, biochemical and molecular characterization which identified them as *Achromobacter marplatensis* (*Am*) and *Pseudomonas azotoformans* (*Pa*) having compatibility for *vice-versa*. This was accompanied with *in vitro* study further establishing the compatibility of efficient OPDBs with PGPMs such as *Pseudomonas flourescens* (*Pf*) and *Trichoderma harzianum* (*Th*). These studies facilitated the development of bioformulation containing PGPMs and OPDBs, finally evaluated for its efficacy against bacterial wilt of brinjal and degradation of OP pesticide. The potted experiment showed that combination of *Pa* + *Pf* + *Th* displaying lowest percent wilt incidence (PWI) of 5% coupled with significantly highest root biomass (5.35g/plant), shoot biomass (36.39g/plant), root length (27.88 cm/plant), shoot length (81.42 cm/plant), leaf number (83.20/plant), fruit number (5/plant), branches number (8.80/plant) and yield (1.42kg/plant) applied as seed treatment+seedling root dip+ soil application. The bioformulation consisting of *Am* + *Pa* + *Pf* + *Th* was observed most effective with 85% degradation of OP at 45 days after application. Such studies would be instrumental in providing novelty in bioremediation of pesticide contaminated soil as well as biological management of bacterial wilt disease with a single formulation.

PP(S2)/24: *In vitrao* evaluation of botanicals and bioagents for the eco-friendly management of anthracnose disease of Sarpagandha (*Rauwolfia serpentine* L.) caused by *Colletotrichum gloeosporioides*

Sanjog Chhetri[1]* and Goutam Mondal[2]
[1]Department of Plant Pathology, [2]All India Coordinated Research Project on Medicinal and Aromatic Plants and Betelvine, Directorate of Research, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia – 741252, West Bengal, India
**Email: sanjogchhetri02@gmail.com*

Rauwolfia serpentine (L.) Benth. Ex Kurz., commonly known as Sarpagandha (Indian snakeroot) is an important medicinal, evergreen perennial shrub that belongs to family Apocynaceae and, mainly found in the Indian subcontinent and Southeast Asian countries. Its root contains many important alkaloids, like ajmalicine, ajmaline, rauvolfinine, reserpine, serpentine, etc which are used as a remedy for curing hypertension, insomnia, sedative insomnia, etc. In this context, like other crops, this important medicinal plant is facing severe problems of diseases that discourage commercial cultivation. Moreover, the pathogens decrease the medicinal value by producing toxic metabolites which are harmful to the human body. Therefore, special care is needed for the management of diseases particularly eco-friendly management perfectly fits the scenario. Among many other diseases, Anthracnose disease caused by *Colletotrichum gleosporoidies* is an important foliar disease. Leaf extract of six medicinal plants namely, Aswhwagandha (*Withania somnifera*), Akanda/Madar *(Calotropis gigantea)*, Tulsi (*Ocimum tenuiflorum*), Ghetu (*Clerodendrum infortunatum)*, Chatim *(Alstonia scholaris)*, and Senna *(Cassia angustifolia)* and five isolates of *Trichoderma* spp were evaluated *in vitro* against the pathogen. Among crude extract of botanicals, Ashwagandha was only able to inhibit the mycelial growth of the tested pathogen after 5 days and 8 days of incubation were 23.69% and 20.83%, respectively. The dual culture test revealed that the maximum percentage of inhibition by T4 (14.8% in 3 days and 51.1% in 7 days after inoculation) and T5 (11.9% in 3 days and 51.1 % in 7 days after inoculation).

PP(S2)/25: Effect of different organic amendments and biocontrol agent on root rot disease complex of tomato (*Solanum lycopersicum* L.) caused by concomitant occurrence of *Rhizoctonia solani* and *Meloidogyne javanica*

Aradhna Sagwal*, Satish Kumar and Kushal Raj
Department of Plant Pathology, College of Agriculture, CCS Haryana Agricultural University, Hisar - 125004, Haryana, India
**Email: aradhnasagwal31@gmail.com*

Tomato is considered an important vegetable crop not only for its economic importance but also for its nutritional value. It remained prone to various fungal, bacterial, nematode and viral diseases and amongst them, root-rot disease complex caused by concomitant occurrence of *R. solani* and *M. javanica* has been key problem in Haryana resultantly reduces yield and production to great extent. The experiment was carried out under screen house conditions, CCS HAU Hisar during 2018-19 with the aim to evaluate the effect of different organic amendments and biocontrol agents on root rot disease complex in tomato cv. Hisar Arun (Selection 7). Tomato seeds were sown @ 10 seeds/pot filled with sterilized sandy loam soil having 1000 mg/kg soil (*Rhizoctonia solani* inoculum level) and 1000 J2/kg soil of (*M. javanica* inoculum level). The minimum disease incidence of 33.3 and 36.6 per cent was observed when the soils were incorporated with Mustard cake @ 2g/kg soil followed by Cotton cake @ 2g/kg soil in comparison to disease incidence of 63.3 per cent in control pots and the soil application of Mustard cake protected 47.4 per cent plants from mortality. The application of *Glomus mosseae* (VAM) at 200, 150, 100 sporocarps/ kg soil managed disease to the extent of 36.8%, 21%, 10.4 % respectively. When *T. harzianum* @ 5g/ kg soil and 10g/kg soil was incorporated then 21 per cent & 42 per cent disease was managed respectively. Hence, systematic approach to manage the root-rot disease complex with the help of organic amendments and bioagents require attention under the current era.

PP(S2)/26: Eco-friendly management of charcoal rot of sesame caused by *Macrophomina phaseolina* (Tassi) Goid

Preeti*, H.S. Sharan and A.S. Rathi
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar - 125004, Haryana, India
**Email: dhimanpreeti45@gmail.com*

The charcoal rot disease caused by *Macrophomina phaseolina* (Tassi) Goid, is the most destructive soil and seed borne disease of sesame (*Sesamum indicum* L.). The present investigation was undertaken to study the eco-friendly management of *M. phaseolina* through botanicals and bio-agents under *in vitro* and *in vivo* conditions. Among the botanicals evaluated, the phytoextract of *Lantana camara* inhibited maximum mycelial growth by 89.43 per cent at 20 per cent concentration followed by *Parthenium hysterophorus* upto 87.21 at 20 per cent concentration. Evaluation of bio-agents for their efficacy against *M. phaseolina in vitro* revealed that *Trichoderma harzianum* showed maximum antifungal activity with 66.94, 59.99, 59.44 per cent of mycelial inhibition by dual culture technique, production of non-volatile and volatile compounds techniques respectively, which was followed by *T. viride* with 59.16, 55.27, 53.00 per cent mycelial inhibition, respectively. *Pseuodomonas fluorescens* was found to be least effective with 30.83, 51.38, 47.77 per cent mycelial inhibition by dual culture technique, production of non-volatile and volatile compounds techniques respectively. Among the combinations of phytoextracts and bioagents tested under screen house conditions, seed soaking in solution of 20 per cent concentration of *L. camara* extract for 5-10 minutes followed by seed treatment with *T. harzianum* @ 10g/kg seed was found most effective in controlling the disease upto 36.43 per cent in HT-1 and 40.92 per cent in HT-2 varieties followed by combination of *P. hysterophorus* + *T. harzianum* which controlled the disease up to 34.28 and 38.53 per cent in HT-1 and HT-2 varieties, respectively.

PP(S2)/27: Improvement of bio-control potential of *Trichoderma asperellum* through mutagenesis

A.G. Gathe* and S.T. Ingle
Department of Plant Pathology, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola – 444104, Maharashtra, India
**Email: aggathe108@gmail.com*

The present investigation aimed to apply the chemical mutagenesis and irradiation technique for genetic improvement of the *Trichoderma asperellum* to enhance its bio-control efficiency and tolerance with fungicides. Identified mother culture of *T. asperellum* was subjected to chemical mutagenesis with ethyl methyl sulphonate (EMS) and hydroxyl amine (HA) @ 200 ìl/ml and physical mutagenesis with gamma radiation (cobalt 60) @ 250 gry and ultraviolet (UV)

rays @ 254 nm wavelength. The time durations for all treatments were 30, 45, 60 and 75 minutes. After mutagenesis 16 mutants were tested for its stability up to seven generation. All mutants and mother culture of *T. asperellum* were differentiated by cultural and morphological characteristics. All mutants showed different colony colour, mycelial growth rate, pigmentation, phialides, conidial size and shape. Entirely mutants recorded significantly higher radial mycelial growth rate than mother culture. The highest average radial mycelial growth rate i.e. 37.93 mm/day was recorded by mutant TaH2(T2) whereas mother culture TaMc (T17) recorded 36.11 mm/day. All the mutants showed strong antagonistic activities against tested soil borne pathogens. The highest per cent growth inhibition of *Sclerotium rolfsii* was recorded in mutant TaH2 (T2) i.e. 88.89 per cent. In case of *R. bataticola* and *Fusarium oxysporum* f.sp. *ciceri* highest per cent growth inhibition was recorded in mutants TaU3(T11) and TaG1(T13) i.e. 62.82 and 75.38 per cent respectively. All the mutants recorded higher chitinase enzyme than mother culture. Mutant TaH2 (T2) recorded highest i.e. 0.98 chitinase enzyme units/ mg of protein whereas mother culture TaMc (T17) contained only 0.62 chitinase enzyme units/ mg of protein.

PP(S2)/28: Biological control of blast disease in finger millet by *Pseudomonas fluorescens* and *Bacillus subtilis*

T.M. Hemalatha*, L. Madhavilatha, B. Vajantha, N.V. Sarala, M. Hemanthkumar, M. Shantipriya and K.R. Tagore
Agricultural Research Station (ANGRAU), Perumallapalle, Tirupati – 517505, Andhra Pradesh, India
**Email: hema.agri@gmail.com*

Finger millet is one of the important millet crop grown by most of the poor farmers in Andhra Pradesh. The crop is most vulnerable to blast disease caused by *Pyricularia grisea* and yield loss of more than 50% is reported. This disease occurs severly during kharif season but the extent of the crop loss depends on the severity and the time of onset of rains. Chemical management of the disease is uneconomical and hence is not quite often considered by marginal and resource poor farmers. A study was initiated at Agricultural Research Station, Perumallapalle to examine biocontrol options for the management of blast disease. A total of 17 Pseudomonas and ten bacillus isolates were isolated from finger millet phyllosphere. In vitro evaluation of phyllosphere microflora against P. grisea revealed that Bacillus isolate-10 and Pseudomonas isolate, P-7, recorded maximum inhibition of 85.54 and 90.4 per cent respectively. These two isolates were further identified as Bacillus subtilis and Pseudomonas fluorescens based on 16S rRNA sequence. Field evaluation of these bioagents revealed that Seed treatment + Seedling dip + Foliar spray with *B. Subtilis* and *P. fluorescens* recorded minimum PDI of leaf (11..19), neck (10.34) and finger blast (12.4) with maximum grain yield (3077 kg ha-1) as against control with leaf blast (74.45), neck blast (56.74) and finger blast (49.65) with grain yield (1566 kg ha-1).

PP(S2)/29: Integrated disease management against stem rot of groundnut caused by *Sclerotium rolfsii* Sacc. in field conditions

Pawar G.S.*, Gholve V.M. and Navale M.D.
Department of Plant Pathology, College of Agriculture, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani – 431402, Maharashtra, India
**Email: ganeshtheplantpathologist@gmail.com*

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop of tropical and subtropical regions of the world. Groundnut is reported to have originated from South America. It is one of the most important food and cash crops of our country. Stem rot caused by *Sclerotium rolfsii* Sacc. is one of the most widely spread and destructive disease of groundnut (*Arachis hypogea*). about 27% or more yield loss due to this disease has been reported from India and 25% yield loss in Maharashtra. The Systemic, Non-Systemic and Combi fungicides, Botanical and Bio-agent found most effective during *in vitro* studies were evaluated under natural field conditions comprised of 14 treatments in

Kharif, 2019. Results revealed that all the treatments significantly influenced the Pre-emergence mortality, post-emergence mortality and incidence of stem rot caused by *S. rolfsii* in groundnut. The percentage reduction of the pre-emergence mortalities were ranged from 35.16 to 65.14 per cent. Highest reduction in pre-emergence mortality (65.14 %) recorded with Mancozeb (ST) + *Bacillus subtilis* (ST) + Vitavax power (SD) + Garlic extract (SA) followed by the treatments *viz*., Mancozeb (ST) + *Bacillus subtilis* (ST) (62.49 %) which were found at par with each other. The percentage reduction of the post-emergence mortality was ranged from 57.48 Garlic extract (SA) to 82.37 Mancozeb (ST) + *Bacillus subtilis* (ST) + Vitavax power (SD) + Garlic extract (SA) per cent. Of all the treatments tested significantly highest reduction in pre-emergence seed rot (82.37 %) was recorded with Mancozeb (ST) + *Bacillus subtilis* (ST) + Vitavax power (SD) + Garlic extract (SA). The treatment combination of Mancozeb (ST) + *Bacillus subtilis* (ST) + Vitavax power (SD) + Garlic extract (SA) was found most effective with least incidence of stem rot (18.09%) upto 49 days after sowing as compared to untreated (33.74%).

PP(S2)/30: *In vitro* efficacy of phyto extracts to control stem rot of groundnut (*Arachis hypogaea* L.) caused by *Sclerotium rolfsii* Sacc.

Pawar G.S.*, Gholve V.M. and Navale M.D.
Department of Plant Pathology, College of Agriculture, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani – 431402, Maharashtra, India
**Email: ganeshtheplantpathologist@gmail.com*

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop of tropical and subtropical regions of the world. Groundnut is called as ‘king’ of oilseeds on account of its diversified uses. Groundnut is the 13th most important food crop and 3rd most important oilseed crop of the world. In India, groundnut is grown in four seasons, namely, *Kharif* (85%), *Rabi* (10%), Summer (4%) and Spring (less than 1%). Stem rot caused by *Sclerotium rolfsii* Sacc. is one of the most widely spread and destructive disease of groundnut (*Arachis hypogea* L.). All of the aqueous extracts of the 8 botanicals evaluated *in vitro* (each @ 15 and 20%) were found antifungal to *S. rolfsii* Sacc. However, on the basis of highest average mycelial growth inhibition recorded at 15% conc., *A. sativum* (90.89%) was the most effective, followed by *O. sanctum* (83.61%), and *C. longa* (1.78%) was found comparatively less effective. At 20% conc., *A. sativum* (93.81 %) recorded highest average mycelial growth inhibition, followed by *O. sanctum* (90.77%), and *C. longa* (25.00%) was found comparatively less effective.

PP(S2)/31: Eco-friendly disease management of southern blight (*Sclerotium rolfsii)* of China aster by incorporation of various soil amendment tactics

Natasha Kashyap* and Sunita Chandel
Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India
**Email: natashakashyap724@gmail.com*

Sclerotium rolfsii Sacc. is one of the most destructive soil borne pathogen affecting extensive variety of crops in India. China aster is an emerging crop in the country and hence increase in the production area implicit higher risk of diseases. Southern blight caused by *S. rolfsii* is a serious problem in the cultivation of China aster because of its wide host range, hard resting sclerotia and hence persistence in the soil for a long time. Therefore, an investigation on Southern blight of China aster was undertaken with reference to its environment friendly management by incorporation of biofumigants and biocontrol agents along with soil solarization. Among different biofumigants, mainly crucifer crop residues (CR) evaluated under pot conditions, radish CR was found to be most effective with mycelial inhibition of 63.00 per cent followed by cabbage CR with mycelial inhibition of 61.00 per cent. However, cauliflower CR was shown to have antisporulant activity with lowest production of sclerotia (4.33). Bio control agents (BCA's) evaluated against test pathogen under in vitro conditions showed maximum efficacy of *Trichoderma viride* with mycelial growth inhibition of 70.83 per cent followed by *T. virens* with an inhibition of 61.66 per cent. The most effective treatments under in vitro and pot conditions were selected for an integrated disease management trial (2020) for incorporation with soil solarization which revealed that cabbage CR+ soil solarization was found to be most effective with disease incidence of 16.26 per cent followed by raddish CR+ soil solarisation with 25.33 per cent disease incidence.

PP(S2)/32: Ameliorative changes in the seed quality parameters in lentil by using *Trichoderma harzianum* (*ThL*-4) bioformulation

Shaily Javeria[1]*, Atul Kumar[2], Amit C. Kharkwal[1], Ngamani Sandra[2], Sunil Kumar[2] and Pratibha Sharma[3]
[1]Amity Institute of Microbial Technology, Amity University, Noida - 201301, Uttar Pradesh, India
[2]Division of Seed Science and Technology, [3]Ex Principal Scientist, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: atulpathiari@gmail.com*

The present investigation was carried out keeping into consideration, development of an improved bio-formulation of *Trichoderma harzianum* with enhanced shelf life. A comparative evaluation of PDB talc-based and sorghum formulations in the form of seed coat and soil treatment demonstrated that, the soil treatment significantly enhanced the plant growth performance of lentil. Between the two formulations, the sorghum based formulation proved better as the rhizosphere competence of sorghum formulation was superior to that of PDB talc formulation. Our results suggest that sorghum residue acts as a better substrate owing to high cellulase and spore production. The biocontrol ability of both formulations was tested against *Fusarium oxysporum* f. sp. *lentis* and it was found that the disease incidence was reduced by 98% when the sorghum formulation was given as soil application. Comparison of Membrane Thermal Stability of *Trichoderma harzianum* (ThL-4) was carried out on different media and its growth on sorghum media was lesser than others which implicit that there was a pronounced permeability of the membrane. This strain of *Trichoderma* in sorghum substrate resulted in enhanced seed quality parameters in the crop. The Sorghum Talc Based formulation enhanced seed vigour I and II of lentil seeds when applied through paper towel method, which leads to better stand establishment resulting into improved productivity. This formulation provided a food substrate for the *T. harzianum* ThL-4 biomass, which led to significant proliferation in the soil and enhanced its shelf life. The present study clearly exhibited that the propagation of *T. harzianum* (ThL-4) in the rhizosphere of lentil plants is dependent on formulation.

PP(S2)/33: Integrated disease management of false smut [*Ustilaginoidea virens* (Cooke) Takahashi] of rice

K.B. Rakholiya*
Department of Plant pathology, N.M. College of Agriculture, Navsari Agricultural University, Navsari – 396450, Gujarat, India
**Email: kbrakholia@gmail.com*

False smut of rice caused by *Ustilaginoidea virens* (Cooke) Takahashi, is an economically important disease in India. False smut disease has been observed in severe form since 2001 due to widespread cultivation of high fertilizer responsive cultivars and hybrids, high yielding varieties, excessive application of nitrogenous fertilizer and an apparent change in climate. In different weather conditions, false smut cause heavy yield loss varies from upto 75 per cent, so integrated diseases management practices is better as compared alone management practices. In the present study, evaluation of various fungicides, phytoextracts and bio-agents under field condition revealed that number of infected panicle per m2, disease incidence per cent, number of smutted ball and disease severity index were reduced in the spray application of trifloxystrobin (25%) + tebuconazole (50%) at 0.05 per cent at booting stage and 50 per cent panicle emergence stage which was at par with azoxystrobin (20%) + difenoconazole (12.5%) at 0.05 per cent, propiconazole (25 EC) at 0.1 per cent and tebuconazole (25.9 EC) at 0.15 per cent and resulted in higher grain and straw yield.

PP(S2)/34: Evaluation of different ecofriendly management aspects against black scurf of potato (*Solanum tuberosum*)

Manoj Kumar*, Anil Kumar, Kushal Raj and Rakesh Punia
Regional Research Station (CCS HAU), Bawal, Rewari – 123501, Haryana, India
**Email: manojbuswal@gmail.com*

To develop eco-friendly disease management options involving fungicides, bioagents and organic amendments applied as tuber dipping, tuber treatment and soil application respectively, for the management of black scurf of potato. The efficacy of promising fungicides, bio-agents and organic amendments which were found best under *in vitro* conditions was further evaluated under field conditions. The infected tubers were planted in the field after dipping in the solution of MEMC-6 FS w/v (0.1%), Monceren 250 EC (0.1%) and *T. harzianum* & *T.viride* (106 conidia/ml) for 10-15 minutes. Organic amendments (@ 20 g/kg soil were applied as soil application 20 days before planting. Experiment was conducted in RBD and the disease incidence (%) and disease over control were recorded after harvesting of the potatoes. Results indicated that treatment of tubers with fungicides, bioagents and incorporation of organic amendments resulted significant reduction in disease incidence. Among fungicides, monceren showed highest reduction in disease (98.58%) over the control with the lowest disease incidence (01.00%), followed by MEMC which reduced black scurf disease up to 83.49 per cent over control with the disease incidence 11.67 per cent. Tubers treated with bioagent *T. harzianum* showed reduction in disease (65.09%) over the control with the disease incidence (24.67%), followed by *T. viride* treatment which reduced black scurf disease up to 60.38 per cent over control with the disease incidence 28.17 per cent. Among organic amendments, incorporation of vermicompost controlled disease up to 48.11 per cent, which was found more effective with the disease incidence 36.67 per cent than neem cake that showed lowest reduction (40.09%) in the disease over control with the highest (70.67%) disease incidence.

PP(S2)/35: Efficacy of different plant exctracts against *Phyllosticta capitalensis*, the causal agent of leaf spot disease of curry leaf plant (*Murraya koenigii*)

Susmita Oraon*, Goutam Mondal, Siddharth Singh
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur - 741252, Nadia, West Bengal, India
**Email: khushioraon97@gmail.com*

Murraya koenigii (L.) Sprengel, commonly known as Curry leaf is a flavoring spice and a medicinally important crop. The essential oil composition of leaves has great industrial importance. Besides, leaves are used in *Ayurveda*, *Siddha* and traditional Chinese treatments for their medicinal properties. It is an important export commodity from India and the country exported 600 tons of curry leaves during 2016-17. Though it has a high market demand, the quality produce is being reduced day by day due to incidence of diseases. One of important pathogen of curry leaf is *Phyllosticta capitalensis* causing leaf spot. In this experiment, 10 *Trichoderma* isolates and 10 plant extracts namely, Aswhwagandha (*Withania somnifera*), Akanda/Madar *(Calotropis gigantean)*, Tulsi (*Ocimum tenuiflorum*), Sarpagandha (*Rauvolfia serpentine*), Bach (*Acorus calmus*), Kalmegh (*Andrographis paniculate*), Betel vine (*Piper betel*), Curry leaf (*Murrya koenigii*), Ajwain (*Trachyspermum ammi*) and *Lantana camara* were used to evaluate their efficacy against the pathogen through dual culture and poison food technique respectively. Besides, 9 fungicides namely, Trifloxystrobin, Thiophanate methyl, Chlorothalonil, Dithianon, Pyraclostrobin, Mancozeb, Trifloxystrobin + Tebuconazole, Carbendazim + Mancozeb, Tebuconazole were also tested. Out of 10 isolates, *Trichoderma* T13 showed maximum inhibition (92.82%) followed by isolates T14, T1, T9 and T10 (88.72%, 87.81%, 87.81% and 87.81% respectively). Among 10 plant extracts, Sarpagandha (68.06%) was found best followed by Aswhwagandha leaf extract (43.73%). All the nine tested fungicides were showed effective. So, biocontrol agent, *Trichoderma* isolate T13 and Sarpagandha leaf extract could be used to manage the leaf spot disease.

PP(S2)/36: Integration of bioagents and fungicides for the management of seedling blight of castor caused by *Phytophthora nicotianae*

B. Vidya Sagar*
Department of Plant Pathology, College of Agriculture, Rajenranagar, Hyderabad – 500030, Telangana, India
**Email: bvidyasagar24@gmail.com*

Seedling blight caused by *Phytophthora nicotianae* is a common disease of castor (*Ricinus communis*) in India. The efficacy of 13 native *Trichodema* sp were evaluated along with two potential biocontrol agents (*Trichoderma harzianum*- 4 (Th4d)d and *Pseudomonas flurescence*-2 (Pf2) developed by IIOR). Among them Trichoderma spp. 6 was found effective followed by Pf2 and Th4d under *invitro* conditions. Nine fungides were also screened at 0.1, 0.2 and 0.3 per cent concentration against the test pathogen, among them Mefenoxam+Mancozeb and Metalaxyl 35%WS recoded more than 90 per cent inhibition at low concentration tested. The native *Trichoderma* sp along with Th4d and Pf2 were integrated with fungicide mefenoxam+ mancozeb and evaluated as seed treatment and foliar application in different combinations against the seed ling blight disease under glass house conditions. Among the various treatments seed treatment with native Trichoderma isolate T6 +foliar application of Mefenoxam+ Mancozeb (0.1%) was found most effective in reducing the disease incidence by 94.82 per cent followed by seed treatment with Pf2 1 per cent + foliar application of mefenoxam+mancozeb (0.1%) when compared to control.

PP(S2)/37: Eco-friendly management strategy for leaf spot disease of Tulsi (*Ocimum tenuiflorum*) caused by *Colletotrichum gloeosporioides*

Soumik Mukherjee* and Goutam Mondal
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur - 741252, Nadia, West Bengal, India
**Email: soumik.m95@gmail.com*

The queen of herbs, Tulsi (*Ocimum tenuiflorum*) is an inherent plant of the Indian subcontinent with both cultural and medicinal significance. The leaf extracts of this herbal plant has been used for ages to cure respiratory ailments, remedies for symptoms of common cold, inflammations and also cancers. Its products, both raw and processed, are exported throughout the world with annual demands meeting up to 3000 MT. Unfortunately, this miraculous plant too is not immune to pathogenic harm. One such fungal pathogen namely *Colletotrichum gloeosporioides* causes severe harm to the plant. Since the leaves of the plant are consumed orally in most parts of India thus it is essential to manage the leaf spot pathogen through non-toxic, eco-friendly amendments. For this purpose five isolates of a biocontrol agent namely, *Trichoderma* spp. and crude extracts of five plants *viz*., Garlic (*Allium sativum*), Turmeric (*Curcuma longa*), Sarpagandha (*Rauvolfia serpentina*), Neem (*Azadirichta india*), and Bael (*Agele marmelos*) were tested against the pathogen to evaluate their efficacy *in vitro*. Among the biocontrol agents highest inhibition potential was observed in isolate T2 (48.1%) followed by isolate T3 (44.4%) in 7 days. Among the plant extracts, Turmeric exhibited highest potential (87.2%) followed by garlic (67.7%) in 7 days. Therefore, isolate-2 of *Trichoderma* spp. and rhizome extract of Turmeric could be used as biofungicide *in vivo*.

PP(S2)/38: Integrated management of banded leaf and sheath blight (*Rhizoctonia solani*) of maize by peat based *Pseudomonas fluorescens* formulation

Bidwan Ranjan Sahoo[1]*, Bignyan Ranjan Sahoo[2], Sobita Simon[3] and Kartik Chandra Sahu[1]
[1]Department of Plant Pathology, Institute of Agricultural Sciences, Sikshya 'O' Anusandhan (Deemed to be University), Bhubaneswar - 751029, Odisha, India
[2]Department of Soil Science and Agricultural Chemistry, Odisha University of Agriculture and Technology, Bhubaneswar - 751003, Odisha, India
[3]Department of Plant Pathology, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad - 211007, Uttar Pradesh, India
**Email: sahoobidwanranjan02@gmail.com*

Banded leaf and sheath blight (BLSB) on maize is a soil borne disease caused by *Rhizoctonia solani* is more prevalent in humid weather condition temperature of 28 0C. It has highly gained economic importance up to 100%. The disease is very difficult to control even through fungicides. Development of resistant cultivar is more ideal but is has not been possible due to non availability of host resistance. Among eight isolates of *Pseudomonas fluorescens* from the crop rhizosphere, three isolates showed high effective against *R. solani* under *in vitro* condition by exhibited inhibitory action against *R. solani* causing BLSB. The disease was significantly controlled by seed treatment of the peat based formulation 15g/kg of seed in field condition.

PP(S2)/39: Mitigation of drought stress by *Trichoderma harzianum* through seed biopriming

Morajdhwaj Singh[1]* and Ramji Singh[2]
[1]Department of Horticulture, Dolphin (PG) Institute of Biomedical & Natural Sciences, Dehradun – 248007, Uttarakhand, India
[2]Department of Plant Pathology, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut – 250110, Uttar Pradesh, India
**Email: dr.umdsingh@gmail.com*

Wheat, the world's most important food crop in terms of production and consumption both, serves as the prime item in the diet of millions of people. Production of wheat in India is limited by several biotic and abiotic stresses. Present study has been focused to investigate the effect of antagonist fungus *viz Trichoderma harzianum* for drought stress management, an abiotic stress, in wheat. Wheat seed biopriming with *T. harzianum*, enhanced drought resistance by affecting stomatal conductance, net photosynthesis, proline content, chlorophyll content, catalase and peroxidase activity. Out of several strains of *T. harzianum* collected from different locations of Uttar Pradesh and from various crop's rhizosphere, most superior six strains (*viz.* IRRI-1, Th-3, Th-21, Th-26, Th-28 and Th-30), on the basis of their growth rate were selected. These selected strains were applied as seed bio-priming to test their efficacy to enhance drought tolerance in wheat at stem elongation/jointing stage. With strains IRRI-1and Th-3, after 14 days of exposure to drought, maximum shoot length, root length, leaf area index, flag leaf area, relative water content, membrane stability index, chlorophyll content, proline content, catalase and peroxidase activity were observed as 83.80 cm, 23.60 cm, 37.91, 31.76, 71.23, 66.36, 45.60, 11.50 µ mol g-1, 104.69 and 202.02 unit with IRRI-1 and 74.30 cm, 19.90 cm, 32.69, 30.82, 66.89, 63.83, 42.60, 12.40, 98.25 and 189.45 with Th-3, respectively. IRRI-1and TH-3 strains of *T. harzianum* have been found to be effective in providing drought tolerance in wheat plants by decreasing the proline content and by enhancing the total chlorophyll content, relative water content, membrane stability index and biochemical properties *i.e.* catalase and peroxidase activity in wheat plants.

PP(S2)/40: Physio-biochemical changes under drought stress as influenced by *Trichoderma* spp through seed biopriming

Morajdhwaj Singh[1]* Ramji Singh[2], Devesh Nagar[3] and D.C. Kala[4]
[1]Department of Horticulture, Dolphin (PG) Institute of Biomedical and Natural Sciences, Dehradun – 248007, Uttarakhand, India
[2]Department of Plant Pathology, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut – 250110, Uttar Pradesh, India
[3]Department of Agriculture, Govt. of Uttar Pradesh
[4]Department of Agriculture, School of Agriculture, Forestry and Fisheries, Himgiri Zee University, Dehradun – 248197, Uttarakhand, India
**Email: dr.umdsingh@gmail.com*

Drought is a major abiotic stresses that reduce crop productivity and weaken global food security and growing impacts of climate change and increases the occurrence and severity of drought stress especially in the current scenario. Plants have developed dynamic responses at the morphological, physiological and biochemical levels allowing them to escape or adapt to unfavorable environmental conditions. Further, several independent studies have shown that increased drought can reduce crop yields by as much as 50%. Response to stress is complex and involves several factors including changes of hormones, enzymes, and secondary metabolites. A wide range of adaptations and mitigation strategies are required to cope with such impacts. *Trichoderma* species, one of the most widely used microbes for the biocontrol of plant diseases, are known to alter the response of plants to drought stress. The recent advances in technology may mitigate the detrimental effects of drought through the use of drought tolerant *Trichoderma* isolates as a seed biopriming biocontrol agent. Growth enhancement strategies under drought conditions for alleviation of drought stress and enhancement of shoot and root biomass of crop increases productivity. Finally, in future, drought tolerant *Trichoderma* strains could be used to improve plant biomass and productivity in crops under drought conditions. Seed biopriming with drought tolerant isolates of *Trichoderma spp.* explore the mechanism underlying plant water stress resilience in response to *Trichoderma* inoculation. Seed biopriming enhanced drought tolerance of crops as drought induced changes like stomatal conductance, net photosynthesis, decrease in proline content, and an increase in total phenolics and chlorophyll content. The accumulation of toxic reactive oxygen species (ROS) negatively affects the plant biomass and root vigour which ultimately affects the yield. Therefore seed biopriming came into practice to reduce the damages resulting from accumulation of ROS in stressed plants. It has also been reported that Seed biopriming in crop plants with drought tolerant *Trichoderma* isolates increased root vigour besides performing the process of osmoregulation. It ameliorates drought stress by inducing physiological and biochemical protection in plants against oxidative damage, due to enhanced capacity to scavenge ROS, a mechanism that is expected to augment tolerance to drought stress.

PP(S2)/41: Effect of different season on yield and biological efficiency of different strains of *Pleurotus* species

Devika Saha*, C.S. Shukla and G.K. Awadhiya
Indira Gandhi Krishi Vishwavidalaya, Raipur- 492012, Chhattisgarh, India
**Email: sahadevika24@gmail.com*

Mushroom is a macro-fungus which is saprophyte in nature that derives its nutrients from ligno-cellulosic substrate. Oyster mushroom (*Pleurotus* species) can be cultivated throughout the year but commercially requires a specific weather condition, temperature and relative humidity. Variation in any of the factors directly influence the primordial initiation, yield and biological efficiency. Different strains of Pleurotus species (PL-16-01, PL-16-02, PL-16-03 and PL-16-04) were cultivated and its spawn run, primordial initiation, yield and biological efficiency were recorded. It was concluded that the growth and yield characters were affected by weather parameters and shows significant difference in the performance of different strains. In winter season, when the temperature is between 14 C -27 C

with 70-80 % relative humidity there was quick spawn run (16.93 days) in PL-16-04 strain with earlier primordial initiation (3.53 days) in PL-16-04. While yield and biological efficiency of PL-16-04 were recorded (396.86 gm and 70.58 %, respectively) to be higher. Key words: Weather parameters, spawn run, primordial initiation, yield, biological efficiency.

PP(S2)/42: *In vitro* evaluation of different crop residues on carpogenic germination of *Sclerotinia sclerotiorum* causing tomato timber rot

Bhagyashree Bhatt* and Geeta Sharma
Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakhand, India
**Email: bhagyashreebhatt15@gmail.com*

With the growing concern towards environment safety, ecofriendly management practices of the plant diseases are gaining a lot of attention. In case of soil borne plant pathogens it is primarily required as it governs the sustainability of other beneficial microbes. *Sclerotinia sclerotiorum* which is a soil borne pathogen, has a wide host range and is known to survive in soil in the form of sclerotia for as long as about ten years. The carpogenic germination of sclerotia under favourable conditions, leads to the production of apothecia and the ascospores released by it forms primary source of inoculum. Since crop residues play a major role in soil borne plant pathogens, a study was conducted to observe the effect of different crop residues (rice, maize, sugarcane, lentil, tomato, brinjal, cauliflower, turmeric, tejpatta and mustard) on the carpogenic germination of the pathogen. Amongst all the treatments, sclerotia kept in soil mixed with rice straw showed delayed stipe formation and no carpogenic germination was observed in soil mixed with crop residues of mustard. The results obtained in the study depicts that carpogenic germination of sclerotia can be hindered by alteration of crop residues in soil.

PP(S2)/43: Bio-fumigation for controlling replant problem in fruit crops

Anshul Shyam*
Department of Fruit Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India
**Email: anshulshyam168@gmail.com*

Replant problem refers to the poor growth of fruit trees when replanted on old orchard site and is widely distributed throughout the fruit growing areas of the world. Temperate fruit crops like apple, plum, peach, cherry are the most affected by this problem. The suppression of growth is brought by various factors involved like abiotic factor including root exudates, deterioration of soil properties and biotic factor refers to increase in population of pathogenic microbial species in rhizosphere. The plants suffer from stunted growth, leaf discolouration, root tip necrosis, reduced number of root hairs which cause poor growth and hamper the establishment of newly planted tree. The management practices mainly comprises of pre planting treatments carried out in old orchard site. Fumigation is an important tool to overcome this problem. Chemical fumigants are commonly used for this purpose but due to its broad spectrum killing most of the soil organism and residual effect more focused is put on biological approach. Bio-fumigation refers to the incorporation of fresh plant mass into the soil particularly belonging to Brassicaceae family which releases several substances such as methyl isothyocianates that are able to suppress soil borne pests. The members of Brassicaceae family have high amount of glucosinolates present in their tissue so when the tissue disruption takes place it leads to hydrolysis of glucosinolates in presence of myrosinase enzyme causing production of isothyocianates compounds. These isothiocyanates compounds have anti-microbial, anti-fungal, and anti-nematicidal properties resulting in soil sterilization.

PP(S2)/44: Inhibitory effect of some botanical extracts on mycelial growth of *Fusarium oxysporum* causing wilt of brinjal (*Solanum melongena* L.)

Sabebaro Namo Das*

Department of Botany, B.P. Chaliha College, Nagarbera, Kamrup - 781127, Assam, India

**Email: sabebaro.das@gmail.com*

Fusarium oxysporum f.sp. *melongenae* is an important disease that caused wilt disease in brinjal crop. The present work carried out with the antifungal activity of three botanical extracts viz.*Allium sativum*, *Lantana camara* and *Cassia alata* at different concentration (5%, 10% and 15%) were tested against *Fusarium oxysporum* under *in vitro* condition by Poisoned Food Technique. Result revealed that there is a marked variation in reduction of mycelial growth of *F. oxysporum*. Among the tested plants extracts *A.sativum* showed significant reduction in the growth of *F oxysporum*. *A. sativum* extracts at 15% concentration completely inhibited the mycelial growth followed by *L. camara* (52.2%); while *C. alata* showed least effect inhibition (41.4%) at the highest concentration over control. Application of plant extracts for controlling pathogens that causes plant disease is an eco-friendly and cost-effective approach.

PP(S2)/45: Biofertilizer made by utilizing poultry feather waste

Arpana Pal[1]*, Keerti Singh[1] and Kunal Kishor[2]

[1]Department of Microbiology, School of Basic and Applied Sciences, Shri Guru Ram Rai University,
Dehradun – 248001, Uttarakhand, India
[2]Department of Microbiology, School of Allied Health Sciences, Sharda University, Greater Noida – 201306,
Uttar Pradesh, India
**Email: aviaru2807@gmail.com*

It has been found over and again that 99% Indian soil responds well to Nitrogen application which is a macronutrient for plant growth. Unless nitrogen deficiency is corrected application of other nutrients might not give fruitful results. To explore nitrogen rich organic sources that can be utilized as bio-fertilizer becomes the need the of hour so as to prevent accumulation of hazardous chemicals in soil. One of the underused potential sources of nitrogen is poultry feather waste (PFW). World wide approximately 3.0- 3.08 lakh metric tones of PFW is generated that can be utilized for generation of various eco-friendly sustainable products one of which is the bio-fertilizer. Since chicken feather is rich in keratin protein it can yield potential micro and macronutrients along with nitrogen. In a study it was found that treated poultry feather waste (TPFW) contains higher percentage of organic matter (35.9%) and total nitrogen (4%). When applied to control field the color of the plants were observed greener in TPFW applied plants than control plants and the green color was pronounced with increasing rate of TPFW application. Plant height (cm/plant), leaf number per plant, weight of plants (g/plant) was also increased due to the application of TPFW at 12 t/ha and above. Thus utilizing PFW as bio-fertilizer will not only help in nutrient enrichment of soil (specifically Nitrogen) but will also help to curb soil pollution which is caused due to slow degradation of PFW in nature.

PP(S2)/46: Biological management of rice sheath blight disease caused by *Rhizoctonia solani* Kuhn.

N.S. Punya[1]*, N. Kiran Kumar[1], V.B. Sanath Kumar[1], S.B. Yogananda[2], K.R. Ashoka[3] and H.B. Mahesh[4]
[1]Department of Plant Pathology, [2]Department of Agronomy, [3]Department of Soil Science and Agricultural Chemistry, [4]Department of Genetics and Plant Breeding, College of Agriculture, V.C. Farm, Mandya – 571401, Karnataka, India
**Email: punyans417@gmail.com*

Rice sheath blight is one of the most economically significant rice diseases worldwide. This disease causes significant grain yield and quality losses. Management of sheath blight primarily relies on chemical control. Use of only fungicides in disease management pose environment pollution and also leads to resistance development in the pathogen. A field experiment was conducted during *kharif* 2020 at College of Agriculture, V. C. Farm, Mandya, to elucidate different eco-friendly strategy in suppression of rice sheath blight disease. Foliar applications of five bioagents and a tropical seaweed (*Kappaphycus alverezii*) at 30 and 60 days after transplanting were evaluated for their efficacy in suppressing the rice sheath blight disease. All the treatments were found to be effective in mitigating the disease severity over the untreated control with enhanced rice growth and yield parameters. Among all the tested bioagents, *Trichoderma harzianum* treatment was significantly effective over untreated control (62.70 %) and showed least disease severity (21.30 %) which was on par with Hexaconazole 5EC (20.48 %), followed by *Bacillus subtilis* (32.4 %), seaweed (33.28 %) and *B. pumilis* (33.8 %). However, *T. viride* treatment was least effect with disease severity of 36.52 % followed by *Pseudomonas fluorescens* (36.11 %). In addition to variation in disease severity these treatments influenced variation in grain yield and chaffiness of the crop also. Maximum per hectare grain yield and least grain chaffiness was obtained in *T. harzianum* treatment (4667 kg/ha & 8.60%) which was almost on par with Hexaconazole 5 EC (5033 kg/ha & 8.00 %) followed by *B. subtilis* (4525 kg/ha & 10.60 %), seaweed (4396 kg/ha & 12.00 %) and *B. pumilis* (4313 kg/ha & 15.30 %) when compared to untreated control (2886 kg/ha & 28.60 %).

PP(S2)/47: Evaluation of bio-control agents against Fusarium wilt of cucumber

Deepika Sharma[1]* and Arti Shukla[2]
[1]Department of Plant Pathology Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan -173230, Himachal Pradesh, India
[2]Horticulture Research & Training Station & KVK (Dr. YSPUHF), Kandaghat - 173215, Himachal Pradesh, India
**Email: ds2037@ymail.com*

Cucumber is an important cucurbitaceous vegetable rich in vitamins and minerals and is affected by various fungal as well as bacterial diseases. Among various diseases affecting cucumber, Fusarium wilt is the most serious disease caused by *Fusarium oxysporum* in long term monoculture causing huge economic losses. Due to environmental and health concerns, non chemical practices are encouraged over the large use of pesticides and chemicals. Among various management methods applied to contain the disease, use of fungal as well as bacterial bio-control agents is an important practice for Integrated Disease Management programme. Soil application of antagonistic microbes with suitable substrate and seed treatment with bio-control agents has been reported to be more effective than the direct application Under *in vitro* conditions, among fungal bio-control agents *Trichoderma harzianum* was found most effective with 61.08 per cent inhibition of mycelial growth of *Fusarium oxysporum* followed by *Trichoderma* virens with 57.51 per cent inhibition whereas, among bacterial bio-control agents, maximum mycelial inhibition of 45.69 per cent was observed in *Pseudomonas fluorescens*. Seed and soil application of *Trichoderma harzianum* followed by *Trichoderma virens* proved to be the most efficacious with 48.25 and 45.42 per cent disease control, respectively. Among bacterial bio-control agents, *Pseudomonas fluorescens* was found most effective with 27.81 per cent disease control followed by *Bacillus* sp.

PP(S2)/48: Assessment of actinomycetes for hydrolytic enzyme production

Umang[1]*, Gourav Chopra[1], Leela Wati[1] and Kushal Raj[2]
[1]Department of Microbiology, [2]Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: lwkraj@hau.ac.in*

Biocontrol of plant pathogen is becoming main component of integrated plant disease management due to hazardous impact of pesticides and other agrochemicals on the ecosystem. Therefore, the focus on management of plant diseases has been shifted from chemical pesticides to more ecofriendly biopesticides to reduce environmental hazards and minimize the risk of development of pesticide resistant strains of plant pathogens. Actinomycetes, a group of Gram positive bacteria found in soil own numerous features for their use as biocontrol agent. Actinomycetes are reported to produce various extracellular metabolites and cell wall degrading enzymes that play an important role in fighting against pathogens. The use of these microbes in controlling plant diseases is the most economic, effective and eco-friendly method of biocontrol. In present study seven actinomycetes strains retrieved from different soil samples of CCS Haryana Agricultural University Farm were evaluated for production of hydrolytic enzymes. Three isolates exhibited cellulose degrading ability, two isolates showed protease and three isolates possessed lipase activity under *in vitro* conditions. The promising isolates having different enzymatic activity could be exploited for biocontrol potential against different plant pathogens.

PP(S2)/49: Isolation and evaluation of actinomycetes for biocontrol attributes

Kavita Rani[1], **Umang[1]*,** Leela Wati[1] and Kushal Raj[2]
[1]Department of Microbiology, [2]Department of Plant Pathology, CCS Haryana Agricultural University,
Hisar – 125004, Haryana, India
**Email: lwkraj@hau.ac.in*

Actinomycetes are aerobic Gram-positive bacteria, having high G+C content belonging to order actinomycetales characterized with substrate and aerial mycelium growth. Actinomycetes play significant roles in the nutrient cycling of organic matter; inhibit the growth of several phytopathogens as these bacteria are important producers of secondary metabolites such as lytic enzymes that have a great diversity of biological activities including antibacterial, antifungal, *etc.*, which could protect the plants against various pathogens. The use of these microbes in controlling plant diseases is the most economic, effective and eco-friendly method of biocontrol. Furthermore, actinobacteria do not contaminate the environment instead, they help sustainably in improving soil health by formation and stabilization of compost piles, formation of stable humus and combine with other soil microorganisms in breaking down the tough plant residues such as cellulose and animal residues to maintain the biotic equilibrium of soil. In present study forty actinomycetes isolates (AK1-AK40) retrieved from soil samples collected from CCS Haryana Agricultural University Research Farm were evaluated for various biocontrol attributes. Among forty isolates three isolates possessed multiple plant growth promoting attributes like indole acetic acid production and phosphate and zinc solubilizing activity. Nine isolates were found to produce hydrocyanic acid and four were found to produce siderophores and inhibit the growth of *Fusarium oxysporum* under *in vitro* conditions. The potential isolates could be explored as biocontrol agent to control various phytopathogens.

PP(S2)/50: Management of major diseases in rapeseed-mustard

R.N. Sharma[1]* and S. Mureliya[2]

[1]*Department Plant Pathology, S.K.N. College of Agriculture (Sri Karan Narendra Agriculture University, Jobner), Jobner - 303329, Rajasthan, India*

[2]*Agricultural Research Station (Sri Karan Narendra Agriculture University, Jobner), Navgaon-Alwar - 301025, Rajasthan, India*

**Email: rnsharma.patho@sknau.ac.in*

A field trial was laid out at Agricultural Research Station (*S.K.N. Agriculture University*, *Jobner*), Navgaon - Alwar (Rajasthan) to test the efficacy of fungicides against white rust and Alternaria blight of rapeseed-mustard using highly susceptible variety 'Varuna' during 2015-16. Five fungicides viz., mancozeb 75% WP (0.2%), metalaxyl 8% + mancozeb 64% WP (0.2%), hexaconazole 5% EC (0.05%), difenconazole 25% EC (0.05%) and propiconazole 25% EC (0.05%) were tested for their efficacy alone as single spray at 45 days after sowing (DAS) and in combination with mancozeb at 45 DAS followed by spray of other four fungicides individually at 60 DAS. The spray of different fungicides alone as single spray treatment or each fungicide in succession with mancozeb (0.2%) significantly reduced the both diseases over control. The treatment containing single spray of mancozeb 75% WP (0.2%) followed by single spray of metalaxyl 8% + mancozeb 64% WP (0.2%) performed best in respect of white rust disease control as well as grain yield concerned, where, lowest white rust disease intensity (1.40%) and highest grain yield (13.48 q/ha) was recorded. In case of Alternaria blight disease, single spray of mancozeb 75% WP @ 0.2% followed by single spray of hexaconazole 5% EC (0.05%) proved most effective which allowed least disease intensity (2.07%). However, maximum IBCR (9.57) was noted in treatment containing single spray of hexaconazole 5% EC @ 0.05% due to low cost of hexaconazole fungicide.

