INDIAN PHYTOPATHOLOGICAL SOCIETY
NORTH-EASTERN ZONE

National Symposium