PP(S2)/51: Botanicals and GRAS (generally regarded as safe) chemicals for the management of *Penicillium digitatum* Sacc. and *P. italicum* Wehmer causing postharvest decay of Kinnow mandarin

Gurwinder Kaur*, Sandeep Raheja, Anita Arora and B.V.C. Mahajan

Punjab Agricultural University, Dr. J.C.B. Regional Research Station, Abohar - 152116, Punjab, India

**Email: sidhugur27@gmail.com*

Post-harvest decay of Kinnow mandarin is an important issue in south western Punjab. It occurs mainly due to Penicillium digitatum and *P. italicum* and cause enormous losses every year. In order to reduce the postharvest losses ten botanicals viz., onion (bulb), neem (leaves and kernel),lantana (leaves and flowers), datura (leaves), aak (flowers), garlic (bulb), eucalyptus (leaves), karanj (leaves) and marigold (flowers) were evaluated at 5, 10, 15 and 20 % concentration under in vitro and 5, 10, 15% concentration under in vivo conditions together with this GRAS chemicals viz., sodium benzoate, copper sulphate, calcium chloride, potassium sorbate, sodium carbonate, sodium bicarbonate and boric acid were evaluated at 50,100,150,200 and 250mM concentration under in vitro and 2, 3 and 4 % concentration under in vivo against *P. digitatum* and *P. italicum*. Among all the tested botanicals, garlic extract was found most promising and showed 100 inhibition of mycelial growth of both *P. digitatum* and *P. italicum* under *in vitro* at 10 and above this concentrations whereas under in vivo garlic extract at 15 concentration showed 100 % and 92.22 % reduction of green and blue mould (*P. digitatum* and *P. italicum*) respectively. Among the GRAS chemicals boric acid, copper sulphate, sodium carbonate and sodium bicarbonate showed 100 % inhibition of mycelial growth of both *P. digitatum* and *P. italicum* under in vitro at 100mM and above concentrations whereas under in vivo at 4% concentration boric acid showed 100 per cent disease reduction followed by sodium carbonate (95.56 %).

PP(S2)/52: Antagonistic effects of bioagents on mycelial growth and carpogenic germination of sclerotia of *Sclerotinia sclerotiorum* on Indian mustard

Jhilmil Gupta*
Department of Plant Pathology, R.B.S. College, Bichpuri, Agra – 283105, Uttar Pradesh, India
**Email: gupta_jhilmil@rediffmail.com*

Sclerotinia sclerotiorum (Lib.) de Bary is a soilborne pathogen capable of infecting more than 400 host plants worldwide. It is a major pathogen that plays a crucial role in reducing the yield in economically important crops. The capability of sclerotia to survive for more than 4 years becomes very difficult to manage the crop from the infection of *Sclerotinia* rot fungus. Stem rot of Indian mustard [*Brassica juncea* (L.) Czern & Cross] caused by *Sclerotinia sclerotiorum* is potentially a serious threat in many mustard growing areas in India. Treatments of seeds and foliar spray with of fungicides applied at regular intervals 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.*, *Coniothyrium minitans*, *Aspergilus nidulans, Trichoderma harzianum,* and *Pseudomonas chlororaphis* were evaluated for the control of stem rot of Indian mustard. Results on bio-efficacy of different bioagents, when evaluated under glass house condition, the *Coniothyrium minitans* was the most effective agent and caused highest reduction (64.7 %) in carpogenic germination of sclerotia followed by *Aspergilus nidulans* (52.5 %) and *Trichoderma harzianum* (48.8 %), over control while *Pseudomonas chlororaphis* (48.3 %) was at par with *T. harzianum*. All the bioagents showed significant reduction effective in controlling the disease. Similar results were achieved when bioagents tested on dual inoculated plates.

PP(S2)/53: Biological control of damping off of okra

Patel Jaina V.*
Department of Plant Pathology, College of Agriculture, C.S.K. Himachal Pradesh Krishi Vishwavidyalaya, Palampur - 176062, Himachal Pradesh, India
**Email: jainapatel31095@gmail.com*

Rhizoctonia solani was found major associated pathogen with damping off of okra in summer season grown crop. Twenty isolates of *Trichoderma* spp. isolated from different rhizosphere soil and five standard isolates of *Trichoderma* spp. already available were evaluated for their antagonistic activity *in vitro* against *R. solani*. Among all the isolates tested, *Trichoderma* sp. -2 was found best bioagents for inhibiting mycelial growth of *R. solani* (67.8%) in dual culture followed by *Trichoderma* sp.-9 (67.0%), *Trichoderma* sp. -6 (64.8%) and *Trichoderma* sp. -11 (61.9%). Significantly, maximum mycelial growth inhibition (42.4%) of pathogen was with volatile compounds activity of *Trichoderma* sp.-2 while, filter sterilized culture filtrate of *Trichoderma* sp. -6 showed maximum pathogen mycelial inhibition. On the basis of morpho-cultural characteristics the potential bioagent isolates, *Trichoderma* sp.-6 and *Trichoderma* sp.-9 were identified as *T. harzianum* and *T. viride*, respectively. In myco parasitic interaction, bioagents hyphae coiled around *R. solani* mycelium and after penetration lysed the pathogen hyphae. Under net house conditions, seed biopriming application method of bioagents was found superior for management of damping off of okra caused by *R. solani* than soil application, seed treatment and drenching.

PP(S2)/54: Effect of commercially available microbial biopesticides on rice pathogens, seed germination and seed vigour index of rice

Mehjebin Rahman*, P.K. Borah and Popy Bora
Department of Plant Pathology, Assam Agricultural University, Jorhat - 785013, Assam, India
**Email: mehjebinr@gmail.com*

With the increase in consciousness of human health, mankind prefers harvests from organic farming. In the present days, biopesticide industry is undergoing a significant growth. Many young entrepreneurs are taking up biopesticide firms as a new scope in the industrial sector. A research was conducted to study the indicated bioagents from the biopesticide products available in the agromarkets. Firstly, the suppressive effects of isolated bioagents were tested *in vitro* against two pathogens of rice by the Dual culture method. Secondly, their effect on seed germination and seed vigour were tested on rice seeds. Seed germination test was done by Between paper method while vigour indices were evaluated according to the protocol proposed by Abdul Baki and Anderson. A total number of ten biopesticides products were evaluated. Biozin – PTB was found to be most effective in inhibiting both the rice pathogens *Rhizoctonia solani* and *Xanthomonas oryzae* pv *oryzae.* Biofor – PF2 promoted highest seed germination percentage and Bioveer highest seed viour I and II in rice seeds.

PP(S2)/55: *In vitro* evaluation of potential fungal and bacterial bio-agents against *Alternaria alternata* (Fr.) Keissler causing leaf blight disease in little millet

Boda Praveen* and A. Nagaraja
Department of Plant Pathology, University of Agricultural Sciences, GKVK, Bangalore – 560065, Karnataka, India
**Email*: praveenboda035@gmail.com

Little millet (*Panicum sumatrense*) is one of the minor cereal crop belonging to the family Poaceae (Gramineae) which is indigenous to Indian sub-continent. The crop is cultivated by tribal and poor farmers for food and feed. It is a rich source of complex carbohydrates, antioxidants and phenolic compounds which help to prevent metabolic disorders like diabetes, cancer, obesity etc. Leaf blight disease is one of the emerging maladies in successful cultivation of little millet. Leaf blight causing pathogen was confirmed as *Alternaria alternata* based on morphological characetiristics and molecular confirmation with internal transcribed spacer region (ITS), smaller sub unit (SSU) and *A. alternata* species specific primer (AAF2/AAR3). Fungicidal sprays for the management of the disease may not be economically viable and feasible. Hence, the present *in vitro* study was carried out to know the antifungal activity of six fungal and ten bacterial bio-agents against *Alternaria alternata* inciting little millet leaf blight disease. Among the six fungal bio-agents tested against *Alternaria alternata*, highest mycelial radial growth inhibition was noticed with *Trichoderma harzianum* (ThB5) 75.18% followed by *Trichoderma harzianum* (Th14) 74.19% and among the bacterial bio-agents, *Bacillus velezensis* strain P42 showed highest mycelial growth inhibition (84.75%) over control.

PP(S2)/56: Evaluation of bio control agents against maydis leaf blight of maize caused by *Bipolaris maydis* (Nisikado and Miyake) Shoemaker

Manjeet Singh* and Rakesh Mehra
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: manjeetsigh@gmail.com*

Maize (*Zea mays* L.) is one of the most important cereal crops in the world and popularly known as queen of

cereals. It is third major crop in India after wheat and rice. About 65 pathogens infect maize and out of these, maydis leaf blight (MLB) caused by *Bipolaris maydis* (Nisikado and Miyake) Shoemaker is considered as one of the most serious disease. The disease is widely distributed in lndia during *kharif* season. MLB appears every year with incidence ranging from 20-85 per cent in Haryana. The disease has the potential to reduce the grain yield upto 4l per cent in susceptible cultivars. Keeping in view of environmental pollution and ecological imbalance caused by the use of chemical fungicides, an effort has been made in the present experiment to control the pathogen by using bio control agents. Five bio-control agents (*Trichoderma harzianum, T. viride, Pseudomonas fluorescens, P. maltophila* and *Bacillus subtilis*) were evaluated against maydis leaf blight of maize under field conditions during *kharif* season. Among the various bio control agents tested, *Trichoderma harzianum* was found to be most effective as it showed minimum Per cent disease intensity and maximum per cent disease control followed by *T. viride*. The bio control agents *Bacillus subtilis* was found least effective with maximum per cent disease intensity and minimum per cent disease control. These finding will be helpful in developing integrated disease management strategies for the control of maydis leaf blight of maize.

PP(S2)/57: Efficacy of botanicals against maydis leaf blight of maize caused by *Bipolaris maydis* (Nisikado and Miyake) Shoemaker

Manjeet Singh* and Rakesh Mehra
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: manjeetsigh@gmail.com*

Maize (*Zea mays* L.) is popularly known as ‘Miracle crop’ due to its high yield efficiency, important human nutrient and basic element of animal feed. About sixty five pathogens infect maize and out of these, maydis leaf blight caused by *Bipolaris maydis* (Nisikado and Miyake) Shoemaker is considered as one of the most serious diseases. The disease is widely distributed in lndia during *kharif* season. Maydis leaf blight appears every year with incidence ranging from 20-85 per cent in Haryana. The disease has the potential to reduce the grain yield up to 4l per cent in susceptible cultivars. Keeping in view of environmental pollution and ecological imbalance caused by the use of chemical fungicides, an effort has been made in the present experiment to control the maydis leaf blight by using botanicals. Twelve botanicals (Garlic clove, neem leaves, onion bulb, eucalyptus leaves, aonla leaves, aak leaves, tulsi leaves, turmeric rhizomes, congress grass, Acacia leaves, jamun leaves and datura leaves) were evaluated at 20 per cent concentration against maydis leaf blight under field conditions during *kharif* season. All the botanicals were sprayed at initiation of the disease followed by second spray at fifteen days interval. Among the botanicals garlic was found to be most effective which gave maximum per cent disease control followed by neem. Next effective plant extract were turmeric, tulsi, onion, aak, datura, eucalyptus, aonla and congress grass. However, jamun and acacia were found least effective. These finding will be helpful in developing integrated disease management strategies for the control of maydis leaf blight of maize.

PP(S2)/58: Harnessing endophytes as biological control agents for bacterial blight disease (*Xanthomonas axonopodis* pv. *punicae*) in pomegranate

Manjunatha N.*, Jyotsana Sharma, Ramakant Gharte and Vijay Lokhande
ICAR-National Research Centre on Pomegranate, Solapur – 413255, Maharashtra, India
**Email: manju.ars@rediffmail.com*

Xanthomonas axonopodis pv. *punicae* (*Xap*) is widely prevalent and causes Bacterial Light Disease (BBD) in pomegranate grown in different areas of India. There is a need to use environmentally safe approaches to overcome the loss of fruit yield in pomegranate due to this disease. In the present study, we have isolated and characterized endophytes associated with medicinal plants (Tulsi, Basil, Pudina, Lemon grass and Amla) that have antibacterial activities against *Xap*. A total of 28 endophytes were isolated from roots, stems and leaves of medicinal plants which comprises of bacterial (19), Actinobacterial (4) and fungal (5) endophytes. Endophytes were tested *in-vitro* for their bio-efficacy against *Xap* and all endophytes significantly inhibited the growth of *Xap*. However, actinobacteria endophytes AE-5, AE-3 and AE-4 were found most effective with *Xap* inhibition of 68.12%, 69.85% and 77.10% (AE-5) respectively. Among bacterial endophytes BE-4, BE-10, BE-5 and BE-2 were most promising with 67.72% 63.97%, 59.09% and 58.22% inhibition of *Xap* growth respectively and 2 fungal endophytes FE-2 and FE-3 with 59.71% inhibition of *Xap*. In a glasshouse trial actinobacteria endophytes (AE-4 and AE-5) reduced BB above 40% with 3 theraputic sprays at 15 days interval, whereas in preventive sprays (3 sprays) bacterial endophytes (BE-2 and BE-4) and actinomycete isolate (AE-5) and fungal endophyte (FE-8) reduced BBD by 40 to 68% up to 30 days and 32 to 51% up to 40 days after *Xap* sprays. As the efficacy was reduced after 30 days, hence sprays need to be repeated after 15–20 days for effective control. These results indicate that endophytes are potential biological control agents against BBD of pomegranate.

PP(S2)/59: Bacteriophages as promising agents for the biological control of bacterial blight disease (*Xanthomonas axonopodis* pv. *punicae*) of pomegranate

Jyotsana Sharma, **Manjunatha N.*,** Vijay Lokhande and Anita S. Aralimar
ICAR-National Research Centre on Pomegranate, Solapur – 413255, Maharashtra, India
**Email: manju.ars@rediffmail.com*

Bacterial blight disease (BBD), caused by the bacterium *Xanthomonas axonopodis* pv.*punicae* (*Xap*) is one of the deadly diseases of pomegranate. Its management is difficult, given its aggressiveness and easy dispersion. Effectiveness of antibiotics and copper compounds is quite low and their use in the field is restricted, given environmental and human health concerns. Bacteriophages have emerged as an alternative for the control of bacterial plant diseases, but their potential for the control of BBD is yet to be tested. Thus, in this study, bacteriophages isolated from infected leaves and soil (below infected plant) and evaluated for their capacity to control both *in vitro* and on pomegranate plants under glasshouse conditions. Five lytic bacteriophages (BP-1, BP-2, BP-3, BP-4, and BP-5) were selected and evaluated against *Xap*. Here, all bacteriophages reduced the growth of the *Xap* in semisolid (nutrient glucose agar) and liquid media (nutrient broth). Pure cultures were sprayed on infected pot culture plants showing BB symptoms under glasshouse conditions. One out of five bacteriophage isolates (BP-1) against *Xap* collected from soil below infected plant showed promise with 44.5% reduction in BBD over a period of one month, whereas control plant recorded 71.1% increase in BBD in the same period. All treatments when compared on a single date after one month, BP-1 recorded 61.55% less BBD than control. These results support that bacteriophages are promising biological control agents against BBD of pomegranate. As these bacteriophages are present in phyloplane and soil of pomegranate orchards, hence these are safe and promising alternatives for pomegranate production.

PP(S2)/60: *In vitro* and field evaluation of compost tea and seaweed formulation on leaf blight of sunflower

Shadab M. Khatib*, K. Karuna and Dattatreya
Department of Plant Pathology, College of Agriculture, University of Agricultural Sciences, GKVK, Bengaluru – 560065, Karnataka, India
**Email: shadab16k@gmail.com*

Sunflower crop suffers from many diseases of which *Alternaria* blight has been considered as a potentially destructive disease. *In vitro* evaluation of compost tea revealed that maximum inhibition of *A. helianthi* was recorded in compost tea at 25 per cent (60.5%) followed by compost tea at 20 per cent (58.5%) and 15 per cent (53.8%). In field conditions, foliar spray of compost tea at the rate of 1:10 ratio at 30, 45 DAS and propiconazole at 1ml/L at 60

DAS increased the growth parameters like plant height (245.93 cm), stem girth (4.60 cm), number of leaves (9.35) and chlorophyll content (42.97). Foliar spray of compost tea with propiconazole was effective in controlling the *Alternaria* blight of sunflower with least disease severity (10.37%) and higher yield (2201.41 Kg/ha) which was on par with foliar spray of seaweed formulation (LBD-1) at 30, 45 DAS and propiconazole at 60 DAS with disease severity 12.32 per cent and seed yield of 1928.04 Kg/ha.

PP(S2)/61: Biochemical changes induced by compost tea and seaweed formulation spray inhibiting *Alternaria* leaf blight of sunflower

Shadab M. Khatib*, K. Karuna and Dattatreya
Department of Plant Pathology, College of Agriculture, University of Agricultural Sciences, GKVK,
Bengaluru - 560065, Karnataka, India
**Email: shadab16k@gmail.com*

Alternaria blight is one of the most important fungal disease of sunflower caused by *Alternaria helianthi* (Hansf.) Tubaki and Nishihara. Peroxidase and superoxide dismutase enzymes were analysed by using guaiacol and nitro blue tetrazolium chloride as the substrate, respectively whereas phenols and flavonoids estimation were carried out by using Folin-Ciocalteau and aluminium chloride as a reagent, respectively. Foliar spray of compost tea (1:10) @ 30, 45 DAS and propiconazole @ 1 ml/L at 60 DAS showed increased defense enzymes such as superoxide dismutase (39.47ìg/50 per cent inhibition) and peroxidase (16.86 ìg/min/mg protein) when compared to superoxide dismutase (59.37 ìg/50 per cent inhibition) and peroxidase (10.76 ìg/min/mg protein) in control plants. Secondary metabolites such as phenolics (67.92 mg/g FW) and flavonoids (60.01 mg/g FW) was maximum in foliar spray of compost tea (1:10) @ 30, 45 DAS and propiconazole @ 1 ml/L at 60 DAS when compared to phenolics (57.48 mg/g FW) and flavonoids (41.87 mg/g FW) in control plants. This study demonstrated that foliar spray of compost tea and propiconazole can be used effectively for the management of Alternaria blight in fields as it exhibited more defense enzyme activity which resulted in least disease severity.

PP(S2)/62: Biochemical and molecular characterization of pearl millet root bacterial endophytes

Pooja Sangwan* and Kushal Raj
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: choudhary.shweta737@gmail.com*

Endophytes are micro-organisms which colonize plants internally without any adverse effect on host. They share an intimate symbiotic association with host which makes them more valuable biocontrol agents and plays significant role in growth and development of host plants by producing a range of nutrient products and facilitating primary and secondary nutrient uptake through atmospheric nitrogen fixation, formation of iron siderophores and solubilization of minerals such as phosphate, potassium and zinc. In the present study, a total of 30 pearl millet root bacterial endophytes (PMRBE1- PMRBE 30) were obtained from crushed roots of pearl millet. On the basis of improved seed germination, positive impact on growth and yield attributes and better disease management two endophytic isolates PMRBE6 and PMRBE23 were selected for biochemical and molecular characterization. Both were positive for Methyl Red (MR) and VP test. They utilized citrate and developed blue colour in Simmon's citrate medium. Intense deep blue colour appeared in isolates PMRBE6 and PMRBE23 when loopful bacterial growth was rubbed on filter paper moistened with Wurster's reagent, indicating that these isolates were oxidase positive. Both isolates liberated effervescence when 3% H2O2 was added on the bacterial growth which indicate positive catalase test. Clear zone around the bacterial isolates after flooding the plate with Gram's iodine indicated that PMRBE6 and PMRBE23 hydrolyzed starch. The isolate PMRBE23 was found motile while PMRBE6 was non motile. PMRBE6 and PMRBE23 were found to utilize gelatin. On the basis partial 16S rRNA sequencing, bacterial isolates PMRBE6, and PMRBE23 were identified as *Bacillus subtilis* strain PD4 (Accession no. MN400209) and *Alcaligenes faecalis* strain HX2016003 (Accession no. MN400208). Hence, it is proposed that potential strains observed in the present study can be deployed as bio-inoculants to improve plant growth and yield, and to manage the disease.

PP(S2)/63: Evaluation of promising pearl millet root bacterial endophytes for the management of downy mildew disease under screen house conditions

Pooja Sangwan* and Kushal Raj
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: choudhary.shweta737@gmail.com*

The use of endophytic bacteria for controlling pathogenic fungi and bacteria is receiving increasing attention as sustainable alternative to synthetic pesticides. Endophytes colonize the internal tissues of plants without causing any visible harm to plants. Endophytic bacteria have been found virtually in every plant, where they colonize internal tissues of their host plant and can form different relationships like symbiotic, mutualistic, commensalistic and trophobiotic. Endophytic microbes play significant role in growth and development of host plants by producing a range of nutrient products and facilitating primary and secondary nutrient uptake through atmospheric nitrogen fixation, formation of iron siderophores and solubilization of minerals such as phosphate, potassium and zinc. They also supply roots with growth promoting phytohormones such as auxin, cytokinin and gibberellin. In the present study, a total of 30 pearl millet root bacterial endophytes (PMRBE1- PMRBE 30) were obtained from crushed roots of pearl millet. Promising endophytes *viz.* PMRBE1, PMRBE4, PMRBE5, PMRBE6, PMRBE7, PMRBE17, PMRBE18, PMRBE20, PMRBE23 and PMRBE24 were selected on the basis of germination (%), seedling vigour index I & II and germination speed for seed treatment as well as foliar spray for screen house experiment. Seeds of pearl millet cultivars *viz*. HHB 226, HHB-67 Imp and 7042S were inoculated with selective active culture of endophytic bacterial isolates independently and in combination. Foliar application of selected endophytes and metalaxyl MZ @ 0.25%, was carried out in respective plots 15 days after sowing and data on germination per cent, downy mildew incidence at 30 and 60 days after sowing was recorded. Maximum germination (%) was achieved on seed treatment with isolate PMRBE6 and with seed treatment + foliar spray with isolate PMRBE6. Minimum downy mildew incidence at 30 and 60 Days after sowing (DAS) was recorded on inoculation of HHB226, HHB67 Imp and 7042 S seeds with isolate PMRBE6 and with seed treatment + foliar spray with isolate PMRBE6. Pearl millet root bacterial endophytes exhibiting biocontrol activities could be exploited in friendly, sustainable organic agriculture.

PP(S2)/64: Fungal endophytes: emerging trends in the field of plant protection

Priyanka Gupta*
College of Agriculture, CCS Haryana Agricultural University, Hisar - 125004, Haryana, India
**Email: priyankagupta@hau.ac.in*

Fungal endophytes have aroused great interest of Plant Pathologists over the past few years because of the benefits they provide to host plants in which they reside. The term “endophyte” has been used since 19th century for endophyte-host interactions when Leveille and de Bary first used it for fungus living inside plants. Fungal endophytes are a source of novel natural compounds or substances which have potential use in agriculture and pharmaceutical industry. Various secondary metabolites viz alkaloids, flavonoids, steroids, terpenoids, phenols and quinols have been extracted which are potentially beneficial for the host plant development and upsurging defence mechanisms against herbivores and stress tolerance. For example, *Phomopsis oblonga* protected Elm trees against beetle *Physocnemum brevilineum* by reducing the spread of elm dutch disease. The enhancement of plant defence due to association with fungal endophytes raises an interesting avenue for their use in pest and disease control strategies for sustainable agriculture. Population’s demand for safe food products free from pesticide residues, makes it necessary to search for alternative control methods over chemical methods which guarantee food safety. Therefore, endophytes prove to be very interesting field with potential benefits to host plant by lowering the losses by phytopathogens, which ensures yield enhancement to the farmers. Thus, their role in plant-pathogen interactions is gaining momentum; however, more about physiology and regulation processes of plant-endophyte interactions is yet to be discovered.

PP(S2)/65: Biological control of *Verticillium* wilt of cotton by antagonistic fungal strains and biochemical formulation under polyhouse and natural field conditions

Kamaldeep Kaur[1]* Ashish Vyas[2*]

[1]Department of Botany, School of Bioengineering and Biosciences, [2]Department of Microbiology and Biochemistry, Lovely Professional University, Phagwara - 144411, Punjab, India

Email: ashish.vyas@lpu.co.in

A study was carried out to test the effect of antagonistic fungal strains in combination with biochemical formulation to suppress the effect of *V. dahliae* under poly house and natural field conditions. Among the five antagonistic fungal strains, most significant biocontrol efficacy has been recorded in *Trichoderma harzianum* followed by *A. terreus* and *A. niger* during pot trials and Most effective biocontrol efficacy has been observed in combinatorial study between biochemical formulation and *T. harzianum* under both poly house and natural field conditions. Effect of antagonistic strains helps to increases height and yield of cotton as compared to control plants. *Aspergillus terreus* was significantly reduced the symptoms of wilt disease with biocontrol protection of 74.5% followed by *Trichoderma harzianum* (72.3%), *Aspergillus fumigatus* (68.8%), *A. niger* (66.2%), *A. nidulans* (61.2%) as compared to control during natural field conditions. During pot trials, most significant biocontrol efficacy has been recorded in *Trichoderma harzianum* followed by *Aspergillus terreus*, *A. niger*, *A. fumigatus* and *A. nidulans* with 70.3, 66.5, 64.2, 61.5 and 59.2 biocontrol protection percent respectively as compared to control plants. Biocontrol protection percent was recorded in *Trichoderma harzianum* with 79.5% percent followed by *A. terreus* (78.3%), *A.fumigatus* (72.8%), *A. niger (69.2%)* and *A. nidulans* (68.2%) when treated with biochemical formulation. This investigation indicates that fungal strains in combination with biochemical formulation have the potential to control *Verticillium* wilt in significant proportion.

PP(S2)/66: Protecting onion seedlings from damping-off under organic cultivation system: A way forward

Kishor Chand Kumhar* and Hans Raj

Deendayal Upadhyay Centre of Excellence for Organic Farming, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India

**Email: kishorkumarc786@gmail.com*

Damping-off is one of the important nursery diseases of onion which affects onion seedlings in terms of quantity as well as its health to the great extent. It is incited by several soil resident fungal species viz., *Fusarium*, *Pythium*, *Phytophthora*, *Rhizoctonia*, etc. Although it can be managed through different chemical fungicides, however under an organic cultivation system such formulations are restricted and hence some alternative approaches are needed to handle the disease problem more safely. Genus *Trichoderma* is a versatile microbial candidate among the successful biological control agents (BCAs) that can manage a wide range of fungal pathogens. To assess the potency of *Trichoderma harzianum* against damping-off, a nursery experiment was laid out in RBD during November 2019 with seven treatments composed of different ways of its application in three replications. Results showed that its application in various ways could promote seed germination as compared to control. Its application laid a reduction

in damping-off incidence when compared with control. The disease incidence ranged from 4.92 (12.78±0.71) to 8.35 (17.40±1.30) which was lower than control where it was 18.76 (25.63±0.92) percent. It is concluded that this fungal antagonist is effective in controlling damping-off disease of onion when it is used for seed treatment, soil application in form of drenching as well as enrichment of organic manures such as farmyard manure and vermicompost. It could be one of the promising strategies under the organic cultivation system to tackle certain disease problems in a much safer way without harming the associated environment.

PP(S2)/67: Management of *Tillitia indica* through host resistance, chemicals, plant extracts and bioagents

Mamta*, Rajender Singh and Man Mohan
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: dahiya107@gmail.com*

Karnal bunt is an important internationally quarantined disease of wheat. Karnal bunt (KB) or partial bunt incited by *Tilletia indica* Mitra [syn. *Neovossia indica* (Mitra) Mundkur] is native to the asian subcontinent. Therefore, Keeping in view of its significance host resistance is done with two hundred seventy nine genotypes showed less than 5 coefficient of infection expressing resistant reaction and 221 genotypes were susceptible having more than 5 per cent coefficient of infection under artificial inoculation condition. Neem seed kernel and neem leaves inhibited teliospore germination whereas propiconazole completely inhibited teliospore germinationn. *Trichoderma harzianum* and *Baccillus* spp. also inhibited teliospore germination to some extent. Maximum disease control was obtained by propiconazole 25% EC (0.1%), followed by combination of propiconazole 25% EC (0.05%), neem seed kernel and *Trichoderma harzianum*. Neem seed kernel and *Trichoderma harzianum* were also able to check the disease. Therefore, combination of plant extract, bioagent along with least amount of chemical application can be best ecofriendly strategy to manage it.

PP(S2)/68: Evaluation of biocontrol agents and botanicals for managing white rot of onion caused by *Sclerotium rolfsii* Sacc. in Manipur

Rimamay Konjengbam[1]* and Rajkumari Tombisana Devi[2]
College of Agriculture, Central Agricultural University, Imphal - 795001, Manipur, India
**Email: rimamay24@gmail.com*

Six locally available botanicals and five biocontrol agents were assessed *in vitro* against *Sclerotium rolfsii* Sacc. causing white rot of onion (*Allium cepa* L.) in Manipur. Seven fungicides were tested *in vitro* against *Sclerotium rolfsii* and the unsuccessful fungicide was selected for comparison with effective botanicals and antagonistic biocontrol agents under field conditions. Field trial was carried out to investigate the efficacy of *Trichoderma harzianum*, *Tricoderma viride*, garlic (*Allium sativum* L.), turmeric (*Cucurma longa* L.) and sweet flag (*Acorus calamus* L.) in comparison to efficacy of carbendazim (50 WP) for the management of white rot of onion. All the treatments reduced percent disease incidence. Carbendazim was more effective than biocontrol agents and botanicals resulting in lowest disease incidence of 10.51% and recorded highest disease control of 79.41%. Highest bulb yield of 19.12 t/ha was also recorded from carbendazim treatment. *Trichoderma harzianum* was next to carbendazim recording second lowest disease incidence of 15.50% and second highest disease control of 69.60%, giving a bulb yield of 17.79t/ha followed by *T. viride* which recorded disease incidence of 19.50% giving bulb yield of 17.56 t/ha . Among plant extracts, garlic was most efficient and recorded disease incidence of 20.00%, disease control of 60.78% and bulb yield of 17.49 t/ha. Among the different treatments, it was observed that the maximum net return per rupee invested was recorded with carbendazim (1:3.25) followed by garlic (1:2.96). Least cost benefit ratio was observed from the plots sprayed with sweet flag extract (1:2.72).

PP(S2)/69: Natural way to management of Fusarium fruit rot disease of banana by plant products

Baria T.T*. and Rakholiya K.B.
Department of Plant Pathology, N.M. College of Agriculture, Navsari Agricultural University, Navsari -396450, Gujarat, India
**Email: bariatushar4@gmail.com*

Use of fungicide on harvested fruits to manage the diseases is not desirable from health point of view, also continuous and indiscriminate use has led to the development of fungicide resistant strains of the pathogens. An attempt was made to explore the possibility of using various phytoe-xtracts for the management of Fusarium fruit rot of banana.Nine different plant extract *i.e.* Garlic, Tulsi, Babul, Turmeric, Periwinkle, Ardusi, Neem, Acalypha and Eucalyptus against *Fusarium musae in vitro* and *in vivo.* Among of different plant extract garlic cloves extract at 10 per cent was recorded highest mycelial growth inhibition (85.71%) followed by neem leaves (79.37%) and eucalyptus leaves (73.54%) extracts at same concentration under *in vitro*. Whereas, *in vivo* condition, lowest fusarium fruit rot severity (11.81%) was recorded in neem leaves extract at 10 per cent concentration and it was found at par with garlic cloves extract and tulsi leaves extract on 8th day after pre- inoculation. While in post- inoculation, lowest severity (12.18%) was recorded under the garlic cloves extract at 10 per cent concentration and it was remained at par with neem leaf extract at 10 per cent on 8th day after inoculation.

PP(S2)/70: SSA novel technique to screen *in vitro* efficacy of *Trichoderma asperellum* in interaction with new combi molecules on the growth of *Sclerotium rolfsii* Sacc. inciting stem rot of groundnut

Arunasri P.*, Padmodaya B., Reddikumar M., Koteswara Rao S.R. and Ravindra Reddy B.
Department of Plant Pathology, S.V. Agricultural College, Tirupati – 517502, Andhra Pradesh, India
**Email: pinagariar7@gmail.com*

Stem rot of groundnut incited by *S. rolfsii* is one of the major disease that causes 60-70 per cent disease incidence and mortality. Among the different *Trichoderma* spp. *T. asperellum* is found to be very successful biocontrol agent to control stem rot of groundnut as this agent is having heat tolerance, saline tolerance besides capable of parasitizing *S. rolfsii* by lysis, mycoparasitism and siderophores (that compete for iron).To overcome fungicidal resistance by the pathogen combination molecules have been recommended. But majority of these effective combi molecules may be incompatible with *T. asperellum* which limits combination of new combi molecules with biocontrol agents. The present investigation was taken up with a novel technique involving dual culture cum poisoned food technique to screen *in vitro* efficacy of *T. asperellum* in interaction with new combi molecules(Azoxystrobin 11%+ Tebuconazole 18.3 %SC, Azoxystrobin 7.1%+ Propiconazole 11.9% SE, Azoxystrobin 18.2% + Difenoconazole 11.4 %SC, Tebuconazole 50% + Trifloxystrobin 25% SC, Mancozeb 63% + Carbendazim 12%WP, Flusilazole 12.5% + Carbendazim 25%WP, Hexaconazole 4% + Zineb 68% WP and Captan 70% + Hexaconazole 5% WP)on the growth of *S. rolfsii*. Both *S. rolfsii* and *T. asperellum* interacted with each other in presence of fungicides and expressed their sensitivity towards eight combi molecules. This one step techniche can be effective and convenient to test both bioefficacy of biocontrol agents and efficacy of fungicides. Hexaconazole 4% + Zineb 68% WP (Avtar) was found to be effective on *S.rolfsii* and compatible with *T. asperellum.* Inhibition of mycelial growth of *S. rolfsii* with avtar at 100 ppm was 100 per cent and sensitivity of *T. asperellum* to avtar was 70.6 percent.

PP(S2)/71: Isolation and evaluation of native bio control agents and endophytes from the rhizosphere of *Cedrus deodara* forest against damping off of *Cedrus deodara* seedlings in Himachal Pradesh

Manica Tomar* and Abhishek Chauhan

Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India

**Email: manicatomar22@gmail.com*

A survey in three different forest ranges in Solan district of Himachal Pradesh was conducted during the year 2018-2019 and 2019-2020 to assess the incidence of damping-off in *Cedrus deodara* seedlings. The incidence of damping-off was found in all the nurseries that were surveyed and the highest disease incidence was recorded in Kandaghat range (45.7%) followed by Chail range (37.98%) and Solan range (27.43%), respectively. Soil samples from the rhizosphere of healthy mature trees, healthy nursery and diseased nursery were collected during the survey to isolate the native micro fauna. Eight fungal isolates and two bacterial isolates were isolated and identified. The native biocontrol agents were tested *in vitro* against the damping-off pathogen of *C. deodara* seedlings i.e., *Fusarium oxysporum* f. sp. *pini*. Out of the eight fungal isolates *Penicillium sp.* was found to be the most effective against the damping-off pathogen followed by *Trichoderma virens*, *Trichoderma harzianum* and *Trichoderma viride* respectively. The tested biocontrol agents were tested for compatibility amongst each other for the preparation of consortium. The four compatible biocontrol agents were mass cultured on wheat grain-sawdust medium separately and used as consortium against the damping-off pathogen *Fusarium oxysporum* f. sp. *pini* of *Cedrus deodara* seedlings. The integration of *Trichoderma harzianum* + *Penicillium sp.* + *Trichoderma virens* resulted in maximum reduction of the disease incidence with only 29.44 per cent incidence followed by *Trichoderma viride* + *Trichoderma virens* + *Penicillium sp.* (31.33%) and *Trichoderma viride* + *Trichoderma harzianum* + *Penicillium sp.* (33.85%), respectively.

PP(S2)/72: Formulating microbes for sustainable plant disease management

Abhishek Sharma*

Amity Food and Agriculture Foundation, Amity University Uttar Pradesh, Noida – 201313, Uttar Pradesh, India

**Email: asharma5@amity.edu*

India, emerging as a global food bowl, faces major biotic stresses in its agricultural production due to various fungal, bacterial, and viral diseases. The conventional chemical pesticides are still used majorly in disease management despite their known detrimental effects and other shortcomings. Substituting conventional plant disease management strategies, microbes-based pesticidal formulations have emerged as a strong possibility. The use of native antagonist microbial formulations in disease management can drastically alter the rhizospheric microbiota in favour of host plants subjected to various diseases. Diverse mode of action imparted by the biocontrol agents involving competition, parasitism, antibiosis, induced resistance, etc., provides a strengthened response to the phytopathogens. A consortium of these biocontrol agents can bestow resistance against multiple disease-causing agents and also avert resistance development in the phytopathogens; a constraint faces by the chemical pesticide. Microbial biocontrol agents in the form of various formulations such as wettable powder, water-dispersible granules, emulsifiable liquid, etc., have shown immense improvement in storability, shelf life, field application, and disease management efficacy. Thus, the microbes-based pesticidal formulations hold a significant role in disease management.

PP(S2)/73: Antagonistic activity of bio-agents against postharvest diseases of mango *in vitro*

A. Ramakrishna*, C.D.Deokar, V.K. Bhalerao, R.M. Naikand S.B.Jadhav

Department of Plant Pathology and Agricultural Microbiology, PGI, Mahatma PhuleKrishiVidyapeeth, Rahuri - 413722, Maharastra, India

**Email:ramakrishnaasu@gmail.com*

Mango (*Mangiferaindica* L.) is an important fruit crop in the world. The world market continues to become more prices competitive in spite of postharvest challenges for example, losses caused by diseases (HCDA, 2011). Mango fruit suffers from many postharvest problems like diseases and disorders, which reduce the value of fruits during storage. In India, major postharvest diseases of mango are anthracnose (*Colletotrichumgloeosporioides*),and black rot (*Aspergillus niger*),which causes substantial losses to the fruit industry.The present investigation was to determine the antagonistic activity of bio-agents against postharvest diseases of mango. The agents *Trichoderma*, *Bacillus*, *Pseudomonas* and yeast isolates were individually screened against a number of postharvest pathogens including *Colletotrichumgloeosporoides*, *Aspergillus niger.*The fungal antagonist *Trichodermaviride* was found the most effective in inhibiting the mycelial growth of pathogens by 60.84 and 63.13 per cent respectively followed by *Trichodermaharzianum* 60.37 and 52.04 per cent respectively.

SESSION 3

Next generation pesticide and application

Biomolecules, immune boosters, nano-molecules, ICT, automization like robotic & drone

Keynote Lectures

KN(03)/01: Next generation RNA based biopesticides

Neena Mitter*
Director, Centre for Horticultural Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, 4072, QLD, Australia
Director, Australian Research Council Industrial Transformation Research Hub for Sustainable Crop Protection, The University of Queensland, St Lucia, 4072, QLD, Australia
**Email: n.mitter@uq.edu.au*

Drought, flood, cyclone, bushfire, pest and disease and the recent pandemic; all these and many more factors are increasingly threatening food and nutritional security. Pests and diseases represent a major constraint for increased productivity. Resistance, lack of pathogen specificity, persistence of residues, run-off and potential harm to human health and the environment are major issues with current crop protection practices. The key question is how innovation in ag-tech can deliver alternatives to reduce the use of chemical-based fungicides, while maintaining crop production, into the future. RNA based biopesticides presents a sustainable next generation platform for crop protection. The discovery of RNAi as a natural regulatory mechanism has proved to be a powerful strategy to engineer disease resistance against viruses, viroids, nematodes, insect pests and fungi. RNAi-mediated protection by topical application of double stranded RNA (dsRNA) was once considered infeasible due to a perceived barrier of uptake in plants. However, a series of papers have shown that exogenous application of dsRNA can induce RNAi-mediated defence. The major limitation however is the instability of topically applied naked dsRNA. BioClay technology using clay particles as carriers has opened the window of opportunity to deliver RNA based biopesticides as a sustainable spray application. RNAi effectors delivered as BioClay are stable, do not get washed off and provide protection to the sprayed and unsprayed leaves against the targeted viruses and insect pests. Real world application of RNA based biopesticides will be governed by factors such as cost-effective production of dsRNA and the regulatory landscape.

Oral Presentations

OP(S3)/01: Zorvec® Active (Oxathiapiprolin) - A new generation chemistry for the management of grape downy mildew

Vinod Singh Mehra*, Basweshwar Ghodki, Bharani Deepan, Ashutosh Bhaik, Edwin Rogbell and Jean-Luc Genet
Corteva Agriscience, The V-Ascendas, Atria Block, 12th Floor, Plot No. 17 Software Units Layout, Madhapur, Hyderabad - 500081, Telangana
**Email: vinod.mehra@corteva.com*

Grape is one of the world’s most produced fruit crops grown for making wines, raisin preparation and as a table fresh fruit. In India, it is mainly grown for table use. Downy mildew disease by *Plasmopara viticola* is an extremely serious fungal disease of grapes that can lead to severe crop losses. Multiple repeated applications of fungicides are required for managing this deadly disease during the crop cycle. This has led to resistance against fungicide groups. Zorvec® active (Oxathiapiprolin) is the first member of a new class of highly active oomycete fungicides, the piperidinyl thiazole isooxazolines. It acts via novel fungal target, an oxysterol binding protein, resulting in excellent preventative and residual efficacy against this oomycete disease of grapes. Zorvec® Enibel (Oxathiapiprolin 0.6% + Mancozeb 60% w/w WG) was evaluated for field efficacy on grape downy mildew in major grape growing geographies across India. Zorvec® Enibel at 1515 gai/ha recorded minimum (0-1.9%) downy mildew infection on the leaves and bunches when compared to untreated (51.1-81% infection). This rate recorded the most effective disease control of 85.7-100% when compared with the standards tested (16.6-84% disease control).

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OP(S3)/02: Evaluating the field efficacy of new and commercially available fungicides against sheath blight of rice caused by *Rhizoctonia solani* Kuhn

S. Lenka*, P.C. Rath, Raghu S, A. Mahanty, T. Adak, A.K. Mukherjee and M.K. Bag
Division of Crop Protection, ICAR-National Rice Research Institute, Cuttack – 753006, Odisha, India
**Email: srikantalenka@yahoo.in*

Sheath blight of rice caused by *Rhizoctonia solani* Kuhn {teleomorph: *Thanatephorus cucumeris*) Frank (Donk)} is a major biotic constraint in almost all the rice growing areas next to blast, reducing both grain yield and quality. This disease generally appears at maximum tillering stage and affects all the plant parts above water line. Yield losses due to this disease alone in India has been reported up to 54.3% (Rajan, 1987; Roy, 1993). Various attempts were made to develop sheath blight resistant varieties, but till date no such varieties have been released. Various cultural practices combined with use of fungicides are the most common option of managing this disease. Chemical control of sheath blight disease is successful in the field conditions in majority of cases. Some combination fungicides were tried with the hope of synergistic action and it was found that Mancozeb + Thiobencarb and Iprodione+Carbendazim were better than several single formulations in disease control and yield protection, while Mancozeb+Carbendazim tank mix was not effective (Rao *et al.*, 1978; Singh and Sethunathan, 1987; Thangaswamy and Rangaswamy, 1989; Torabi and Binesh, 1987). One field experiment was conducted at ICAR-National Rice Research Institute, Cuttack during *kharif*, 2020 with eight treatments and four replications in which seven new and commercially available fungicides namely, difenoconazole 25EC @0.5ml/l, isoprothilane 40EC @1.5ml/l, kasugamycin 3%SL @2.0ml/l, kitazin 48EC @1.0ml/l, propineb 70WP @3.0g/l, tebuconazole 25.9EC @1.5ml/l and thifluzamide 24SC @0.8g/l were evaluated under artificial inoculation with taking of susceptible check var. Tapaswini. From the critical observations and computed analysis, among eight treatments including control, best treatment was T-2, isoprothilane 40EC @1.5ml/l showing 18.4% disease severity, 72.6% reduction in disease severity over control; 22.5% disease incidence, 68.3%reduction in disease incidence over control. Second significant treatment was T-1, difenoconazole 25EC @0.5ml/l which showed 19% disease severity, 67.2% reduction in disease severity over control; 26.8% disease incidence, 64.6% reduction in disease incidence over control. The untreated control showed 69.4% disease incidence and 72.5% disease incidence. Out of seven new and commercially available fungicides, isoprothilane 40EC @1.5ml/l and difenoconazole 25EC @0.5ml/l can be taken for another season for conformity in evaluating their field efficacy against sheath blight disease.

OP(S3)/03: Comparative efficacy of plant extracts and fungicides for management of wilt of chilli

Sanjeev Kumar*
Department of Plant Pathology, Office of Dean Faculty of Agriculture, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur - 482004 Madhya Pradesh, India
**Email: sanjeevcoa@gmail.com*

Wilt diseases has become a major problem in chilli cultivation throughout Madhya Pradesh and causes 10-50 per cent loss. Limited work has been done in management of Fusarium wilt of chilli. The present investigation was undertaken to sort out the most effective chemicals and botanicals for management of disease. Seven fungicides, *viz.*, Azoxystrobin, Propineb, Thiophanate Methyl, Difenoconazole, Mancozeb, Mancozeb + Thiophanate Methyl, Boscolid + Pyraclostrobin and seven plants extracts namely *Allium sativum*, *Azadirachta indica*, *Polyalthia longifolia*, *Allium cepa*, *Gingiber officinalis*, *Withania somnifera* and *Asparagus racemosus* were evaluated against wilt of chilli caused by *Fusarium oxysporum* f. sp. *capsici* (sacc.) under *in vitro* and *in vivo* condition. Mancozeb + Thiophanate Methyl, Difenoconazole and Thiophanate Methyl were found most effective fungicides which completely inhibited the radial growth of *Fusarium oxysporum* f.sp. *lycopersici* under *in vitro* condition. Two consecutive soil drenching with Mancozeb + Thiophanate methyl was found most effective in reducing the impact of disease (5.3%) as well as enhancing the yield (470.9 q/ha). Garlic clove extract was found promising in inhibiting the growth of test pathogen *as* it produced 24.52 percent growth inhibition of test pathogen followed by *Azadirachta indica* (22.96%) *under in vitro condition* .Two soil drenching of garlic clove extracts @ 15% concentration showed minimum disease incidence of (16.33%) with maximum yield (60 q/ha) under field condition.

OP(S3)/04: Evaluation of fungicides in reducing disease progress and rate of infection of *Phytopthora infestans* in potato

Vinod Upadhyay*, Sunil Kumar Paul and Ashok Bhattacharyya
Regional Agricultural Research Institute (AAU), Gossaigaon – 783360, Assam, India
**Email: vinodupadhyay148@gmail.com*

Late blight disease of potato (caused by *Phytophthora infestans*) is a polyclic disease with high rate of infection and can only be effectively manage through fungicide application. Total of seven different fungicides namely, Fenamidone + Mancozeb, Dimethamorph, Tebuconazole + Trifloxystrobin, Azoxystrobin, Mandipropamid, Mancozeb and Metalaxyl + Mancozeb. and non-treated control (NTC) has been evaluated against late blight pathogen in potato under natural epiphytotic condition from the year 2017-2020. Experiments were replicated four times in a randomized block design planted with late blight susceptible cultivar Kufri Jyoti. All the fungicides tested provide effective preventive control as compare to non-treated control (NTC). Dimethamorph, Mandipropamid and azoxystobin show considerably low area under disease progress curve (AUDPC) value (152, 397and 359) and infection rate (r) (0.060, 0.075 and 0.066) as compare to Fenamidone + Mancozeb, Metalaxyl + Mancozeb, Tebuconazole + Trifloxystrobin and mancozeb showing AUDPC value of 453,638,776 and 901 and infection rate of 0.083, 0.062, 0.097 and 0.074 respectively whereas, Non treated control show maximum AUDPC value of 1635 and rate of infection of 0.164. Application of dimethamorph showed maximum percent increase in tuber yield over control (163.73) followed by Mandipropamid (144.24), Fenamidone + Mancozeb (117.89), azoxystobin (117.41), Metalaxyl + Mancozeb (114.69), Mancozeb (97.92), Tebuconazole + Trifloxystrobin (72.52). The benefit cost ratio was found highest for dimethamorph and Mandipropamid as compare to all other treatments. These results show the efficacy of dimethamorph and Mandipropamid in effectively managing the late blight severity with increase tuber yield in potato.

OP(S3)/05: Potentiality of new fungicide Mefentrifluconazole 400 g/l SC to curtail sheath blight and grain discoloration of paddy

V. Prakasam*, C. Priyanka, K. Chakrapani, D. Ladha Lakshmi, G.S. Laha, C. Kannan, D. Krishnaveni, K. Basavaraj, G.S. Jesudasu and M. Srinivas Prasad
ICAR-Indian Institute of Rice Research, Hyderabad – 500030, Telangana, India
**Email: vprakasam.iari @gmail.com*

Rice is affected with number of diseases, among them sheath blight caused by a fungus *Rhizoctonia solani* AG1 IA causes yield loss upto 70% in advance stages of disease development. Apart from sheath blight, grain discolouration has become a serious problem in recent years in India especially when there is post-flowering rain. Effective management of these two diseases through applying fungicides is the better option because developing resistant/ tolerant variety against these diseases is very difficult. Present investigation has been taken to assess the bio-efficacy and phytotoxicity of new fungicidal molecule Mefentrifluconazole 400 g/l SC against sheath blight under artificial inoculation and grain discoloration under natural incidence of rice during *Kharif*-2016 and 2017 in vitro and in vivo at ICAR-IIRR, Hyderabad. It is evident from the results, application of Mefentrifluconazole 400 g/l SC @ 140, 120 and 100 gm/ha active ingredient was found effective in reducing of disease severity of sheath blight and grain discolouration compare to other standard fungicides and untreated control. Besides, this molecule also increased the grain yield. Besides, Mefentrifluconazole 400 g/l SC @ 120 gm/ha and 240 gm/ha active ingredient do not cause any kind of phytotoxicity in rice (*Cv*. BPT 5204). Hence, application of Mefentrifluconazole 400 g/l SC @ 120-100 gm/ha of active ingredient or 250-300 ml/ha formulation is safe to rice crop and it can effectively manage the sheath blight and grain discolouration diseases of rice.

OP(S3)/06: Efficacy of different fungicides/chemicals under in vitro conditions against *Rhizoctonia solani* causing black scurf of potato (*Solanum tuberosum*)

Manoj Kumar*, Anil Kumar, Narender Singh and Jagdeep Singh
Regional Research Station (CCS HAU), Bawal (Rewari) – 123501, Haryana, India

Efficacy of fungicides was tested under *in vitro* conditions for the per cent mycelial growth inhibition of *Rhizoctonia solani* causing black scurf of potato (*Solanum tuberosum*). The efficacy of six chemicals/ fungicides *viz*., boric acid, methoxy ethyl mercuric chloride (MEMC), mancozeb, monceren, hexaconazole and propiconazole was tested *in vitro* condition on the radial growth inhibition of *R. solani* at four different concentrations *viz*., 100, 250, 500 and 1000 ppm by employing poison food technique. Observations on colony diameter of the fungus were recorded after fifth day of incubation. There was significant decrease in mycelial growth with increase in concentration of fungicides. The extent of growth inhibition, however, varied among all the six fungicides. The experimental results clearly showed that monceren fungicide completely inhibited mycelial growth followed by 81% inhibition MEMC at 100 ppm concentration, whereas, boric acid, propiconazole 25%, hexaconazole 5% and mancozeb 75% were responsible for 76.00, 72.33, 70.00 and 45.00 per cent inhibition of mycelial growth of *R. solani*, respectively at 100 ppm concentration. MEMC at 500 ppm concentration completely inhibited mycelial growth as compared 97.33% inhibition by boric acid as similar conditions. An inhibition of 94.33 and 89.67 per cent was observed at 250 ppm concentration of MEMC and boric acid, respectively. The complete growth inhibition of *R. solani* was observed with MEMC showed at 500 ppm followed by boric acid, propiconazole 25% and hexaconazole 5% at 1000 ppm. Mancozeb 75% (74.33% inhibition @ 1000 ppm) was found least effective at all the concentrations indicating their in effectiveness in checking radial growth of the fungus. The *in vitro* evaluation of the fungicides against the test fungus indicated that monceren 250 EC, MEMC-6 FS were more promising compared to others and intermediate response in suppressing growth of the test fungus was observed with the other fungicides *viz*., boric acid, propiconazole 25%, hexaconazole 5%, whereas, mancozeb 75% was least effective at all the concentrations.

OP(S3)/07: Bio-efficacy of promising fungicides for management of coffee leaf rust disease caused by *Hemileia vastatrix* B. & Br.

M. Sudha*, Santoshreddy Machenahalli, Madhu S. Giri, A.P. Ranjini and N. Suryaprakash Rao
Central Coffee Research Institute, Chikkamagaluru District, C.R. Station – 577117, Karnataka, India
**Email: sudhaccri@gmail.com*

Coffee is a tropical and global commodity crop. *Coffea arabica* and *Coffea canephora* are the commercially cultivated species, however, *Coffea arabica* is susceptible to pest and diseases. Coffee Leaf Rust (CLR) is considered as one of the important diseases and prevails in all coffee growing countries. CLR management strategies are based on cultural operations, resistant cultivars, and chemical control. In India, much research has been done regarding the fungicides to combat the disease including Bordeaux mixture. CLR control in India is accomplished using 2-3 sprays in a season with contact and systemic fungicide depending on the tolerance of the cultivars. The present study was investigated to evaluate the ability of different triazole and strobilurin fungicides either alone or combination spray to manage CLR. Hence, a field experiment was laid out as bulk trial to assess the bio-efficacy of promising systemic fungicides hexaconazole 5EC, hexaconazole 75WG, pyraclostrobin (133 g/L)+epoxiconazole (50 g/L) w/v SE, tebuconazole 430SC, propiconazole 25EC against CLR disease at Central Coffee Research Institute, Chikkamagaluru District, Karnataka, during 2019-20 and 2020-21. Experiment had eight treatments with susceptible arabica cultivar Sln.3. Treatments were imposed during pre & post monsoon periods and rust incidence was recorded at monthly intervals. The statistical analysis of data indicated that these systemic fungicides are almost on par with each other and superior to contact fungicide Bordeaux mixture. However, combi-product fungicide pyraclostrobin 133g/L+epoxiconazole 50g/L @ 1.0 ml/L showed minimum incidence in both the years of study. A mixture of triazole and strobilurin fungicides prevents the fungus from developing resistance.

Poster Presentations

PP(S3)/01: Efficacy of different fungicides on juice quality of sugarcane against pokkah boeng disease (PBD)

Vishal Gandhi[1]* and Rakesh Mehra[2]
[1]*Department of Plant Pathology, CCS Haryana Agricultural University, Hisar - 125004, Haryana, India*
[2]*Regional Research Station (CCS HAU), Karnal - 132001, Haryana, India*
**Email: vishalgandhi1991@gmail.com*

Sugarcane is one of the important cash-cum-industrial crops in India affected by several pathogens viz; fungus, bacteria, virus and phytoplasma. Among these pokkah boeng disease (PBD) caused by *fusarium sp*. complex is considered a serious and emerging threat to its cultivation in terms of quality and production. The disease caused 5-90 % reduction in yield and quality parameters by reducing plant height, number and lenght of internodes, stem diameter, brix %, sucrose %. and purity %. An experiment was conducted to manage the disease through different fungicides and to find out the effect on juice quality. The disease incidence varied from 4.07 to 29.77 per cent during the course of study. Among all the treatments T1 (Sett treatment with carbendazim 0.2% followed by three spray with carbendazim 0.2 % at 15 days interval) was found significantly superior over all the treatments in respect of qualitative attributes of the sugarcane in crop being brix % (21.93 %), sucrose % (18.86 %) and purity % (86%).

PP(S3)/02: Potassium phosphite: A novel blasticide enhances blast disease resistance in *ptxD*-OE transgenic rice

Sahil Mehta[1]*, A. Kumar[2], G. Prakash[2], Asmita Singh[2], Neelmani Rathi[3], V. Mohan Murali Achary[1], T.K. Das[3] and M.K. Reddy[1]

[1]*Crop Improvement Group, International Centre for Genetic Engineering, and Biotechnology, New Delhi - 110067, India*
[2]*Division of Plant Pathology,* [3]*Division of Agronomy, ICAR-Indian Agricultural Research Institute,*
New Delhi - 110012, India
**Email: sahilmehtasm21@gmail.com*

Rice is the second-most widely grown cereal nourishing more than 60 % of the human population in the world. In rice farming, the blast disease caused by *Magnaporthe oryzae* is one of the major production constraints responsible for approximately 30 % of productivity losses. As the current management options including host resistance and fungicides application are either non-durable or unacceptable owing to the multitude of factors, there is a growing consensus devising new strategies. Considering this, in the present study, a series of experiments was conducted on *ptxD*-OE transgenic rice (Cultivar BPT5204) to assess the efficacy of potassium phosphite (Phi) as a plant protection agent against the blast (Virulent isolate PB1637). The *in vitro* assessed minimum inhibitory concentration of 400 mM Phi was applied prophylactically, *i.e.* before rice blast inoculation as well as curatively, *i.e.* after rice blast inoculation as a foliar spray. Application of Phi in both ways resulted in a reduction in blast disease (incidence, severity, and lesion score). Furthermore, the prophylactic application of Phi outperformed the curative application of Phi as well as positive chemical control (Tricyclazole, currently under a ban) in terms of reductions in blast severity as well as incidence. Apart from these, the foliar application of Phi also induced positive effects on leaf total chlorophyll content, carotenoid content, and enhanced the activity of multiple defense-related genes, and enzymes. Taken together, the significant reductions in blast disease, the present study gives credence to the potential of Phi for the ecofriendly management of blast disease in the integrated crop management approach for improving the rice yield and productivity.

PP(S3)/03: Management of citrus root rot by using non conventional chemicals under nursery conditions

Y.V. Ingle[1]*, D.H. Paithankar[1], S.B. Bramhankar[2], S.S. Mane[2] and A.G. Gathe[2]

[1]*AICRP on Fruits,* [2]*Department of Plant Pathology, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola - 444104, Maharashtra, India*
**Email: yog_ingle@rediffmail.com*

Phytopthora spp. causes root rot, foot rot, crown rot and gummosis diseases in citrus. It reduces life expectancy, quality and yield potential of trees. It attacks citrus species right from damping off in nursery beds to fibrous root rot, crown rot, premature leaf fall, foot rot and gummosis in mature orchards and infect almost every part of citrus plants. At present only Cymoxanil + mancozeb fungicides reported to be in label claim for management of root rot and gummosis. In search of newer chemical, certain non-conventional chemicals tried to manage the citrus root rot disease in nursery conditions. All tested chemicals showed significantly differences compared with control. Non conventional chemical Potassium phosphonate @ 5ml/liter water/plant produced the best effect in disease reduction (70.0%) with only 10.0% seedling mortality which is at par with fungicides Metalaxyl + Mancozeb (combi product) @ 2g/liter water and Sodium hypochlorite 5 ml/ liter water/plant recorded 10.0 and 13.33% reduction in mortality over control.

PP(S3)/04: Characterization of Turmeric based curcumin content against *Taphrina maculans* by HPLC and spectrophotometer

Mukul Kumar[1]*, A.K. Mishra[2], Pooja Kumari[3] and S.K. Biswas[2]
[1]Department of Plant Pathology, C.S. Azad University of Agriculture and Technology, Kanpur – 208002, Uttar Pradesh, India
[2]Department of Plant Pathology, Tirhut College of Agriculture, Dholi, (R.P.C.A.U.) Pusa, Samastipur - 848125, Bihar, India
[3]Department of Entomology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: emailofmukul@gmail.com*

Turmeric (*Curcuma longa*) is known to be used successfully in Ayurvedic formulations from ancient times. Now, recently it is proved to be very much effective against covid-19. It is a rich source of many bioactive phytoconstituents like curcuminoids, turmerone and many more. Curcuminoids is the group of chief dynamic components and has number of medicinal properties such as anti-inflammatory, antitumour, antiviral, anticancer, antifungal and antiparasitic. Different analytical methods have been developed in recent year for the estimation of quality control of curcuminoids in Curcuma longa extract including HPLC, HPTLC and UV-Visible Spectrophotometry. While the primary component curcumin from curcuminoids is still lacking for its analytical method development along with validation. Therefore, in the present study was conducted during 2018-19 through simple UV visible and HPLC method was developed and validated according to international conference harmonization (ICH) guidelines for the quantitative estimation of curcumin in Curcuma longa extract. The linear response for the curcumin content ranges from 1.25 to 7.5 ìg/ml. The precision (R.S.D.) among thirty sample preparations was 0.42%. The LOD and LOQ are 0.06 and 0.18 ìg/ml, respectively. The recovery of curcumin was about 99.45%. Key Words: Curcuma longa, Taphrina maculans, Curcumin, Spectrophotometer.

PP(S3)/05: Management of necrosis and leaf curl diseases of sunflower under field conditions

K. Venkataramanamma*, S. Neelima, K. Prabhakar and D. Lakshmi Kalyani
Regional Agricultural Research Station (ANGRAU), Nandyal – 518502, Andhra Pradesh, India
**Email: kvrag84@gmail.com*

Virus diseases are causing more yield losses in sunflower crop. Among the virus diseases necrosis and leaf curl diseases are very important. A field experiment was conducted during rabi, 2017-18 with seven different treatments having insecticides in three replications for management of these diseases. Necrosis is transmitted through thrips and leaf curl is transmitted through whiteflies. Among the different treatments for necrosis disease, necrosis incidence was less in the treatment i.e., T2 (Seed treatment with Imidacloprid 600FS @ 5ml/kg seed + foliar spray with Fipronil 5SC @ 1ml/lit at 30, 45 and 60 days after sowing), which recorded 3.25%, followed by treatment T1 (Seed treatment with Imidacloprid 600FS @ 5ml/kg seed + foliar spray with Imidacloprid 17.8SL @ 0.5ml/l at 30, 45 and 60 DAS) recorded necrosis incidence of 4.35%. Regarding leaf curl disease, the treatment T6 (Seed treatment with Imidacloprid 600FS @ 5ml/kg seed + foliar spray with Spiromesifen 24SC (Oberon) @ 1ml/l at 30, 45 and 60 DAS) recorded low leaf curl incidence of 7.88 % followed by the treatment T5 (Seed treatment with Imidacloprid 600FS @ 5ml/kg seed + foliar spray with Flonicamide 50WG (Ulala) @ 0.25g/l at 30, 45 and 60 DAS) recorded leaf curl incidence of 13.58% which are on par with each other and not significant over other treatments. Yield was high in the treatment T6, which recorded 1717 kg/ha and also high B: C ratio of 2.04. Next higher yield was recorded in the treatment T4, recorded yield of 1684 kg/ha with B: C ratio of 1.98. So for management of necrosis disease, the treatments T2 and T1 performed better and for leaf curl disease, T5 and T6 performed better and in the experimental filed leaf curl incidence was more than that of necrosis and B:C ratio was also higher for the same treatments.

PP(S3)/06: *In-vitro* efficacy of plant extracts and fungicides against *Ceratocystis fimbriata* (Ellis & Halst.) inciting wilt of pomegranate

Rajat Sharma*
Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India
**Email: sharmarajat.ysp@gmail.com*

Wilt incited by *Ceratocystis fimbriata* is a major disease of pomegranate. Efforts were made to evaluate extracts of six locally sourced plants and eleven fungicides under *in-vitro* conditions by poisoned food technique, against *Ceratocystis fimbriata*. Amongst the plant extracts evaluated, *Nerium indicum* at 30% concentration was most active in restricting mycelial growth of *Ceratocystis fimbriata* (40.98%), followed by *Adhatoda vasica* (19.63%). Amongst systemic fungicides, carbendazim (Bavistin 50 WP), propiconazole (Tilt 25% EC) and hexaconazole (Contaf 5% EC) gave 100% mean growth inhibition of *Ceratocystis fimbriata* at all concentrations, followed by fosetyl-Al (Aliette 80% WP) (58.39%). Non-systemic fungicides, mancozeb (Dithane M-45 75% WP) and propineb (Antracol 70% WP) were most effective with 100% mean growth inhibition of *Ceratocystis fimbriata* followed by copper oxy chloride (Blitox 50 WP) (75.67%) and captan (captan 50 WP) (55.55%). The combi fungicides *viz.* carbendazim 12%+ mancozeb 63% (Companion 75 WP) gave absolute (100%) inhibition of test fungus followed by captan 70%+ hexaconazole 5% WP (Taqat) and metiram+pyraclostrobin (Cabrio Top 60 WG) with mean per cent inhibitions of 62.59 and 45.67% respectively. The plant extracts and fungicides varied in their inhibitory effect at different levels of concentrations. These treatments may therefore, be used to bestow antifungal action due to their antimicrobial activity on metabolic developments of *Ceratocystis fimbriata*.

PP(S3)/07: Management of pod blight complex of soybean

D.L. Wasule*, P.R. Shingote, R.M. Shinde and K.D. Thakur
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola - 445001, Maharashtra, India
Vasantrao Naik College of Agricultural Biotechnology (Dr PDKV, Akola), Yavatmal - 445001, Maharashtra, India
**Email: wasuledhiraj@pdkv.ac.in*

Pod blight complex disease is a major threat to soybean cultivation. Seed born nature, and attack later growth stage leads to severe economic losses. Field trial was conducted to evaluate the efficacy different fungicide and bio agent as seed dresser and foliar sprays of fungicides and bio agent, Combination of seed dressing and foliar spray for in consecutive three years for integrated management of Pod blight complex of soybean. The pooled results of three years revealed the highest seed germination was observed in treatment seed dressing with Carboxin + Thiram @2g/kg seed (94.39%). The minimum disease index, least per cent pod infection and maximum grain yield was recorded in treatment Carboxin + Thiram @2g/kg seed + spray with Thiophanate methyl @0.1% (8.74%), (12.83%), and (1628kg/ha) respectively at 55 and 75 DAS. This combination was also found impressive in improving seed germination. Seed dressing with Carboxin + Thiram @2g/kg seed + spraying with Thiophanate methyl @0.1% at 55 and 75 DAS recommended for integrated management of Pod blight complex of soybean.

SESSION 4

Host-pathogen interaction and genomics of plant pathogens

Molecular basis of host-pathogen interaction, genome announcement, patho-genomics, functional genomics

Keynote Lectures

KN(S4)/01: Host-pathogen interactions in the rust pathogens of wheat and barley

Robert F. Park*
Plant Breeding Institute, The University of Sydney, Australia
**Email: robert.park@sydney.edu.au*

Maintaining the current yield and quality of cereal crops and reducing the current impact of diseases to meet future demand and achieve Zero Hunger by 2030 will require sustained commitment, sound science, and good policy. The rust pathogens remain especially damaging to cereal production; the global impact of wheat stripe rust alone was estimated at 2.08% yield losses and annual losses of 5.47 million tonnes of wheat valued at some USD $979 million. This presentation will provide examples from our recent research into genetic variability and genomics of the three rust pathogens that infect wheat: *Puccinia graminis* (Pg), *P. triticina* (Pt), and *P. striiformis* (Ps). Long-term pathogenicity surveys of Pg and Pt (since 1921) and of Ps (since 1979) in Australia have formed the basis of the genetic control of the diseases they cause. These studies have shown clear evidence of periodic exotic incursion and the establishment and expansion of clonal lineages of each via simple mutation and somatic hybridisation. Whole genome sequencing of historical collections of each rust have allowed the origins of many of exotic rust isolates to be determined, and confirmed the importance of both somatic exchange and mutation in the development of new virulence in Pg and Pt, and of mutation in Ps.

KN(S4)/02: Recognition and specificity: Gene-for-gene concept of resistance and beyond

R. Sridhar*
Independent Researcher, Chennai, Tamil Nadu, India
[*Formerly with ICAR-National (Central) Rice Research Institute, Cuttack 753006, Odisha, India*]
E-mail: rangsridhar@yahoo.com

Gene-for-gene resistance hypothesis is based on the direct pathogen recognition, and this specificity operates in a receptor–ligand model wherein plant resistance proteins are direct receptors for pathogen avirulence factors. Approaching this further, in the plant immunity perspective, has brought in a lot of change in our knowledge resulting in unfolding a new paradigm of plant immune system, projecting indirect pathogen recognition (guard, decoy, integrated decoy models with intrinsic variations) in plant immunity. Along with direct recognition, the indirect pathogen recognition is not uncommon in plant-pathogen interactions, and the direct recognition is viewed as an exception rather than the rule. The indirect pathogen recognition operates through a distinctly different host protein (without any other function, termed as guardee or decoy) other than the resistance protein. This decoy protein serves as the unintended target for the pathogen elicitor/effector resulting in its modification. This modified form then activates the resistance gene for expression. The translation of the “decoy approach” to diverse crop species possessing native endogenous orthologs of the *Arabidopsis* decoy protein, has been shown. The availability of precise gene editing techniques has opened up new approaches for taking these phenomena into the next level of genetic engineering for engineering GMO-free genetic resistance in plants through protein engineering (specifically "decoy engineering" in this context) allowing the modification of recognition specificity to suit for different pathosystems with diverse pathogens besides nematodes and sap-sucking insects involving this specific protease-mediated decoy modification in host-parasite interaction using protease activity for their infection/infestation cycle or replication machinery.

KN(S4)/03-04: Exploring the genomic landscapes of *Rhizoctonia solani* and development of RsolaniDB - a comprehensive omic resource for the soilborne Basidiomycetous phytopathogen

Kaushik, A.[1], Roberts, D.P.[2], Ramaprasad A.[1], Mfarrej, S.[1], Mridul Nair[1], Lakshman, **D.K.[2]*** and **Pain, A.*[1,3]**

[1]*Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology, Saudi Arabia*

[2]*Sustainable Agric. Systems Lab., USDA-ARS, Beltsville, USA*

[3]*Res. Center for Zoonosis Control, Hokkaido University, Japan*

**Email: dilip.lakshman@usda.gov; arnab.pain@kaust.edu.sa*

Rhizoctonia solani Kühn (tele: *Thanatephorus cucumeris*) is a collective name for a group of ubiquitous basidiomycetous soilborne fungi, which cause up to 50% agricultural damages annually on a wide range of economically important plants. The limited availability of genome sequences and predicted proteomes areimportant barriers hindering understanding of functional complexity and temporal dynamics in *R. solani*. To further mobilize research with *R. solani* we present data on genomes and transcriptomes of 12 *Rhizoctonia* isolates covering seven anastomosis groups (AGs) and selected subgroups, seven of which are presented for the first time. RsolaniDB (http://rsolanidb.kaust.edu.sa/RhDB/) is a large-scale, integrative web repository for hosting the *R. solani* pangenome project which includes detailed information on each *R. solani* isolate, such as genome properties, predicted transcript/protein sequences, predicted function, and protein orthologues among other AG sub-groups, along with tools for Gene Ontology and PANTHER pathway enrichment analysis, and Integrative Genome Viewer visualization of gene models. By adding the six previously reported genome assemblies, RsolaniDB stands as the universal platform for accessing *R. solani* resources with single identifier format. Since none of the existing databases host such a large repertoire of *Rhizoctonia* genome assemblies and accessory web-tools for functional enrichment analysis of gene set, RsolaniDB positions as a unique and valuable resource for formulating new hypotheses and understanding the unique or conserved pathosystem of *R. solani* groups. The associated gene-set enrichment analysis tool further sets RsolaniDB apart from the existing fungal databases.

KN(S4)/05: *Xanthomonas oryzae* pv. *oryzae*-effectors vs rice immunity: understanding and scope for bacterial blight management

Kalyan K. Mondal

Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India

**Email: mondal_kk@rediffmail.com*

Xanthomonas oryzae pv. *oryzae* (Xoo), the causal bacterium of bacterial blight (BB) of rice, engages T3SS-effectors to suppress rice PTI for its own growth and subsequent proliferation in the invaded tissues. Our group screened T3SS-effectors repertoire of a virulent Indian strain Xoo race 4 that contains both Xop and TALE effectors. Among TALEs, both complete (tTALEs) as well as incomplete/pseudo/iTALEs are identified. The functional studies based on loss-and-gain of effector indicated that amongst 21 Xop effectors, only two namely, XopF and XopR contribute immensely during BB development. Xoo mutants (Xoo "*xopF* or Xoo "*xopR*) showed significant reduction *in planta* colonization, BB intensity but induced more callose deposition. Rice transcripts analysis indicated a significant fold increase of PTI marker genes by Xoo mutants. The effectors were shown to localize to plasma membrane. We identified two rice interactors for XopF, namely photosystem-I reaction subunit V (PSI-G) and cyclophilin II. PSI-

G interacts with many proteins of photosystem I, while cyclophilin II associates with proteins involved in protein-folding, signal transduction and ubiquitination. This suggests that XopF interacts with the two interactors to fulfil its common goal of subverting the plant immunity, either through interfering photosystem I or through destabilising plant immune protection system like cyclophilin. Altogether, our detailed insight into the Xoo-effectors vs rice immunity leads to sensible scope for improving BB resistance through modifying those rice interactors.

Invited Lectures (Lead Lectures)

IP(S4)/01: Begomovirus species-specific detection by PCR

Bikash Mandal*
Advanced Center for Plant Virology, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012
**Email: leafcurl@rediffmail.com*

Multiple begomoviruses are known to infect a single crop species with similar symptoms, it is necessary to have a sensitive and specific detection for each begomovirus species. PCR is a preferred diagnostic technique for plant virus detection as it is more sensitive than ELISA. However, the species-specific detection of begomoviruses by PCR is not available. As multiple begomoviruses are known to infect a single crop, rapid and specific diagnostic methodology for differentiating these begomovirus species is required. The species demarcation criteria in the genus *Begomovirus* is <91% genome sequence identity of DNA-A component. The 9.0% nucleotide dissimilarity is distributed randomly over the genome, but not in a continuous stretch. So, it is difficult to prepare primers that can differentiate begomovirus species by PCR. In order to overcome this problem, we identified 1-3 unique nucleotide sequence in the DNA-A genome of the begomovirus species infecting tomato and chilli in India through multiple sequence alignment. The specific primer was designed considering these few polymorphic sequences at the 3´ end of each primer for the differential detection of closely relating begomovirus species. The PCR optimization was carried out for each primer pair with the respective cloned DNA-A of the above viruses. The optimum quantity of template DNA and specific annealing temperature were identified for each virus species detection. The methodology resulted in specific amplification without any cross reactivity with the cloned DNA-A of the other begomovirus species. A generic method of PCR also was developed to detect any begomovirus in the sample in order to use it as a parallel confirmatory test with the species-specific PCR. The specific PCR amplification for each of the six begomovirus species was validated based on the testing of tomato and chilli leaf samples collected from the different states of India. The cloning and sequencing of the specific amplified DNA band in the selected field samples revealed 92-99% sequence identity with the respective begomovirus species; this further confirmed the specificity of the tests. In conclusion, a principal concept of species-specific diagnosis of begomovirus has been demonstrated here using half a dozen of begomovirus species, this further can be used for the development of specific-diagnosis of other closely related begomoviruses or any other virus.

IP(S4)/02: Piper DNA virus 1 is an endogenous para retro virus integrated in the chromosome 14 of black pepper (*Piper nigrum* L.)

A.I. Bhat*, A. Mohandas, B. Sreenayana, T.S. Archana and K. Jasna
ICAR-Indian Institute of Spices Research, Kozhikode - 673012, Kerala, India
**Email: Ishwarabhat.a@icar.gov.in*

A 7178 base pair contig obtained during high-throughput sequencing (HTS) of black pepper that showed similarities with pararetroviruses was named as piper DNA virus 1 (PDV-1). In the present study HTS results were confirmed through polymerase chain reaction carried out using primers designed to various regions of PDV-1 and total DNA isolated from black pepper. Cloning and sequencing of PCR products resulted in a sequence of 5961 bases that showed 98% identity with PDV-1, 65–66% (with sequence coverage of 12–21%) with different strains of rice tungro bacilliform virus and 32–36% with badnaviruses, respectively. The sequenced region contained motifs characteristic of zinc finger, retroviral aspartyl protease, reverse transcriptase-RNaseH of pararetroviruses. But efforts to get complete genome of the virus isolate did not yield any results indicating non-circular nature of the virus. Further, analysis of the complete genome sequence of black pepper showed integration of fragmented, sense and antisense oriented PDV-1 sequence at 22 loci in the chromosome number 14 of black pepper. Lack of PDV-1 specific transcripts both in reverse transcription (RT)-PCR and RNA-sequencing combined with integration of PDV-1 sequence in the black pepper chromosome indicate that PDV-1 exists as an endogenous pararetrovirus for which we propose the name Piper nigrum virus (PnigV).

IP(S4)/03: Role of small RNAs in plant-virus interaction with special reference to cassava mosaic virus – cassava system

Makeshkumar T.*, Sumayya Mohamed and Asha Srinivasan
ICAR-Central Tuber Crops Research Institute, Thiruvananthapuram – 695017, Kerala, India
Email: makeshctcri@gmail.com; makeshkumar.t@icar.gov.in

Plants are constantly under threat from various pathogens from the environment which they survive. Diseases caused by these pathogens in crop plants evidently affect agricultural production by reducing the yield and quality of crops. Several plant viruses cause range of diseases in plants and many of them has wide host range. Plants initiate complex defence mechanisms to prevent, or resist, damage during the onset of a viral infection. Most of them are unique compared to other plant-pathogen interactions which involves various cellular and physiological changes. In general, plant defense responses against pathogens are mediated by effector-triggered immunity (ETI), R- gene mediated responses and RNA silencing of viruses. Host small RNAs have a critical role in the gene expression events during plant immune responses, pathogen virulence, and communications in plant-microbe interactions. Endogenous small RNAs are 20 to 40 nucleotide (nt)-long noncoding RNA molecules present in most eukaryotic organisms that regulate gene expression in a sequence-specific manner either transcriptionally or post-transcriptionally. They include microRNAs (miRNAs) and small interfering RNAs (siRNAs) based on their biogenesis and precursor structure. While miRNAs are derived from imperfectly base-paired hairpin loop structures, siRNAs are derived from paired double-stranded RNA (dsRNA) precursors. Four different types of siRNAs are known in plants: trans-acting siRNAs (ta-siRNAs), natural antisense transcripts (NATs)-derived siRNAs (nat-siRNAs), heterochromatic siRNAs (hc-siRNAs) or repeat-associated siRNAs (ra-siRNAs), and long siRNAs (lsiRNAs). Plants infected with viruses acquire immunity by producing Dicer-Like Proteins (DCL) dependent and virus-derived siRNAs, which guide argonautes (AGO) proteins to viral RNAs and thus help to arrest the infection. AGOs are associated with small RNAs and form RNA-induced silencing (RISC) complexes to induce silencing of target genes. The putative targets of microRNA (miRNA) families include conserved domains in these NB-LRRs (ETI) and trigger the production of trans-acting siRNAs. DCL2 and SGS3 transcripts were also cleaved by these 22-nt miRNAs, generating phasiRNAs, suggesting interplay between silencing and pathogen defense pathways. In our study, 158 conserved miRNAs belonging to 22 families were identified in leaf library of cassava line CMR123, a cassava mosaic disease (CMD) tolerant cassava variety using deep-sequencing data. Cassava microRNA mes-miR159b, was the most abundant followed by mes-miR166e, mes-miR9386, mes-miR395d, mes-miR167c. MicroRNAs having targets in immune receptors like leucine rich repeats (LRR) and nucleotide binding site (NBS) encoded by resistance (R) genes, and pathogenesis related (PR) proteins and defensins were identified. Identification of additional miRNAs and other pathogen-responsive small RNAs regulated by viral infection can be identified using new technologies, such as high-throughput deep sequencing which will help better uunderstanding of the mechanism of plant defense responses against viruses.

Oral Presentations

OP(S4)/01: Candidate flowering genes expression during the battle of pigeonpea sterility mosaic virus in pigeonpea (*Cajanus cajan* (l) Millsp.)

R.L. Chavhan[1]*, P. Yeswanth[1], V.R. Hinge[1], A.S. Deshmukh[1], H.B. Patil[1] and P.K. Chakrabarty[2]
[1]*Vilasrao Deshmukh College of Agricultural Biotechnology, Nanded Road, Latur – 413512, Maharashtra, India*
[2]*Agricultural Scientist Recruitment Board, DARE, ICAR, New Delhi - 110012, India*
**Email: rlchavhan@gmail.com*

Pigeonpea (*Cajanuscajan* (L.) Millsp) is widely recognized as red gram and grown as tropical and sub-tropical legume crop. The Pigeonpea sterility mosaic virus (PPSMV) is an important biological threat causes losses to the extent of 30-100%. The study was attempted to disclose key genes which are influenced by Pigeonpea sterility mosaic virus during infection battle with pigeonpea. The virus resistant cv. IPA-16-F and susceptible cv. ICP-8863 was inoculated separately by PPSMV with three biological replications along with control plants. The cDNA synthesized from infected leaf samples at seedling and flowering stages were utilized in semi qPCR and RT PCR analysis. The 18S rRNA was utilized as housekeeping gene and normalized the data of real-time gene expression experiment. Moreover protein was isolated and differential protein expression profiling was analyzed. The differentially expressed proteins revealed an elevated expression of defense proteins or PR protein during their course of interaction. The Semi qPCR and Real-time PCR analysis exhibited high change fold gene expression under the battle of PPSMV with important host genes assisted during flower development pathway namely flowering time control protein (FCA and FPA) gene, pollen development SF3 gene, flowering promoting factor (FPF), and Floral promoter (AP1) gene. Thus this is the first report on identification of key genes which are regulated by PPSMV during seedling as well as flowering stage of Pigeonpea. The identified genes would be providing as potential target sitesand further perpetuation of Pigeonpea sterility mosaic virus in pigeonpea. Hence, further studies are required to mine and discriminate their actual roles in engineering of resistance against Pigeonpea sterility mosaic virus.

OP(S4)/02: Emerging virus and virus-like pathogens prevalent in north east region of India: characterization and simplified diagnostics

Susheel Kumar Sharma[1]*, S.S. Roy[1], K. Sarda Devi[1], Baby Wangkhem[1], A. Ratankumar Singh[2] and Raghuveer Singh[3]
[1]*ICAR Research Complex for NEH Region, Manipur Centre, Lamphelpat, Imphal – 795004, Manipur, India*
[2]*ICAR Research Complex for NEH Region, Umiam - 793103, Meghalaya, India*
[3]*ICAR Research Complex for NEH Region, Arunachal Pradesh Centre, Basar - 791101, Arunachal Pradesh, India*
**Email: susheelsharma19@gmail.com*

Virus and virus-like pathogens are a serious challenge to the successful production of different crops in North East Region (NER) India. The region encompasses large biodiversity of plants as well as pathogens infecting them. Characterization of the exact viral agents associated with the economically important diseases of crops grown in the region and development of simplified diagnostics is a major challenge. Present study focused on characterization of exact etiological agents associated with the viral disease complex of passion fruit, chilli & citrus and development of simplified diagnostics for the characterized viruses. Out of 857 symptomatic and asymptomatic chilli samples collected across the NER, 60.09% were tested positive for chilli veinal mottle virus (ChiVMV), 46.09% for cucumber mosaic virus (CMV), 10.38% for capcicum chlorosis virus (CaCV). 24.7% of the tested samples had mixed infection of ChiVMV and CMV. This study also confirmed the infection of large cardamom chirke virus (LCCV) in chilli of NER. Genetic characterization of representative ChiVMV, CMV and CaCV isolates indicated their distinctness. The potyvirus associated with yellow mottle and fruit deformation disease of passion fruit shared a similarity of 66 to 70% with bean common mosaic virus (BCMV) indicating its novelty and genetic distinctness. Genetically distinct

strains of citrus tristeza virus (CTV) and huanglongbing-associated Ca. Liberibacter asiaticus and their prevalence in citrus orchards of NER were detected. A simplified multiplex-PCR assay for the simultaneous detection of six chilli viruses in a single tube was developed. Simplified recombinase polymerase amplification (RPA) assays were developed for ChiVMV, passion fruit potyvirus and CTV wherein crude sap extracted from infected tissues was successfully used as template to perform RPA reaction at an isothermal temperature of 37 ÚC. The developed RPA assay could detect the target pathogens up to 10^{-6} to 10^{-8} dilution of crude sap and was as sensitive as bench mark PCR. These assays were validated using field samples and found highly sensitive and robust. These diagnostic assays will have application in routine indexing and production of virus-free plantlets in NER.

OP(S4)/03: Evaluation for host resistance in muskmelon, cucumber and bitter gourd against Fusarium wilt disease

Shumaila Shahid*
Division of Plant Pathology, Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: shumaila24amu@gmail.com*

Fusarium wilt of cucurbits is a widespread disease which causes significant losses to the crop. With the better understanding of pathogen virulence strategies and the multiplicity of their host, it becomes easy to discern host-resistance mechanism. An experiment was carried out to identify resistance in 60 cucurbit germplams, 20 each of muskmelon, cucumber and bitter gourd for their resistance against Fusarium wilt disease. Screening was conducted with artifitial inoculation of Fusarium wilt pathogen. Two methods i.e. soil inoculation and root-dip inoculation were used. The resistance has been recorded on a disease rating scale (0-5) and the germplasms has been categorized as highly resistant (0=0%), resistant (1=0-10%), moderately resistant (2=10.1-25%), moderately susceptible (3=25.1-50%), susceptible (4=50.1-75%) and highly susceptible (5=75.1-100%). Based on host-pathogen reaction of Fusarium disease on the cucurbit germplasms, 8 germplams of muskmelon were found highly susceptible to *Fusarium oxysporum* f. sp. *melonis*, 3 as moderately susceptible, while 1 germplasm was found resistant. Among cucumber germplams, 6 were found highly susceptible to *Fusarium oxysporum* f. sp. *cucumerinum*, 1 as moderately susceptible while 1 as resistant. In case of bitter gourd, 6 germplasms were found highly susceptible against *Fusarium oxysporum* f. sp. *momordicae*, while 1 was moderately susceptible and 1 germplasm was found resistant to Fusarium wilt pathogen. The study revealed few resistance sources against the virulent pathogen which urges to study its molecular basis of host-pathogen interaction. This will help in breeding for resistance sources to Fusarium wilt pathogen which is an effective and sustainable management of this disease.

OP(S4)/04: Localization of tospovirus nucleocapsid protein (N) in cells of *Thrips palmi in-vitro*

Sumit Jangra, Heena Dhall, Basavraj Y.B., R.K. Jain and **Amalendu Ghosh***
Insect Vector Laboratory, Advanced Centre for Plant Virology, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: amal4ento@gmail.com*

Tospoviruses (Bunyaviridae: Tospovirus) are one of the most important plant viruses affecting the yield of several field and horticultural crops. They are transmitted by thrips in a persistent propagative manner. *Thrips palmi* Karny (Thysanoptera: Thripidae) is a predominant tospovirus vector in Asia. *T. palmi*-transmitted groundnut bud necrosis virus (GBNV) causes losses of more than US$ 89 million per annum across Asia. Yield losses up to 100% have been reported due to infection of watermelon bud necrosis virus (WBNV). Little is known about the relationship of *T. palmi* and tospovirus. One of the possible reasons is unavailability of cell line of *T. palmi* to study the cellular interactions of tospoviruses with its vector. We, for the first time, report a primary cell culture of *T. palmi* established from embryonic tissues. An artificial oviposition setup was developed to collect the intact eggs of *T. palmi*. Embryonic tissue of 4 60-70 h old was implanted in a modified Kimura's medium (pH 7.0). Round-shaped cells of varying sizes and tissue clumps were observed immediately after implanting. Fibroblast-like cells started generating within 3 h of tissue implantation. The fibroblast grew in size and number with time and networking of fibroblast was observed post 5 days of implantation. Fresh media was supplemented at 2-3 days interval. A 48 h old primary cell culture of *T. palmi* was transfected with semi-purified groundnut bud necrosis virus (GBNV). The virus localization in cells was visualized using GNBV-nucleocapsid protein antibody and FITC conjugated secondary antibody. The N-protein of GBNV was localized in nucleus of *T. palmi* cells 24 h post-transfection. This is the first report of localization of N-protein of GBNV in its vector cells.

OP(S4)/05: Hybrid de novo assembly and functional annotation of rice blast-causing *Magnaporthe oryzae* reveals versatile metabolic pathways and pathogenicity factors

Bhaskar Reddy*
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: 24breddy@gmail.com*

Being one of the putative centers of origin for blast disease-inciting filamentous fungus, *Magnaporthe*, is a major threat to the Indian productivity of agriculturally important cereal crops including rice. This is because of wide-distribution, rapid aerial transmissions, seed-borne latent infection, and associated yield losses. In order to better understand the genetic variability, host specificity and molecular basis of the pathogenicity-associated traits, the whole genomes of rice infecting *Magnaporthe oryzae* (Strain RMg-Dl) was sequenced using the Illumina and PacBio platforms. The high-throughput hybrid denovo assembly of short and long reads resulted in a total of 375 scaffolds. The analysis revealed genome size of *M. oryzae* (Strain RMg-Dl) was 42.43 Mb and genes content was 10553. Furthermore, comparative genome analysis revealed 99 % average nucleotide identity among other fungal genomes. Among the detected transposable elements in RMg-Dl genome, LTR/Gypsy and Type LINE showed higher occurrence. Similarly, the InterProScan of predicted protein sequences of annotated genome revealed that 3774 protein family (PFAM), and 2079 CDD were present in RMg-Dl genome. The prevalence of virulence factors determination revealed that 50 different VFs were found in the genome. The biochemical pathway such as mTOR signaling, cAMP signaling, MAPK signaling– yeast, pathway related genes were identified in RMg-Dl genome. Taken together, the generated information will be useful to develop a specific marker for diagnosis, pathogen surveillance and tracking, molecular taxonomy, and species delineation which ultimately leads to device better management strategies for blast disease.

OP(S4)/06: Characterization of pseudoTALEs of Indian strain of *Xanthomonas oryzae* pv. *oryzae* race 4, the bacterial blight pathogen of rice

Thungri Ghoshal[1,2]*, Kalyan K. Mondal[1] and Seema Bhatnagar[2]
[1]*Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India;* [2]*Amity Institute of Biotechnology Amity University, Noida, Uttar Pradesh*
**Email: ghoshal.thungri@gmail.com*

TALEs are the Type III secretion system (T3SS) effector proteins of *Xanthomonas oryzae* pv. *oryzae* (Xoo) that helps the pathogen to establish infection in susceptible varieties of rice. Xoo strain contains two types of TALE, namely typical TALE (referred to as tTALE) and incomplete/truncated/pseudo TALE (referred to as iTALE). tTALE helps the bacterium to cause infection in rice by hijacking the transcription of SWEET genes (required for bacterial nutrition in the apoplast). While the iTALEs effectively infringe the host immunity through interfering the host transcription for *R* genes or so called *E* genes. Unlike tTALEs, iTALEs do not have complete domain but are shorter in 58 aa at the N terminal and do not have any AD domain. However, they possess NLS like tTALEs. The iTALEs are demonstrated to compete the binding site for tTALEs and thereby it interferes the tTALE-induced transcription of *R* genes. Race 4 is a predominant Indian Xoo strain causing notoriety in many susceptible rice cultivars. AnnoTALE based analysis revealed that Xoo race 4 contains 5 incomplete or pseudo TALES that harbour CRR sequences ranging from 0-19 repeats. Xoo race 4 have 11, 13, 0, 2 and 19 repeats in the CRR regions of TALE1, TALE2, TALE3 TALE4 and TALE5, respectively. The phylogeny drawn from the amino acid sequence of these TALEs indicated that the pseudo TALE1, TALE2 and TALE4 of Xoo race 4 were shown identity with TalBK1, a pseudoTALE from Korean strain KACC10331. Also TALE3 of Xoo race 4 shared identities with the TalAH3 of the Korean strain KACC10331. While TALE5 of Xoo race 4 gave identity with TAL5A of the Philippines strain PXO99A. Our study, thus suggest that Xoo race 4 shared a high degree of homology with reference to the prseudoTALEs of other Asian strains. This insight would help in predicting the possible role of iTALEs/pseudoTALEs of Xoo race 4, particularly in deciphering their role as a suppressor or competitor for *R* gene-induced rice resistance.

Poster Presentations

PP(S4)/01: Draft genome sequence analysis of *Bipolaris sorokiniana* causing spot blotch of wheat to understand host pathogen interaction

Shweta Agarwal*, Sapna Sharma, Malkhan Singh Gurjar, Bishnu Maya Bashyal, Sarika Sahu, M.S. Saharan and Rashmi Aggarwal
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: sinni.vits13@gmail.com*

Spot blotch disease of wheat caused by *Bipolaris sorokiniana* Boerma (Sacc.) is an emerging problem in South Asian countries. In this study, whole genome of highly virulent isolate of *Bipolaris sorokiniana* (BS112) was sequenced and assembled with Illumina Hiseq, Oxford Nanopore Sequencing and Ion-Torrent platform technologies. Hybrid Assembly through MaSuRCA tool was created using Trim-galore, and nanopore fast5 data were base called using Albacore. Hybrid assembly strategy produce assembly size of 35.64Mb providing coverage of 97.6% on reference ND90Pr genome (GenBank accession number AEIN00000000) with GC content of 50.2%. Average gene density predicted was 250-300 genes/Mb. A total of 235 scaffolds were obtained using pyscaf assembler with N50 of 16,54,800 bp. Paired end library data generated using illumina Hiseq platform. Total 5996 simple sequence repeats were identified in the genome assembly, and the most abundant simple sequence repeat type was tetra nucleotide having 37.49% of total SSRs. It is predicted to contain a total of 10460 protein-coding genes, from which total protein annotated against fungal database is 10141. The comparative genome analysis suggested 11874 proteins of *B. sorokiniana* is orthologous in four species of *Bipolaris*, whereas 8370 form single copy gene cluster. In addition, 152 transcription factors involved in various biological processes were identified and a total of 682 secretory proteins were predicted using secretome analysis. 216 CAZy were predicted using CAZy database which is involved in cell wall degradation and storage components. This genomic resource will provide a new insight into better understanding of spot blotch disease and *B. sorokiniana* of wheat.

PP(S4)/02: Characterization of chili leaf curl virus complex infecting chili in Maharashtra

Prashant R. Shingote*, Dhiraj L. Wasule and Kuldeepsingh D. Thakur
Vasantrao Naik College of Agriculture Biotechnology (Dr PDKV, Akola), Waghapur Road, Yavatmal – 445001, Maharashtra, India
**Email: shingoteprashant@pdkv.ac.in*

Chili leaf curl disease (ChiLCD) has been a major limitation to chili cultivation and production in India. Chili is prominently cultivated in Maharashtra, Telangana, Andhra Pradesh, Karnataka, and Tamil Nadu states. The present study detected the presence of Chili leaf curl virus (ChiLCV) associated with ChiLCD in Maharashtra. The ChiLCD

affected chili plants were exhibiting various symptoms including leaf curling, smaller leaves, stunted growth bearing of least flowers and fruits. A total of nine infected samples 5 from the Vidarbha region and 4 from the Marathwada region were collected and subjected to polymerase chain reaction using CP, specific primers. The six samples detected with 520 bp size amplicon corresponding to the CP gene. The 520 bp amplicon was gel eluted and sequenced. BLAST results of the sequence information revealed a 99% similarity with ChiLCV isolates from the GenBank database. Sequence analysis of the coat protein (CP) gene revealed the identity of ChiLCV associated with the ChiLCD in chili in Maharashtra, India. Moreover, the phylogenetic analysis suggested the clustering of these isolates from two different regions within the same clade and corresponds to the chili leaf curl virus Geminiviridae. The PCR results indicated that ChiLCV from Maharashtra governs DNA-A genome along with the beta satellite molecule.

PP(S4)/03: Upregulation in expression profile of heat shock protein genes in *Pentalonia nigronervosa* upon acquisition of Banana Bunchy Top Virus (BBTV) under temperature susceptibility

Swati Chakraborty[1]*, Mritunjoy Barman[2], Snigdha Samanta[2], Moupiya Roy[3], Sarbani Das[1], Subham Dutta[1] and Jayanta Tarafdar[1]

[1]Department of Plant Pathology, [2]Department of Agricultural Entomology, [3]Department of Agricultural Statistics, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur - 741252,West Benga, India

**Email: swatichak777.sc@gmail.com*

The intricate relationship between plant-pathogen-vector systems is still an ambiguous mechanism to understand. Banana Bunchy Top Disease (BBTD) caused by Banana Bunchy Top Virus (BBTV) is transmitted only by the banana black aphid, *Pentalonia nigronervosa* and its effect on vector's developmental biology, fecundity and its overall fitness is poorly understood. In our present experiment, temperature susceptibility of *P. nigronervosa* by comparing mortalities as well as heat shock protein (hsp) mRNA levels between Non Viruliferous (NVr) and Viruliferous (Vr) aphids were investigated. The lifespan of Vr aphids was 5.33 days shorter than that of NVr ones. Both NVr and Vr aphids were exposed for 3 hr at 4, 25, and 35æ%C respectively. The mortality rate of Vr aphids was higher than NVr ones, following exposure at respective temperatures with no significant difference at 25æ%C. Analysis of the expression level of heat shock protein (hsp) genes using quantitative real-time PCR showed that both cold and heat shock treatments stimulated higher expression of hsps (hsp40, hsp70, and hsp90) at various rates in Vr aphids than NVr ones, but there was no difference at 25æ%C. All together, our results showed that BBTV acquisition accelerated the rate of the developmental stages and increased susceptibility to thermal stress in *P. nigronervosa*. Therefore, this modification may result in reduced vector longevity due to increased metabolic energy utilization. Our results provide insights into the complex interaction between vector fitness and thermal stress in relation to the acquisition and transmission of BBTV.

PP(S4)/04: Identification and validation of germination-related genes in teliospores of *Tilletia indica* causing Karnal bunt of wheat using RNA seq approach

Haritha Mohan M.[1]*, Malkhan Singh Gurjar[1], Prachi Jain[1], Shweta Agarwal[1], Naresh Kumar[2], M.S. Saharan[1] and Rashmi Aggarwal[1]

[1]Division of Plant Pathology, [2]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India

**Email: mharithamohan58@gmail.com*

Karnal bunt of wheat is an important quarantine disease of wheat which interrupts India's wheat trade in international market. The mystery of spore dormancy and germination a key question remains unresolved till now. The whole

transcriptome of germinating and dormant teliospores of *Tilletia indica* was performed using RNA Seq. The transcriptome data of teliospores of *T. indica* submitted to the database (NCBI SRA accession: PRJNA522347). The unigenes from the pooled teliospores were 16,575 having unigenes length of 28,998,753 bases. Maximum number of unigenes were about 5,696 with bases between 1000 and 2000. Functional annotation showed 14,784 CDS in pooled teliospores whereas 6,812 CDS had no significant BLAST hits. The high-quality reads of germinating teliospores mapped on to 21,505 predicted CDSs. 9,680 CDSs were common between dormant and germinating teliospores. 11,825 CDSs were found to be in germinating teliospores while only 91 were unique in dormant spores. The pathway analysis showed highest number of pathways were found in germinating spores than dormant spores. Highest numbers of CDS were found to be associated with translation (431), transport and catabolism (340), signal transduction (326)and carbohydrate metabolism (283). The differential expression analysis (DESeq) of germinating and dormant teliospores showed that 686 CDS were up-regulated and 114 CDS were down-regulated in the germinating teliospores. 38 genes were selected from up regulated and down regulated genes for the relative expression analysis in the teliospores of 2015 and 2018. *Ti3931* (7.88), *Ti6828* (7.06 fold), *Ti7098* (6.16), *Ti7462* (5.81), *Ti752 2*(7.97), *Ti9289* (10.05), *Ti8670* (4.95), *Ti7959* (6.34), *Ti7809* (7.75), *Ti10095* (6.34), *Ti9297 (9.31*), *Ti8696 (5.13*), *Ti7959 (6.34), Ti7809* (7.75), *Ti10095* (6.34), *Ti9297* (9.31), *Ti8696* (5.13), *Ti7699* (8.9), *Ti7858* (10.33), *Ti7954* (7.46), *Ti7739* (5.46),*Ti9665* (10.74), *Ti9335* (6.75), *Ti8396* (9.35), *Ti8126* (8.87), *Ti7326* (6.04), *Ti10208* (13.83), *Ti12356* (7.83), *Ti14271* (9.98) and *Ti9234* (11.2) genes were found to be highly expressed in the germinating spores. These genes showed a very less expression in the dormant teliospores. Eight genes *viz. Ti508* (0.77 fold), *Ti4152* (0.68), *Ti5346* (0.51), *Ti2375* (0.69), *Ti3739* (0.21), *Ti1134* (0.45), *Ti4399* (0.43), *Ti4422* (0.93) which were down-regulated in germinating teliospores showed a very less expression in the germinating teliospores. In conclusion, transcriptome analysis revealed that 30 genes up-regulated in germinating teliospores are supposed to be involved in the process of germination and the 8 genes down-regulated are supposed to be related to the process of dormancy of teliospores. Further, mechanism of teliospores germination and dormancy in *T. indica* will be understood by functional genomics approach and to devise the anti-sporulation strategies.

PP(S4)/05: Genetic and molecular basis of gene-for-gene relationship a way of understanding the plant and pathogen interaction

Parvesh Kumar* and Pankaj
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: parveshchauhan777@gmail.com*

Plants are primary producers known as base of most food chains in the ecosystem and constantly threatened by an array of biotic stress in their natural environment. The bacteria and fungi that colonize in the living plant tissues of apoplastic region. Secreted molecules, derived from the pathogens, are the key factors which determine their pathogenicity and allow their successful colonization inside the host while the plant derived molecules are involved in the recognition of these pathogens in order to elicit the defense response. In plant-pathogen interactions, a single plant disease resistance gene *R* and a single complementary avirulence gene in pathogen *Avr* account for pathogen recognition resulting in *Avr-R* mediated resistance known as gene-for-gene model. The *Avr* gene products (elicitors), also known as pathogen-associated molecular patterns (PAMPs), are recognized by the membrane-localized pattern recognition receptors (PRRs) of plants. The successful recognition of microbial derived PAMPs by PRRs of the plants activates a first line of defense which is known as PAMP- triggered immunity (PTI). To counter-attack the PTI, many pathogens deliver various “effector” proteins inside the host cell, which suppress the components of PTI. The resistance R proteins of plants recognize these effector proteins of pathogens and can induce a second line of defense which is known as the effector-triggered immunity (ETI). PTI and ETI together constitute a major innate immune response, enabling plants to recognize and battle against the pathogen attack. However, the components of *Avr-R* mediated resistance in response to different pathogens remain unknown, requiring a large-scale investigation.

PP(S4)/06: Evaluation of interaction among pathogens of ginger rhizome rot complex

Patil, A.C.*, Kawathe, N.D. and Apet, K.T.
Department of Plant Palthology, Vasantrao Naik Marathwada Agricultural University, Parbhani – 431402, Maharashtra, India
**Email: aashutoshppatil2254@gmail.com*

Ginger crop is one of the most important spice crop cultivated in India. Which suffers from several diseases, among which rhizome rot complex caused by *P. aphanidermatum*, *F. oxysporum* f.sp *zingberi*, *S. rolfsii*, *R. solanacearum* and *M. arenaria* is one of the serious diseases observed regularly in ginger growing areas. Pot culture experiment were conducted in three replication and nineteen treatments to investigate interaction among the rhizome rot pathogens was applied to plants individually and also in combinations to find the major pathogen from those interactions which were responsible for rhizome rot. Results found that maximum plant disease incidence were recorded with the treatment *P+F* and *P+N* with (63.48%) followed by *P* (62.54%), *F* (60.03%). Minimum plant disease incidence was recorded by Control (21.41%) followed by *P+F+S* (27.25%), *P+F+S+R+N* (36.23%), Nematode (38.57%) and remaining treatments were recorded in between (58.25%) to (39.93%). Similarly the rhizome rot percentage in interaction were calculated. The maximum rhizome rot incidence were recorded with the treatment *P+F* with (73.4%) followed by *P* , *F*, *P+N* and *S+N* with (66.6%), S, P+R, *F+S*, *S+R* with (60%). Minimum rhizome rot incidence was recorded by Control (26.6%) followed by *P+F+S* (33.4%), Nematode (40%) and remaining treatments were recorded in between (53.4%) to (46.6%).

PP(S4)/07: Dynamic role of studies on interaction between *Meloidogyne javanica* and *Rhizoctonia solani* on tomato

Aradhna Sagwal*, Satish Kumar and Kushal Raj
Department of Plant Pathology, College of Agriculture, CCS Haryana Agricultural University, Hisar - 125004, Haryana, India
**Email: aradhnasagwal31@gmail.com*

Tomato (*Solanum lycopersicum* L.) is one of the major vegetable crop widely grown in almost every country in the world. It belongs to family Solanaceae and is universally considered as protective food. India ranks second in the area as well as in production of tomato after China. Amongst the various soil borne diseases, root rot disease complex considered as the most devastating disease complex in Haryana and the crop is prone to attack of various pathogens from early sowing of crop till maturity. A fungus is an essential component of the interacting system of a fungus—nematode complex disease and plays an important role in the disease etiology. The experiment was conducted under screen house conditions to know the effect of concomitant occurrence of *Rhizoctonia solani* and *Meloidogyne javanica* on root rot disease complex in tomato. Seeds of tomato cv. Hisar Arun (Selection 7) was inoculated with the nematode or fungus individually or simultaneously in various combinations and observations on per cent pre-emergence and post-emergence mortality were recorded after 30 days of sowing. It was found that that maximum pre emergence plant mortality (30 per cent), post emergence plant mortality (53.3 per cent) and 83.3 per cent disease incidence occurred when *M. javanica* (1000 J2/kg soil) was inoculated one week prior to *R. solani* (1000 mg/kg soil) followed by occurrence of 63.3 per cent disease incidence when *R. solani* and *M. javanica* were inoculated simultaneously. The simultaneous inoculations by both pathogens have synergistic effect in causing root rot disease complex in tomato. The severity of disease incidence was further enhanced when the inoculation of *M. javanica* preceded *R. solani*. *M. javanica* predisposed the roots for further infection by *R. solani* and act as an incitant for the entry of *R. solani*. Hence, it is imperative that interaction of both the pathogens require consideration for management strategies.

PP(S4)/08: Functional characterization of an avirulence (*AvrBs1*) gene of *Xanthomonas campestris* pv. *campestris* to black rot disease in cauliflower

Amit Kumar Kesharwani[1,2]*, Dinesh Singh[1] and Anupama Sharma Avasthi[2]
[1]*Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
[2]*Amity Institute of Biotechnology, Amity University, Noida - 201313, Uttar Pradesh, India*
**Email: amit.kesharwani@student.amity.edu*

Xanthomonas campestris pv. *campestris* (Xcc) (Pammel) Dowson is a gram-negative bacterium. It is a vascular pathogen that causes the most destructive disease -black rot in cruciferous plants including cauliflower worldwide. The nine *avr* genes such as (*AvrBs1*, *AvrBs2*, *XopE*, *XopH*, *XopAc*, *XopAG*, *XopAH*, *AvrXccA*, *AvrXccA2*) were annotated after the sequencing of reference genomes of Xcc strain ATCC33913, B100 and 8004. These *avr* genes may be involved in the development of pathogenicity according to the host specificity in cruciferous crops. To characterize the role of one of the pathogenicity-causing factor, an avirulence gene *avrBs1* was amplified at 1338 bp, cloned, and sequenced from the Indian isolate of Xcc-C1 (Race 1) isolated from leaf of cauliflower plant. However, *AvrBs1* has 1338 bp long nucleotide sequences and 445 amino acids. Although, *AvrBs1* of Xcc-C1(Race 1) – (MN117727) India, showed 99% sequences similarity with XccB100 – (AE008922) race 1, Xcc ATCC33913–(AM920689) race 3, and Xcc 8004 (CP000050) race 9. The marker-free deletion mutant construct of *AvrBs1* gene (>1200bp) was prepared in suicide vector pk18mobSacB via electroporation. The restriction digestion of mutant plasmid construct with *Eco*RI confirmed the integration of targeted *avr* gene in suicide vector. However, the positive construct was confirmed by the DNA sequencing with vector-specific primers (M13F and R). This deletion mutant construct was used to develop a deletion mutant of Xcc via electroporation at 1.5KV, 5ms, 25 μF. The mutants of Xcc are using for the functional analysis of *avrBs1* protein in cauliflower during pathogenicity. This study will elucidate the role of *avrBs1* in the development of pathogenicity in crucifer crops.

PP(S4)/09: Molecular basis of host- pathogen interaction in plants

Pooja Sharma*
Department of Biotechnology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173223, Himachal Pradesh, India
**Email: 10pooja.sharma94@gmail.com*

Food security has become an issue of global importance and major price spikes for staple food have occurred in recent years. These price spikes are partly due to impact of plant diseases, such as spread of wheat stem rust pathogen that has increased focus on improving crop protection approaches. Plant breeders have been using ‘resistance’ genes to control diseases in crop plants for almost 100 years and its effectiveness is based on ‘gene-for-gene’ relationships between host and pathogen. However, only through recent molecular studies it become apparent that host resistance genes encode components of plant immune system which recognize conserved molecular patterns and effector proteins in pathogens. The primary immune response is called PAMP triggered immunity (PTI). At the same time, pathogens acquired the ability to deliver effector proteins to plant system to suppress PTI allowing pathogen growth and disease. In the “gene-for-gene” interaction, the host plant becomes resistant when its dominant *resistance* (*R*) gene matches dominant *avirulence* (*AVR*) gene present in pathogen. Such host-pathogen combination is called “incompatible” interaction. When either or both *R*-gene and *AVR* gene are absent, host plant becomes susceptible, resulting in “compatible” interaction. Widespread genome sequencing of host and pathogen genomes will facilitate the identification of effector proteins, expression patterns and gene homology of host target proteins. An integrated approach based on the combined knowledge of molecular basis of ‘defense systems’ used by plant and ‘assault systems’ used by pathogens will help to design novel methods for plant disease management.

PP(S4)/10: *In vitro* infection models of sheath blight useful to evaluate the infection behavior and efficacy of fungicides against sheath blight disease of rice

Amit Mahilang*, Sumit and Anil Kotasthane

Department of Plant Pathology, Indira Gandhi Krishi Vishwavidyalaya, Raipur – 492006, Chhattisgarh, India
**Email: amitmahilang100@gmail.com*

Sheath blight (ShB) disease, caused by *Rhizoctonia solani*, is an economically important rice disease worldwide, and causes 5 to 10% yield losses in the lowland rice of tropical Asia 5-20% in Chhattisgarh. Resistance inducing chemicals that are able to induce broad disease resistance offer an additional option for the farmer to complement genetic disease resistance and the use of fungicides. In this article, we describe a simple germinated paddy seed roll technique for sheath blight infection development which formed the basis to drive the component of fungicide evaluation in moist chamber. Curative effects of fungicides (azoles, strobilurins and antibiotics) at two spray intervals on sheath blight development varied significantly and was significantly reduced after second spray.

PP(S4)/11: *Candidatus Liberibacter asiaticus* manipulates the expression of vitellogenin, cytoskeleton, and endocytotic pathway-related genes to become circulative in its vector, *Diaphorina citri* (Hemiptera:Psyllidae)

Damini jaiswal[1,3]*, V. Kavi Sidharthan[1], Richa Rai[1], Susheel Kumar Sharma[2], Nandlal Choudhary[3], Amalendu Ghosh[1] and Virendra Kumar Baranwal[1]

[1]Advanced Center of Plant Virology, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
[2]ICAR-Research Complex for NEH Region, Manipur Center, Imphal – 795004, Manipur, India
[3]Amity Institute of Virology & Immunology, Amity University, Noida – 201313, Uttar Pradesh, India
**Email: daminidiksha@gmail.com*

Citrus greening disease or huanglongbing (HLB) caused by *Candidatus* Liberibacter asiaticus (*C*Las) is very economically important bacterial disease causing production constraint worldwide. It is transmitted by the Asian citrus psyllid (ACP), *Diaphorina citri* (Hemiptera: Psyllidae) in a persistent propagative manner. Therefore, it is prerequisite to understand the molecular interaction between *C*Las and ACP and insight of interrupting the interrelationship can provide an alternative to insecticides for managing citrus greening disease. In the present study transcriptome data analysis of ACP in response to *C*Las revealed differential expression of 3911 genes (in which 2196 up-regulated, and 1715 down-regulated) that includes the functionally important key genes of ACP for instance; genes involved in cytoskeleton synthesis and nutrition-related proteins, such as vitellogenins, extensin, laminin, tropomyosin, troponin C, and lightin. Majority of the differentially expressed genes were categorized under molecular function followed by cellular components and biological processes. Further, KEGG pathway analysis showed differential regulation of carbohydrate, nucleotide, and energy metabolic pathways, the endocytotic pathway, and the defense-related pathways. The present study provides an understanding of genes involved in circulation or systemic propagation of *C*Las in ACP. The candidate genes involved in key physiological processes and *C*Las transmission by ACP would be potential targets for sustainable management of ACP and *C*Las.

PP(S4)/12: Chilli leaf curl virus manipulates the gene expression of its vector, *Bemisia tabaci* for successful transmission

Aarthi Nekkanti[1], Prosenjit Chakraborty[1], V.K. Baranwal[1], Vinay Kalia[2], Subhash Chander[2] and **Amalendu Ghosh[1]***

[1]Division of Plant Pathology, Indian Agricultural Research Institute, New Delhi - 110012, India

[2]National Centre for Integrated Pest Management, Pusa Campus, New Delhi - 110012, India

**Email: amal4ento@gmail.com*

Begomoviruses (genus: *Begomovirus*, family: *Geminiviridae*, order: *Geplafuvirales*) are transmitted by whitefly (*Bemisia tabaci*, Hemiptera: Aleyrodidae) in a persistent circulative manner. The relationship of begomoviruses with *B. tabaci* is very specific and thought to be mediated by many unidentified genes and receptors. Chilli leaf curl virus (ChiLCV) is one of the important begomoviruses responsible for recent epidemics of leaf curl disease in chilli. Understanding the molecular interaction between ChiLCV and *B. tabaci* and interrupting the interrelationship can provide an alternative to pesticide-based management of virus-vector complex. We observed significant changes in the transcripts of *B. tabaci* in response to ChiLCV infection. A total of 81 genes of *B. tabaci* were differentially expressed immediately after acquisition of ChiLCV. Among them, 29 and 52 genes are significantly up- and down-regulated, respectively. The expression of ten highly regulated genes was validated in RT qPCR. The majority of the differentially expressed genes were categorized under cellular components followed by biological processes and molecular functions. KEGG pathway analysis showed differential regulation of metabolic pathways, transforming growth factor (TGF) â signaling pathway, regulation of actin cytoskeleton, cytokine-cytokine receptor interaction, cell adhering molecules (CAM), and adherens junction related pathways. The key genes that were highly regulated involved in receptor binding, antigen binding, epithelial cell differentiation, extracellular matrix organization, intracellular membrane transport, cell to cell and cell surface receptor signaling such as tob1 protein, down syndrome cell adhesion molecule 1 isoform BD, adenosine deaminase, propyl 4 hydroxylase alpha 1 subunit, 1- acyl-sn-glycerol-3 phosphate acyltransferase, inhibin beta chain. Differential regulations of genes involved in key pathways might favor the ChiLCV to get entry and circulate in *B. tabaci* system. The candidate genes involved in key physiological processes and ChiLCV transmission by *B. tabaci* would be novel targets for sustainable management of whitefly-begomovirus complex.

PP(S4)/13: Viral suppressors of RNA silencing - the protagonists of plant viral synergisms

Malavika M.*, Dibyendu Ghosh and Supriya Chakraborty

School of Life Sciences, Jawaharlal Nehru University, New Delhi – 110067, India

**Email: supriyachakrasls@yahoo.com*

Synergistic interactions among plant viruses are one of the major causes of exacerbation of disease symptoms leading to severe economic loss in the community. These viruses encode suppressor proteins that can compete with and neutralize the host's immune responses. These viral suppressors have evolved with the host plant in a way that they can interfere with biogenesis and spread of RNA silencing signals employed by the host against the invading viruses. They can interfere with the Transcriptional gene silencing (TGS) as well as Post transcriptional gene silencing (PTGS) mechanisms in a variety of ways thereby manipulating host defense responses. Some synergistic interactions have been reported in the case of helper dependence where the helper virus facilitates the dependent viruses in accumulation and altering their tissue tropism by allowing them access throughout the host. There are reports of asymmetric synergism between viruses where one virus reaps the benefits by enhancing its viral titer while the other interacting partner has no significant change. Studies have stated that these suppressor proteins produced by viruses are very distinct and a single mutation can have a substantial effect on its function. Synergisms, in few cases, have been established based on the order in which the viruses enter the host. The role of viral

suppressors on RNA silencing on plants has been analyzed by various researchers. This paper highlights viral suppressors of RNA silencing especially those involved in synergistic interactions and analyzing their mode of action, development of symptoms, and their impact on host plants.

PP(S4)/14: Host-pathogen interaction and genomics of plant pathogens

Ragani kumari*
Department of Mycology and Plant Pathology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi – 221005, Uttar Pradesh, India
**Email: kragani20@gmail.com*

Host pathogen interaction are at the heart of our understanding of infectious disease, including their spread, development, diagnosis and treatment. As such, the study of these interaction is essential to modern medicine especially in the face of increasing antibiotic resistance and requires significant attention. Today exists a spread spectrum of tools to be used in pathogen identification. Traditional staining and microscopic methods as well as modern molecular method are presented in this chapter. Pathogen identification is only the beginning to obtain information related to pathogenicity of the microorganism in the near future. A variety of novel genomics technique has transformed the identification, detection and classification of both hosts and pathogens, allowing a greater resolution that helps decipher their underlying dynamics and provided novel insight into their environment. Molecular factors enabling microbial pathogens to cause plant diseases have been sought with increasing efficacy over three research era that successively introduced the tools of disease physiology, single gene molecular genetics and genomics.

PP(S4)/15: Fungal proteomics as a tool to study plant microbe interactions

Manjari* and Ram Chandra
Department of Mycology and Plant Pathology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi – 221005, Uttar Pradesh, India
**Email: mishramm1596@gmail.com*

Proteomics is defined as the systemic analysis of the proteome, the protein complement expressed by a genome, cell, tissue or organism. Proteins play critical role in diverse biological processes through interactions with other proteins, DNA and other molecules .Consequently ,fungal proteomics is defined as the study of the intracellular and extracellular protein complement of fungi .Fungi are responsible for causing harmful diseases in plants ,therefore a detailed analysis of their biochemistry is important to understand the mechanism of disease caused by them .Multiple techniques including mass spectrometry ,genome and transcriptome sequencing and advances in bioinformatics are used to study fungal proteomics .Recent advancement in proteomic technologies offers an exciting opportunity to reveal the fluctuations of fungal proteins and enzymes .An alternate approach is to tag proteins of interest with epitopes that can be detected with commercially available antibodies .Proteomics will play a major role in future research in disease management and biotechnological uses of fungi. Although the assignment of biological roles of both *in silico* annotated and un annotated genes, remains a significant challenge but it is clear that this phenomenon will accelerate our understanding of fungal biology and yield identification of many new enzymes for biotechnological uses.

PP(S4)/16: Extracellular vesicles from *Fusarium oxysporum* f. sp. *cubense*, a banana wilt pathogen

Lizelle B. Fernandes, Jacinta S. D'Souza and **Siddhesh B. Ghag***
School of Biological Sciences, UM-DAE Centre for Excellence in Basic Sciences, University of Mumbai, Kalina campus, Santacruz (East), Mumbai - 400098, Maharashtra, India
**Email: siddhesh.ghag@cbs.ac.in*

Fusarium wilt disease of banana is a destructive disease caused by a hemibiotrophic filamentous fungus, *Fusarium oxysporum f. sp. cubense* (Foc). It has devastated banana plantations globally and has led to a threat of extinction. Studies have demonstrated the role of several transcription factors, effectors and small RNAs in pathogenicity. However, the precise mechanism involved in Foc-banana crosstalk at the interface and secretion of virulent factors remains elusive. Current findings emphasize on the significance of extracellular vesicles (EVs) in trafficking these virulent factors that modulate the host defence system and physiology promoting host-pathogen interactions. EVs are ubiquitous communicators involved in both inter and intracellular communication across all three kingdoms. This study focuses on the optimization of Foc EVs isolation using different methods; these include precipitation using polyethylene glycol and sodium acetate, high speed centrifugation and phase separation using ethyl acetate. Isolated EVs were microscopically visualized using Nile red staining. Transmission electron microscopy revealed and confirmed the presence of typical circular, double-membrane layered, vesicular-like structures ranging between 50-200 nm. The protein content of the isolated EV fractions from all procedures was estimated and phase separation using ethyl acetate produced highest yield. Further, the extracted EVs were separated using SDS-PAGE and proteins ranging from 11-240 kDa were observed. These fractions will be further processed for western blotting (using HSP70 antibody as a marker) and mass spectrometry analysis. Results obtained through this study evidently demonstrated the secretion of EVs by Foc and hints its significance in pathogenicity.

PP(S4)/17: Deciphering the mystery of long non-coding RNAs in plant-virus interactions: a new paradigm

Kamal Kumar* and Supriya Chakraborty
School of Life Sciences, Jawaharlal Nehru University, New Delhi – 110067, India
**Email: supriyachakrasls@yahoo.com*

The tussle between the plants and viruses began ever since these pathogens started parasitizing their hosts. The plant viruses cause havoc and economical loss, ultimately reduce crop productivity and yield. This association is an emerging field that gives insights on the emergence of diseases, the occurrence of genetic changes, and underlying defensive mechanisms of both plants and viruses to subdue virus-induced gene silencing in hosts. Long non-coding RNAs (LncRNAs) are a group of approximately 200 nucleotide long RNA transcripts which have been described as non-functional genic regions, having a multilevel regulatory function in eukaryotes. They also play crucial roles in plant development, including flowering, root organogenesis, seedling photomorphogenesis, reproduction, and defense against biotic stress. Being sessile, plants must continuously adapt to occasional and inevitable abiotic and biotic environmental conditions during their life cycle. To cope up with the continuous changes, plants have developed several layers of sophisticated molecular mechanisms and possess hidden mysteries to mitigate the challenges against stresses. The resistance mechanisms can undoubtedly be of benefit in controlling diseases and minimizing crop losses. There is a paucity of understanding the roles of lncRNAs during the pathogenesis of viruses in plants. Some known functions of viruses include acting like endogenous target mimics of miRNAs which activate the expression of defense-related genes and regulator of mRNA expression. Therefore, unraveling the lncRNAs and their functional roles in host-virus interactions will certainly help to develop new techniques for protecting plants against invading viruses.

PP(S4)/18: Genome editing a promising technology: development of disease-resistant soybean

A. Ramlal* and Ambika Rajendran

Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India

**Email: ramlal.ayyagari@gmail.com*

Soybean (*Glycine max* (L.) Merrill) is a functional leguminous vegetable crop and a rich source of proteins, lipids, lecithin, vitamins (A, B, B2, D, E), and minerals (Ca, Fe, K). It is a widely consumed and economical crop. It is highly prone to various kinds of diseases caused by viruses like soybean mosaic virus (SMV), soybean vein necrosis virus, soybean dwarf virus, bean pod mottle virus (BPMV) and bacteria include bacterial blight (*Pseudomonas syringae* pv. *glycinea*) and bacterial pustule (*Xanthomonas campestris* pv. *glycines*). SMV, blight and pustule are some of the most devasting and common diseases in soybean which cause a heavy loss in yield and production. The co-evolution of both avirulence and resistance (Avr – R genes) have led to the rapid emergence of resistance in susceptible individuals and classical breeding programs are not sufficient to overcome this hurdle. India is based on agriculture for both economy and survival and the outbreak of diseases may decline growth, development and quality of crops and weakens the nation’s economy and food security. Genome editing is a powerful method which has widen the field of plant biology and biotechnology making it possible for targeted gene modifications. Crop improvement using editing techniques has immensely increased the scope by enhancing breeding and developing new resistant varieties against diseases for sustainable agricultural practices. The concept of genetic breeding will provide effective strategies and overcome the limitations of classical breeding.

SESSION 5

Diagnostics and genetic variability

Diagnostics, genetic variability, sensor based detection viz., nano-sensors, e-nose

Keynote Lectures

KN(S5)/01: Advances in genomics and diagnostics of fungal plant pathogens and their management

Rashmi Aggarwal*
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: rashmi.aggarwal2@gmail.com*

During the Genomics era, a need is felt to increase crop production and productivity using genomics led modern tools and techniques particularly in wheat and rice as both crops are export oriented. In this endeavor, constant research efforts to counter emergence of earlier less known diseases and new races/pathotypes of existing pathogens, which are potential threat to production, are needed. Monitoring plant health and detecting the pathogen early are essential to reduce the disease spread, and facilitate effective management practices. DNA-based methods now provide essential tools for accurate plant disease diagnosis. Recently, effective amplification platforms, probe development, various quantitative PCR, DNA barcoding and RNA-Seq-based next-generation sequencing have revolutionized the research in fungal detection field, and differentiation area. Hence, genome sequence led diagnosis and management strategies have a major role to curtail losses due to the diseases. This development has also rapidly increased our understanding of the molecular mechanisms underlying 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 data has helped genomics-based approaches to improve disease resistance in crops. The genomes of more than1100 fungal species are available in the public domain and plant pathogenic fungi comprised the largest category (35.5 %). Plant disease diagnosis and pathogen detection are fundamental components of successful agriculture. Management practices in crop health and food safety are critically linked with detection of plant pathogens at the early stages of the diseases. At present specific, fast and sensitive technologies which should be simple and grower friendly are very valuable, requiring no specialized staff for diagnosis of a disease in the field. This is essentially required in the recent scenario of changing climatic conditions, which is causing the appearance of a pathogen in areas where years ago they were unexpected. Biosensors based on highly selective bio-recognition elements are being developed as new tools for the early identification of crop diseases. Some of the promising techniques that can be applied to in-field molecular detection of plant pathogens and how these techniques can change the way farmers and pathologists are diagnosing plant diseases further impacts the management. Loop mediated isothermal amplification and recombinase polymerase amplification, are already being successfully used for routine diagnosis. However, most technologies still need validation in the field, where they have a promising future for in-field diagnosis when combined with simple DNA extraction methods, reagent stabilization techniques and their integration into portable devices. Further, with the increasing computational power, areas such as machine learning, image processing, deep learning, etc are also potential tools for plant disease diagnosis. Finally, molecular diagnostic techniques used in plant disease diagnostic clinics need to be robust, reliable, inexpensive and easy to be used that they can compete with, and complement traditional techniques. In this presentation, applications of these techniques for accurate identification and quantification of plant diseases /pathogens and challenges for management shall be discussed.

KN(S5)/02: Recent developments in plant disease diagnostics using laboratory and artificial intelligence dependant IoT methods

R. Selvarajan*

ICAR-National Research Centre for Banana, Tiruchirapalli – 620102, Tamil Nadu, India

**Email: selvarajan.r@icar.gov.in; selvarajanr@gmail.com*

Agriculture plays a vital role in the economy of developing countries and protecting the crop health helps in achieving the food security. The production and productivity of field and horticultural crops are highly affected by the biotic and abiotic factors. Among the biotic factors, plant diseases cause severe threats by devastating crop production in every region of the world and annually, FAO estimated that the loss due to plant diseases is around $220 billion. Effective and efficient diagnostic tools for timely determination of plant diseases become essential to deploy management measures to assure the sustainability and food security. Plant pathogen detection is heavily dependent on a wide variety of molecular assays and immunological dependent methods. Recently CRISPR-Cas based on-site detection also been applied the detection of human and plant pathogens. Both laboratories based and on-site diagnostics are applied for effective management of the plant diseases. A more recent technology is the detection of volatile organic compounds (VOCs) released from plants, and cost-effective smartphone-based VOC fingerprinting platform that allows non-invasive diagnosis of plant diseases. Technological advancement in the field of information and communication technologies (ICT) made possible to develop IoT enabled devices to identify the plant diseases more precisely. Machine or deep learning tools are exploited for developing the detection models and are deployed in a smartphone for on-site disease identification. Researchers have applied deep convolutional neural networks and deep transfer learning for digital mobile app-based disease detection in banana and other crops. Many plant diseases are influenced by weather parameters and modelling is necessary to predict and forecast the diseases and develop an IoT enabled decision support systems. Both image and non-image-based sensor methods are reported for fungal diseases in rice and other crops. In this lead talk both laboratory dependant methods of detection of plant pathogens, on-site detection and IoT based methods of plant disease diagnostics are dealt in detail.

Oral Presentations

OP(S5)/01: Multilocus sequence typing and simple sequence repeats analysis in *Tilletia Indica* isolates inciting Karnal bunt of wheat

Malkhan Singh Gurjar[1]*, Shekhar Jain[2], Prachi Jain[1], Shweta Aggarwal[1], Jagmohan Singh[1], Sangeeta Gupta[1], Tej Pratap Jitender Kumar[1], Naresh Kumar[3], Mahender Singh Saharan[1] and Rashmi Aggarwal[1]

[1]Fungal Molecular Biology Laboratory, Division of Plant Pathology, [3]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India

[2]Department of Biotechnology, Mandsaur University, Mandsaur - 458001, Madhya Pradesh, India

**Email: malkhan_iari@yahoo.com*

Karnal bunt of wheat is an internationally quarantined disease affecting the trade; quality and production of wheat. The present study was undertaken to decipher genetic variation in Indian isolates of *Tilletia indica* collected from different locations. Seven multilocus sequence fragments were selected to differentiate and characterize these *T. indica* isolates. A phylogenetic tree constructed based on pooled sequences of actin-related protein 2 (ARP2), â-tubulin (TUB), eukaryotic translation initiation factor 3 subunit A (EIF3A), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), histone 2B (H2B), phosphoglycerate kinase (PGK) and serine/threonine-protein kinase (STPK) showed that isolate KB-11 (Kaithal, Haryana) was highly conserved as it was located in cluster 1 having maximum sequence similarity with the reference strain. Other isolates in cluster 1 included KB-16 and KB-17 both from Uttar Pradesh and KB-19 from Haryana. Isolates KB-07 (Jind, Haryana) and KB-18 (Mujaffar Nagar, Uttar Pradesh) were the most diverse and grouped in a subgroup of cluster 2. Maximum numbers of SNPs (675) were in the PGK gene across the

T. indica isolates. The minimum numbers of SNPs (67) were in KB-11 (Kaithal, Haryana) while the maximum number of SNPs (165) was identified in KB-18 followed by 164 SNPs in KB-14. KB-18 isolate was found to be the most diverse amongst all *T. indica* isolates. The whole-genome of *Tilletia indica* has been sequenced using Illumina and PacBio platforms. So far, SSR markers have not been developed for *T. indica* population. A total of 5,772 simple sequence repeat loci were identified in the *T. indica* genome assembly. Majority SSRs were tri-nucleotide (42 % of total SSRs). Forty (40) microsatellite markers (SSRs) were developed for *Tilletia indica* to analyze the population structure of 20 isolates from the northwestern plain zone of India. The number of alleles ranged from 2 to 6 in *T. indica* isolates. The highest number of alleles was 6 in TISSR1 and TISSR34 markers. The frequency of 2 loci was very high in the *TI* population. The polymorphic information value content (PIC) values ranged from 0.20 to 0.81 with an average of 0.51. The highest PIC value was 0.81 in TISSR34 followed by TISSR1 (0.75). This first study on multilocus sequence typing (MLST) and SSR analysis revealed that the population of *T. indica* was highly diverse. This genetic information will be helpful in understanding the epidemiology and in devising management strategies for Karnal bunt disease.

OP(S5)/02: Morpho-molecular characterization of *Alternaria alternata* associated with the blight of linseed

Yaswant kumar Pankaj, M.S. Saharan and **Lakshman Prasad***
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: laxmanprasad25@yahoo.com*

Linseed (*Linum usitatissimum* L.) is an *rabi* oilseed crop and a major source of oil and fiber. Alternaria blight is major biotic factor limiting crop yield in hot and humid environments. Present study is the morpho-molecular characterization of linseed blight causing fungi. The infected plant samples were collected and fungi were isolated. Preliminary identification was done on the basis of colony and conidial morphology using compound microscope and Molecular characterization of the same fungus was done by grown onto the PDB for mass growth till 07 days' incubation at 25±20C. Mycelial mat were collected for DNA extraction using CTAB method and extracted DNA was amplified with ITS 1 and ITS 4 primers in PCR machine. Results indicates the visual appearance of colony was olive-green to black in color with circular in shape. Conidial characteristics were olivaceous to dark brown, produced in simple or branched chains of 2-7, and vary in shape and dimensions (average 37 x 13 µm, including the beak when present). Amplified PCR product was found of 543 base pair. Such amplified product was eluted from the agarose gel and sequencing was carried out with both the primers, ITS 1 and ITS 4. Both sequences were blasted on NCBI to validate and found that ITS 1 and ITS 4 accounted for 93% and 90% of query coverage from the blast search result, respectively, which showed higher similarity of resulted sequence with the *Alternaria alternata* (MW487251). Hence, morphological and molecular identification reveal similar patterns of *A. alternata* in Linseed.

OP(S5)/03: Association of *F. oxysporum* with basal rot of garlic and effect of different soil temperature and moisture levels on its development

Meenu Gupta*, Sonakshi, Arti Shukla and HR Sharma
Department of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India
**Email: meenugupta1@gmail.com*

Garlic (*Allium sativum* L.) is the most widely cultivated *Allium* species after onion belonging to the family Amaryllidaceae. During its cultivation, garlic crop is attacked by a number of fungal, bacterial and viral diseases of which basal rot of garlic has been found to be predominant and destructive. During the survey in Solan and Sirmour districts, maximum disease incidence (58.64%) of basal rot of garlic was observed at Nauhradhar followed by Batyuri (54.49%) and Thadi (52.48%) in Sirmour district. Symptoms of the disease were observed on above as well as underground plant parts of garlic. Initial symptoms appeared as yellowing of leaves starting from tip which progressed downward and plant showed wilting symptoms. Affected plants could be easily uprooted and infected bulbs showed rotting symptoms with brown flattened roots. Under severe conditions, yellow patches of plants were seen in the field. The associated fungi were isolated in pure culture on PDA and based on cultural and morphological characters, these were identified as *F. oxysporum*. Presence of macro-conidia, micro-conidia and chlamydospores was recorded. Its identity was further confirmed using molecular characterization. Pathogenicity tests revealed that soil inoculation with mass culture on sand:corn media was better in disease development over conidial suspension used as inoculum for soil inoculation and pre-planting clove inoculation. Epidemiological studies of disease revealed that disease incidence was maximum at 30oC soil temperature and 45 per cent of soil moisture level under *in vivo* conditions.

OP(S5)/04: Characterization of *Ralstonia solanacearum* isolated from coastal area of Odisha infecting solanaceous crops

G. Biswal[1]*, D. Singh[2], S. Sahoo[1], A. Nayak[1] and K. Sinha[1]
[1]*College of Agriculture, Odisha University of Agriculture & Technology, Bhubaneswar – 751003, Odisha, India*
[2]*Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, NewDelhi – 110012, India*
**Email: gayatribiswal1965@gmail.com*

The bacterial isolates were collected from wilted brinjal, chilli and tomato plants from Bhubaneswar and adjoining coastal regions were undergone different tests for their identification and characterization. These isolates were rod shaped, gram negative and presence of polar flagella. The bacterial isolate collected from wilted brinjal, chilli and tomato plant were virulent in nature to cause disease in respective healthy plants. Carbohydrate utilization tests of isolates showed positive reactions towards glucose, maltose, sucrose, trehalose, mannitol, fructose, galactose, dextrose, arabinose and sorbitol but they showed negative reaction against lactose, raffinose, melibiose, L-Arabinose, mannose, adonitol, erythritol, alfa-methyl-D-glucoside, lactose, raffinose, adonitol, erythriol, alfa-methyl-D – mannoxide. Among different biochemical tests, the isolates showed positive response to citrate utilization, Voges prosker and Methyl red tests and showed negative reaction to indole production, gelatine liquefaction, H2S production, phenylalanine deamination, urease reduction, lysine and orinthine decarboxylation tests. The physiological studies, *i.e.* thermal death point, thermal death time and effect of pH on growth of the isolates were done and 600 C was found to be the thermal death point of the isolates. Thermal death time was recorded as 8 minutes at 60o C and the pH range was 4 to10. All these studies conducted showed that causal organism for wilting in brinjal, chilli and tomato was *Ralstonia solanacearum.*

OP(S5)/05: ZYMV-Trini: An emerging genotype of Zucchini yellow mosaic virus causing severe mosaic in cucurbits in Trinidad and Tobago

Chinnaraja Chinnadurai*
The University of the West Indies, Department of Life Sciences, Faculty of Science and Technology, St Augustine,
0 N/A,Trinidad And Tobago
**Email: cchinnaraja86@gmail.com*

The newly emerging potyviruses such as Zucchini yellow mosaic virus (ZYMV) and Squash mosaic virus (SqMV) causing severe mosaic in cucurbits were identified in Trinidad. Further studies were carried out for the molecular characterization of the full-length genome of the Zucchini yellow mosaic virus. In this study, four Zucchini yellow mosaic virus (ZYMV) isolates infecting pumpkin in Trinidad and Tobago were characterized by complete genome sequencing for the first time. Phylogenetic analyses of the isolates showed variability of 5.9–6.0 % nt and 7.7-7.9 % aa sequences with the most closely related isolates NAT and AG (Israel) and SE04T (Slovakia). Based on the variations in the complete genome as well as gene sequences, a new genotype designated ZYMV-Trini is proposed for these isolates. Among the gene sequences of ZYMV-Trini isolates, maximum variations were noticed in the HC-Pro gene with 20.8 % aa sequence divergence from their closest relatives whereas the least variations were with the P1 (2.0 to 2.3 % aa divergence) and CP (2.9 % aa divergence) genes. This study also proved that transmission of ZYMV can also occur through seeds (2 %), but this was less common than transmission via the aphid species *Aphis gossypii*. The progression of ZYMV in pumpkin seedlings was quantified by RT-qPCR which showed a rapid surge in viral load after 37 days. From the recombination analyses, it could be concluded that isolates SE04T from Slovakia, NAT from Israel and AP Gherkin from India have major contributions in the genome architecture of ZYMV-Trini isolates.

OP(S5)/06: Intra-regional population biology of *Xanthomonas oryzae* pv. *oryzae* causing bacterial blight of rice in the Andaman Islands, India: revelation by pathotyping and Multilocus Sequence Typing (MLST)

Sakthivel K.[1]*, Kumar A.[2], Gautam R.K.[1], Manigundan K.[1], Laha G.S.[3], Velazhahan R.[4], Reena Singh[1] and Inderjit Singh Yadav[5]

[1]Division of Field Crop Improvement and Protection, ICAR-Central Island Agricultural Research Institute, Port Blair - 744 101, Andaman and Nicobar Islands, India
[2]Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
[3]Division of Crop Protection, ICAR- Indian Institute of Rice Research, Hyderabad, Telangana - 500030, India
[4]Center for Plant Protection Studies, Tamil Nadu Agricultural University, Coimbatore - 644101, Tamil Nadu, India
[5]School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana – 141004, Punjab, India
**Email: veluars@yahoo.in*

A total of 27 yellow pigmented bacterial isolates inciting rice bacterial blight from diverse rice fields of Andaman Islands were characterized. All isolates could incite blight on susceptible-rice cultivar, C14-8. Phenotypic, pathogenic traits and 16S rRNA sequences revealed their identity as *Xanthomonas oryzae* pv. *oryzae*. Virulence-profiling on standard differentials indicated prevalence of seven pathotypes of *X. oryzae* pv. *oryzae* on the Island. Pathotypes-VI and -VII were highly-virulent whereas the Pathotype-I was less-virulent. Multi-locus sequence typing (MLST) based on nucleotide sequence polymorphism in nine housekeeping genes*dna*K; *fyu*A;*gyr*B (two loci): *rpo*D; *fus*A; *gap*A; *glt*A; and *lep*Aclustered 27 isolates into 17 sequence types (STs) segregated into two Clonal-Complexes (CC).While CC-I comprised of isolates from Andaman Island, the CC-II is mixture of isolates representing mainland India and Andaman Island. Genetic and virulence analysis of *X. oryzae* pv. *oryzae* in Andaman revealed introduction and host mediated regional diversification and local adaptation of *X oryzae* pv. *oryzae*. The study calls for need of multi-gene pyramiding for durable disease resistance and establishing stringent quarantine measures for safeguarding island agricultural practices in the future.

OP(S5)/07: Development of one step reverse transcriptase-recombinase polymerase amplification method for the detection of potato virus S in potato leaves and tubers

Ravinder Kumar*, Priyanka Kaundal, Rahul Kumar Tiwari, Sundaresha S., Kailash C. Naga, Sanjeev Sharma and Vinay Sagar

ICAR-Central Potato Research Institute, Shimla - 171001, Himachal Pradesh, India
**Email: chauhanravinder97@gmail.com*

Potato virus S (PVS), belonging to the order *Tymovirales*, family *Betaflexiviridae*, genus *Carlavirus* is the most common viruses affecting potatoes worldwide. Currently, PVS is detected by enzyme-linked immunosorbent assays (ELISA) and reverse transcription polymerase chain reaction (RT-PCR) assays. ELISA is time-consuming and RT-PCR requires skilled manpower and complex procedures of RNA isolation as well as a thermal cycler. To overcome

these difficulties, a one step reverse transcription- recombinase polymerase amplification (RT-RPA) was developed to detect potato virus S (PVS) in leaves and tubers of potato using paper based RNA extract as template. Three primer pairs were designed from coat protein gene of the virus, one primer pair gave specific and sharp amplification with RNA isolated from infected plant but not with healthy plant. A magnesium acetate concentration of 14 mM, 30 min of incubation time and a temperature of 37–420C was found optimum for detection of the PVS and there was no cross-reactivity with other common potato viruses. The one step RT-RPA could detect the virus up to 10-5 dilution of the total RNA, while regular RT-PCR could detect the virus up to 10-3 dilution indicating that RPA is 100 times more sensitive than RT-PCR. RT-RPA was further simplified using paper based extracted RNA as template which could detect the virus up to 10-4 dilution. RT-RPA assays were validated using field samples of potato representing different varieties and geographical regions. Our study showed that newly developed one step RT-RPA assay is rapid, sensitive, and reliable method for detection of PVS in leaves and tubers of potato and can be utilized as an effective technique in virus free seed potato certification processes as a substitute to RT-PCR.

OP(S5)/08: Deciphering the morphological and genetical variability among the isolates of *Fusarium oxysporum* f.sp. *lentis* causing wilt of lentil

Arya A.[1]*, Kushwaha K.P.S.[2] and Bohra Y.[3]
[1]*FASC, SGT University, Gurugram - 122505, Haryana, India*
[2]*Department of Plant Pathology, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakhand, India*
[3]*College of Agriculture, Punjab Agriculture University, Ludhiana - 141004, Punjab, India*
**Email: anshularyapp.23@gmail.com*

Lentil wilt is caused by the fungal pathogen *Fusarium oxysporum* f.sp. *lentis* which is the imperfect stage of the fungi, however it shows the great diversity in the morphology as well as at genetical level. The current study was conducted to explore the genetical as well as morphological diversity among the twenty two isolates of the same pathogen collected from lentil growing areas of Uttarakhand and Uttar Pradesh. The wilt pathogen is a soil and seed borne in nature and has lentil as its only host even though variability among the pathogen isolates has been observed due to the several factors affecting its growth, reproduction and survival at different environmental conditions. The present study is conducted to study the morphological and genetical variability among the twenty two isolates of the pathogen collected from different lentil growing areas of Uttarakhand and Uttar Pradesh. The isolates showed huge difference in the cultural growth i.e. difference in the pigmentation (purple, Pink and yellow etc.), size (1.47 X 1.05 µm to 20.37 X1.67 µm) of macro and microconidia and also on the growth pattern (fluffy and appressed). The diversity among the isolates were studied using ISSR and SSR primers.The results obtained from the ISSR (PIC ranged from 0.65 to 0.93) and SSR primer (Jaccard's similarity coefficient ranged from 0.41 to 1.0) showed versatility in the genome of the different isolates of the pathogen. The collected data also revealed the huge diversity among the population of the pathogen collected from two different states i.e. Uttarakhand and Uttar Pradesh. Thus the present study revealed the morphological and genetical variability existing among the different isolates of the pathogen, moreover, it's impact on selection and discovery of different management strategies for the disease in future.

Poster Presentations

PP(S5)/01: Transmission efficiency of a peanut witches' broom phytoplasma strain associated with sesame phyllody by dodder, grafting and leafhoppers

Hemavati Ranbennur[1]*, Kirti Rawat[1], Ashutosh Rao[2], Celia Chelam[2], Meshram N.[3] and G.P. Rao[1]
[1]Division of Plant Pathology, [3]Division of Entomology, ICAR-Indian Agricultural Research Institute,
New Delhi - 110012, India
[2]ICAR-National Bureau of Plant Genetic Resources, New Delhi - 110012, India
**Email: hemaiari@gmail.com*

During survey of sesame crops in August-December 2020, severe incidence of sesame phyllody and witches' broom symptoms were recorded in twenty accessions with incidence upto 60 percent. The symptomatic samples were processed for DNA extraction and PCR assays with P1/P7 and R16F2n/R16Rn primer pairs. Peanut witches' broom phytoplasma (PWBP) strain (16SrII-D) was identified and confirmed associated with all the symptomatic sesame accessions employing 16S rRNA sequence analysis comparison. Two major leaf hopper species *Orosius albicintus* and *Hishimonus phycitis* were identified feeding in sesame field. Both the leaf hopper species were found efficient in successful transmission of PWBP from sesame to brinjal and sesame to sesame plants. Various transmission methods were tested to check the transmission efficiency of phytoplasma through seed, grafting (wedge, patch, leaf disc and plugging), dodder and insects. The transmission studies revealed that PWBP strain was not seed transmitted. Our results confirmed that the sesame PWBP strain was efficiently transmitted by dodder (90%), insect (65%), and by grafting methods (wedge and leaf disc grafting)(66.67%). These methods will help in maintaining the phytoplasma strain in glasshouse and suitably used for indexing of sesame germplasm accessions.

PP(S5)/02: Morphological and biochemical characterization of *Dickeya zeae* a causal agent of bacterial stalk rot disease in maize

J. Rajender*, Dinesh Singh and Lokesh babu
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: jraj.ra0680@gmail.com*

Maize bacterial stalk rot caused by *Dickeya zeae* is becoming a destructive disease in some maize growing regions of India. Disease may reduce up to 98.8% crop yield and more prevalent in the rainy season. The localized occurrence of the bacterial stalk rot of maize was noticed in recent years and causes significant losses of the yield during the rainy season under specific condition of high temperature and dry humidity. Even though frequent occurrence of this disease in major maize growing areas, very few morphological and biochemical studies were reported until. In order to identify stalk rot bacterial strains morphology, The pathogen was isolated from infected maize plants on a semi-selective CVP (Crystal Violet Pectate) medium followed by morphological biochemical and molecular assays were conducted. The isolated bacterial colonies were whitish grey, shiny, non-mucoid, round with irregular margins and a characteristic raised center on nutrient agar medium whereas, on PDA medium produced fried egg colonies. On Logan's medium all strains of bacteria were produced intensive red 2 mm colonies. The strains were Gram and oxidase-negative, non-fluorescent, facultative anaerobic gelatine, catalase and indole positive. All strains were grown at 37 °C and caused potato tuber rot while variable growth was observed in medium containing 5% NaCl. The phenotypical characterization and amplification of the specific 420-bp fragment in PCR assay revealed that the isolated strains belong to genus *Dickeya zeae*.

PP(S5)/03: Specific detection of *Fusarium fujikuroi* causing bakanae of rice through recombinase polymerase amplification

Prashantha S.T., **Bashyal B.M.*** Sangeeta Gupta and Rashmi Aggarwal
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: bishnumayabashyal@gmail.com*

Bakanae of rice is a major devastating disease caused by *Fusarium fujikuroi.* The disease causes a significant yield loss in major rice growing parts of the country. Symptoms of the disease include yellowish leaves, elongation, rotting and adventitious roots formation. These visible symptoms are helpful in identification of the pathogen associated with the disease. Several workers attempted to identify the pathogen based on PCR, real time PCR, LAMP techniques. But a rapid point of care diagnostics to identify the pathogen in rice seed/infected plants is not available. The isothermal amplification techniques like RPA, LAMP are useful in development of field based detection of the pathogen. These techniques can be integrated with lateral flow devices for rapid identification in field samples. The unique secondary metabolite gene cluster present in *Fusarium fujikuroi* has been utilized in this study to amplify the NRPS31 in *Fusarium fujikuroi* isolates. The gene sequence was downloaded from NCBI database and identified a unique region through in silico analysis. Five set of RPA primers were designed to amplify the NRPS31 gene. Among them, only one manually designed primer amplified the target gene. The target gene was amplified only in *Fusarium fujikuroi* and did not amplify in other sps of *Fusarium* such as *Fusarium proliferatum, Fusarium verticillioides, Fusarium thapsinum, Fusarium andiyazi, Fusarium mangiferae* and *Fusarium oxysporum.* The amplification produced a 280bp product in *Fusarium fujikuroi* isolates. The technique described here is specific, sensitive and useful in developing rapid diagnostic tools.

PP(S5)/04: Genetic variability of *Sugarcane bacilliform virus* causing leaf fleck of sugarcane in India

Janiga Gopinath, K. Nithya and **R. Viswanathan***
ICAR-Sugarcane Breeding Institute, Coimbatore – 641007, Tamil Nadu, India
**Email: rasaviswanathan@yahoo.co.in*

Sugarcane bacilliform virus (SCBV) (Genus: *Badnavirus*, Family: *Caulimoviridae*), a plant pararetrovirus which causes leaf fleck in sugarcane considered as economically important pathogen, limiting the exchange of its germplasm worldwide. To explore the prevalence and genealogies of SCBV from germplasm and cultivated varieties, 358 leaf fleck affected samples from cultivars and germplasm were collected and subjected to PCR to amplify 726bp reverse transcriptase/ribonuclease H region of ORF3. 104 PCR amplicons were sequenced and the contigs derived from each fragment was assembled using CAP3 contig assembly and variability analysis was performed in MEGA X using the maximum likelihood method with tamura-Nei model. Phylogenetic analyses of the sequences revealed formation of three major groups, in which CBJ 46 alone formed a separate group with 40% similarity to the remaining isolates. The sequences had shown 85-99% similarity with other SCBV partial sequences (ORF 3 region) from NCBI genbank. Overall, SCBV-BT and SCBV-BRU genotypes are found to widely present in India and existence of newer genotypes viz. CHN 1, CHN 2 from China, SCBV-IM and SCBV MO from Australia were identified from India for the first time. Even though the isolate CBJ 46 showed >80% similarity to ORF 3 of SCBV YN –YZ 20602 from China, in phylogenetic analysis it has formed a clear distinct separate group which indicates the possible emergence of new SCBV variant. Huge phylogenetic diversity existing among the SCBV isolates throws light on the variation within the SCBV species in India and their variation from the other genera of Badna viruses. Thus the present study helps to understand the SCBV population structure in India and will address the spread of new genetic variants from other countries through germplasm exchange.

PP(S5)/05: Damping-off of small millets caused by *Sclerotium* sp.

Rajesha G.*, Das I.K., Sunil Kumar Sharma, Ganapathy K.N., Amasiddha B. and Vilas A. Tonapi
ICAR-Indian Institute of Millet Research, Rajendranagar, Hyderabad - 500030, Telangana, India
**Email: rajesha@millets.res.in*

Small millets are resurging as important food, feed, fuel and fodder crops cultivating in India. The seedling of Barnyard millet, Little millet and Finger millets showing the symptoms of damping-off and seedling rot caused by *Sclerotium* sp. was observed during rabi season of 2019 and 2020 at ICAR-IIMR Research Farm, Hyderabad. The incidence was observed after 15 days of sowing in all the millets. Initially the leaves were pale yellow and dried from bottom to top. The discoloration and rotting of young roots turned into root rot was observed in infected seedlings. Later the presence of white mycelial growth and formation of sclerotia was also observed led to wilting and premature death of seedlings under field condition. The incidence of 21%, 17% and 14% was recorded in Barnyard millet, Little millet and Finger millet respectively under field condition. The disease incidence under field condition was observed upto 32 days after sowing in barnyard and little millet whereas upto 38 days in Finger millet. All the three isolates of small millets produced the white mycelia and formation of sclerotia on PDA plates. The size of sclerotia were small (0.5 to 1.5 mm) and pale brown in colour covered with thin outer layer. Infection of *Sclerotium* was recorded in small millets and reporting as a first report in India in millets.

PP(S5)/06: Identification and characterisation of peanut witches' broom Phytoplasma associated with witches' broom disease of bamboo

R. Manish* and G.P. Rao
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: manishnivas9@gmail.com*

Bamboos, called as poor man's timber has multifaceted uses from construction to culinary purposes. Suspected phytoplasma like symptoms of witches' broom and leaf yellows were observed in the bamboo species, *Dendrocalamus strictus*, in Karnataka and Delhi. Symptomatic samples were collected and the whole genomic DNA was extracted. Preliminary test for detection of phytoplasma was conducted by PCR amplification of the phytoplasma specific universal primer pairs P1/P7 followed by nested primer pair R16mF2/R16mR1. The expected amplicons of 1.4 kb were obtained from all the symptomatic samples and were sequenced. Pairwise sequence comparison of the *16S rRNA* gene sequences showed 100% similarity with that of peanut witches' broom (16SrII-D) phytoplasma strain. Phylogenetic analysis by neighbour-joining method based on *16S rRNA* gene sequences clustered the bamboo phytoplasma strains from Karnataka and Delhi with strains of 16SrII-D subgroup. Virtual RFLP conducted using *i*PhyClassifier online tool with 17 restriction enzymes confirmed the identity of 16SrII-D subgroup of phytoplasma associated with the bamboo samples. Further validation is in progress using other housekeeping genes (*rp* operon, *secY* gene, *tuf* gene) and could be used for finer classification of the phytoplasma strains.

PP(S5)/07: Studies on *in vitro* growth parameters affecting *Botryodiplodia theobromae* (Pat.) Griff and Maubl. causing mango dieback and gummosis

Shalini Verma*, Ankita Thakur and H.R. Gautam
Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni Solan -173230, Himachal Pradesh, India
**Email: shaleiniverma@gmail.com*

Mango (*Mangifera indica*) is the most important fruit of India. The fruit suffers from several diseases due to various biotic as well as abiotic stresses. However, the mango dieback and gummosis (*Botryodiplodia theobromae*)

is an important disease which causes mango decline and post-harvest losses. The present study was conducted in May-September 2019 at the Fruit Pathology Laboratory of Department of Plant Pathology, Dr YS Parmar University of Horticulture and Forestry, Solan, HP. The fungus *B. theobromae* was isolated from infected shoots and maintained on PDA medium. The growth of the fungus was assessed *in-vitro* under different temperature, pH and light conditions. The culture was grown between 0o to 40oC. However, maximum mean mycelial growth (83.40mm) was observed at 40oC. Whereas, maximum mean growth rate of 0.75mm/h was observed at 15oC. The temperature of 30oC exhibited good sporulation and pycnidia production. Significant differences were observed for various pH levels in our study. The pH 7.0 showed maximum mean diametric growth of 32.20mm, whereas, pH 7.0 and 7.5 showed maximum mean growth rate of 0.74mm/h and 0.70mm/h respectively. The pH 6.5 showed good pycnidia production. There was no significant effect of duration of light periods on the fungus growth, sporulation and pycnidia production, however, maximum mean diametric growth was recorded on continuous light exposure to the fungus (81.20 mm) followed by 24 hours light and 24 hours dark (81.10 mm), 16 hours light and 48 hours dark (80.85 mm) and 8 hours light and 16 hours dark (80.30 mm).

PP(S5)/08: Occurrence of spindle dry rot disease in coconut seedlings

Prathibha V.H.*
ICAR-Central Plantation Crops Research Institute Kasaragod – 671124, Kerala, India
**Emal: prathibhacpcri@gmail.com*

Coconut (*Cocos nucifera* L.) is an important plantation crop and popularly known as 'Kalpavriksha'. Even though coconut palm is hardy and adaptable to varied climatic conditions, it is counteracted by many pests and diseases. Recently, severe spindle dry rot type of disease has been observed in two to three years old coconut seedlings in Coimbatore, Pollachi and Tirupur districts of Tamil Nadu during 2019 and 2020. Symptoms were characterized as wilting of spindle leaf followed by drying and dark brown to black color discoloration near the base of the spindle. Disease affected samples were collected and isolated the pathogen from all the infected parts. The associated pathogen was characterized using morphological and molecular traits. Eight fungal isolates were consistently isolated from the infected samples. These were characterized as whitish grey color colonies and later turn to dark grey with dense aerial mycelium. Ellipsoidal shaped, unicellular hyaline conidia raised from cylindrical shaped conidiogenous cells. Mature conidia were brown in color (19-25×10-17ìm) with single septum and longitudinal striations. Identification was confirmed by sequencing internal transcribed spacer rDNA region and blast analysis of sequences showed 99% identity to *Lasiodiplodia theobromae* (CBS164.96). Based on morphological and molecular characterization, pathogen associated with dry spindle rot disease of coconut seedlings was identified as *Lasiodiplodia theobromae* Pat. In Pathogenecity test recorded typical symptoms of spindle dry rot on twelve days after incubation. To our knowledge, this is the first report of *L. theobromae* causing spindle dry rot disease of coconut seedlings. The disease is under check by treatment with Hexaconazole 5EC.

PP(S5)/09: Significance of biological and serological studies to unravel the prevalence of tomato yellow leaf curl virus in Himachal Pradesh

Shalaka Ahale* and Anil Handa
Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India
**Email: shalakaahale135@gmail.com*

Begomoviruses are known to cause huge economic losses in Solanaceous vegetable crops particularly tomato, capsicum and potato. Tomato is one of the most important vegetable crops of hill state of the Himachal Pradesh and tomato yellow leaf curl virus was observed to be associated with tomato. Extensive surveys were conducted during cropping seasons of 2020-2021 in major tomato growing areas of the state. It was observed that maximum diseases incidence of TYLCV was recorded in Una district followed by Solan and Sirmaur districts. Based on the symptoms isolates were collected from different locations. Typical symptoms observed on infected plants were curling, yellowing of leaves from margins, reduction in leaf size resulting in shoe-stringing. Infected plants were drastically stunted and were easily recognizable in the field. Host range studies were conducted using mechanical sap transmission on different hosts belonging to *Solanaceae*, *Amaranthaceae* and *Chenopodiaceae* families, besides different indicator hosts namely *Chenopodium amaranticolor, Chenopodium quinoa, Capsicum annuum, Nicotiana tabacum, Dhatura stramonium, Amaranthus viridis.* However, the virus was not transmissible to any of the indicator hosts and other plants inoculated for establishing the host range. DAS-ELISA further confirmed that TYLCV was not transmitted to these hosts as indicated by low optical density values recorded at 405 nm.

PP(S5)/10: A duplex PCR for the simultaneous detection of CMV and PVY in Bhut Jolokia (*Capsicum chinenese* Jacq)

Ch Inao khaba* and P.D. Nath
Department of Plant Pathology, Assam Agricultural University, Jorhat – 785013, Assam, India
**Email: inaokhaba11@gmail.com*

The major growing region of Bhut Jolokia (Solanaceae) is North Eastern Region (NER) of India. The chemical compound (Capsaicin) is used to help relieve of pain known as neuralgia. Approximately 76 viruses have been reported in pepper. Viral diseases had been reported as a major threat to sustainable and productive agriculture worldwide. The production of Bhut Jolokia is drastically reduced due to viral disease complex (more than two virus). Among them CMV and PVY were the major RNA viruses of Bhut Jolokia in NER of India and other Asian countries. Rapid, Reliable, Specific and Sensitive diagnostic methods are very much needed for integrated disease management. Simplex and duplex polymerase chain reaction (PCR) methods were developed by designing a specific primer. The PCRs targeted CP gene of CMV (633bp) and PVY (386bp). Both simplex and duplex PCRs detected the CP gene of CMV and PVY in a 20ìL PCR reaction system. Sanger sequencing was done for accurate confirmation. The confirmed nucleotide sequences of CMV and PVY had been submitted to gene bank (Accession: MW597406, MW597407) respectively. The duplex PCR method provide us time-saving and convenient, and may prove to be an invaluable tool for molecular detection and epidemiological investigation of CMV and PVY in endemic area.

PP(S5)/11: *Candidatus* phytoplasma trifolii: A 16Sr VI group of phytoplasma posing threat to brinjal cultivation in Assam

Dibya Sree Dutta*, Manoj Kumar Kalita and Palash Deb Nath
Department of Plant Pathology, Assam Agricultural University, Jorhat – 785013, Assam, India
**Email: dibya.sreedutta01@gmail.com*

During 2018 to 2020, roving survey was conducted in seven major brinjal growing districts of Assam namely, Biswanath, Darrang, Golaghat, Jorhat, Nagaon, Sibsagar and Sonitpur to study the incidence, natural transmission, yield loss assessment and molecular characterization of brinjal little leaf disease (BLL). The disease was prevalent in all the fields surveyed with disease incidence varying from 3.62 to 23.63 per cent. Among the four predominant leafhopper species *viz*., *Amrasca biguttula biguttula* (Ishida), *Exitianus indicus* (Dist.), *Hishimonus phycitis* (Dist.), *Nephotettix nigropictus* (Stal) collected from the farmer's field, only *Hishimonus phycitis* (Dist.), could successfully transmit the pathogen from diseased to healthy brinjal plants. Total genomic DNA extracted from symptomatic and asymptomatic brinjal plants collected from different districts of Assam were subjected to PCR assays using phytoplasma specific universal primers. All the symptomatic brinjal plants yielded an expected amplicon size of ~1.5 kb from PCR confirming the presence of phytoplasma. Sequencing and phylogenetic analysis has revealed the association of '*Candidatus* Phytoplasma trifolii' (16SrVI) (clover proliferation group) with the brinjal little leaf disease in Assam. The disease severely affected both the growth and yield attributing parameters of brinjal plants which varied depending upon the age of the plant during infection. Highest reduction of fruit yield (94.79%) over healthy plant was observed when plants were infected at 65-70 days after transplanting.

PP(S5)/12: Molecular detection of *cucumber mosaic virus* in a monocrop pumpkin (*Cucurbita moschata*) from Assam

Kulumanali Gogoi*, Ranima Mishra, Munmi Borah and P.D. Nath
Department of Plant Pathology, Assam Agricultural University- Jorhat – 785013, Assam, India
**Email: kulumonali.gogoi.amj19@aau.ac.in*

Pumpkin (*Cucurbita moschata*) is an important vegetable crop of *Cucurbitaceae* family which is grown worldwide. In Assam, it's mostly cultivated in the *kharif* and summer season. In the recent years, it has been observed that the pumpkin fields were infected by some yellow mosaic type diseases. The production of pumpkin is generally challenged by diseases especially those caused by viruses. Among the list of viruses infecting pumpkin, *Cucumber mosaic virus* (CMV) is a major cosmopolitan virus causing high yield losses in many crops including pumpkin. This study determines the presence or the absence of CMV in pumpkin monocrop field. The survey was conducted in various pumpkin growing areas *viz*; Golaghat, Jorhat, Karbi Anglong, Sivasagar and Biswanath Chariali districts of Assam. The symptomatology revealed reduced leaf size with mosaic and mottling in the diseased plants. These samples randomly collected and tested by double antibody sandwich- enzyme linked immunosorbent assay (DAS- ELISA). The samples showing positive results in DAS-ELISA were then indexed by Reverse transcription polymerase chain reaction (RT-PCR) method. Total RNA from virus infected plants were extracted and purified by standard TRIzol reagent method. After the RNA isolation, TaKaRa cDNA synthesis kit was used to prepare the cDNA, which was further utilized in PCR using the specific primers for CMV coat protein gene, viz., S1 Forward and S2 Reverse. The PCR assay showed a band size of 593 base pairs specific to CMV and confirmed the presence of the virus.

PP(S5)/13: Variability in yellow mosaic virus infecting blackgram from Andhra Pradesh, India

D. Vijay Kumar Naik*, B.V. Bhaskara Reddy, R. Sarada Jayalakshmi Devi, L. Prasanthi, Lakshminarayana R. Vemireddy and A. Srividhya

Regional Agricultural Research Station (ANGRAU), Tirupati – 517502, Andhra Pradesh, India
**Email: dvnaik24@gmail.com*

Yellow mosaic disease (YMD) cause severe yield loss and it is caused by yellow mosaic virus (YMV) belongs to family Geminiviridae, genus begomovirus. YMV infected blackgram samples were collected from East Godavari, Kurnool and Prakasam districts of Andhra Pradesh. The total DNA was isolated by CTAB method and used in rolling circle amplification (RCA). The RCA based full length *Mungbean yellow mosaic India virus* (MYMV) DNA-A and *Mungbean yellow mosaic virus* (MYMV) DNA-B of three isolates (East Godavari, Kurnool and Prakasam) were cloned and sequenced. The nucleotide sequence data were assembled and analyzed ORF wise using BioEdit software. Multiple nucleotide sequence of full length DNA-A of MYMIV-EG (MT312254) isolate showed >96% similarity at nucleotide and >90% at amino acid level with other MYMIV isolates in NCBI database. The complete DNA-A nucleotide sequence of MYMIV-KNL (MT350281) and MYMIV-PRA (MT300190) isolates shared >99% similarity at nucleotide and >98% at amino acid level with other MYMIV isolates. Among the three isolates, the maximum similarity was shared between the MYMIV-KNL and MYMIV-PRA isolates, hence MYMIV-KNL and MYMIV-PRA isolates treated as same variant whereas MYMIV-EG isolate treated as different variant. The MYMV-B of MYMV-EG (MT312255), MYMV-KNL (MT318837) and MYMV-PRA (MT318839) isolates shared >97% identity at nucleotide level and >96% at amino acid level with other MYMV-B isolates. DNA-B isolates cloned from East Godavari, Kurnool and Prakasam districts were partially sequenced and were closely related to MYMV-B than MYMIV-B.

PP(S5)/14: Genetic variability analysis of *Apple stem grooving virus* isolates in India

Asha Rani*, Vanita Chandel, Sunny Dhir and Narayan Rishi
Amity Institute of Virology & Immunology, Amity University Uttar Pradesh Noida – 201313, Uttar Pradesh, India
**Email: sdhir1@amity.edu*

Apple stem grooving virus (ASGV), genus *Capillovirus*,belongs to the family *Betaflexiviridae*and has single stranded RNA genome. An apple isolate of ASGV from cv. Maharaji from Srinagar (J&K) was molecularly characterized. Complete genome analysis revealed ASGV-K matched 97% to an apple isolate p12cv. Red Chief fromPalampur (H.P., India) and BR isolate cv. Gala from Brazil. It also matched 93% to HPKu2 isolate from Kullu (H.P., India). An intriguing finding was thatisolate K matched 82% to another Kashmir isolate CITH from apple cultivar Oregon spur. When ORF1 for both the isolates were aligned, high variability was observed at region VI (515-590 amino acids) and region VII (1595-1850 amino acids), already reported variable regions among *Capilloviruses*. A phylogenetic analysiscomprising of all the available 38 complete genome sequences of ASGV isolates clustered them in two groups. Isolates p12, HPKu2 and K clustered together in group B while isolate CITH belonged to group A in confirmation to the above analysis. These analyses confirm the presence of two distinct ASGV genotypes in India. The results are helpful to understand the genetic diversity of ASGV in orderto develop effective virus management strategies.

PP(S5)/15: Use of machine learning to improve plant health

Srija Chakraborty*
Indian Institute of Technology Delhi, New Delhi - 110016, India
**Email: srijaciitd@gmail.com*

Economy of our country is majorly dependent on agriculture, which contributes to the livelihood of over 50% of our population. Not just economy, everyone’s daily food consumption is affected by the fruits of the labors of our farmers. As a result, crop diseases are a huge threat to our country’s food as well as economic security. Constant monitoring of plant health and detection of plant diseases is extremely crucial factors while following sustainable agricultural practices. To prevent losses in yields of the agricultural produce, it is important to diagnose the diseases at the right time and take steps to cure them. Unfortunately, many farmers all around the world find it extremely cumbersome to carry out rapid identification, primarily due to lack of affordable and accessible infrastructure. Manually monitoring the plants is nearly impossible. In large-scale farming, the tremendous amount of required work and expertise, along with excessive processing time, makes it a herculean task. Here, image processing and machine processing plays a huge role. A system based on the concept of multiple linear regressions has been used for image recognition. Various steps such as image acquisition, pre-processing, segmentation of image, feature extraction and finally classification are carried out in ways so as to maximize accuracy and intelligence of the model. The system has proven to have an effective ability for image recognition, reliability and precision. Further, this entire system can be modeled into a mobile application, for an effective smartphone-assisted diagnosis of plant diseases for the farmers.

PP(S5)/16: Molecular detection of cow pea mild mottle virus infecting soybean crop in Assam, North East India

Bishakha Deb*, Munmi Borah, Gowthamkumar Routhu and P.D Nath
Department of Plant Pathology, Assam Agricultural University, Jorhat - 785013, Assam, India
**Email: bishakhadeb4@gmail.com*

Soybean, being a leguminous crop is an important soil enriching seed legume which significantly contributes towards the productivity of the crop as well as soil. A crop native to East Asia, is widely cultivated across the globe and India holds the position of being the 4th largest producer. The production of the crop significantly contributes to the country's economic growth. The green foliage has been subjected to many diseases and other abiotic stresses, impacting the yield of the crop. In this study, we aimed to detect the mosaic symptoms exhibited by the soybean plant. *Cow pea mild mottle virus*, a Carlavirus transmitted by whiteflies is an important disease of soybean affecting the yield of the crop. A survey was conducted in the soybean growing areas of Jorhat and the symptoms exhibiting mosaic and mild mottle were collected. Total RNA was extracted from the collected samples and the NABP gene was amplified by RT-PCR using gene specific primers. The RT-PCR results revealed a ~216nt band size, thus confirming the presence of the virus in the infected samples. To the best of our knowledge, this is the first report of *Cow pea mild mottle virus* infecting soybean crop from North East India.

PP(S5)/17: Studies on diagnosis and transmission of *Colletotrichum capsici* (Sydow.) in chilli and its effect on seed quality parameters and its eco-friendly management

Balachandan Gowda C.[1]*, Atul Kumar[1], Sandeep K. Lal[1], Arpita Srivastava[2], Jameel Akhtar[3], Gyan P. Mishra[4] and Shaily Javeria[1]
[1]Division of Seed Science and Technology, [2]Division of Vegeatble Science, [4]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
[3]Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi – 110012, India
**Email: atulpathiari@gmail.com*

The anthracnose or fruit rot disease caused by *Colletotrichum capsici* (Sydow.) is a wide spread problem, limiting the profitable cultivation and seed production throughout the chilli growing regions of India. The present study was conducted to evaluate the seed quality parameters in healthy and diseased seeds, seed health testing, antioxidant enzymes activity, component plating studies, seedling symptom test, pot culture study and microscopic visualization of diseased seeds surface of the variety Pusa Jwala, during 2018- 2020. The results shows that healthy seeds exhibited good germination percentage (77.50 %), Seedling Vigour index-1 (751.85), Seedling Vigour index-2 (2,404.38) and Electrical conductivity (1.145 milli Siemens), whereas the infected chilli seeds exhibited poor germination percentage (57 %) less than IMSC standards. In addition the diseased seeds showed reduced vigour of 370.30 (SVI-1), 960.35 (SVI-2) and EC (2.429 milli Siemens). It clearly elucidates that the pathogen was responsible for reduction in seed quality parameters of chilli. The analysis of activity of antioxidant enzymes (SOD and Catalase) shows that the diseased seeds reported nearly doubled enzyme activity as compared to healthy seeds. Among the different seed health testing methods, the standard blotter method was most suitable for detection of seed borne infections. The seed borne nature of *C. capsici* was proved by seedling symptom test and also in pot culture study. Study on the location of seed borne fungi in the infected chilli seeds revealed that *C. capsici* was noticed both in the pericarp and embryo. Microscopic observation of infected seeds revealed the presence of fruiting body, acervuli on seed surface, which contained abundant dark brown setae with several septations and pointed brown tips.

PP(S5)/18: Pathogenic variability among isolates of *Xanthomonas axonopodis pv. punicae* in India and its correlation with genetic diversity revealed by ISSR markers

Jyosthna, M.K.[1]*, Reddy, N.P.E.[2], Padmodaya, B.[3], Hariprasad, K.V.[4] and Naidu, G.M.[5]

[1]Department of Plant Pathology, [4] Department of Entomology, Sri Venkateswara Agricultural College, Tirupati – 517502, Andhra Pradesh, India

[2]Regional Agricultural Research Station, Tirupati – 517502, Andhra Pradesh, India

[3]District Agricultural Advisory and Transfer of Technology Centre, Kadapa, Andhra Pradesh, India

Sri Venkateswara Agricultural College, Tirupati

[5]Statistics and Computer Applications, College of Agriculture, Naira - 522101, Andhra Pradesh, India

**Email: jyothsnamk78@gmail.com*

Forty seven *Xanthomonas axonopodis* pv. *punicae* (Xap) isolates collected from four important pomegranate growing states of India were subjected for pathogenic diversity analysis and further correlated with genetic diversity using inter simple sequence repeat (ISSR)—PCR analyses. Among the 47 isolates tested for virulence, four isolates *viz*., A_9L, B_{10}F, Sa_2L, NRCP were categorized as highly virulent based on disease severity rating of detached assay of both leaves and fruits. ISSR analysis revealed the presence of 2 clusters, 25 per cent similarity in dendrograms. The dendrogram revealed that, all the isolates were not clustered in accordance with geographical location of isolation and specificity of location of isolation *i.e* leaf and fruit isolates, because all the isolates from different geographic locations isolated from fruit were clustered in all groups along with isolates from leaves. The highest polymorphic information content (PIC) value 0.7 was obtained with two primers, ISSR 857, UBC 8932800. No correlation was observed in grouping of the isolates based on geographical origin, irrespective of virulence. The spread of the pathogen isolates in India might be due to the transport of clonal propagating material of a single cultivar, Bhagwa from one place to another, carrying latent infection and resulting in disease outbreaks.

PP(S5)/19: Morphological, biochemical, and molecular characterization of soft rot and black leg diseases of potato

Basavaraj Chilazari*, Dinesh Singh, V.K. Baranwal, Neelam Geat, Amit K. Kesharwani, J. Rajender and Lokesh Babu

Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India

**Email: chbasavaraj883@gmail.com*

The bacterial genera *Pectobacterium*, *Dickeya* and *Enterobacter* are plant pathogens that cause soft rot and blackleg of potato. In the present study, 5 soft rot bacteria were isolated from potato tubers showing typical tuber soft rot and blackleg symptoms. The samples were obtained from different locations in India. The initial identification was based on morphological and biochemical characteristics. The isolates were able to cause soft rot on potato tuber in 48 h after inoculation under conditions of high relative humidity. Colony morphology on nutrient agar medium shown characteristic perfect round with raised centre for *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc) while Dickeya spp. shown fried egg colonies with irregular margin. On logans medium, colonies appeared non fluidal with red to pink centre having transparent margin with size 0.5 mm in diameter for Pcc and 2.0 mm diameter for *Dickeya* spp. They were gram negative, facultative anaerobe, oxidase negative, catalase positive, nonfluorescent on King's B medium, levan and arginine dehydrolase negative. Pcc was negative for gelatin and starch. *Dickeya* spp. was positive for gelatin and negative for starch. Molecular characterization (PCR analysis) revealed the identification of *Pectobacterium carotovorum subsp. carotovorum* and Dickeya spp. The primer (pmrAF/pmrAR) selected for the detection of *Pectobacterium carotovorum* subsp. *carotovorum* specifically amplified a 666-bp region in only two out of 5 soft rot isolates. Two single 320-bp band was produced from 5 isolates of *Dickeya* spp. using primer fliCF/fliCR.

SESSION 6

Plant quarantine

Agro-terrorism, regulatory rules, amendments, certification, global threat and containment, invasive pests & diseases

Keynote Lectures

KN(S6)/01: Ensuring biosecurity through effective policy framework and stringent quarantine of plant genetic resources

S.C. Dubey[1]* and Kavita Gupta[2]

[1]Indian Council of Agricultural Research, KrishiBhawan, New Delhi – 110001, India

[2]Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi – 110012, India

**Email: scdube2002@yahoo.co.in*

Biosecurity policies including quarantine play an important role in facilitating transboundary exchange of plant genetic resources (PGR) by preventing introduction of pests into new geographical areas.With the coming of the Convention on Biological Diversity (CBD) in 1992 and World Trade Organization (WTO) in 1995, international exchange of PGR has been altered. Under WTO, the aim is to promote trade by undertaking quarantine and influencing trade policies while CBD aims at protection and conservation of biodiversity.International exchange of PGR as governed by the biosecurity policies has contributed significantly towards crop improvement and increasing crop production. Even the PGR being exchanged under the International Treaty on Plant Genetic Resources of Food and Agriculture are governed by the respective national biosecurity regulations of the nations. Being a signatory to both International Plant Protection Convention and WTO, India needs to comply with their requirements. The Plant Quarantine (Regulation of Import into India) Order, 2003 has been legislated and came into force from April 1, 2004, under which import of commodities, additional declarations for freedom from quarantine pests is based on a standardised pest risk analysis (PRA. More than 84 amendments of the PQ Order 2003 have so far been notified to the WTO revising quarantine pest lists; recognition of irradiation and cold treatments; pest free areas; revising the lists of crops under Schedule VI and VII to include 699 and 519 crops/ commodities, respectively and 57 weed species. ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) is authorized to issue import permit and undertake quarantine of plant germplasm including transgenics and for issue of Phytosanitary Certificate for material under export. Adopting a systematic workable strategy, using a combination of conventional and modern techniques, over the past forty years, a total of 75 exotic pests including fungi (5), viruses (17), insects/ mites (25), nematodes (9) and weeds (16) of great quarantine significance to the country have been intercepted. All efforts are made to salvage the infested/ infected materials; however, if the material is unsalvageable, it was incinerated. The interceptions made signify the potential dangers in import of planting material if proper quarantine measures had not been followed. India also has other national regulations related to biosecurity which provide a fragmented legislative system which needs to be harmonized and integrated in to a holistically deal with biosecurity while complying with international norms. The establishment of National Agricultural Biosecurity Board and enactment of Seed Bill needs to be taken up to holistically deal with biosecurity. Also, there is a need to support research, training, capacity-building, networking and information sharing activities at both national and regional levels.

KN(S6)/02: High throughput sequencing as diagnostics of known and novel plant viruses/viroids and its application

V.K. Baranwal*
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: vbaranwal2001@yahoo.com*

Plant viruses often get introduced through seeds or planting materials in newer geographical regions due to lack of capabilities to detect and intercept them. Diagnostics play an importanat role in preventing such introduction of plant viruses. However, the common diagnostic methods such as ELISA, PCR or variants of PCR are used for detection of single virus or a few viruuses. DNA microarray chip has been developed for parallel detection of multiple infections of viruses/viroids. All these methods can not detect novel and highly divergent viruses as they depend on prior availability of specific antibodies or genome sequences. High-throughput sequencing (HTS) technologies, allow the sequencing of the whole genome and can be used as a diagnostic tool to identify a plant virus when no prior knowledge of the virus is available. Using available RNA seq data, we could identify nine grapevine viruses and viroids for the first time in grapevine cultivars grown in Indian soil. Using HTS, genome of two new viruses and a viroid were detected in apple cultivars. These pathogens were possibly introduced through import of planting materials. In another study where mining of water hyssop (a medicinal herb) transcriptome was undertaken, genome sequences of two novel rhabdoviruses and a solendovirus were revealed. Even though HTS-based diagnostic is very useful and strong tool to detect known and unknown/novel viruses/viroids, the outcomes may or may not be associated with evidence of living viruses or damage to the plant. Therefore, a detailed guideline for its application is required.

KN(S6)/03: Detoxification of aflatoxins: A promising approach to reduce the risk of aflatoxin contamination of foods and feeds

R. Velazhahan*
Department of Plant Sciences, College of Agricultural and Marine Sciences, Sultan Qaboos University, P.O. Box 34, Al-Khoud, Muscat 123, Sultanate of Oman
**Email: velazhahan@squ.edu.om*

Mycotoxins are low molecular weight secondary metabolites of fungi which are produced under favourable conditions on agricultural commodities. These include aflatoxins, deoxynivalenol, fumonisins, ochratoxin A, patulin and zearalenone. Among them, aflatoxins are the most poisonous mycotoxins. *Aspergillus flavus* and *Aspergillus parasiticus* are the major producers of aflatoxins that contaminate a wide range of agricultural commodities including corn, peanuts, chilli, tree nuts, figs, sorghum and rice. These fungi invade the agricultural commodities at pre-harvest stage or during post-harvest operations and storage and produce aflatoxins. These aflatoxins are highly toxic, hepatocarcinogenic, mutagenic and teratogenic compounds. Aflatoxins belong to the group of difuranocoumarins. More than 18 different types of aflatoxins have been characterized. The major aflatoxins are aflatoxin B1(AFB1), aflatoxin B2 (AFB2), aflatoxin G1(AFG1) and aflatoxin G2 (AFG2). Aflatoxin M1 (AFM1) is the major metabolite of AFB1 that is found in milk of animals that have consumed feed contaminated with AFB1. Among the various aflatoxins, AFB1 is highly toxic and carcinogenic to animals and humans. Humans are exposed to aflatoxins directly by consumption of aflatoxin-contaminated foods, or indirectly by consumption of foods from animals (egg, milk, meat) previously exposed to aflatoxins in feeds. Aflatoxin contamination in milk products such as cheese, yogurt and cream has also been reported. Aflatoxin contaminated diet has been linked with the high incidence of liver cancer in humans. Hence, over 100 countries have set regulatory limits on permissible levels of aflatoxins in foods. The regulations on the import of aflatoxin contaminated food products results in huge losses each year to the agriculture and feed industries. Aflatoxins are extremely durable under storage and processing of foods or feeds. Management of aflatoxin contamination at pre-harvest stage can be achieved by either controlling aflatoxigenic fungi or controlling production of aflatoxin. At post-harvest stage, strategies such as reducing moisture content of the agricultural products, proper storage, treatment with electromagnetic radiation, ozone fumigation, adoption of improved sorting technologies and detoxification can reduce aflatoxins to acceptable levels. Various physical, chemical and biological methods have been used for detoxification of aflatoxins in foods and feeds. The use of plant products for detoxification of aflatoxins has been suggested as biologically safe and cost-effective method.

KN(S6)/04: Maize Lethal Necrosis (MLN): Effort towards containing the spread and impact of a devastating transboundary disease in sub-Saharan Africa

Suresh L.M.*, Yoseph Beyene, Manje Gowda, Michael Olsen, MacDonald Jumbo, Dan Makumbi, Mosisa Worku, Francis Mwatuni and B.M. Prasanna
International Maize and Wheat Improvement Center (CIMMYT), ICRAF Campus, UN Avenue, Gigiri,
PO Box 1041-00621, Nairobi, Kenya
**Email: l.m.suresh@cgiar.org*

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.

Invited Lectures (Lead Lectures)

IP(S6)/01: International and national regulatory framework for transboundary movement and quarantine of living modified organisms

V. Celia Chalam*, Kavita Gupta, J. Akhtar, Z. Khan and A.K. Maurya
Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi 110 012, India
E-mail: celia.chalam@icar.gov.in; mailcelia@gmail.com

The Cartagena Protocol on Biosafety (CPB) to the Convention on Biological Diversity (CBD), an international agreement governs the transboundary movement of living modified organisms (LMOs). Article 18 of CPB sets forth rules related to handling, transport, packaging and identification requirements of LMOs. Documentation requirements vary according to intended use of LMOs.Article 18 (2b) gives necessary documentation to accompany the shipment of LMOs for contained use.In compliance to this, import of GMOs/ LMOs in India is governed by the provisions of Environment Protection Act, 1986 and Rules 1989. Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources(ICAR-NBPGR), New Delhi is the nodal organization for import and quarantine of transgenic planting material meant for contained use and isgoverned by the provisions of Plant Quarantine (Regulation of Import into India) Order 2003 and its amendments (herein after referred to as PQ Order 2003). Import permit (IP) is issued subject to import Clearance issued by the Review Committee on Genetic Manipulation (RCGM), Ministry of Science and Technology, Govt. of India.The documents, which should essentially accompany the consignment meant for contained use are: IP issued by Director, ICAR-NBPGR and Phytosanitary Certificate (PC) issued by the NPPO of the country of origin. IP is issued as per the PQ Form 09 of PQ Order 2003, giving information about common/scientific name of material, country of origin, name and address of exporter and importer etc., including name and address of individual/ institution to whom the LMOs are consigned, number of samples, type of material- trial/ germplasm etc., transgene (s)/ trait, additional declaration that material should be free from specific pests (as per PQ Order 2003); Import clearance from RCGM giving information about new or modified traits, transformation events, risk class, specification of use, specifies requirements, if any for the safe contained use, handling, storage, transport and use of LMOs; declaration by the indenter that the material is free from embryogenesis deactivator gene. PC issued by country of origin, giving details of material and treatment as per the format of International Plant Protection Convention (IPPC) of FAO. Commercial invoice giving details of material from the country of export; Red/White tag in PQ form 11.

Keeping in view the biosafety requirements, National Containment Facility of level-4 (CL-4) has been established at ICAR-NBPGR to ensure that no viable biological material/ pollen/ pathogen enters or leaves the facilityduring quarantine processing of transgenics. Quarantine processing involves detection of pests in imported germplasm using conventional. Serological and molecular techniques and salvaging of infested/ infected material by using suitable detection and disinfestation procedures/ techniques. In addition, post-entry quarantine growing/inspection of the transgenics is also undertaken by ICAR-NBPGR. During 1997-2020, >16,000 samples of different transgenic crops, comprising *Arabidopsis thaliana*, *Brassica* spp., *Cicer arietinum*, *Eucalyptuscamaldulensis*, *Glycine max*, *Gossypiumhirsutum*, *Manihot esculenta*, *Nicotiana tabacum*, *Oryza sativa*, *Solanumlycopersicum*, *S. tuberosum*, *Triticum aestivum* and *Zea mays* with different traits imported into India for research purposes were processed at ICAR-NBPGR for quarantine clearance. As per the Plant Quarantine (Regulation of Import into India) Order 2003, 1,284pests are regulated pests, which are of quarantine significance for India.A number of economically important pests (insects, mites, nematodes, fungi, bacteria and viruses) were intercepted including the ones not reported from India such as fungus: *Peronospora manshurica* on soybean and nine viruses viz., *Barley stripe mosaic virus*, *Bean mild mosaic virus*, *Cherry leaf roll virus*, *Cowpea severe mosaic virus*, High plains virus, *Maize chlorotic mottle virus*, *Raspberry ringspot virus*, *Tomatoringspot virus* and *Wheat streak mosaic virus*. Besides, *Arabis mosaic virus* and *Maize dwarf mosaic virus*are not known to occur in Indiaon soybean and wheat, respectively, were intercepted.Other important interceptions were, insects- *Cryptolestes ferrugineus*, *Rhizopertha dominica* and *Sitophilus oryzae*; nematode- *Aphelenchoides besseyi*; fungi- *Alternaria brassicae*, *A. brassicicola*, *Phoma lingam*; bacterium- *Xanthomonas campestris* pv. *Campestris*. The infected plants were uprooted and incinerated. Also, the pest risk associated with the import of these crops from the source countries was evaluated. India need to establish a network of interconnected diagnostic laboratories and strong surveillance programme to identify new pests. Adopting the reliable techniques with an appropriate strategy for pest detection would go a long way in ensuring biosecured agriculture against transboundarypests through quarantine, pest-free trade and exchange of germplasm.

Oral Presentations

OP(S6)/01: First report of *Dickeya fangzhongdai* causing bacterial soft rot disease on *Dendrobium nobile* in India: A new invasive pathogen

A. Balamurugan[1,4]*, A. Kumar[1], K. Sakthivel[1,2], M. Ashajyothi[3], Kuleshwar Prasad Sahu[1] and M. Karthikeyan[4]

[1]*Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India*
[2]*Crop Protection Section, ICAR-Indian Institute of Oilseed Research, Hyderabad - 500030, Telangana, India*
[3]*Plant Protection Lab, ICAR-Central Agroforestry Research Institute, Jhansi - 284003, Uttar Pradesh, India*
[4]*Department of Plant Pathology, Tamil Nadu Agricultural University, Coimbatore - 641003, Tamil Nadu, India*
**Email: abalamurugan555@gmail.com*

Soft-rot disease on *Dendrobium nobile* observed in a commercial farm in the Nilgiris district of Tamil Nadu, India. Polyphasic characterization of the causal agent coupled with a detailed investigation established the disease etiology. Infected leaves showed rot symptoms characterized by irregular water-soaked lesions on the leaf margin that rapidly spread entire leaf. Milky exudation on the cut end of infected leaves indicated the bacterial etiology. Bacterial colonies isolated were irregular, whitish-yellow with a characteristic raised center. All isolates showed identical phenotypic traits and induced a hypersensitive reaction on *Nicotiana tabacum*. Pathogenicity assay performed on *D. nobile* confirmed their pathogenic nature as all three isolates incited typical soft-rot within 12 h post-inoculation. *In vitro* host range studies revealed that all the isolates could cause rot on potato, carrot, onion and *Aloe vera*, but not on chrysanthemum and banana. The identity of the bacterial isolates was confirmed as *Dickeya fangzhongdai* using 16S rRNA gene sequences by closest match with database. The bacterial pathogen is a new record on *Dickeya fangzhongdai* in India in *Dendrobium* orchid. The bacterial pathogen appears to have gained entry into our country through imported orchid planting units. Complete understanding of the etiology of the disease and of the pathogen would be useful to devise suitable management practices for the containment of disease spread in the future.

Poster Presentations

PP(S6)/01: Agroterrorism and food safety

N. Yamini Sousheel*
College of Agriculture, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad - 500030 Telanagana, India
**Email: nysousheel1308@gmail.com*

Food and agriculture are key elements of the critical infrastructure of every country because they provide products that are essential for life. India is a country with a highly developed agricultural sector. Terrorist attacks against crops or livestock could be carried out with a variety of harmful agents, including viruses, bacteria, fungi, nematodes, and insect pests. Most serious plant diseases are caused by fungal pathogens, such as wheat smut, rice blast, brown stripe mildew of corn, and karnal bunt of wheat. Fungal spores can be grown in large quantities, are stable under different weather conditions, and are naturally transmitted through the air. These agents dramatically reduce the yields of corn, rice, and wheat. Small amounts of fungal pathogens could spread to large areas of cropland, and their long incubation period makes them hard to detect at an early stage. The accidental or intentional release of a major agricultural pathogen would have serious economic effects, resulting in production losses, market declines, and increased unemployment in the food and agriculture sector. Quarantines and restrictions on animal movement in the disease-affected regions would paralyze the rural economy. The food supply chain is a key element of the critical infrastructure of every country, yet it is vulnerable to natural diseases and infestations as well as to deliberate attack. Criminals or terrorists could target multiple entry points along the complex supply chain extending from "farm to fork," ranging from the deliberate introduction of anti-crop and livestock pathogens to the adulteration or contamination of processed foods in pursuit of illicit profit or political goals. Although the magnitude of the current threat to food and agriculture is hard to assess, the vulnerabilities are real, and there are clear steps that can be taken to protect the food supply and to deter potential attacks.

SESSION 7

Microbial biodiversity

Diversity in fungi, bacteria & viruses, systematics, edible fungi, medicinal fungi

Keynote Lectures

KN(S7)/01: Microbial diversity in India: challenges and issues

C. Manoharachary*
Applied Mycology & Plant Pathology Lab, Department of Botany, Osmania University, Hyderabad -500007, Telangana, India
**Email: cmchary@rediffmail.com*

The importance of diversity, conservation, and utilization of microbes, fungi and lichens is growing as the number of preserved strains are continuously increasing by isolation and genetic manipulation. 5-50 million species of living biota might exist in globe, of which 1/3 of global diversity is in India. Indian gene centre is one of the mega diversity centres of the world which include North Eastern Himalays and Western Ghats as biodiversity hot spots. The country is endowed with enormous variability In actinomycetes, bacteria, cyanobaceteria, fungi, lichens, viruses and others. (Approximately viruses -2250, bacteria-800, Actiomycetes-80, Fungi-29000, Lichens-2300). All the above living organisms are involved in organic matter decomposition N2-fixation, “P” solibulization, soil and plant health, in industry, medicine, pharmaceuticals, agriculture, bioremediation, Dye industry, food industry, fermentation and in various other activities related human welfare. In-situ and ex-situ conservation methods need to be employed for germplasm maintenance. High throughput sequencing methods along with traditional and innovative methods need to be employed to discover culture dependent and culture independent organisms. Morphotaxonomy and molecular techniques along with other methods are to be employed to study microbes, fungi and others. As on today only a fraction of microbes, fungi, lichens and other biotic communities are enlisted and much needs to be discovered. There is a great need to employ indigenous strains to boost our crop productivity and economy. In this presentation the diversity status of microbes fungi and lichens, their taxonomic aspects and their utilization for human welfare will be discussed. Pertinent challenges and issues also will be discussed.

KN(S7)/02: Aflatoxigenic potential of *Aspergillus flavus* isolates from maize in the Philippines and investigation of predators effect on aflatoxin production

Christian Joseph R. Cumagun*
College of Agriculture, University of the Philippines Los Banos College, Laguna 4031, Philippines
**Email: cumagunc@byui.edu*

Aflatoxin infections in food and feed, and the considerable risks on human health surrounding them have made this one of the most addressed topic for the last decade. Aflatoxin B1 is classified as a carcinogenic molecule, it causes hepatoxicity and could be lethal when high quantities of it is ingested. Economical losses are added up on repercussions on human health. Large outbreaks around the world proved that bad management of stock and inappropriate control of aflatoxin producing species can amplify the risk to a large extent. *Aspergillus flavus* is one of many *Aspergillus* species that are aflatoxin producers, and it is known to produce aflatoxin chemotype B. In this study the aflatoxin production of 74 isolates of *A. flavus* from maize, from different regions of the Philippines was tested. Furthermore, the effect of predators on levels of *A. flavus* aflatoxin production was investigated. Great diversity between isolates that originated from different regions of the Philippines was recorded. Isolates from eastern regions of the country showed the highest aflatoxin production levels (>20 µg/kg). *A. flavus* isolates with medium to low production (from 2 to 5 µg/kg) were spread in all regions of the Philippines. Two isolates with no detectable aflatoxin production were found, which could be used in biological control against aflatoxigenic strains. In the second part, fungal cultures of *Aspergillus flavus* were exposed to isopods (*Trichorhina tomentosa*) and collembolans (*Folsomia candida*) predation, and induction of the aflatoxin production after 24 hours was demonstrated. Aflatoxins production decreased after 48 hours of testing, and the same results were obtained with artificial mechanical injury. Until now, there has not been any study reporting similar results. These results are discussed and recommendations for future research subjects are made.

Oral Presentations

OP(S7)/01: Survey for association of plant parasitic nematodes and *Fusarium oxysporum* with banana in Panama wilt affected areas of Uttar Pradesh, India

P.K. Shukla[1]*, Nidhi Kumari[1], Tahseen Fatima[1], Haripal Singh[1], Harish Pal, Ram Gopal[2] and Shailendra Rajan[1]
[1]*ICAR-Central Institute for Subtropical Horticulture, Rehmankhera, PO Kakori, Lucknow - 226101, Uttar Pradesh, India*
[2]*Regional Research Station (ICAR-CSSRI), Lucknow - 226002, Uttar Pradesh, India*
Email- Prabhat.Shukla@icar.gov.in

Severe incidence of banana wilt caused by *Fusarium oxysporum* f.sp. *cubanse* race TR4 (FocTR4) has recently been reported in several districts of Uttar Pradesh, India. Since, the role of plant parasitic nematodes in aggravating the Fusarium wilt is well established, we conducted survey and collected 155 samples from 67 villages in 9 banana growing districts during September to November 2020. Among plant parasitic nematodes, *Xiphinema* was found most widely (75.5%) distributed followed by *Meloidogyne* (64.5%), *Helicotylenchus* (45.2%), *Tylenchus* (32.3%), *Hoplolaimus* (28.4%), *Tylenchorhynchus* (18.1%), *Rotylenchulus* (15.5%) and *Pratylenchus* (12.9%) respectively. *F. oxysporum* was quantified in the soil samples through dilution plating method on Komada medium where the presence of FocTR4 has already been confirmed using the TR4 specific primers. The CFU of *F. oxysporum* per g of dry soil were recorded maximum in Barabanki (8.5×10^3) followed by Ayodhya (5.0×10^3), Gorakhpur (1.5×10^4), Maharajganj (3.3×10^4), Sant Kabir Nagar (3.6×10^4) and Amethi (2.6×10^4) districts respectively. However, the isolated colonies are subjected for molecular identification for confirmation of race TR4. Maximum population buildup (per g of soil) of *Pratylenchus* (6.50), *Rotylenchulus* (5.75) and *Meloidogyne* (4.38) in the rhizosphere of banana indicated the possibility of their synergistic role in enhancement of banana wilt. Higher percent incidence of *F. oxysporum* and *Meloidogyne* in FocTR4 wilt reported districts *viz.* Maharajganj (93 and 70), Sant Kabir Nagar (89.5 and 73.6), Ayodya (69.6 and 73.9) and Gorakhpur (84.6 and 64.5) confirmed their synergistic effect in disease progression. Results indicate the need of adopting proper management of nematodes for reducing Panama wilt incidence.

OP(S7)/02: Cultural variability, genetic diversity and population analysis of *Ustilaginoidea virens* in India

Manas Kumar Bag[1]*, P. Dey[1], A. Ray[1], P. Masurkar[1,2], R.K. Singh[2] and P.C. Rath[1]
[1]*ICAR-National Rice Research Institute, Cuttack - 753006, Odisha, India*
[2]*Institute of Agricultural Science, Banaras Hindu University, Varanasi - 221005, Uttar Pradesh, India*
**Email: manas.bag@gmail.com*

Rice false smut (RFs) disease, one of the most limiting factor of yield and rice qualities, shows high degree of variability in the field. Adoption of resistant variety to RFs is the best method to combat the disease and that needs thorough knowledge of cultural variability, genetic diversity and population analysis of the pathogen. Information on these aspects is very limited. Present study was targeted to find out the said information from Indian *U. virens* populations. Altogether 113 isolates of *U. virens* were collected from different rice fields of different states of north, east and north-east India. Lots of variabilities (size, texture, color and sporulation time) of cultures of same ages were observed. Majority isolates are moderate to fast growing. Colony texture of most of the isolates were compact, followed by fluffy and few were cottony. U. virens isolates has shown wide variation in incubation period. Fsm 3, Fsm 5 and Fsm 8 showed slow growth upto 7 days but after14 days the growth rate was faster whereas Fsm 6 showed slow growth upto 14 days but at later stage the growth was faster. Fsm 87 showed regressed growth upto 14 days but later on changed to faster growth after 21 days. Populations were analysed based on 17 polymorphic and highly informative microsatellite markers (SSR) based data. A high within-populations genetic diversity (90%) was confirmed with gene diversity index and PPL values of 0.46 and 100% respectively. The dendrogram showed three main clusters, comprised mainly isolates from North-India (C-I), Odisha and Bihar (C-II) while WB and North-Eastern India (C-III). The Neighbor joining based Cluster, PCoA and Structure analyses grouped the populations geographically but not into sharp genetically distinct clusters according to their geographical origins. May be geographical environments have some influence on genetic variation. These baseline informations are useful for designing effective management strategies.

OP(S7)/03: Diversity of the rhizosphere fungal community edifice of upland cotton in North India

S.K. Sain*, Prahlad, V. Kumar, A.P. Singh, D. Paul, S. Gawande, P. Valarmathi, R. Kumar, S.K. Verma, O.P. Tuteja, N.G. Narkhedkar and Y.G. Prasad

Regional Station (ICAR-CICR), Sirsa – 125055, Haryana, India

**Email: sain.skumar@gmail.com*

Rhizosphere fungi (RF) play a vital role in promoting plant growth, health and act as pathogens. The microbial biodiversity of soil depends on soil health and cropping system and healthy soil is good habitat for microbial community and sustain life for the perpetuation of microbes. However, information on the dynamics of the rhizosphere fungal community structure of the worldwide economic upland cotton (*Gossypium hirsutum*) is limited. Therefore, an investigation was conducted to understand RF biodiversity in the upland cotton cropping system. A survey was conducted to collect cotton rhizosphere soil samples from different cotton cropping systems in North India during October-November 2020. The samples were inoculated in Potato Dextrose Agar (PDA) medium supplemented with streptomycin by using the soil dilution plate method. Among 63 samples, 575 colonies of 18 genera including *Aspergillus* spp.(26.1%), *Fusarium* spp.(11.3%), *Mortierella* spp. (11%), *Penicillium* spp. (9.3%), *Acremonium* spp.(5.5%), *Cladosporium* spp. (4.3%), *Rhizoctonia* spp. (2.6%) *Macrophomina* (2.6%), *Trichoderma* spp. (2%), *Rhizopus* spp.(2.0%), *Sclerotium* spp.(1.7%), *Curvularia* spp.(0.9%), *Bipolaris* spp. (0.6%), *Phomopsis* spp. (0.9%), *Metarhizium* spp. (0.9%), *Paecilomyces* spp. (0.9%); *Nigrospora* spp.(0.6%), *Colletotrichum* spp. (0.3%),and non-sporulation (19.1%) were recorded. The average RF colonies in samples 9.1 and 9.9(104c.f.u./ml) were recorded from Haryana and Rajasthan, respectively with an average RF biodiversity of 2.7 in both. The percent contribution of RF was higher (78.3%) in fields that adopted the cotton-wheat-cotton cropping system for the last five or more years compared to the crop rotation. Also, the RF contribution was higher in the soils with pH less than 8 (94.5%) compared to higher pH (>8). The soils with low phosphorus (<23kg/ha) and low organic matter (OM) (0.5%) showed higher contributions of RF, 58.8% and 86.1%, respectively compared to soils with medium phosphorus (23-56 kg/ha) and medium OM (0.5-0.75%). Aspergillus, *Fusarium*, *Penicillium*, *Acremonium*, *Cladosporium* were dominant genera and contributed 67.5% of the total RF. The genera *Acremonium, Trichoderma*, *Metarhizium, Paecilomyces, Nigrospora*, *Mortierella*, *Penicillium*, *Aspergillus* are known to plays a vital role in decomposition, preventing biotic stresses and promoting plant growth. Findings suggest the soil microbial community is a potential microbial indicator helping to improve agricultural management, further study needs to be carried out for exploring their roles in plant growth and health.

OP(S7)/04: Identifying indigenous substrates for the cultivation of *Pleurotus sajor-caju*

Priya John*, Shivangi Kansara, K.B. Rakholiya and Megha Vyas
Department of Plant Pathology, N.M. College of Agriculture, NAU, Navsari - 396450 Gujarat, India
**Email: priyajohn75@gmail.com*

The fact that basidiomycetes convert waste materials into a highly favoured proteinaceous food which is clearly relevant to the requirements of both the developing and developed countries. They have a high saprophyte colonizing ability and can grow on virtually any agricultural waste. The oyster mushroom belongs to the genus *Pleurotus sajor-caju*. An attempt was made in Navsari region of South Gujarat to grow oyster mushroom on locally available substrates. Seven selected substrates (Paddy straw, Wheat straw, Sugarcane bagasse, Sugarcane trash, Cotton stalk, Finger millet straw and Banana pseudostem stretcher) were evaluated for their days for colonization spawn run, days for pinhead formation, days for harvest, weight of fruiting bodies and biological efficiency. The experiment was conducted under controlled condition during 2016-17, 2017-18 and 2018-19. The pooled analysis showed that days for colonization, pinhead formation days for first harvest, weight of fruiting bodies and biological efficiency ranged from 11.58 to 17.83 days, 13.33 to 24.17 days, 1.83 to 627.33 gm and 0.22 % to 64.27 % , respectively. Among the different substrates selected for the cultivation of oyster mushroom, wheat straw gave the highest yield of 627.33 gm and the least yield was obtained in the case of banana pseudo stem stretcher (1.83gm).

OP(S7)/05: Evolutionary relationship among spatio temporally diverse heterothallic *Alternaria alternata* isolates

Deeba Kamil[1]*, Shiv Pratap Choudhary[1], Sushma[2], Shrawan Singh[2], Amrita Das[1], R. Sudeep Toppo[1] and T. Prameela Devi[1]
[1]Division of Plant Pathology, [2]Division of Vegetable Science, ICAR-Indian Agricultural Research Institute,
New Delhi – 110012, India
**Email: deebakamil@gmail.com*

Alternaria alternata is diverse species group, saprophytically found in soil and decaying plant tissues. Taxonomically, several host specific *A. alternata* species group have been studied but genetic evolution and their virulence not yet completely documented and cannot be distinguished by conventional methods. It is very important to study their genomic evolution from saprophytes to endophytes and development of successful fungal pathogen by molecular approaches. The pathogenesis of *A. alternata* species group depends on host susceptibility or resistance as well as quantitative production of HSTs and nHST. The genes responsible for the production of HSTs are found on the conditionally dispensable chromosomes (CDCs) which have been well characterized. Hence, the current study was also conducted to characterize fifty Indian isolates of *A. alternata* species group isolated from diverse hosts. All the isolates were identified as *A. alternata* based on their cultural, morphological and Internal transcribed spacer (ITS) region sequences. The pathogenicity was also conducted for all fifty isolates on cauliflower (var. meghna) and out of them, only 6 showed their pathogenicity. Furthermore, all the isolates were screened for both mating type idiomorphs and toxin gene markers. Three isolates were showed in both MAT idiomorphs. The presence of both MAT idiomorphs within *A. alternaria* isolates indicates that genetic exchange (sexuality or parasexuality) has occurred since the evolution of CDCs, providing a mechanism of transfer of CDCs.

OP(S7)/06: Morphological description of sugarcane wilt pathogen in sub-tropical India

Sanjay Kumar Goswami*, Dinesh Singh, Deeksha Joshi, S.P. Singh, Chandramani Raj and Shweta Singh
ICAR-Indian Institute of Sugarcane Research, Rai Bareli Road, Dilkusha, Lucknow – 226002, Uttar Pradesh, India
**Email: sanjay.goswami@icar.gov.in*

Sugarcane is one of the important cash crops in India and the world. The crop is affected by many devastating diseases like red rot, wilt, smut, RSD, GSD, YLD, rust, etc. Wilt is one of the important fungal diseases of sugarcane affecting its production and productivity. Since the associated pathogen in sub-tropical conditions has not been clearly established with the disease, the studies were conducted to identify and confirm the sugarcane wilt pathogen under sub-tropical conditions. The survey was done to collect 25 wilt diseased sugarcane samples from Co-7717, Co1336, Co0238, I-41-56R, LG-17132, and LG-16138 varieties/genotypes in the year 2020-2021 from Lucknow and Faizabad (UP). Disease incidence ranged from 5-60% in different varieties. The pathogen was isolated using PDA culture medium and characterized morphologically. Out of 25 cultures, 12 (48%) were identified as *Fusarium* sp. Seven (58.3%) of 12 cultures were cottony and fluffy pinkish-white, 3 (25.0%) cultures were cottony and fluffy white, while 2 (16.6%) cultures were cottony dull white. All the 12 cultures showed light yellow colour at the bottom of the Petri plates. Microconidia were oval in shape with a single septum, while macroconidia were sickle-shaped with 2-3 septa. No phialides and chlamydospores were observed in 7 days old cultures. The growth rate of the fungus ranged from 0.6-0.8 cm/day at 27oC.

Poster Presentations

PP(S7)/01: Characterization of *Rhizoctonia solani* isolates collected from different hosts

Priya Chandra[1], **B.M. Bashyal[1]*,** Amar Bahadur Singh[2], S. Gopala Krishnan[3], Pooja Parmar[1] and Rashmi Aggarwal[1]
[1]Division of Plant Pathology, [3]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
[2]College of Agriculture, Agartala – 799210, Tripura, India
**Email: bishnumayabashyal@gmail.com*

Rice (*Oryza sativa* L.) is one of the most important and cultivated crop consumed by nearly half of the global population of the world. Sheath blight disease of rice is caused by *Rhizoctonia solani* Kuhn [teleomorph: *Thanatephorus cucumeris* (Frank) Donk] reported from many states of India. *R. solani* is a destructive fungal pathogen having wide host range and infects the plant in the form of mycelia and sclerotia. Total of 36 isolates of *R. solani* were collected from rice and other hosts in the Kharif and Rabi season of 2018-2020. Isolates were characterized morphologically and molecular through internal transcribed spacer (ITS) region amplification and Universal Rice primers (URP) marker. Considerable amount of morpho-cultural variability has been observed in the isolates in terms of colony color, growth rate and sclerotial characters. Phylogenetic tree using neighbour joining method was constructed on the basis of sequencing data confirmed the identity as *Rhizoctonia solani*. Molecular diversity of the isolates was also evaluated using URP marker. Data obtained was used for construction of UPGMA dendrogram based on Jaccard's similarity coefficient to determined genetic similarity. Total 11 primers were used in the study, out of which only 6 were able to generate PCR products. Total number of bands amplified by 6 primers were 60 and each primer produced polymorphic band. Hence, resulting in an estimation of 100% polymorphism. Results indicated genetic similarity of the isolates existed in the range of 33 % to 92%. Maximum similarity was observed in isolate TP 28 (92%) and TP35 (92%) while least similarity was observed in TP12 (33%) and TP36 (33%). The analysis also revealed dendrogram obtained using data of URP-2F primer clustered 11 isolates of different hosts in one group and 21 isolates of same host (rice) in another group. Results confirmed the genetic diversity among the *R. solani* isolates and its existence in different hosts. The information obtained will be helpful for creating future management strategies against pathogens.

PP(S7)/02: Cultural characteristics of *Cercospora canescens* causing leaf spot of mungbean [*Vigna radiata* (L.) Wilczek] in Bundelkhand

Durga Prasad*
Department of Plant Pathology, College of Agriculture, Banda University of Agriculture & Technology, Banda – 210001, Uttar Pradesh, India
**Email: dp.shubh@gmail.com*

Cercospora leaf spot is the most important fungal disease of Mungbean occurring regularly in Bundelkhand region of Uttar Pradesh. The disease is caused by *Cercospora canescens* Ellis and Martin. Cercospora leaf spot disease appears during warm and humid weather leading to Chlorosis, defoliation and low yield. The pathogen isolated onto potato dextrose agar medium was slow growing; white in colour and puffy growth was observed which was slightly raised on the upper side. Mycelium was hyaline to light brown in color and septate. Conidiophores were straight or flexuous, light brown to brown in color and multi-septate. Conidia were hyaline to light brown, straight to curved with 5-10 septate measuring 3-5 x 40-130 um with delicate tip. The inoculated leaves showed small brown spots in the initial stage which were turned into dark brown and enlarged spots. Closely located spots coalesced and formed large necrotic patches. Developed spots had grey colored center and brown margin. The size of the spots varied from 3- 10mm in diameter. Out of 5 media viz., potato dextrose agar, potato sucrose agar, oat meal agar, mungbean decoction agar and v-8 juice agar medium tested for growth of the *C. canescens,* the highest radial growth of mycelia (87.67mm) recorded in v-8 juice agar medium which was almost equal to growth of mycelia observed on potato dextrose agar (86mm), potato sucrose agar (86.50mm) and mungbean decoction agar (86.50mm). The least radial growth (41.17) of mycelia exhibited in oat meal agar medium. White color colony of *C. canescens* was seen in three media viz., potato dextrose agar, mungbean decoction agar and v-8 juice, while, creamy white and light yellow colored colony were observed in potato sucrose agar and oat meal agar medium, respectively.

PP(S7)/03: Economic empowerment of rural landless women through mushroom cultivation

Harbinder Singh*, Satpal Singh, Prashant Chauhan and Namita Soni
Department of Plant Pathology, Regional Research Station (CCS HAU), Karnal - 132001, Haryana, India
**Email: hsypatho@gmail.com*

Rural women play key role in supporting their households and communities in achieving food and nutritional security, generating income, improving rural livelihoods and overall well being but limited access to land, credit, health care and education are among the many challenges they face in daily life. These constraints prevent them from fully enjoying their human rights and hamper their efforts to improve their lives as well as those who directly or indirectly depend on them. Mushroom cultivation is a women friendly profession. Mushroom cultivation is one agricultural activity in which rural farm women can play a pivotal role without sacrificing their household responsibilities. Mushroom cultivation is simple, low cost, and suitable for rural areas, is less labour intensive and can provide employment to rural landless woman. Mushroom cultivation will improve the socio-economic condition of farmers, families and solve employment problems of both literate and illiterate, especially rural farm women. Mushroom cultivation as an entrepreneurship development among rural women and suitable approach for economic empowerment. Krishi Vigyan Kendra, Karnal took up an initiative for economic empowerment of Schedule Caste rural women by motivating them to adopt mushroom cultivation as an income generating activity. KVK has conducted six training programme each of five days duration for 180 schedule caste women since 2018-19 & 2019-20 and 100 bags (10 Kg each) of spawn run pasteurised compost with casing mixture were provided to each trainee to develop their interest and practical experience. Woman showed keen interest and a sense of belongingness has been made among the trained women towards mushroom cultivation. Total 81 per cent of the trained women revealed that mushroom cultivation is a good enterprise for improving livelihood of schedule caste women and 79 per cent of trainees shared that it require lesser time and space for production. Mushroom yield of these trainees ranges from 180-300Kg/100 bags and total net income ranges from Rs. 8000-12000. It is concluded that mushroom cultivation for economic empowerment of schedule caste women is a profitable activity.

PP(S7)/04 First report of *Ganoderma orbiforme* on arecanut from India

N. Boopathi*, T.K. Bag, T. Prameela Devi, Amrita Das, Deeba Kamil and R. Sudeep Toppo
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: boopathipks15@gmail.com*

Ganoderma is one of the most devastating diseases affecting production and productivity of the many crops by decomposing lignin, cellulose and related polysaccharides. Since a number of *Ganoderma* species are reported to cause the Basal Stem Rot (BSR), also called foot rot in arecanut, a survey was conducted during 2019-20 to collect the basidiocarps of *Ganoderma* spp. from Eastern India (West Bengal and Assam) where arecanut cultivation is predominant. The collected samples were examined for its morphological characteristics. Isolation of fungus from basidiocarp was done using *Ganoderma* Selective Medium (GSM) and further sub-culturing was done on potato dextrose agar (PDA) slants. The observed morphological parameters such as spore size and shape were matched with the established taxonomical characters of *Ganoderma orbiforme*. The morphologically identified fungus was further confirmed by molecular method. Total DNA was extracted from the mycelial mat grown on Potato Dextrose Broth by using CTAB method. DNA was also extracted from the dried basidiocarp samples. Molecular identification of the fungus was done by using the Internal transcribed spacer (ITS1 & ITS 2) regions. The obtained amplicon of 650 bp was sequenced. The sequence showed 100% similarity with *Ganoderma orbiforme* isolate BCC22325 (GenBank No. KX421867.1) through NCBI BLAST analysis. The phylogenetic tree was constructed using ITS sequence of isolated fungus and related sequences available with GenBank by using Maximum likelihood (ML) analysis with 1000 bootstrap replications. As per our knowledge, this is the first report of *Ganoderma orbiforme* causing foot rot on Arecanut from India.

PP(S7)/05: An art from waste- discovery of two putative novel rhabdoviruses and a solendovirus from the transcriptome dataset of a medicinal herb, water hyssop (*Bacopa monnieri*)

V. Kavi Sidharthan* and V.K. Baranwal
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India
**Email: kavisidharthan.v@gmail.com*

Bacopa monnieri (L.) Wettst. (commonly known as brahmi or water hyssop) belonging to the family Plantaginaceae, is an aquatic perennial creeping herb native to Australia and India. Traditionally, water hyssop is regarded as memory revitalizer and mental stress reliever in Indian Ayurvedic medicine. In the current study, a publicly available transcriptome dataset of water hyssop (SRR2826837) was mined for the presence of viral sequences. Through *de novo* assembly using SPAdes and Trinity followed by BLASTn analysis against viral reference genome sequences, the genomes of three putative novel viruses tentatively named as Bacopa monnieri virus 1 (BmV1), Bacopa monnieri virus 2 (BmV2) and Bacopa monnieri virus 3 (BmV3) were discovered. BmV1 and BmV2 genomes resembled those of plant rhabdoviruses. The 13.3 kb long BmV1 genome contained eight antisense ORFs in the order 32 l–N–P’–P–P3–M–G–P6–L–t 5’ with P’ ORF overlapping with P while the 13.2 kb BmV2 genome contained six interspersed ORFs in the antisense orientation (32 l–N–P–P3–M–G–L–t 5’). The 8 kb BmV3 genome possessed five overlapping ORFs with ORFs 2 to 5 similar to solendoviruses. Based on genome organization, sequence similarities and phylogeny, BmV1, BmV2 and BmV3 can be regarded as new members of the genus *Cytorhabdovirus*, *Betanucleorhabdovirus* and *Solendovirus* respectively. The current study will serve as a base for initiating further studies on understanding the distribution and biological properties of the identified viruses.

PP(S7)/06: Studies on anthracnose disease of some selected minor fruits grown in Nadia district of West Bengal

Suryakant Manik*, S. Rizal, P. Sarkar, B.N. Panja and J. Saha
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur - 741252, West Bengal, India
**Email: suryamanik94@gmail.com*

Most of the minor tropical and subtropical fruits have long, well known, good nutritional and medicinal values and contribute to the total fruit production but their importance is confined to local and is within the reach of poor and common people. These minor fruit crops are known to attack by several fungal pathogens that have been reported from various countries including India. But very limited works have been done on the diseases of these minor fruits so far from the state of West Bengal. Isolation, and identification of the pathogens isolated from the diseased samples have been carried out. Some selected minor fruit crops namely Barbados cherry (*Malpighia glabra* L), Litchi (*Litchi chinensis*) and Bael (*Aegle marmelos*) belonging to different families having commercial importance were studied. On Barbados cherry *(Malpighia glabra* L.), the pathogen *Colletotrichum graminicola* was isolated from anthracnose leaf spot. The same pathogen was grown in five (Potato Dextrose Agar, Czapek Dox Agar, Oat Meal Agar, Peptone salt Agar and V8) different media for 10 days of incubation and observed that minimum growth in V8 medium (av. 6.825 cm) and maximum in Potato Dextrose Agar medium (av. 8.875 cm). Litchi plants were also found to be showing typical anthracnose symptoms on their leaves and from morphological studies of the isolated pathogen it was found to belonging to the genus *Colletotrichum* and the from radial growth analysis it was observed similar result obtained in anthracnose disease of barbadose cherry. In case of bael anthracnose, the isolated pathogen was found to be similar to the morphology of *Colletotrichum gloeosporioides* as described by Sutton (1980), but seta was absent in the isolated pathogen. So, the pathogen was considered to be under the genus *Gloeosporium* as it normally lacking seta.

PP(S7)/07: Macroscopic and microscopic vegetative reactions in *Rhizoctonia solani* Kuhn isolates associated with rice, cowpea and amaranth in Southern Kerala

Haritha J. Kumar* and Susha S. Thara
Department of Plant Pathology, College of Agriculture (KAU), Vellayani - 695522, Kerala, India
**Email: harithajkumar666@gmail.com*

Rhizoctonia solani is an economically important, devastating pathogen of a large number of agricultural crops. An examination of macroscopic and microscopic vegetative reactions was carried out in College of Agriculture, Vellayani between paired isolates of *R. solani* associated with rice, cowpea and amaranth in Southern Kerala (171 combinations). Macroscopic vegetative reactions were analyzed using dual culture experiment in two per cent agar medium. The reactions observed were merge (93 combinations), merging line (31), tuft (3), barrage (14), barrage line (30). Microscopic hyphal anastomosis reactions were analyzed using modified cellophane technique in two per cent agar medium. The reactions observed were C0 (No fusion-47 combinations), C1 (Contact fusion-11), C2 (Imperfect fusion-67) and C3 (Perfect fusion-46). C3 reaction was vegetatively compatible and C0, C1 and C2 reactions were vegetatively incompatible. The frequency of anastomosis reactions were less between amaranth and rice isolates and amaranth and cowpea isolates (C0 and C1) and more between rice and cowpea isolates, and within the anastomosis reaction between same hosts (C2 and C3). In the present study, there is no strict correlation exist between microscopic C2 and C3 reactions and macroscopic tuft and merge reactions respectively. These reactions also differentiate the races present in the *R. solani* isolates as they were belonging to different anastomosis groups. This can be correlated to some extent in terms of pathogenicity and host specialization.

PP(S7)/08: A study on biochemical analysis and nutritional value of *Macrocybe giganteum* - A giant mushroom

Megha Suman[1]*, Ishwar Prakash Sharma[2] Shagun Gupta[1]
[1]Shri Guru Ram Rai University, Dehradun - 248001, Uttarakhand, India
[2]Patanjali Herbal Research Department, Patanjali Research Institute, Haridwar - 249405, Uttarakhand, India
**Email: meghasuman90@gmail.com*

Macrocybe giganteum a giant mushroom is a tropical mushroom, that can be cultivated in India during the summer season (April-September). It is similar to *Calocybe indica* in its appearance and production technology. An experiment was carried out with four *Macrocybe giganteum* strains (MA-1, MA-2, MA-3, MA-4) and one *Calocybe indica* strain (CI). The nutritional significance of *Macrocybe giganteum* was also assessed in terms of carbohydrate (TSS), reducing sugars, non-reducing sugars and protein. The total soluble sugars varied among the strains (20.90-26.04%), reducing sugars (3.91-4.37 %) and non-reducing sugars (16.54-22.03%). The protein content reported between 73.20-81.07 mg/g. Nutshell, this study gained the importance of *Macrocybe giganteum* in food industry due to the rich presence of protein and carbohydrate. And the study may conclude that it can be used for protein supplementation in the regular diet.

PP(S7)/09: A macromophological record of wild macro fungi from Chhattisgarh

Pradeep Kumar Badhai*, Harvinder Kumar Singh and C.S. Shukla
Department of Plant Pathology, College of Agriculture, Indira Gandhi Agricultural University, Raipur - 492012, Chhattisgarh, India
**Email: p.badhai27@gmail.com*

In the present investigation a systematic survey was carried out during 2018 and 2019 to prepare an inventory as well as document the wild macrofungi of Chhattisgarh. The first macrofungi appearing post first rains both on forest floors as well as in the Chhattisgarh markets were *Amanita loosii* (Sugamunda), *Amanita caesarea* (Haldi phutu), *Amanita vaginata*, *Agaricus perobscurus*, *Astraeus hygrometricus* (Sal boda, Sarai boda), *Russula rosea* (Paan Phutu), *Russula xerampelina*, *Russula emetica*, *Boletus* sp. (Jam phutu), *Boletus edulis*, *Bovista dermoxantha*, *Russula congoana*, *Lactarius piperatus*, *Lactarius* sp. (Light yellow), *Russula albonigra* (Black), *Cantharellus subalbidus* (Baans phutu). Most of them were found to be in symbiotic association with roots of Sal (Sarai) trees as well as with bamboo plantations. They were documented as ectomycorrhizal fungi contributing to the biomass of Chhattisgarh forests. Other edible and some non-edible fungi recorded were *Auricularia* sp., *Dacryopinax spathularia*, *Ganoderma lucidum*, *Hericium erinaceus*, *Lycoperdon pyriforme*, *Lentinus cladopus*, *Lentinus tigrinus*, *Macrocybe gigantea*, *Macrolepiota procera*, *Pleurotus ostreatus*, *Trametes versicolor*, *Sparassis* sp., *Schizophylum commune*, *Ramaria* sp., *Volvariella bombycina*, *Volvariella volvacea* and *Xylaria* sp.

PP(S7)/10: Morpho-Molecular characterization of different isolates of *Beauveria bassiana* (Bals.) Vuill. as assessed using Internal Transcribed Spacer (ITS) region

Chaithra, M.*, T. Prameela Devi and Deeba Kamil
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India
**Email: chaithram06@gmail.com*

A promising alternative for insect pest control in agriculture is the use of entomopathogenic fungi. The objectives of this work were to isolate and identify morphologically and molecularly the strains of *Beauveria bassiana* from different sources. Nine strains of *B. bassiana* have been partially characterized using morphological traits *viz.*, colony morphology, size and shape of conidia grown on PDA at 27°C. The colony of all the isolates appeared white with different growth pattern. Among them only BbIII and BbVIII isolates showed concentric circles. At 16 DAI, all the nine isolates showed significant difference in the growth rate. Among them, BbIV isolate recorded highest mycelial growth (8.5cm) and lowest was in BbVII isolate (3.5cm). Under compound microscope, all the isolates showed conidia with single cell and oval to round or ellipsoidal with hyalin color and 2-3 µm in diameter. Further, the identification was confirmed by BLAST analysis of amplified 5.8S-ITS region using ITS-1and 4 primers. All the isolates exhibited 5.8S Identity values greater than 99% with strains of *B. bassiana* obtained from NCBI database. Further, confirmed by phylogenetic methods using the Maximum Parsimony algorithm in MEGAX-10.2.4. Our study showed the nine isolates the clear differentiation of nine isolates which were formed into 5clades. Among the nine isolates, BbIX formed separate clad. Which was also different in cultural characters from other isolates by producing dotted type of mycelial growth. But, BbIV and BbVII isolates formed same clad even though they have the different mycelial growth rate. Hence, it is important to note that molecular techniques do not replace or eliminate the need use classical morphological taxonomy tools, but instead, they should be used to complement the studies to achieve a complete, accurate and sufficiently descriptive identification.

PP(S7)/11: Cultural and morphological variability of *Fusarium oxysporum* f.sp. *ciceri*, incitant of wilt of chickpea

K. Venkataramanamma[1]*, B.V. Bhaskara Reddy[2], R. Sarada jayalakshmi[3] and V. Jayalakshmi[1]
[1]*Regional Agricultural Research Station (ANGRAU), Nandyal – 518502, Andhra Pradesh, India*
[2]*Regional Agricultural Research Station (ANGRAU), Tirupati - 517502, Andhra Pradesh, India*
[3]*Department of Plant Pathology, ANGRAU, Tirupati - 517502, Andhra Pradesh, India*
**Email: kvrag84@gmail.com*

Fusarium wilt caused by *Fusarium oxysporum* f.sp. *ciceris* (Foc) is one of the major disease of chickpea and causes significant yield losses. A total of 12 Foc isolates collected from wilt infected plants of chickpea from six districts of Andhra Pradesh. Cultural and morphological characters of different Foc isolates were observed in cultures grown on PDA at 25oC ± 2oC. In all the isolates mycelium was aerial and the texture in different cultures was fluffy, appressed, and less fluffy. In majority of isolates colony colour was white, and in some isolates it was violet, pink, yellowish pink and cream white. Different types of pigmentation such as orange, light yellow, pink, dark brown and purple were observed. Among all the isolates, in seven days, the isolate from Kalyandurgam (Foc-3) grew fast (80 mm) and another isolate from Cumbum (Foc-6) grew slowly (40.5 mm). Under 40 x caliberation mean macro conidia length varied from 16.09 to 28.72 µm, mean width varied from 3.04 to 4.64 µm, having 3 septa in majority of the isolates. Mean micro conidia length varied from 7.1 to 13.36 µm and width varied from 2.2 to 4.5 µm. The diameter of chlamydospores varied from 2.6 to 4.62 µm, located terminally or intercalary. Sporulation was measured under haemocytometer and it was observed in the range of 0.4x106 to 1.3x106 (Foc-9) per ml. This study was clearly indicated that the isolates of Fusarium differed from each other in terms of cultural and morphological characters.

PP(S7)/12: Occurrence and distribution patterns of banded leaf and sheath blight of maize (*Zea mays* L.) incited by *Rhizoctonia solani* Kühn in Uttarakhand, India

Sadhna Chauhan* and Rajesh Pratap Singh
Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar – 263145, Uttarakhand, India
**Email: chauhansadhana19@gmail.com*

Banded leaf and sheath blight (BLSB) is a menacing disease of maize incited by *Rhizoctonia solani* Kühn [teleomorph *Thanatephorus cucumeris* (Frank) Donk] threatening maize cultivation and production in country. Almost little to no information is available on the occurrence and distribution patterns of this disease particularly in various districts of Uttarakhand region. So, in order to establish an understanding of the distribution patterns of this disease, extensive surveys were conducted during the 2017–2019 cropping seasons in all the maize producing regions of the state to record occurrence of this disease as well as diversity in *R. solani* among the naturally occurring populations. Also, forty isolates of the fungus were characterized from 70 diseased samples based on cultural, morphological and pathogenic variability. BLSB has the potential for extensive yield losses up to 40–70% in currently grown cultivars. The survey revealed that this disease exhibits wide range spread with the disease severity ranging from 20 to 80 per cent and gaining the economic importance in the state of Uttarakhand. Such surveys will hold utmost importance for devising disease management strategy and better understanding of its epidemiological aspects as well.

PP(S7)/13: Biology of *Erysiphe cichoracearum* causing powdery mildew of Ivy gourd (*Coccinia grandis*) from West Bengal, India

Goutam Mondal[1] and **Siddharth Singh[2]***
[1]All India Coordinated Research Project on Medicinal and Aromatic Plants and Betelvine, Directorate of Research,
[2]Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Kalyani - 741235, West Bengal, India
**Email: siddharthsingh0459@gmail.com*

Ivy gourd (*Coccinia grandis*) is a climber, trailer, dioecious, and perennial plant. *Coccinia grandis* is a native of East Africa and also found in tropical Asia including India, Pakistan, Bangladesh, Sri Lanka, Indonesia, Malaysia etc., Australia, America and Pacific. The young, tender stem tops, leaves, and tuberous roots of *C. grandis* are used as culinary as well as for pharmacological purposes. Plant preparations from *C. grandis* are indigenously used for various skin diseases, bronchitis, anorexia, cough, asthma, epilepsy, wound healing, leprosy, snakebite, malarial infection, infective hepatitis, and jaundice. During a survey work, the powdery mildew disease was recorded on ivy gourd at Kalyani, Nadia, West Bengal, India (22°59’20"N latitude and 88°27’18"E longitude). The disease symptoms and the morphology of pathogen were studied. The fungi grew ecto-parasitically particularly on the leaf lamina and other tender parts of the host producing enormous superficial mycelium, which appear like a mass of white powder. Severe infection caused leaf distortion, yellowing and withering. Under microscopic study, it was revealed that numerous colourless, thin walled and barrel shaped oidia were produced on the erect conidiophores. The cleistothecia developed in the mycelia mass were tiny, globose and shiny yellow in colour which turned into brown to brownish pink. There were about 13 asci containing two ascospores in each cleistothecium. The average size of oidia and cleistothecia were 31.32 µm x 14.37 µm and 153.49 µm respectively. The pathogen was identified as *Erysiphe cichoracearum* on morphological basis. This is the first report of powdery mildew on Ivy gourd from West Bengal state of India.

PP(S7)/14: Occurrence of rust (*Coleosporium plumeriae*) on Temple tree (*Plumeria acuminata)* in West Bengal, India

Goutam Mondal, Siddharth Singh and **Bandana Mayanglambam***
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia - 741252, West Bengal, India
**Email: bandanamay@gmail.com*

Plumeria acuminata, commonly known as "Temple tree" or "Champa" in India, is native to Mexico, Central America, the Caribbean and South America and spread throughout the tropics. It is a popular landscape, ornamental and medicinal plant with vast economic importance. Many parts of the plant are considered as medicinal and are used traditionally as purgatives, in rheumatism, asthma, piles, gonorrhea, blood disorders and tumors. The occurrence of rust disease on *Plumeria* caused by *Coleosporium plumeriae* was observed at Nadia district of West Bengal, India since, 2018 during the month of December to March with a severity was 5-30%. The symptoms appeared as tiny, raised, rusty, bright yellow or yellow-orange, punctiform, erumpent, and smooth uredinial pustules on lower surface of leaves and corresponding small yellowish lesions on the upper surface. Urediniospores were hypophyllous, elliptical to sub-globose and echinulate and the sizes were 20.26-35.41ìm (Mean-27.33ìm ±3.50) x 15.36-26.07ìm (Mean-20.24ìm ±1.94). Telia formed later on diseased leaves among the uredinia on leaf undersides and were punctiform, erumpent, and smooth. They are not easily rubbed from leaves. Teliospores are smooth, oblong or club-shaped, orange-yellow, oily, and refractile. In advance stage, the diseased leaves became curled, distorted and turned to yellow due to complete leaf chlorosis and necrosis, which ultimately caused to defoliation. Spermagonial and aecial stages of the rust fungus were not observed. It was reported throughout the world. In India, it was reported from Kerala, Meghalaya and Haryana.

PP(S7)/15: Cultural and morphological studies of various isolates of *Fusarium moniliforme* var. *subglutinans* causing Pokkah boeng disease of Sugarcane

Hina Kausar, Geeta Sharma and **Bhagyashree Bhatt***
Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakhand, India
**Email: bhagyashreebhatt15@gmail.com*

Pathogen is a living organism which is dynamic in nature and is subjected to the evolutionary process. It helps a pathogen to survive under stress condition and produce more virulent races, thus studies on variability gives us an idea of population dynamics of the pathogen. *Fusarium moniliforme* var. *subglutinans*, causing Pokkah boeng disease of Sugarcane, is an important pathogen and has reported to cause heavy yield losses. Therefore, a study was conducted to identify the variability in pathogen *Fusarium moniliformae* var. *subglutinans.* 20 isolates of the pathogen, designated as FmU1-FmU20 were collected from different locations of district Udham Singh Nagar and their cultural and morphological variability was studied. To see the variation among conidial characters all the isolates were studied under microscope and found that the fungus produces micro and macro conidia, both varied significantly with respect to shape and size of conidia. On the basis of growth rate, all the isolates were grouped in 3 categories, fast, medium and slow growing, the maximum colony diameter was recorded in isolates, FmU2, FmU10, FmU12, FmU17 and FmU18 after 10 days of inoculation. On the basis of colony texture and pigmentation, a wide range of colour variation was also observed.

PP(S7)/16: A roving survey for fungal foliar diseases of sorghum in Uttarakhand

B.K. Namriboi* and Yogendra Singh

Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar – 263145, Uttarakhand, India

**Email: bknamriboi@gmail.com*

A roving survey for different fungal foliar diseases of sorghum was conducted in different sorghum growing areas of Uttarakhand. A total of 53 farmers' fields were covered in the districts of Udham Singh Nagar, Dehradun, and Haridwar during the Kharif season of 2019 and 2020. The foliar diseases anthracnose, zonate leaf spot, and grey leaf spot were widely distributed. The disease incidence and percent severity of the diseases were recorded in the surveyed areas in both years. The prominent disease recorded was anthracnose with disease incidence as high as 88.7 % and percent severity ranging from 42.7-71.6 %. Zonate leaf spot and grey leaf spot were also recorded with the disease incidence of as high as 67 % and 30 % with percent severity (32-64.4 %) and (11.6-36 %) respectively. Leaf blight was also recorded with <10 % severity in three locations (Khatima, Netanagar, and Chandipur). Further, the samples for these foliar diseases were collected from the surveyed area and the causal organism associated with them was isolated in the laboratory condition. The result depicted that among the isolated pathogens, the most dominant was *Colletotrichum graminicola*, *Gloeocercospora sorghi*, *Curvularia* spp. and *Fusarium* spp. and other fungi found to be associated were *Alternaria* spp. and *Helminthosporium* spp.

PP(S7)/17: Effect of different nutrient media on mycelial growth of blue oyster mushroom [*Hypsizygus ulmarius* (Bull.: Fr.) Redhead]

Aditya*, R.S. Jarial and Kumud Jarial

Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, College of Horticulture and Forestry, Neri, Hamirpur - 170001, Himachal Pradesh, India

********Email: adityabhatia29@gmail.com*

Mushrooms are globally appreciated for their nutritional value and medicinal properties. Their cultivation is an effective bio conversion technology of transforming wastes and woods into highest quality of proteins per unit area. The study was aimed to find out the effect of different solid nutrient media on mycelial growth of *Hypsizygus ulmarius*. Among the different media tested for the mycelial growth of *H. ulmarius*, Potato dextrose agar medium was found to be the best medium (76.20 mm) followed by Malt extract agar medium (59.40 mm) and Czapek's dox agar medium (57.00 mm). These were followed by Asthana and Hawker's medium (46.02 mm) and Carrot agar medium (42.60 mm) which differed significantly with each other after 5 days of inoculation. The mycelial growth in Potato dextrose agar medium was absolutely white having cottony but suppressed ray pattern while Malt extract agar medium showed abundant cottony but fluffy growth with circinate pattern. The growth pattern in Czapek's dox agar medium was however, thin and transparent. The mycelial growth in Carrot agar medium was cottony and compact whereas in Asthana & Hawker's medium it was light thin transparent white and become visible only when seen under light.

PP(S7)/18: Effect of physiological parameters on mycelial growth of blue oyster mushroom [*Hypsizygus ulmarius* (Bull.: Fr.) Redhead]

Aditya*, R.S. Jarial and Kumud Jarial
Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, College of Horticulture and Forestry, Neri, Hamirpur - 170001, Himachal Pradesh, India
**Email: adityabhatia29@gmail.com*

Hypsizygus ulmarius also known as 'blue oyster' or 'elm oyster' is a high yielding mushroom gaining popularity now a days. This mushroom has attractive shape, excellent consistency of cap and stipe, culinary qualities and longer shelf-life. Despite these attractive qualities its production in sub tropical climate has not fully explored. Variability studies on physiological aspects are of immense use to identify the most favorable growing conditions of the mushroom. Hence six level of temperature (10, 15, 20, 25, 30 and 35oC) and five level of pH (4.0, 5.0, 6.0, 7.0 and 8.0) were studied to find out the best temperature and pH for the mycelial growth of *H. ulmarius*. The experiment was conducted in a completely randomised design having four replication of each treatment. *Hypsizygus ulmarius* achieved maximum mycelial growth when the pH of the medium was 8.0 (84.6 mm) followed by pH 7.0 (77.0 mm), pH 6.0 (57.9 mm), pH 5.0 (50.1 mm) and pH 4 .0 (29.3 mm). A temperature of 25oC was found optimum at which maximum diametric growth (77.7 mm) was observed in Potato dextrose agar medium after 5 days of incubation.

PP(S7)/19: Association of arbuscular mycorrhizal and dark septate endophytic fungi in two bamboo species of Manipur

N. Babita Devi* and R.R. Pandey
Department of Life Sciences, Manipur University, Canchipur, Imphal - 795003, Manipur, India
**Email: babi103naorem@gmail.com; rrpandey.mu@gmail.com*

The composition of arbuscular mycorrhizal (AM) fungi in rhizosphere soil and the colonization patterns of AM and dark septate endophytic (DSE) fungi in the roots of two bamboo species viz. *Chimonobambusa callosa* and *Schizostachyum fuchsianum* from Leimakhong Kounu hills of Manipur were assessed. Maximum AM spore density was occurred in *S. fuchsianum*. Altogether, 16 AM fungal species belonging to six genera i.e., *Acaulospora*, *Funneliformis*, *Glomus*, *Rhizophagus*, *Sclerocystis* and *Septoglomus* were isolated from natural field and trap culture soils of both bamboos. Out of all, *Glomus* was the dominant genus represented with five species. Maximum relative abundance (%RA) and isolation frequency (%IF) were recorded with the spores of *Funneliformis geosporum*. However, highest species richness (13 species) was recorded in *C. callosa* soil. The examined root fragments of *C. callosa* and *S. fuchsianum* had dual colonization of AM and DSE fungi and exhibited *Paris*- type of AM morphololology. Incidence of total AM (%RLTC), DSE fungal colonization (%RLDC) and distribution of different fungal structures in the roots of two plant species varied significantly, except that of %RLV and %RLMI (P>0.05). Thus, the presence of AM and DSE associations in selected bamboo species grown in hilly terrains indicate the possibility of utilizing them in agroforestry development.

PP(S7)/20: Prevalence of arbuscular mycorrhizal and dark septate endophytic fungal association in three *Kaempferia* species (Zingiberaceae) of Manipur

L. Surbala* and R.R. Pandey
Department of Life Sciences, Manipur University, Canchipur, Imphal - 795003, Manipur, India
**Email: surbalaloushambam@gmail.com; rrpandey.mu@gmail.com*

Kaempferia species (Zingiberaceae) found in Manipur are well known for their medicinal properties. Hence, we examined the diversity of arbuscular mycorrhizal (AM) fungi in rhizospheric soils and the colonization patterns of AM and DSE fungal structures in the roots of three important ginger species viz. *Kaempferia galanga*, *K. parviflora* and *K. rotunda*, collected from Thoubal District of Manipur, North Eastern (NE) India. A total of 11 AM fungal spore morphotypes belonging to six genera i.e. *Acaulospora*, *Funneliformis*, *Glomus*, *Sclerocystis*, *Scutellospora* and *Septoglomus* were isolated from the rhizosphere of studied gingers. Maximum spore density of AM fungi was recorded in the root-zone soils of *K. rotunda*. The highest percentage of relative abundance (RA%) and isolation frequency (IF%) was recorded with the spores of *Funneliformis geosporum*. The distribution and species richness of AM fungal community was dominated by the members belonging to order Glomerales which was represented by seven species. The examined root fragments of ginger species studied had Intermediate- type of AM morphology. Total root length with AM colonization (%RLTC) and DSE (%RLDC) were highest in *K. rotunda*. Pearson's correlation analysis also revealed the significant positive and negative interactions with some of the soil properties, AM and DSE fungal colonizing variables, respectively. Thus, the occurrence of native AM fungal association in three ginger species suggest that the studied hotspot region harbours a diverse AM fungal community relative to other tropical and subtropical habitats and also reveals the possibility of utilizing them in future for conservation programs.

PP(S7)/21: Preliminary studies on diversity of fungal endophytes from *Coleus forskohlii* (Willd.) Briq.

Grace Leena Crasta[1,2]* and K.A. Raveesha[3,2]
[1]*Department of Botany, St. Joseph's College, Bangalore - 560027, Karnataka, India*
[2]*Department of Studies in Botany, University of Mysore, Mysore - 570005, Karnataka, India*
[3]*Department of life sciences, JSS Academy of Higher Education and Research, Mysuru - 570015, Karnataka, India*
**Email: graceleena11@gmail.com*

Plants inhabit diverse communities of microorganisms such as bacteria, fungi, archaea & protists. The medicinal value of plants could be because of their association with endophytes. Understanding the diversity of culturable endophytic fungi of *Coleus forskohlii* and screening them to yield bioactive compounds would be highly useful for herbal drug industry. The present study throws light upon the diversity of fungal endophytes associated with the leaves of *Coleus forskohlii*. Healthy, Undamaged leaves of *Coleus forskohlii* were collected, washed and surface sterilized using standard protocols. Clean leaf discs were plated on PDA media. The fungal endophytes that emerged from leaves were isolated and identified using 18S rRNA sequencing technique. About 85 fungal endophytes were isolated from 250 leaf bits of *Coleus forskohlii*. Molecular identification using 18S rRNA sequencing revealed 34 different genera of endophytic fungi. The occurrence of *Cladosporium sp.* was found to be highest, and the other predominant genera were found to be *Alternaria sp., Aspergillus niger, Aspergillus sp., Colletotrichum sp., Nigrospora oryzae, Penicillium sp.* & *Phyllosticta fallopiae*. Colonization frequency of the endophytic fungi associated with the leaves of *Coleus forskohlii* was found to be 30.35%. The percentage distribution of members of Ascomycota was the highest, with 96.47% and members of Basidiomycota were distributed least with 3.53%. To bring out the efficacy of the endophytes associated with *C. forskohlii*, various studies can be conducted to benefit the field of herbal drugs.

PP(S7)/22: Cultural, morphological and molecular characterization of *Rhizoctonia* isolates causing banded leaf and sheath blight of maize

Manjunatha S.E.[1]*, Yadahalli K.B.[1], Kalappanavar I.K.[1] and Kachapur R.M.[2]
[1]Department of Plant Pathology, [2]AICRP on Maize, College of Agriculture, University of Agricultural Sciences, Dharwad – 580005, Karnataka, India
**Email: manjunatha932@gmail.com*

Twenty isolates of Rhizoctonia isolates causing banded leaf and sheath blight of maize were collected from different agro-climatic zones of India and were subjected for cultural, morphological, sclerotial and molecular characterization. The results showed the wide variation with respect to cultural, morphological and sclerotial characters. Some of the isolates showed white to light brown and dark brown colony colour, mycelial dispersion varied from aggregate to moderate, colony texture differed from cottony fluffy to sparse fluffy, growth pattern varied from abundant to moderate, hyphal width in the range of very narrow to narrow, the nuclear condition varied from multinucleate to binucleate, sclerotial clump and sclerotia formation varied from slow to moderately fast, sclerotial number per Petri plate varied from excellent to moderate category, sclerotial position differed from central and peripheral to scattered position, sclerotial colour varied from white to dark brown colour, sclerotial size varied from macro or sasakii type to micro size and sclerotial shape was irregular in all the twenty isolates. Molecular characterization revealed that, 13 isolates were identified, confirmed and characterized as *Rhizoctonia solani* AG-1 IA, 5 isolates as *Ceratobasidium* sp. AG-Ba, one isolate as *Ceratorhiza oryzae-sativae* AG-Bb and one isolate was confirmed as *R. solani* AG 2-2-IIIB by using anastomosis (AG) subgroup specific primers for AG-1 IA, AG-Ba, AG-Bb and AG 2-2-IIIB, respectively.

PP(S7)/23: Diversity and characterization of endophytic fungi associated with roots of crop plants cultivated in *Jhum* fields of Manipur, North Eastern India

K. Surendirakumar* and R.R. Pandey
Department of Life Sciences, Manipur University, Canchipur, Imphal - 795003, Manipur, India
**Email: surenderpbt@gmail.com; pandey.rr@rediffmail.com*

Fungal endophytes are known to be diverse and establish a mutualistic relationship with the host plant and protect them from the soil borne pathogens. In this study, we isolated a total of 247 fungal strains belonging to 15 different genera and 29 morphotypes from 300 root tissue segments of selected crop species viz. *Vigna unguiculata*, *Zea mays* and *Oryza sativa* cv. ‘Chakhao amubi’ (aromatic black rice) grown under *Jhum* (shifting cultivation) lands of Manipur, North Eastern (NE) India and identified them based on cultural morphology and molecular rDNA analysis. The endophytic fungal isolation rate (40%) and colonization rate (73%) was maximum in the roots of *O. sativa* cv. The relative abundance (%RA) of endophytic fungi in selected crop plant roots varied from 3.48% to 44.72%. Among all, *Fusarium oxysporum* (28.57%) was the most dominant species with high RA, while *Aspergillus niger* revealed maximum isolation frequency (IF %). Furthermore, the differences in the species distribution of endophytic fungi isolated from different crop species were also recorded. *Aspergillus niger* was commonly recorded with all examined plant roots. Whereas, *Cladosporium cladosporioides, Penicillium ochrochloron, Phialophora mustea* and *Talaromyces assiutensis* were only recovered from the roots of *V. unguiculata*. *Aspergillus* sp.2, *Hypocrea atroviridis* and *Penicillium expansum* were recorded exclusively from the roots of *Z. mays*. Likewise, *Cladosporium tenuissimum*, *Epicoccum nigrum*, *Fusarium* sp.1, *Penicillium sclerotiorum*, *Phoma* sp.1, and *Phomopsis* sp.1 were specifically isolated from *O. sativa* cv. roots. Maximum species richness (SR) of endophytic fungi was recorded with the root segments of *O. sativa* cv. (21) followed by *V. unguiculata* (15) and *Z. mays* (8). In addition, the diversity indices of isolated fungal endophyes were also calculated. Thus, the present findings reveal the crop plants cultivated at highlands (stressed conditions) harbors many different fungal species and that can be explored by different biological applications.

SESSION 8

Climate change impact on pests and diseases
Epidemiology, disease forecasting, modelling, crop loss assessment

Keynote Lectures

KN(S8)/01: Modelling yield losses caused by wheat rusts

L Willocquet* and Serge Savary
INRAE, Centre Occitanie Toulouse, UMR AGIR, 31320 Castanet-Tolosan, France
**Email: laetitia.willocquet@inrae.fr*

Wheat rusts have been the cause of severe epidemics in several parts of the world since the beginning of this century, and it is necessary to produce reliable yield loss analyses in order to develop effective strategies to improve disease management. A powerful approach to design and to evaluate the efficiency of disease management strategies involves yield loss modelling using process-based models in which the physiological consequences of disease on the functioning of crop stands are explicitly incorporated as damage mechanisms. In this presentation, yield loss modelling for wheat rusts is first discussed on the basis of the two damage mechanisms that are most frequently considered. First, a reduction in green Leaf Area Index (LAI) occurs as a result of the loss of photosynthetic tissues which are covered by rust lesions, and this reduces the fraction of radiation intercepted by the crop canopy. Second, assimilates produced by photosynthesis are diverted to the rust pustules, mainly in order to produce uredospores. The special case of stem rust is then especially considered. Stem rust causes lesions on leaf blades, but it typically also causes lesions on sheaths and stems. This brings about the need to incorporate the effects of lesions developing on sheaths and stems. The impact of rusts under climate change is finally discussed, with emphasis on the interaction between disease severity and drought intensity. Rust pustules may act as breaches in the cuticle, which may increase plant transpiration in diseased plants. This third mechanism could lead to massive impact of rusts on plant physiology, and ultimately on yield losses, especially when plants are exposed to drought stress.

KN(S8)/02: Adaptation strategies for plant disease management under climate change

Karen A. Garrett*
University of Florida, Gainesville, Florida, USA
**Email: karengarrett@ufl.edu*

The risk of crop losses to disease and insect pests is strongly tied to weather, so climate and climate change are key risk factors.Crop breeding for resistance to pathogens and herbivores is one of the most important tools for adaptation to climate change, and breeding strategies also must grapple with climate variability.Adaptation by farmers includes decision-making about crop variety and on-farm management, but the regional landscape of farms and farm management will often determine how successful an individual farmer can be. Decision support tools can aid in regional management strategies, such as scenario analysis to determine the likely outcomes of policies intended to support adaptation to climate change.For example, impact network analysis (INA) is a framework for evaluating how successful regional disease management strategies are likely to be, and what sorts of adjustments are necessary under climate change and climate variability.Three key examples of such impact networks are system-level management of new invasive diseases, seed systems which may or may not reduce the spread of disease through seed, and crop breeding networks that determine how limited pools of disease resistance genes are deployed across landscapes.Many diseases with major impacts on farmers are currently spreading into new agricultural regions.Climate change can play a role in their spread, along with the important role of increased human transport.Effective management of newly introduced pathogens often depends on cooperation by a critical proportion of farmers, and by the managers of seed systems.Farmers choose among crop varieties in a context of variable environments, where key diseases and pests may only be important in some years.In crop breeding networks, good decisions about resistance gene deployment must be made by a critical proportion of crop breeders, or lack of resistance must be compensated by improved on-farm management.Plant pathologists can support the development of communities of practice for adapting regional disease management to new global scenarios.

KN(S8)/03: Microbe-mediated adaptation strategies to minimize climate change impacts on crops

Suseelendra Desai*
Division of Crop Sciences, ICAR-Central Research Institute for Dryland Agriculture, Santoshnagar,
Hyderabad – 500059, Telangana, India
**Email: desai1959@yahoo.com*

Plant-microbiome interactions are imminent as they have co-evolved. The diverse Indian agriculture spread across 127 agro-climatic zones offers a vast diversity of microbiomes. The Crop-microbiome interactions have immense potential in terms of plant growth promotion, nutrient management, biological control and imparting host plant resistance against biotic stresses and abiotic stresses due to extreme weather events like drought, salinity, high and low temperature stresses, and floods. Several of the beneficial microorganism species have been shown to possess one or many of the above-mentioned traits. *Trichoderma*, *Pseudomonas*, *Verticillium*, *Fusarium*, *Pasteuria*, and *Bacillus* are known potent biocontrol agents against plant pathogens, insect-pests, nematodes and weeds. *T. harzianum* ameliorated drought stress effects on tomato plants through growth regulation, protected membranes from reactive oxygen species (ROS) and enhanced plant growth through increased nutrient uptake. Similar results were reported with different microbes on chickpea, maize, wheat, common bean and brassica. VAM fungi are known to not only mobilize phosphorus but also impart drought tolerance in maize and other crops. Inoculation of wheat plants with *Pseudomonas putida* strain AKMP7 reduced membrane injury and the activity of SOD, APX and CAT under heat stress and improved the levels of cellular metabolites like proline, chlorophyll, sugars, starch, amino acids, and proteins. Species of *Bacillus*, *Azospirillum*, and *Pantoea* singly or as a consortium imparted salinity stress tolerance in soybean, wheat, thyme, cotton lavender, rock rose, sage and giant reed by modulating phytoharmone signals, nutrient acquisition, osmolyte accumulation, plant ion homeostatis, and production of extracellular polymeric substances. *Enterobacter cloacae* UW4, *E. cloacae* CAL2, and P. putida ATCC17399/pRKACC imparted flood tolerance in tomato plants. Biochemical, physiological and molecular studies of the plant–microbe interactions could activate Induced Systemic Resistance (ISR) against abiotic and biotic stresses. Recent advances in molecular microbiology research provide several insights and tools for understanding plant-microbiome interactions. The evolving microbiome research suggest presence of ‘core microbiomes’ and ‘keystone species’ among microbial communities. While broadly host-associated core microbiome refers to the common groups of microbes particularly important for host biological function, ‘keystone species’ has a large effect on its environment and the rest of the microbial community in the ecological networks. Research is underway to characterize the core microbiomes of the crop species and also target keystone species for rational manipulation of the structure and function of microbiomes. In this paper, the recent advances basic and applied aspects of plant-microbiome research with a perspective of climate-change induced stress management in crops is discussed

Oral Presentations

OP(S8)/01: Virulence screening of wheat powdery mildew (*Blumeria graminis* f.sp. *tritici*) pathogenic isolates from different agro-climatic regions of India

P. Nallathambi[1]*, C. Uma Maheswari[1], Santosh Watpade[2], Prem Lal Kayshap[3], Sudeer Kumar[3], B. Aarthy[1], Priya Ravikumar[1], Anju Sharma[3] and Rishav Kumar[2]

[1]ICAR-Indian Agricultural Research Institute, Regional Station, Wellington (Nilgiris) - 643231, Tamil Nadu, India
[2]ICAR-Indian Agricultural Research Institute, Regional Station, Shimla - 171004, Himachal Pradesh, India
[3]ICAR-Indian Institute of Wheat and Barley Research, Karnal - 132001, Haryana, India
**Email: nallathambiiari@gmail.com*

Wheat powdery mildew (PM) pathogen emerged as major threat due to climate change in some of the Indian wheat cultivars. It disseminates huge number of asexual conidia and infects susceptible genotypes. A candidate race or virulent isolate of *Bgt* is prerequisite to test true resistance. Hence, a total of 85 *Bgt* isolates representing 3 agro-climatic zones were screened for virulence using host differentials constituted at Wellington. Differentials with 'R' genes (*Pm*) were successful to demarcate the virulence efficacy *Pm* genes and PM population. The virulence was indentified based on Decanary values of individual *Bgt* isolates after artificial inoculations. All these PM isolates expressed diversity in symptoms expression with severity under controlled conditions created at Wellington. Out of 85 *Bgt* isolates, 28 expressed incompatible reactions over 20 *Pm* gene(s) with immune or resistance as avriulent (AVR) isolates. Some isolates expressed virulence efficacy of 40-50% against 'R' genes which are grouped as highly virulent isolates after 7-10 days of artificial inoculations. About 50 % of all the *Pm* genes were overcome such virulence factors (VFs). Results further demonstrated that possibility on inheritance of different avirulent factors (AVFs) within the incompatible population of *Bgt* which might have evolved over the period of infections and establishment. Also combination of *Pm* gene(s) in incompatible host lines effectively counteracted the infection process of *Bgt* isolates. This inherited virulence gene(s) are effective against avirulent isolates of *Bgt* which was indirectly evidenced from low range of Decanary values. All isolates are maintained as seedlings culture for further genetic analysis.

OP(S8)/02: Prevalence of postharvest diseases of Khasi mandarin fruit in Siang region of Arunachal Pradesh

Gireesh Chand[1]*, R.C. Shakywar[2] and Pushpendra Kumar[2]

[1]College of Agriculture, [2]College of Horticulture and Forestry, Central Agricultural University, Pasighat - 791102, Arunachal Pradesh, India
**Email: gireesh_76@rediffmail.com*

The postharvest losses are often more harsh in developing countries due to lack of storage and transportation facilities. Fruit infections by fungi may appear during the growth period, harvesting, handling, transportation and post-harvest stockpile and marketing conditions and after procuring by the consumer. The relatively short shelf-life period provoked by pathogens is one of the most important limiting factors that impact the economic value of mandarin fruits. The Khasi mandarin fruits purchased from local market of Siang regions of Arunachal Pradesh to study the biodiversity of fungal post-harvest decay of Khasi mandarin. A total of 200 infected fruits samples were collected from different local market, small pieces of decay part were inoculated on prepared plates of Potato Dextrose Agar (PDA) media, after 7 days of incubation, pure isolated fungi were identified according to the recommended references. Most common decay fungi are isolated and identified as *Penicillium*, *Aspergillus*, *Geotrichum*, *Colletotrichum*, *Alternaria*, *Botrytis*, and Mucor. Several fungal species (25) belonging to 7 fungal genera could be regarded as post-harvest decay of Khasi mandarin fruits in Siang regions of local market. Proper

measures should be adopted to protect fruits from fungal decay in local market facilities. In recent years, storing mandarin fruit in local market facilities has become *Penicillium sp.* (32.25%) was most prevalent followed by *Aspergillus sp.* (25.50%) and *Geotrichum sp.* in both grower lots of the fruit season of the year 2020 and 2021 respectively. Although, maximum fruit decay incidence (38.46%) recorded from East Siang local market in both the fruit season of the year 2020 and 2021. The purpose of this study of Khasi mandarin; fruit decay diseases is threat to mandarin growers because there is no cost effective fruit decay disease management method to the growers of Khasi mandarin, which is the post harvest mandarin losses in Siang regions of Arunachal Pradesh.

OP(S8)/03: Emerging threat of chickpea rust caused by *Uromysis ciceri* due to climate change

Mallikarjun Kenganal*
AICRP on Chickpea and Pigeonpea Zonal Agricultural Research Station, Aland Check Post, Kalaburagi - 585101 Karnataka, India
**Email: mallikarjun_nss@rediffmail.com*

Chickpea is source of vegetarian protein across the country, its area stands next to pigeonpea, but self-sufficiency in its production is yet to be achieved in India. Pests and diseases are collaterally limiting chickpea production. The current study focuses on spatial and temporal epidemics of chickpea rust caused by *Uromysis ciceri* influenced by climate change. Over the past five years, the lesser known chickpea rust has increased in its incidence severity in North Karnataka popularly known as pulse bowl and has become a threat in its cultivation in Bellary, Koppal, Raichur, Belgaum, Dharwad, Gadag and Haveri districts. The disease during 2015-16 was sparsely seen in Bellary (8.45%), Belgum (14.11%) and Dharwad (9.27%) has increased over the years both in its severity and speared. During 2017-18 it was noticed in all the districts except Haveri. The disease pressure was low except Bellary and Belgum during 2018-19 due to severe drought. It was at exponential rate during 2019-20 and 2020-21. Incidence was recorded on all the cultivated varieties *viz*., JG-11, JAKI, GBM-2, BGD-103 and Annigeri, even during 2019-20 and 2020-21, the recently released cultivars *viz*., NBeG 47, NBeG 49 and Super Annigeri-1were also severely infested. Disease incidence has reached up to 87 per cent in 2020-21 in Bellary (Bellary and Shiraguppa taluks). The changing climate is the main driving force in these recurring rust epidemics recorded. In all the study locations, warmer day temperature and declining night temperatures during the growing season are on record contributing to rapid multiplication and spread of uredospores. Over the four years, the disease incidence was found increasing from December and was spreading till end of February. There is a threat to economical yield of chickpea and if not curtailed shall affect the nutritional security and self reliance of pulses in the country. Study observations hints immediate attention to identify resistant cultivars, suitable management strategies and manipulating date of sowing if can sustain yield potential.

OP(S8)/04: Perceptions on disease and pest status of major cultivated crops in north-western Himalayas under changing climate

Krishna Kant Mishra*
Crop Protection Division, ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora – 263601, Uttarakhand, India
**Email: mishrakkpatho@gmail.com*

Agriculture in Indian Himalayan region is basically subsistence farming challenged by a variety of biotic and abiotic stresses. Himalayas are considered as chief hotspot for majority of diseases and insect-pests which are endemic in nature. In recent years, the region experienced fluctuations in disease and insect-pest scenario. Changing climatic conditions not only influence the phenology of insect-pests and diseases but also their time of appearance/ emergence consequently favouring their increased spread and damage potential. Rice blast and brown leaf spot diseases of rice are endemic in nature and their occurrence in particular season depends on prevailing weather conditions owing to

its severity. False smut and leaf scald diseases were considered as minor and now become major diseases for rice cultivation. In wheat, in addition to yellow and brown rust, black rust has also been observed. Similarly, with respect to insect-pests attacking hill crops, minor pests becoming major has become a common phenomenon. Recent past experienced an outbreak of brown plant hoppers in rice, prolonged emergence periods of white grubs, increased incidences of shoot flies in different crops, which clearly explains the phenomenon. The major cause of these outbreaks can be explained by the alterations in microclimate regimes which in turn under the direct influence of changing climates and altered abiotic environments experienced over the globe. This chapter reviews pest and disease dynamics in relation to the magnitude of variations observed in climatological data. The climate change experienced by Indian Himalayas is severe which is already evidenced as aberrations in rainfall, increased drought years, cold and terminal heat stresses and extreme weather events. Being biological entities, crops and associated insect pests, pollinators and diseases are bound to adjust to these anomalies. With changing climatic conditions, different components of agriculture got affected; therefore, there is an urgent need to study the extent of variability in North-Western Himalayas with climate change along with scientific interventions to combat the yield losses.

OP(S8)/05: Studies on epidemiology of leaf, panicle and fruit blights of litchi caused by *Alternaria alternata* in Bihar state, India

Vinod Kumar[1]***** and Ajit K.D. Anal[2]
[1]*ICAR-National Research Centre on Litchi, Mushahari, Muzaffarpur - 842002, Bihar, India*
[2]*Amity Institute of Microbial Technology, Amity University, Noida - 201313, Uttar Pradesh, India*
**Email: vinod3kiari@yahoo.co.in*

Co-evolution of pathogens with changing climate has affected disease dynamics in litchi (*Litchi chinensis*) and *Alternaria alternata* has emerged as the most important pathogen since 2014 causing leaf, panicle and fruit blights in field and fruit decay at post-harvest stage. Aim of this research was to study some of the epidemiological aspects of the disease. The results showed that 63.6-86.7% blighted panicle samples had association of *A. alternata*. At ambient conditions *A. alternata* propagules (conidia) were viable in infected leaves up to 5 month. The pathogen survived throughout the year on infected leaves in lower canopy of trees and also on nursery plants which acted as primary source of inoculums for infection of panicles and fruits during fruiting season. Results showed that the maximum numbers of conidia were present below tree canopy at 3-6 feet height. Temporal variation showed that the maximum conidia in air were present between 6.00-10.00 AM in morning hours. It was evident that the maximum mycelia growth rate and germination of conidia were at 30 °C. The thermal death point of conidia was found to be 45°C with 10 min. exposure under *in vitro* condition. The maximum mean growth rate and germination percent was recorded at 100% relative humidity. The analysis of prevailing weather conditions throughout flowering and fruiting period of litchi during 2016-2019 revealed that a temperature of about 28-30°C and humidity 60-85% was congenial for panicle and fruit blight disease. The disease severity was more between Tmin 20-22°C and Tmax 32-35 °C.

OP(S8)/06: Analysing influence of temperature on virulence and incidence of blight on mustarad caused by *Alternaria brassicicola*

Chanda Kushwaha[1]***,** Diksha Sinha[1], R.S. Singh[2] and Chandan Kishore[2]
[1]*Department of Plant Pathology,* [2]*Department of Plant Breeding and Genetics, Bihar Agricultural University, Sabour, Bhagalpur – 813210, Bihar, India*
**Email: chanda.kushwaha@gmail.com*

Among the various oilseed crops Indian mustard 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.

According to the Intergovernmental Panel on Climate Change reports; by the end of twenty second 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 present greenhouse emissions. A significant shift in global temperature is likely to affect fungal growth patterns and as a result a pathogen might shift to newer locations or evolve itself. Such evolutions might have significant changes with respect to virulence in the pathogen. Investigations were undertaken to find out the likely effect of warmer condition on the production of extracellular enzymes and its association with melanin production. Results indicated that restricted radial growth and diminished melanin production upon exposure to warmer conditions of 35 °C when compared to those at 25 °C accompanied with enhanced extracellular release of enzymes. Artificial Inoculations of leaves of *Brassica juncea var varuna* with *A. brassicicola* at 35°C. resulted in larger chlorotic zones with reduced incubation period. Indicating increased virulence of the pathogen at higher temperature 35°C. Diverse genotypes of mustard were planted at four dates of planting and were artificially inoculated with *A. brassicicola* at 65 days after sowing. Data on Alternaria blight severity and AUDPC, lesion size and number of spots/ leaf. were noted. Significant effect of Date of sowing on Alternaria blight incidence, AUDPC, lesion size and number of spots/leaf were observed. Date of sowing also affected primary, tertiary branching and test weight of mustard genotypes. Mean number of spots/leaf ranged from 8.29 to 18.68 in first and fourth date of sowing respectively. Genotypes BRRM108, BRRM101 and BRRM yielded well in first date of sowing whereas BRRM106 and BRRM 105 yielded well under forth date of sowing and can be consider for late sown conditions when the sensitive floral development phase is exposed to warmer conditions.

Poster Presentations

PP(S8)/01: Isolation, identification and molecular characterization of *Ustilaginoidea virens* isolates collected from India

Pooja Parmar[1], **B.M. Bashyal[1]*,** Najam Waris Zaidi[2], Rohith, M.[1], S. Gopala Krishnan[3] and Rashmi Aggarwal[1]
[1]*Division of Plant Pathology,* [3]*Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
[2]*International Rice Research Institute, New Delhi – 110008, India*
**Email: bishnumayabashyal@gmail.com*

Ustilaginoidea virens is a plant pathogenic fungus responsible for false smut disease of rice. It is an emerging sporadic disease recorded with an incidence of 0-50% in major rice growing countries. The occurrence of disease was the initially thought to be an indicator of good harvest however, the change in global climatic conditions and introduction of new high yielding varieties have led to change in the disease status from minor to major. Hence, we elucidate a comparatively fast and novel method for isolation of the fungal pathogen followed by morphological and molecular characterization. The developed methodology relies on dusting of spores from the inner surface of sterilized smut balls on the Petri plate containing ampicilllin added potato sucrose agar. The method is recorded with a marked success rate of 80-85%. The microscopic observations showed oval and globose shape of conidia and thick walled chlamydopores at 40x magnification. The identity of the pathogen was confirmed through internal transcribed spacer (ITS) region. Isolates were further characterized using different molecular markers like TEF, ITS, â-tubulin and actin. Germination studies were also carried out with different spores and conidia of *U. virens* in different host extracts (panicle, leaf and stem)**.** The germination of conidia and chlamydospores was significant in panicle extract and significant germination of chlamydospores was observed in yellow color smut balls in comparison to dark green color smut balls. In conclusion, the present study could be useful in *U. virens* isolation, pathogenicity testing and genetic studies may aid in devising management strategies.

PP(S8)/02: Impact of different host plants on oviposition and feeding preference of Lemon butterfly, *Papilio demoleus* Linnaeus (Papilionidae: Lepidoptera)

Meenakshi Devi*, R.S. Jaglan and S.S. Yadav
Shree Guru Gobind Singh Tricentenary University, Gurugram – 122505, Haryana, India
**Email: meenakshihau@gmail.com*

Studies of oviposition and feeding preference of citrus butterfly, *Papilio demoleus* Linnaeus, on Kinnow mandarin (*Citrus nobilis* × *Citrus deliciosa*) were conducted during 2016 and 2017 in the Department of Entomology, CCS Haryana Agricultural University, Hisar. The study on host preference of citrus butterfly (*Papilio demoleus* Linnaeus) revealed that among the four host plants, lemon (*Citrus limon*) was the most preferred host plant for egg laying (21.80 eggs/plant) followed by mandarin (Kinnow) (19.76 eggs/plant) and sweet orange (mosambi) (13.16 eggs/plant), while minimum number of eggs were recorded on grapefruit (4.28 eggs/plant). The maximum numbers of eggs were laid on second day on all host plants by *P. demoleus*. The more number of eggs were laid on the under surface of leaves and stems than other parts. The investigation indicated significant differences in egg laying among different hosts by citrus butterfly. Food consumption and utilization studies indicated that food consumption of *P. demoleus* increased significantly from first to fifth instar. Food consumption was 42.037±4.61 g/larva on grapefruit, while 66.535±5.87 g/larva on lemon. The consumption index (CI) of *P. demoleus* was 7.726±0.787 on grapefruit, while it was 23.783±2.019 on lemon. Relative growth rate (RGR) of *P. demoleus* was 0.465±0.046 on grapefruit whereas it was 1.864±0.147 on lemon. Thus lemon was found to be the most preferred host for growth of *P. demoleus* larvae.

PP(S8)/03: Epidemiological studies on the development of mango dieback and gummosis caused by *Botryodiplodia theobromae* (Pat.) Griff and Maubl

Ankita Thakur*, Shalini Verma and H.R. Gautam
Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan - 173230, Himachal Pradesh, India
**Email: ankitath.16@gmail.com*

Mango (*Mangifera indica*) is one of the prime fruits of India economically, culturally and as well as in terms of area and production throughout the world. It suffers from numerous diseases and post-harvest losses. *Botryodiplodia theobromae* causes mango dieback and gummosis and plays a major role in a disease complex of mango sudden decline in several provinces of India. Various biotic and abiotic stresses on a plant lead to disease progression and ultimately render it sick. The detached twig method (Verma and Singh, 1970) was adopted to study different temperature and relative humidity regimes on the development of dieback. These twigs were replicated thrice and kept under 15, 20, 25, 30 and 35oC with 90% humidity maintained. The effect of relative humidity ranging (76-100%) on disease development was evaluated by using different concentrations of sulphuric acid (McLean and Cook, 1941). A significant difference in the incubation period and the rate of lesion development of *B. theobromae* was observed. At 30oC and 35oC, the shortest incubation period (48 hours) was recorded whereas the maximum mean rate of lesion development (0.54mm/h and 0.53mm/h) was observed at a temperature of 30oC and 25oC, respectively. The shortest incubation (29 hours) was observed at 100 per cent relative humidity, while the maximum mean rate of lesion development (0.53mm/h) was observed at 98.5 per cent relative humidity.

PP(S8)/04: Effect of epidemiological factors on the disease development and progression of Alternaria blight and fruit rot of brinjal under *in-vitro* conditions

Sunil Kumar*, Sandeep Kansal, Chidembra Bhardwaj and Sonia Kaushal
Department of Plant Pathology, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan - 173230, Himachal Pradesh, India
Email: s.k.sharma1194@gmail.com*

Brinjal is a highly cosmopolitan and popular vegetable that is grown for short durations in different seasons of the year and fetches high economic returns. Being a perishable crop it is always subjected to high yield losses due to biotic and abiotic factors. Among the biotic factors, Alternaria leaf blight and fruit rot is one of the most destructive diseases. To study the disease development and progression, an experiment was conducted at different levels of temperature, relative humidity, and leaf wetness under *in-vitro* conditions. The maximum disease progression with the highest apparent rate of infection (0.035mm/ hour) and minimum incubation period (62.07 hr) was recorded at 25 ºC, covering the maximum proportion of leaf area (89.71%) after 6 days of incubation. 35 ºC of temperature and 75 per cent of relative humidity were found least congenial for disease development and covered the minimum leaf area (44.47%) after 117.78 hr of incubation and minimum apparent rate of infection (0.021mm/hr). The study also indicated that the disease progressed in increasing *consonance* with the increase in relative humidity and duration of leaf wetness, and required a minimum temperature of 15 ºC and leaf wetness more than 4 hours for initiation of disease and its development.

PP(S8)/05: Survey and identification of bacterial blight of soybean in Uttarakhand

Kumari Surbhi*, K.P. Singh, Aravind T. and Pooja Bhatt
Department of Plant Pathology, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar - 263145, Uttarakahnd, India
**Email: surbhi.gbpuat2018@gmail.com*

An extensive survey was conducted during *Kharif* season 2019 and 2020 in different districts of Uttarakhand for recording the incidence and severity of bacterial blight of soybean. The disease was found to be more prevalent in hilly regions of Kumaon as compared to Garhwal hills. Average incidence of the disease was recorded to be highest in Udham Singh Nagar (22-24 per cent). In distrct Chamoli comparatively higher incidence of 20 per cent was recorded. In four districts of Kumaon hills i.e. Almora, Bageshwar, Champawat and Pithoragarh fairly a medium incidence of disease was recorded in the range of 10 to 18 per cent. Lowest incidence of the disease (less than 5 per cent) was recorded from Rudraprayag. In Tehri and Haridwar districts, no incidence of the disease was recorded. The difference in severity of disease in these regions is attributed to the differences in their respective altitudes and prevailing conditions of temperature and relative humidity. Disease is found to be more prevalent at places with high humidity and warm temperature. Samples collected from different districts were used for isolation of the pathogen (*Psedomonas savastanoi* pv. *glycinea*). The colonies obtained on King's B medium were found similar in morphology to Psedomonas savastanoi pv. Glycinea and were further tested by biochemical methods.

PP(S8)/06: Fenugreek (*Trigonella foenum-graecum)* powdery mildew development vis-a-vis weather parameters

Kushal Raj* and Rakesh Kumar Chugh
Department of Plant Pathology, College of Agriculture, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: kushalraj@hau.ac.in*

Fenugreek (Trigonella foenum-graecum) popularly known as methi is an important legume with multifarious uses. Its seeds and green leaves used in food as well as in medicinal application, is an old practice of human history. The fresh green leaves of *T. foenum-graecum* consumed as vegetables, dried seeds are used as spice in food preparation, and both leaves and seeds are used in flavouring foods in many countries including India. *Trigonella foenum-graecum* has also been reported to exhibit pharmacological properties including antiviral, antimicrobial, hypotensive, antioxidant, anti-inflammatory, and antitumor activity. The productivity of fenugreek in our country is low due to its cultivation under rainfed, marginal and sub-marginal lands and also due to various diseases *viz.*, Cercospora leaf spot, Charcoal rot, Powdery mildew, Downy mildew, rust, collar rot, damping off, Fusarium wilt and yellow vein mosaic. Amongst those, Powdery mildew caused by *Leveillula taurica* and *Erysiphe polygoni* is a common and destructive disease of fenugreek which causes damage to all above ground parts and losses in seed yield may go upto 50%. It is obligate parasite and the disease is affected by some factors relating to weather parameters. Therefore, the present study was carried out to find out the correlation matrix between weather parameters and disease intensity at different date of sowings. The powdery mildew was favoured when average maximum temperature ranged 25 to 30oC and average minimum temperature ranged 8 to 18oC. It was observed that powdery mildew disease has +ve and highly significant correlation with TMax, TMin and evaporation whereas it have-ve and significant with RhM and RhE.

PP(S8)/07: Impact of weather and crop growth stages on the progression of brown spot disease in basmati rice

H.S. Viswanath* and Ramji Singh
Department of Plant Pathology, College of Agriculture, Sardar Vallabhbhai Patel University of Agricultural Sciences and Technology, Meerut – 250110, Uttar Pradesh, India
**Email: shanmukha.viswanath92@gmail.com*

The present study was carried out at basmati rice growing fields at Crop Research Centre of SVPUAT Meerut, U.P during two consecutive years i.e. 2019 and 2020 .The study was primarily focused upon the combined effect of weather parameters and crop growth stages of rice crop on the progression of brown spot disease. It was noticed that disease was first observed at late vegetative stages in both years i.e. 2019 and 2020 and reached its maximum during ripening phase of the crop with total AUDPC'S of 1190.52 and 873.6 respectively during these two seasons. Significant negative correlations of disease intensity with maximum and minimum temperatures of -0.635 & -0.980 and -0.883 & -0.987 during 2020 and 2019 respectively were recorded indicating reduction in maximum and minimum temperatures during end of the crop season greatly favored disease progression, whereas, no significant correlation was observed with morning relative humidity and progress of disease during both years. Highly significant negative correlation of disease severity with evening relative humidity (-0.803) was recorded during year 2020 and non-significant correlation of e-RH (-0.477) was observed during 2019 which might be the reason for comparatively lower level of disease during year 2020. Although non-significant negative correlation of disease severity with overall rainfall during the entire crop season was recorded during both years, highly significant positive correlation of 0.988 and negative correlation of -0.547 was observed from late vegetative to early reproductive stage during 2019 and 2020 respectively, indicating high intermittent rainfall during initial reproductive stage of crop might be responsible for large amount of spore dispersal (high inoculum pressure) leading to greater disease progression during 2019.

PP(S8)/08: Epidemiology of *Tillitia indica* inducing Karnal bunt

Mamta*, Rajender Singh and Man Mohan
Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004, Haryana, India
**Email: dahiya107@gmail.com*

Karnal bunt disease of wheat continues to be a potential threat to production and trade of wheat. Weather play a crucial role in disease development, therefore to analyse the effect of various weather parameters such as minimum and maximum temperature, minimum and maximum relative humidity, total rainfall and rainy days of February to mid March were correlated with Karnal bunt incidence of wheat from wheat samples collected from different grain market of Haryana. Karnal bunt incidence had significant positive correlation with maximum temperature (0.629), rainy day(0.207) and total rainfall(0.637) from February to mid March 2016-17 and 2017-18. On the basis of these weather parameters and KB incidence, regression equation Y (Prediction) = $0.629 + 0.023\ T_{max} + 0.008_{rainfall} – 0.012_{rainy\ days}$, $R^2 = 0.67$ was developed. Thus, these weather parameter may be predetermining of KB occurrence which can be harnessed by seed grower and policy makers.

PP(S8)/09: Prevalence of soybean diseases in north eastern state, Assam

Munmi Borah[1]* and Shamarao Jahagirdar[2]
[1]Department of Plant Pathology, Assam Agricultural University, Jorhat - 785013, Assam, India
[2]Department of Plant Pathology University of Agricultural Sciences, Dharwad - 580005, Karnataka, India
**Email: munmi.borah@aau.ac.in*

There were very few reports of North East India, which explained disease occurrence in soybean. Survey and identification of soybean diseases were made from soybean fields in Assam during the year 2018-2019 and results revealed, soybean in Assam as disease stressed crop. Seed rot (*Pythium*, *Phytophthora*), Seedling mortality (*Phytophthora*, *Rhizoctonia*, *Pythium*) and Root & lower stem decay (*Fusarium*, *Rhizoctonia*, *Phytophthora*) were common during rainy days viz. July 25th to until August 2nd week. Collar rot (Coll.R.) observed during August 15th Onward at seedling to Vegetative growth stage of the crop. Weather data revealed that in the month of July- August maximum rainfall was experienced resulting in severity of many diseases. Among foliar diseases Alternaria leaf spot appeared during first week of September vegetative growth stage of the crop. Comprehensively analyzing the relationship between crop disease and weather conditions, we could draw with the conclusion that due to heavy rain during the month of July –August there is occurrence of most of the fungal diseases in Assam. Our study showed interesting fact about weather co-relation with pathogenic microbes in soybean crop. Furthermore Mungbean yellow mosais disease was identified by Polymerase Chain Reaction (PCR) using primers targeting the Coat protein region of the virus. The PCR results revealed a ~524 bp band size, thus confirming the presence of the virus in the infected samples. This is the first report of *Mungbean yellow mosaic virus* infecting soybean crop from Assam using molecular tool.

SESSION 9

Impact of COVID -19 on Indian agriculture

Delivery system, export -import hindrance, labour crisis, production systems

Oral Presentations

OP(S9)/01: Consumer producer co-opted linkage through e-resources for farm solutions and marketing of produces during COVID-19 pandemic

Mallikarjun Kenganal*

AICRP on Chickpea and Pigeonpea, Zonal Agricultural Research Station, Aland Check Post, Kalaburagi – 585101, Karnataka, India

**Email: mallikarjun_nss@rediffmail.com*

Crop cultivation has suffered worst during COVID-19 outbreak but marketing had ruined lives of many who directly and indirectly depended on production and supply chain of farm produces. Growers and consumers were the worst affected and study focuses on special initiatives undertaken during the pandemic period by the Agricultural institutes. Kalaburagi is the first district to record death of human being due to COVID19 in India and trauma of the disease could be imagined out of it. Rural areas were no exception of it. Farmers who depend upon APMC and rural hats for marketing their farm produce witnessed closure of these marketing facilities, restrictions on transportation facilities, movement of labors and individuals left everyone stressed. On the other hand, consumers irrespective of rich poor and middleclass struggled to source daily food needs. These difficulties on dual side were solved by proactive intervention and involvement of Zonal Agricultural Research Station (ZARS), Krishi Vigyan Kendra, along with government officials of agriculture, horticulture and revenue departments in Kalaburagi district. Farmers under distress were given fixed mobile number to register their grievances on mobile number at Agri-war room either by calling or Whats-app message to get their problems resolved without physical movement or contact. Queries related to pest and disease management were solved using e-sap and Whats-app messages, photos, video calls and providing you tube videos on proper managements. Those approaching with difficulties to sell their farm produce especially fruits and vegetables were provided single platform on Whats-app group to put their detailed information. Each farmer was to provide details of types of produce available, quantity, quality, frequency of availability, packing size, grade and distance from ZARS and KVK. On the other side, consumers in Kalaburag city were given wide publicity about door delivery of kitchen needs especially fruits and vegetables at affordable price and informed to register their demand in a specified Whats-app group. The ZARS & KVK warehouses were temporarily served as aggregating points for all the farm produces from different farmers registered in the producers group and segregating in to customized packs as per each consumer demand. This unique system helped in avoiding social gatherings, congregation of public; maintain hygiene, 2m social distancing with each other which were all essential at the moment and prescribed by the government. In order to transport produces, Tata trust “Kalike” was roped in to get their pickup vans for transportation of produces. The Agriculture, Horticulture department officials issued necessary passes for free movement of vans on roads and permission from revenue department for staff engaged in had helped in operating the system hassle free. The entire system was guided by ZARS and KVK engaging FPO and SHG member volunteers. Results were beyond expectations and had opened new way of marketing farm produces without middlemen. The use of e-platform and gadgets helped in avoiding spillage of farmers profit and consumers’ savings into many hands in between production and door delivery of farm produces. There was only 12 per cent extra price the consumers paid over what farmers gained and that extra was paid towards volunteers engaged and transportation. The system adopted at the time helped more than 370 farmers with 8000 consumers with a turnover of more than 12.7 corers was very much appreciated by both GOK and GOI. The model entered in to the collections of best practices for marketing farm produces during COVID-19 outbreak compilations of ICAR. This shall be continued in future also suits well under the new farm laws being implemented by Indian government.

OP(S9)/02: Impact of COVID-19 on Indian floriculture industry

Ch. Sai Ratna Sharavani[1]* and K. Gopal[2]

[1]Deparment of Floriculture and Landscape Architecture, [2]Department of Plant Pathology, Dr. Y.S.R. Horticultural University, Venkataramannagudem, West Godavari Dist – 534101, Andhra Pradesh, India

**Email: chnani11@gmail.com*

Floriculture is one of the important commercial trades in Agriculture owing to steady increase in demand of flowers. India has exported 16,949.37 MT of floriculture products to the world for the worth of Rs. 541.61 Crores/75.89 USD Millions in 2019-20. The flower industry in India caters to a huge domestic market and provides livelihoods to workers and farmers in rural areas. But after the outbreak of COVID 19 Pandemic, Floriculture sector is also badly affected as any other sector. There was a complete collapse of the market as a result of the nationwide lockdown in two phases (Phase I - 25 March to 14 April 2020 and Phase II – 15 April to 3 May 2020), restricting all social gatherings, weddings, cultural activities, religious places and the closing of the hotel and hospitality industry, has destroyed the demand for flowers. The highly perishable nature of the floriculture produce requires quick sales or a cold chain for distant markets. Due to closure of air and surface transport and also lack of labour, farmers has dumped their produce which brought the flower industry to a standstill. The Government of India (GoI)'s decision to partially open retail shops from 25 April 2020 with some restrictions has helped to resume the supply chain though to a limited extent. But it is unlikely that the demand would build up to pre-lockdown levels. The Government of India should initiate various schemes and programs to help the flower farmers to cope up from the biological disaster and make floriculture sector to rise again.

Poster Presentations

PP(S9)/01: COVID-19: Impact on Indian Agriculture Sector

Dinesh Kumar*, Debanjan Mahapatra and Omprakash

Department of Plant Pathology, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur - 848125, Bihar, India

**Email: dineshmarhi1998@gmail.com*

Farming remains the central pillar of Indian economy. The country like India is mainly dependent on agriculture. COVID-19 has vanished many things while in some part it is returning also. Due to COVID-19 it came into focus that the new technology should be adopted in agriculture to have timely operations in maximum conditions. Use of advanced machinery also reduces the demand of labour, mainly useful in area where there is the insufficiency of labour. It also decreases the wages spent on labour. There is interruption of supply chain which leads to think upon the proper transport chain of the perishable products. Farmers also adopted various online learning platforms for getting updated information about market, timely operations on fields. It also leads to negative impact on agriculture. Like farmers do not get information for timely spray of different chemicals on crop which leads to loss of crop. It also generated unemployment among various labourers and small farmers. Similarly, Punjab, Haryana and other north states of India are among India's agricultural powerhouses, although in these states most of the work is done by migrant labour from East side. Thus COVID-19 has positive as well as negative effect on agriculture.

SESSION 10

Stakeholders meet on plant protection issues
Industry, academia, government, farmers interface

Keynote Lectures

KN(S10)/01: Plant clinic diagnosis worldwide and amateurs plant doctors versus phytiatry doctors

Pratibha Sharma*
Department of Plant Pathology, SKN College of Agriculture, Jobner, Jaipur – 303329, Rajasthan- India
**Email: psharma032003@yajoo.co.in*

Plant clinic or plant health clinic concept is emerging area in modern agriculture which provides crop care solutions for the farming community and also links the farmers with scientific community. In India Plant Health Clinic is a part of Plant Protection department of Agricultural Universities. Global Plant Clinic (GPC), a part of CABI and agricultural organizations in different countries provides training on agriculture farming to the farmers and also train the plant doctors and agricultural scientist for the betterment of practical advices to the farmers. Another important aspect is who should be a Plant Doctor. Plant Doctors, plant health practitioners academically trained across agricultural science discipline, including both pest-related (entomology, plant pathology, nematology, weed science, and other pests) and plant-related (agronomy, horticulture, soil and water science, etc.) disciplines, need to be the important components for Plant Doctor courses which directly serve agriculture and the general public, through the prevention, diagnosis and management of plant health problems. Plant Medicine or Phytiatry as Medicine in Plants and Veterinary in animals could be a University science directly connected with all aspects of basic and applied topics of various related sciences. Farmers need to follow scientific methods and technologies for the successful agriculture outputs. This is indeed very essential since presently youth is not attracted towards the farming sector. .Lack of Plant Medicine Doctors allows amateurism and unqualified non technical persons to teach and guide farming community which may lead to several losses to the crop.

INDIAN PHYTOPATHOLOGICAL SOCIETY

National e-Conference

Plant Health and Food Security: Challenges and Opportunities

March 25-27, 2021

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Hall 1	https://us02web.zoom.us/j/86303302267?pwd=OUZYd2xEaHRobHdoRHVoMDJPM0ptQT09	**ID:** 863 0330 2267 Passcode: 102370
Hall 2	https://us02web.zoom.us/j/81186328790?pwd=aEFDRUNNbWJwaGwvUDN1TUdCTExzUT09	**ID:** 811 8632 8790 Passcode: 955155
Hall 3	https://us02web.zo.us/j/83078388487?pwd=eFFmWDlna1F1REp3czVUMEE0UVZLdz09	**ID:** 830 7838 8487 Passcode: 618202
Hall 4	https://us02web.zoom.us/j/81782330937?pwd=aHVMYkZ2bGwrdEFaZmNEUXhlamdCZz09	**ID:** 817 8233 0937 Passcode: 417006

PROGRAMME OF TECHNICAL SESSIONS

Day 01 (Thursday, March 25, 2021)		
10.00-11.30	**Mundkur Memorial Award Lecture** by **Dr. C. Chattopadhyay**, Joint Director Academic (Acting), ICAR-IIAB, Ranchi, Jharkhand Plant Pathology in the Era of New Education Policy: challenges and opportunities **M.S. Pavgi Memorial Award** by **Dr. R. Viswanathan**, Principal Scientist & Head, Division of Crop Protection ICAR-SBI, Coimbatore, Tamil Nadu Impact of yellow leaf disease in sugarcane and successful disease management to sustain crop production **Plenary Lecture 1: Dr. Ravi Khetarpal**, Asia-Pacific Association of Agricultural Research Institutions (APAARI), Bangkok Asia Pacific Scenario on Plant Health and Food Security Challenges	**Hall 1** **Chairs:** Prof. Anupam Varma Prof. B.L. Jalali
12.00-13.30	**Inauguration Session**	**Hall 1**
13.30-14.15	**Lunch Break**	
14.15-15.00	**Presidential Address** by Dr. P.K. Chakrabarty, Member, ASRB, KAB, New Delhi, India	**Hall 1** **Chair:** Dr. C.D. Mayee
15.00-17.30	**Technical Session 3: Next generation pesticide and application** (Biomolecules, immune boosters, nano-molecules, ICT, automization like robotic & drone)	**Hall 1** **Chairs:** Dr. T.S. Thind Dr. Madhuban Gopal

		Rapporteurs: Dr. Srikanta Lenka Dr. Jameel Akhtar
	Keynote Lectures (01)	
	Dr. Neena Mitter, Director, Australian Research Council Industrial Transformation Research Hub for Sustainable Crop Protection, The University of Queensland, St Lucia, Australia Next generation RNA based biopesticides	
	Oral Lectures (07)	
	Dr. Vinod Singh Mehra, Corteva Agriscience, The V- Ascendas, Hyderabad, Telangana, India Zorvec® Active (Oxathiapiprolin)- A new generation chemistry for the management of Grape Downy mildew	
	Dr. Srikanta Lenka, Crop Protection Division, ICAR-NRRI Cuttack, Odisha, India Evaluating the field efficacy of new and commercially available fungicides against sheath blight of rice caused by Rhizoctonia solani Kuhn	
	Dr. Sanjeev Kumar, Department of Plant Pathology, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, Madhya Pradesh, India Comparative Efficacy of Plant extracts and fungicides for Management of Wilt of Chilli	
	Dr. Vinod Upadhyay, Regional Agricultural Research Institute (AAU), Gossaigaon, Assam, India Evaluation of fungicides in reducing disease progress and rate of infection of Phytopthora infestens in potato	
	Dr. Prakasam Vellaichamy, ICAR-Indian Institute of Rice Research, Hyderabad, Telangana, India Potentiality of new fungicide Mefentrifluconazole 400 g/l SC to curtail sheath blight and grain discoloration of paddy	
	Dr. Manoj Kumar, CCS HAU, Regional Research Station, Bawal (Rewari), Haryana, India Efficacy of different fungicides/chemicals under in vitro conditions against Rhizoctonia solani causing black scurf of potato (Solanum tuberosum)	
	Dr. Sudha M., Division of Plant Pathology, Central Coffee Research Institute Coffee Research Station, Chikkamagaluru, Karnataka, India Bio-efficacy of promising fungicides for management of coffee leaf rust disease caused by Hemileia vastatrix B. & Br.	
15.00-17.30	**Technical Session 4: Host-pathogen interaction and genomics of plant pathogens** (Molecular basis of host-pathogen interaction, genome announcement, patho-genomics, functional genomics)	**Hall 2** **Chairs:** Dr. V.G. Malathi Dr. J. Kumar **Rapporteurs:** Dr. Basavaraj Dr. Susheel Kumar Sharma
	Keynote Lectures (05)	
	Prof. Robert F. Park, The University of Sydney, Faculty of Science, School of Life & Environmental Sciences, Plant Breeding Institute, NSW Host-pathogen interactions in the rust pathogens of wheat and barley	

	Dr. R. Sridhar, Independent Researcher, Plot No. 54, Padmavathy Street Santosh Nagar Extn. Madanandapuram, Chennai, Tamil Nadu Recognition and specificity: Gene-for-gene resistance and beyond	
	Dr. Dilip Lakshman, Sustainable Agric. Systems Lab., USDA-ARS, Beltsville, United States Exploring the Genomic Landscapes of Rhizoctonia solani and Development of RsolaniDB - a Comprehensive Omic Resource for the Soilborne Basidiomycetous Phytopathogen	
	Prof. Arnab Pain, Pathogen Genomics Laboratory, Biological and Environmental Sciences and Engineering (BESE) Division, KAUST, Jeddah, Saudi Arabia, Exploring the Genomic Landscapes of *Rhizoctonia solani* and Development of RsolaniDB - a Comprehensive Omic Resource for the Soilborne Basidiomycetous Phytopathogen	
	Dr. Kalyan K. Mondal, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India *Xanthomonas oryzae* pv. *oryzae*-effectors vs rice immunity: Understanding and scope for bacterial blight management	
	Invited Lectures (03)	
	Dr. Bikash Mandal, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Begomovirus species-specific detection by PCR	
	Dr. Ishwara Bhat, ICAR-Indian Institute of Spices Research, Kozhikode, Kerala, India Piper DNA virus 1 is an endogenous pararetrovirus integrated in chromosome 14 of black pepper (Piper nigrum L)	
	Dr. Makeshkumar T., ICAR-Central Tuber Crops Research Institute, Sreekariyam, Thiruvananthapuram, Kerala, India Role of small RNAs in plant-virus interaction with special reference to cassava mosaic virus – cassava system	
	Oral Lectures (04)	
	Dr. Rahul Chavhan, V.D. College of Agricultural Biotechnology, Vasantrao Naik Marathwada Krishi Vidyapeeth, Latur, Maharashtra, India Candidate flowering genes expression during the battle of Pigeonpea Sterility Mosaic Virus in Pigeonpe a (*Cajanus cajan*(l) Millsp.)	
	Dr. Susheel Kumar Sharma, ICAR Research Complex for NEH Region, Manipur Centre, Imphal Emerging Virus and Virus-like Pathogens Prevalent in North East Region of India: Characterization and Simplified Diagnostics	
	Dr. Shumaila Shahid, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi Evaluation for host resistance in muskmelon, cucumber and bittergourd against Fusarium wilt disease	
	Dr. Sumit Jangra, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Localization of tospovirus nucleocapsid protein (N) in cells of Thrips palmi in-vitro	
	Dr. Bhaskar Reddy, Division of Plant Pathology, ICAR-Indian	

	Agricultural Research Institute, New Delhi, India Hybrid de novo assembly and functional annotation of rice blast-causing *Magnaporthe oryzae* reveals versatile metabolic pathways and pathogenicity factors	
	Ms. Thungri Ghoshal, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Characterization of pseudoTALEs of Indian strain of *Xanthomonas oryzae* pv. *oryzae* race 4, the bacterial blight pathogen of rice	
15.00-17.30	**Technical Session 5: Diagnostics and genetic variability** (Diagnostics, genetic variability, sensor based detection viz.,nano-sensors, e-nose)	**Hall 3** **Chairs:** Dr. R.K. Jain Dr. M.P. Thakur **Rapporteurs:** Dr. M.S. Gurjar Dr. K. Sakthivel
	Keynote Lectures (02)	
	Dr. Rashmi Aggarwal, ICAR-Indian Agricultural Research Institute, New Delhi, India Advances in Genomics and diagnostics of fungal plant pathogens and their management	
	Dr. Ramasamy Selvarajan, ICAR NRC Banana, Tiruchirapalli, Tamil Nadu, India Recent developments in plant disease diagnostics using laboratory and artificial intelligence dependant IoT methods	
	Oral Lectures (08)	
	Dr. Malkhan Singh Gurjar, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Multilocus Sequence Typing and Simple Sequence Repeats Analysis in *Tilletia Indica* Isolates Inciting Karnal Bunt of Wheat	
	Dr. Lakshman Prasad, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Morpho-molecular characterization of Alternaria alternate associated with the blight of Linseed	
	Dr. Meenu Gupta, Department of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India Association of *F. oxysporum* with basal rot of garlic and Effect of different soil temperature and moisture levels on its development	
	Dr. Gayatri Biswal, Department of Plant Pathology, Odisha University of Agriculture & Technology, Bhubaneswar, Odisha Characterization of *Ralstonia solanacearum* isolated from coastal area of Odisha infecting solanaceous crops	
	Dr. Chinnaraja Chinnadurai, The University of the West Indies, Department of Life Sciences, Faculty of Science and Technology, St Augustine, Trinidad And Tobago ZYMV-Trini: An emerging genotype of Zucchini yellow mosaic virus causing severe mosaic in cucurbits in Trinidad and Tobago	
	Dr. Sakthivel K., Crop Protection Section, ICAR-Indian Institute of Oilseed Research, Hyderabad, Telangana, India Intra-regional population biology of *Xanthomonas oryzae* pv. *oryzae* causing bacterial blight of rice in the Andaman Islands, India: revelation by Pathotyping and Multilocus Sequence Typing (MLST)	

	Dr. Ravinder Kumar, Bemloe CPRI Shimla 171001 Himachal Pradesh, India Development of one step reverse transcriptase-recombinase polymerase amplification method for the detection of potato virus S in potato leaves and tubers	
	Dr. Anshul Arya, FASC, SGT University, Gurugram, Haryana Deciphering the Morphological and Genetical variability among the isolates of *Fusarium oxysporum* f.sp. lentis causing wilt of lentil	
15.00-17.30	**e-Poster Presentation Session (Session 3, 4, 5)**	**Hall 4** **Chairs:** Dr. G.P. Rao Dr. M.S. Saharan **Rapporteurs:** Dr. Gireesh Chand Dr. Vinod Kumar

Day 02 (Friday, March 26, 2021)		
10.00-11.30	**Plenary Lecture 2: Dr. Serge Savary**, INRA, UMR1248 AGIR, Université Toulouse, INPT, UMR AGIR, F-31029 Toulouse, France The State of Global Plant Health and the Consequences of Global Changes	**Hall 1** **Chairs:** Dr. S.S. Chahal Dr. D.V. Singh
	Sharda Lele Memorial Award by **Prof. V. Devappa**, Professor & Head, Department of Plant Pathology, College of Horticulture (UHS Campus), Bengaluru, Karnataka, India Status of pomegranate wilt (*Ceratocystis fimbriata*) in Karnataka and it's management strategies	
	J.P. Verma Memorial Award by **Dhruva Kumar Jha**, Professor, Department of Botany, Gauhati University, Guwahati, Assam, India Problems and Prospects of Utilization of Bacterial Endophytes for the Management of Plant Diseases	
10.00-13.00	**Technical Session 2A:** Eco-friendly management (Biocontrol, organic farming, conservation agriculture, biopesticide, IPM/IDM)	**Hall 2** **Chairs:** Dr. A.N. Mukhopadhyay Dr. H.B. Singh **Rapporteurs:** Dr. Mehi Lal Dr. Amalendu Ghosh
	Keynote Lectures (04)	
	Dr. Becky Westerdahl, Extension Specialist and Professor of Nematology, Department of Entomology and Nematology, University of California, Davis, USA Eco-friendly Management of Plant Parasitic Nematodes	
	Dr. Daniel P. Roberts, Research Leader, Sustainable Agricultural Systems Laboratory, USDA-ARS, USA Precision agriculture and geospatial techniques for sustainable disease control	
	Dr. R.N. Pandey, Department of Plant Pathology, B.A. College of Agriculture, Anand Agricultural University, Anand, Gujarat *Trichoderma* spp. in the management of stresses in plants, their commercialization for sustainable agriculture and rural prosperity	
	Prof. M.S. Reddy, Asian PGPR Society for Sustainable Agriculture, Department of Entomology & Plant Pathology, Auburn University, AL, USA Integrated nano-based microbiome and smart agriculture for plant health management	
	Dr. Ranajit Bandyopadhyay, International Institute of Tropical Agriculture (IITA), Oyo, Nigeria	

	Research to commercialization pathway of a public biocontrol innovation: The case of aflatoxin biocontrol in Africa	
	Invited Lectures (04)	
	Dr. D.J. Patel, Nico Orgo Manures, Dakor, Dist. Kheda, Gujarat Integrated nano-based microbiome and smart agriculture for plant health management	
	Dr. Jyotsana Sharma, ICAR-National Research Centre on Pomegranate, Solapur, Maharashtra, India SIX-STEP management practices: An effective, economical and eco-friendly technology to control bacterial blight in Pomegranate	
	Dr. Mujeebur Rahman Khan, Department of Plant Protection, Aligarh Muslim University, Aligarh, Uttar Pradesh, India Important nematode problems in cereal crops and their management	
	Dr. Gururaj Sunkad, University of Agricultural Sciences, Raichur Karnataka, India Prospects of Plant Growth Promoting Microorganisms for the management of Plant Diseases under Changing Scenario	
	Oral Lectures (05)	
	Dr. Kushal Raj, Department of Plant Pathology, CCS Haryana Agricultural University, Hisar, Haryana, India Exploring biocontrol potential for management of alternatria leaf spot of aloe vera	
	Dr. Mahender Singh Yadav, ICAR-National Research Centre for Integrated Pest Management, New Delhi, India Bio-intensive strategy for sustainable management of disease in *Brassica juncea*	
	Dr. Bishnu Maya Bashyal, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Molecular programming of drought challenged *Trichoderma harzianum* bioprimed rice (*Oryza sativa* L.)	
	Dr. Veena S.S., Division of Crop Protection, ICAR-Central Tuber Crops Research Institute, Sreekariyam, Thiruvananthapuram, Kerala, India Eco-conscious approaches to manage fungal diseases of aroids	
	Dr. Mehi Lal, ICAR- Central Potato Research Institute, Regional Station, Meerut, Uttar Pradesh, India Antagonistic and phosphorus solubilizing activities of native Pseudomonas spp. Against soil and tuber-borne diseases of potato (*Solanum tuberosum* L.)	
10.00-11.30	**Technical Session 6: Plant quarantine** (Agro-terrorism, regulatory rules, amendments, certification, global threat and containment, invasive pests & diseases)	**Hall 3** **Chairs:** Dr. S.C. Dubey Dr. K.P. Singh

		Rapporteurs: Dr. Pardeep Kumar Dr. Amrita Das
	Keynote Lectures (04)	
	Dr. S.C. Dubey, Assistant Director General (Plant Protection & Biosafety), Indian Council of Agricultural Research, New Delhi, India Ensuring biosecurity through effective policy framework and stringent quarantine of plant genetic resources	
	Prof. Virendra Baranwal, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India High throughput Sequencing as diagnostics of known and novel plant viruses/viroids and its application	
	Dr. R. Velazhahan, Department of Plant Sciences, Sultan Qaboos University, Muscat, Oman Detoxification of aflatoxins: A promising approach to reduce the risk of aflatoxin contamination of foods and feeds	
	Dr. L.M. Suresh, International Maize and Wheat Improvement Center (CIMMYT), Nairobi, Kenya Maize Lethal Necrosis (MLN): Effort towards containing the spread the spread and impact of a devastating transboundary disease in sub-Saharan Africa	
	Invited Lecture (01)	
	Dr. V. Celia Chalam, Principal Scientist & Head, Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India International and national regulatory framework for transboundary movement and quarantine of living modified organisms	
	Oral Lecture (01)	
	Dr. Balamurugan A., Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India First report of Dickeya fangzhongdai causing bacterial soft rot disease on Dendrobium nobile in India: A New Invasive Pathogen	
11.30-13.00	**Technical Session 7: Microbial biodiversity** (Diversity in fungi, bacteria & viruses, systematics, edible fungi, medicinal fungi)	**Hall 1** **Chairs:** Dr. B.N. Chakraborty Dr. L. Daiho **Rapporteurs:** Dr. Deeba Kamil Dr. Sanjay Goswami
	Keynote Lectures (02)	
	Dr. C. Manoharachary, Applied Mycology & Plant Pathology Lab, Department of Botany, Osmania University, Hyderabad, Telangana, India Microbial diversity in India: challenges and issues	
	Dr. Christian Joseph R. Cumagun, Adjunct Professor,	

	Brigham Young University, Idaho, College of Agriculture and Life Sciences, Department of Biology, Rexburg, ID 83460, USA Aflatoxigenic potential of *Aspergillus flavus* isolates from maize in the Philippines and investigation of predators effect on aflatoxin production	
	Oral Lectures (06)	
	Dr. Prabhat Kumar Shukla, Division of Crop Protection, ICAR-Central Institute for Subtropical Horticulture, Lucknow, Uttar Pradesh, India Survey for associated of plant parasitic nematodes and Fusarium oxysporum with banana in Panama wilt affected areas of Uttar Pradesh, India	
	Dr. Manas Bag, Crop Protection Division, ICAR- National Rice Research Institute, Cuttack, Odisha, India Cultural variability, genetic diversity and population analysis of Ustilaginoidea virens in India	
	Dr. Satish Kumar Sain, ICAR-CICR Regional Station, Sirsa, Haryana, India Diversity of the rhizosphere fungal community edifice of upland cotton in North India	
	Dr. Priya John, Department of Plant Pathology, N.M. College of Agriculture, NAU, Navsari, Gujarat, India Identifying indigenous substrates for cultivation of Pleurotus sajor-caju	
	Dr. Deeba Kamil, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Evolutionary relationship among spatiotemporally diverse heterothallic *Alternaria alternata* isolates	
	Dr. Sanjay Goswami, Crop Protection Division, ICAR-Indian Institute of Sugarcane Research, Lucknow, Uttar Pradesh, India Morphological description of sugarcane wilt pathogen in sub-tropical India	
12.00-13.30	**Technical Session 8: Climate change impact on pests and diseases** (Diversity in fungi, bacteria & viruses, systematics, edible fungi, medicinal fungi)	**Hall 3** **Chairs:** Dr. C. Chattopadhyay Dr. S.K. Gupta **Rapporteurs:** Dr. Chanda Kushwaha Dr. G. Prakash
	Keynote Lectures (03)	
	Dr. Laetitia Willocquet, AGIR, INRA, Université de Toulouse, Castanet-Tolosan, France Modelling yield losses from wheat rusts	
	Dr. Karen A. Garrett, University of Florida, Gainesville, Florida, USA Adaptation strategies for plant disease management under climate change	
	Dr. Suseelendra Desai, Head (Plant Pathology), ICAR-CRIDA, Hyderabad, Telangana Microbe-mediated adaptation strategies to minimize	

	climate change impacts crops	
	Oral Lectures (06)	
	Dr. P. Nallathambi, ICAR-IARI Regional Station, Wellington, Tamil Nadu, India Virulence screening of wheat powdery mildew (Blumeria graminis f.sp. tritici) pathogenic isolates from different agro-climatic regions of India	
	Dr. Gireesh Chand, College of Agriculture, Central Agricultural University, Pasighat, Arunachal Pradesh, India Prevalence of Postharvest Diseases of Khasi Mandarin Fruit in Siang Region of Arunachal Pradesh	
	Dr. Mallikarjun Kenganal, AICRP on Chickpea and Pigeonpea Zonal Agricultural Research Station, Kalaburagi, Karnataka, India Emerging threat of chickpea rust caused by Uromysis ciceri due to climate change	
	Dr. Krishna Kant Mishra, Crop Protection Division, ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarakhand, India Perceptions on disease and pest status of major cultivated crops in north-western Himalayas under changing climate	
	Dr. Vinod Kumar, National Research Centre on Litchi, Muzaffarpur, Bihar, India Studies on epidemiology of leaf, panicle and fruit blights of litchi caused by Alternaria alternata in Bihar state, India	
	Dr. Chanda Kushwaha, Department of Plant Pathology, Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India Analysing influence of temperature on virulence and incidence of blight on mustarad caused by Alternaria brassicicola	
13.00-14.30	**Lunch Break**	
14.30-17.00	**Technical Session 1: Plant disease resistance** (Resistance breeding, MAS, virulence screening, race profiling)	**Hall 1** **Chairs:** Dr. Rashmi Aggarwal Dr. Harbans Bariana **Rapporteurs:** Dr. V.K. Vikas Dr. J. Nanjundan
	Keynote Lectures (03)	
	Prof. Dr. Karl-Heinz Kogel, Institute of Phytopathology, Centre for BioSystems, Land Use and Nutrition, Justus Liebig University (iFZ), Giessen, Germany Plant protection by double-stranded RNAs, a novel biofungicide for sustainable crop protection: mechanisms and activities	
	Dr. Dilantha Fernando, Dean of Studies (St. Paul's College) & Professor, University of Manitoba, Canada Resistance breeding, MAS, virulence screening, race profiling	

	Dr. S.C. Bhardwaj, ICAR-IIWBR, Regional Station, Flowerdale, Shimla, Himachal Pradesh, India Integration of resistance in wheat to counter fast evolving rusts	
	Invited Lectures (03)	
	Dr. Robin Gogoi, Division of Plant Pathology ICAR-Indian Agricultural Research Institute, New Delhi, India Unfurling maydis blight resistance in maize germplasm of India	
	Prof. Shekar Shetty, Department of Studies in Applied Botany & Biotechnology, University of Mysore, Manasagangotri, Mysore, Karnataka, India Innate immunity in plants and systemic acquired resistance for plant health – Challenges and opportunities to ensure food security	
	Dr. Mahender Singh Saharan, Division of Plant Pathology ICAR- Indian Agricultural Research Institute New Delhi, India Studies on occurrence, variability and sources of resistance for head scab of wheat in India	
	Oral Lectures (06)	
	Dr. Philomin Juliana, Wheat breeder, Global Wheat Program, CIMMYT, Mexico Enhancing genetic gain for wheat blast resistance in bread wheat using genomics	
	Dr. Neeraj Dwivedi, The Energy and Resources Institute, New Delhi Parental polymorphic survey and screening of F2 mapping population derived from a cross between Bhut Jolokia (CC0164) X IVPBC- 535 against anthracnose (fruit rot) in chilli	
	Dr. J. Nanjundan, ICAR-Indian Agricultural Research Institute, Regional Station, Wellington, Tamil Nadu, India Identification and characterization of Indian mustard accessions with novel resistance against multiple isolates of Albugo candida occurring at Wellington	
	Dr. Vikas VK, ICAR-Indian Agricultural Research Institute (IARI), Regional Station, Wellington, Tamil Nadu, India Marker assisted pyramiding of stem rust, leaf rust and powdery mildew resistance genes for durable resistance in wheat (*Triticum aestivum* L.)	
	Mrs. Mounika Kollam, The University of the West Indies, Department of Life Sciences, Faculty of Science and Technology, St Augustine, Trinidad and Tobago Molecular characterization of tobacco etch virus (TEV) virus infecting hot peppers (*Capsicum Chinense*) in Trinidad and Tobago	
	Mrs. Ashajyothi Mushineni, ICAR-Central Agroforestry Research Institute, Jhansi, Uttar Pradesh, India Black pepper endophytic Pseudomonas putida BP25 modulates defense elicitation in rice against fungal blast	

14.30-17.00	**Technical Session 2B:** Eco-friendly management (Biocontrol, organic farming, conservation agriculture, biopesticide, IPM/IDM)	**Hall 2** **Chairs:** Dr. Prasun Mukherjee Dr. Pratibha Sharma **Rapporteurs:** Dr. Mukesh Kumar Khokhar Dr. Sumit Aggarwal
	Keynote Lectures (05)	
	Dr. Prasun Mukherjee, Scientific Officer G, Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Mumbai, Maharashtra	
	Dr. Jayaraj Jayaraman, Professor of Biotechnology and Plant Microbiology, Dept. of Life Sciences, The University of the West Indies, St. Augustine, Trinidad and Tobago Developing Integrated disease management systems for sustainable vegetable production in the tropics	
	Dr. D.B. Olufolaji, Department of Crop, Soil and Pest management, The Federal University Technology, Akure, Nigeria The impact of biocontrol of plant diseases on increasing food crops in Nigeria; Sub-Saharan Africa	
	Dr. Gomathinayagam Subramanian, Director, University of Guyana Guyana, South America *Trichoderma harzianum*, a multipotential organism for biological control of Plant Pathogens	
	Dr. Hesham Ali El Enshasy, Institute of Bioproduct Development, Universiti Teknologi Malaysia, Malaysia Platform Technology for Large Scale Production of Biological Control Agents for Fungal Oil Palm Diseases	
	Invited Lectures (04)	
	Dr. Lata, Principal Scientist, Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi Mitigating environmental pollution and improving soil health using fungal resources	
	Dr. A.K. Chowdhury, Professor & Head, Department of Plant Pathology, UBKV, Coochbehar, West Bengal Disease dynamics and associated soil health parameters in rice wheat cropping systems under conservation agriculture	
	Dr. Savarni Tripathi, ICAR-Indian Agricultural Research Institute, Regional Station, Pune, Maharashtra, India Viral disease scenario in solanaceous vegetable crops in western Maharashtra and developing effective management strategies	
	Oral Lectures (06)	
	Dr. Amalendu Ghosh, Advanced Centre for Plant Virology, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Controlling the transmission of chilli leaf curl virus by	

	exogenous application of dsRNA targeting hsp70 gene of its vector, *Bemisia tabaci*	
	Dr. Mukesh Kumar Khokhar, ICAR-National Research Centre for Integrated Pest Management, New Delhi, India Impact of IPM intervention on inoculum density and disease development relationship between pathogen and antagonistic microbials in transplanted and direct seeded Rice	
	Dr. R. Thava Prakasa Pandian, ICAR-Central Plantation Crops Research Institute Regional Station, Vittal, Karnataka, India Identification of an effective isolate of *Trichoderma asperellum* AT172 for the management of arecanut basal stem rot disease	
	Dr. Rekha Balodi, ICAR-National Research Centre for Integrated Pest Management, New Delhi, India Monitoring of native Trichoderma species population in tomato field	
	Dr. Sumit Kumar Aggarwal, ICAR-Indian Institute of Maize Research PAU Campus Ludhiana, Punjab, India Adoption of modules for Management of Banded Leaf & Sheath Blight of Maize in India	
	Ms. Shivani Gupta, Department of Plant Pathology, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India Status of Cercospora (*Cercospora tageticola* Fresen.) leaf spot of marigold in Himachal Pradesh and its novel management strategies	
14.30-17.00	**Technical Session 9: Impact of COVID -19 on Indian agriculture** (Delivery system, export -import hindrance, labour crisis, production systems) **Technical Session 10: Stakeholders meet on plant protection issues** (Industry, academia, government, farmers interface)	**Hall 3** **Chairman:** Dr. M.K. Naik Dr. S.K. Malhotra **Rapporteurs:** Dr. Susanta Banik Dr. N. Srinivasa
	Keynote Lectures (01)	
	Dr. Pratibha Sharma, Division of Plant Pathology, SKN Agricultural University, Jobner-Jaipur, Rajasthan Plant clinic diagnosis worldwide and amateurs plant doctors versus phytiatry doctors	
	Invited Lecture (03)	
	Shri R.G. Agarwal, Group Chairman, Dhanuka Agritech Limited, 14th Floor, Cyber City, DLF Ph:-III, Gurgaon, Haryana Transfer of new pesticides technology	
	Dr. Keshav Deshmukh, Bayer Crop Science Limited, Maharashtra, India Crop protection solutions for integrated disease management	
	Oral Lectures (02)	

	Dr. Mallikarjun Kenganal, AICRP on Chickpea and Pigeonpea Zonal Agricultural Research Station, Kalaburagi, Karnataka, India Consumer producer Co-opted linkage through e-resources for farm solutions and marketing of produces during COVID-19 pandemic	
	Dr. Sai Ratna Sharavani Channapurapu, Department of Floriculture and Landscape Architecture, Dr. Y.S.R. Horticultural University, Venkataramannagudem, West Godavari, Andhra Pradesh, India Impact of COVID-19 on Indian floriculture industry	
10.00-11.30	**e-Poster Presentation Session (Session 2 S2(01-50))**	**Hall 4** **Chairs:** Dr. Dinesh Singh Dr. R.M. Gade **Rapporteurs:** Dr. Ravindra Kumar Dr. Rahul Chavan
14.30-17.00	**e-Poster Presentation Session (Session 1, 2(S251-72), 6)**	**Hall 4** **Chairs:** Dr. Dinesh Singh Dr. R.M. Gade **Rapporteurs:** Dr. Ravindra Kumar Dr. Rahul Chavan

Day 03 (Saturday, March 27, 2021)		
10.00-11.00	**J.F. Dastur Memorial Award** by **Dr. Kajal Kumar Biswas**, Principal Scientist, Division of Plant Pathology ICAR-Indian Agricultural Research Institute, New Delhi Understanding of sleeping giant-virus in citrus and cotton: perspective to economic losses in India and a challenge to battle	**Hall 1** **Chairs:** Dr. S.M. Paul Khurana Dr. C. Manoharachary
	S. Sinha Memorial Award by **Dr. Pramod Kumar Gupta**, Scientist, JNKVV, Jabalpur, Madhya Pradesh Current status of Cercosporoid fungi in India, effective management strategies and future directions	
11.00-13.00	**MJN Academic Award Contest (16)**	**Hall 2** **Chairs:** Dr. R. Selvarajan Dr. A.K. Chowdhury
	Ms. Kakumoni Saikia, Department of Plant Pathology, Assam Agricultural University, Jorhat, Assam Antibiotic exuding Rhizospheric Streptomyces for biological management of Xanthomonas oryzae pv. oryzae in rice	North-Eastern Zone
	Ms. Arti Kumari, School of Crop protection, CPGSAS, Central Agricultural University (Imphal), Umiam, Meghalaya Synthesis and characterization of biogenic silver nanoparticles: its assessment as antipathogenic activity against Rhizoctonia solani and Xanthomonas oryzae pv. oryzae and toxicity on beneficial microbes and mammalian cells	North-Eastern Zone
	Dr. Darshan K., Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Transcriptomic analysis of Chaetomium globosum Kunze. for bioprospection of antagonistic related gene(s)	Delhi Zone
	Dr. Sajad Un Nabi, ICAR-Central Institute of Temperate Horticulture, Srinagar, Jammu & Kashmir, India Comparative Virome analysis in mosaic infected and asymptomatic apple cultivars using RNA sequencing: development of multiplex RT-PCR and evaluation of rootstocks for sensitivity to mosaic disease	Delhi Zone
	Mr. Debayan Mondal, Department of Biochemistry, Uttar Banga Krishi Viswavidyalaya, Coochbehar, West Bengal, India Enzyme kinetics and gene expression analysis reveals differential response of aromatic rice landraces from sub -Himalayan Terai region of India to rice blast disease	Eastern Zone
	Ms. Mehulee Sarkar, Advanced Centre for Plant Virology, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi Suppressor activity analysis of Tomato leaf curl New	Eastern Zone

	Delhi virus gene(s) and development of RNAi construct to evaluate their efficacy in inhibiting the virus	
	Dr. Scindiya Mohandoss, ICAR-Sugarcane Breeding Institute, Coimbatore, Tamil Nadu, India Molecular characterization and functional analysis of pathogenicity related genes in Colletotrichum falcatum causing red rot in sugarcane	Southern Zone
	Dr. Amoghavarsha Chittaragi, Department of Plant Pathology, University of Agricultural and Horticultural Sciences, Shivamogga, Shivamogga, Karnataka, India Characterization and virulence profiling of Magnaporthe oryzae isolates from diverse rice ecosystems of Karnataka	Southern Zone
	Mr. Rathod Parashuram, Department of Plant Pathology, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India Exploring Potential Pseudomonas for Plant Growth Promoting traits and invitro Suppression of Charcoal Rot in Soybean (Glycine max (L.) Merrill)	Central Zone
	Dr. Chaithanya B.H., Regional Agricultural Research Station (ANGRAU), Nandyal, Andhra Pradesh, India Development of DNA based screening method for Yellow Mosaic Virus infecting Black gram and studies on vector (*Bemisia tabaci*) biotypes in Andhra Pradesh	Central Zone
	Dr. Tanveer Fatima, Aligarh Muslim University, Aligarh, Uttar Pradesh Effect of elevated levels of CO_2 on the development powdery mildew in cucumber species	Mid-Eastern Zone
	Ms. Ruchi Srivastava, ICAR- National Bureau of Agriculturally Important Microorganism, Kushmaur, Mau, Uttar Pradesh Secretome analysis reveals effector candidates associated with broad host range necrotrophy in *Fusarium udum*	Mid-Eastern Zone
	Mr. R.S. Lad, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra Seasonal effects on population dynamics of Phytophthora spp. and disease development in mandarin	Western Zone
	Mr. R.C. Agale, Department of Plant Pathology, VNMKV, Parbhani, Maharashtra Variability among Rhizoctonia bataticola isolates, causing dy root rot of soybean and its management	Western Zone
	Ms. Ayesha Nabi, Division of Plant Pathology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Jammu & Kashmir Optimizing the *Agrobacterium tumefaciens*-mediated transformation conditions in *Colletotrichum lindemuthianum* for uncovering the functionality of pathogenicity arsenals	Northern Zone
	Ms. Jashanpreet Kaur, Department of Plant Pathology, Punjab Agricultural University, Ludhiana, Punjab	Northern Zone

	Characterization and mapping of Spot blotch in *Triticum durum -Aegilopes speltoides* introgression lines using genotyping by sequencing	
11.00-13.00	**APS Travel Grant Award Contest (05)**	**Hall 1** **Chairs:** Dr. R.N. Pandey Dr. A.K. Misra
	Mr. Jagmohan Singh, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India Deciphering the Chaetomium globosum induced signaling network in tomato against early bight	Delhi Zone
	Mr. Gowtham Kumar Routhu, Assam Agricultural University, Jorhat Jorhat, Assam, India Post transcriptional gene silencing using Coat protein gene specific dsRNA molecules against cognate Cucumber mosaic virus (CMV) infecting Bhut jolokia crop of Assam	North-Eastern Zone
	Sumaih Wani, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar J&K Status and molecular characterization of potato virus Y strains in Kashmir valley	Northern Zone
	Ms. Sabiha Sayeed, Department of Plant Protection, Faculty of Agricultural Sciences, Aligarh Muslim University, Aligarh, Uttar Pradesh Efficacy of plant extracts against *Mungbean Yellow Mosaic India Virus* (MYMIV) in urdbean (*Vigna mungo* L.)	Mid-Eastern Zone
	Mr. Vaibhav Pratap Singh, Department of Plant Protection, Faculty of Agricultural Sciences, Aligarh Muslim University, Aligarh, Uttar Pradesh Effect of temperature and pH on mycelial growth and sporulation of *Alternaria brassicae* (Berk.) Sacc. causing Alternaria blight of rapeseed-mustard	Mid-Eastern Zone
10.00-13.00	**e-Poster Presentation Session (Session 7, 8, 9)**	**Hall 3** **Chairs:** Dr. Naresh Mehta Dr. D.B. Parakh **Rapporteurs:** Dr. Bishnu Maya Bashyal Dr. Sanjeev Kumar
13.00-14.00	**Lunch Break**	
14.00-17.00	**Annual General Body Meeting of the Society**	**Hall 1**
	Valedictory Session	**Hall 1**

INDIAN PHYTOPATHOLOGICAL SOCIETY

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e-POSTERS PRESENTATION SESSION

Day 01 (Thursday, March 25, 2021)	
15.00- 17.30	**Technical Session 3: Next generation pesticide and application** (Biomolecules, immune boosters, nano-molecules, ICT, automization like robotic & drone) **Poster No. PP(S3)/01-07** **Technical Session 4: Host-pathogen interaction and genomics of plant pathogens** (Molecular basis of host-pathogen interaction, genome announcement, patho-genomics, functional genomics) **Poster No. PP(S4)/01-18** **Technical Session 5: Diagnostics and genetic variability** (Diagnostics, genetic variability, sensor based detection viz.,nano-sensors, e-nose) **Poster No. PP(S5)/01-18** **Chairs:** Dr. G.P. Rao, Dr. M.S. Saharan **Rapporteurs:** Dr. Gireesh Chand, Vinod Kumar
Day 02 (Friday, March 26, 2021)	
10.00-11.30	**Technical Session 2:** Eco-friendly management (Biocontrol, organic farming, conservation agriculture, biopesticide, IPM/IDM) **Poster No. PP(S2)/01-50** **Chairs:** Dr. A.I. Bhat, Dr. Usha Chakraborty **Rapporteurs:** Dr. Meenu Gupta, Dr. Pramod Kumar Gupta
14.30-17.00	**Technical Session 1: Plant disease resistance** (Resistance breeding, MAS, virulence screening, race profiling) **Poster No. PP(S1)/01-28** **Technical Session 2:** Eco-friendly management (Biocontrol, organic farming, conservation agriculture, biopesticide, IPM/IDM) **Poster No. PP(S2)/51-71** **Technical Session 6: Plant quarantine** (Agro-terrorism, regulatory rules, amendments, certification, global threat and containment, invasive pests & diseases) **Poster No. PP(S6)/01** **Chairs:** Dr. Dinesh Singh, Dr. R.M. Gade

	Rapporteurs: Dr. Ravindra Kumar, Dr. Rahul Chavan
Day 03 (Saturday, March 27, 2021)	
10.00-13.00	**Technical Session 7: Microbial biodiversity** (Diversity in fungi, bacteria & viruses, systematics, edible fungi, medicinal fungi) **Poster No. PP(S7)/01-23** **Technical Session 8: Climate change impact on pests and diseases** (Diversity in fungi, bacteria & viruses, systematics, edible fungi, medicinal fungi) **Poster No. PP(S8)/01-09** **Technical Session 9: Impact of COVID -19 on Indian agriculture** (Delivery system, export-import hindrance, labour crisis, production systems) **Poster No. PP(S9)/01** **Chairs:** Dr. Naresh Mehta, Dr.D.B. Parakh **Rapporteurs:** Dr. Bishnu Maya Bashyal, Dr. Sanjeev Kumar

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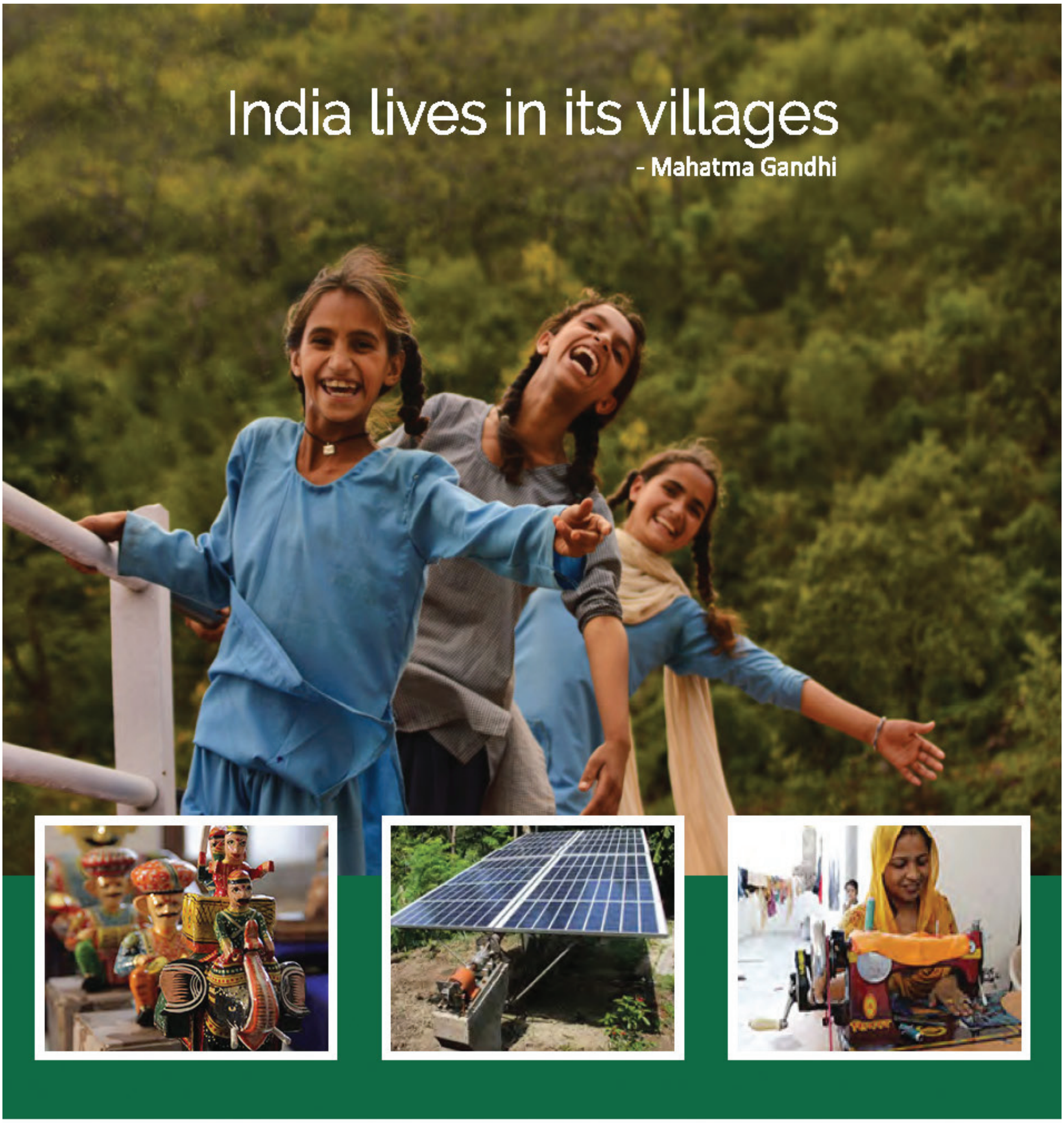
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- Mahatma Gandhi


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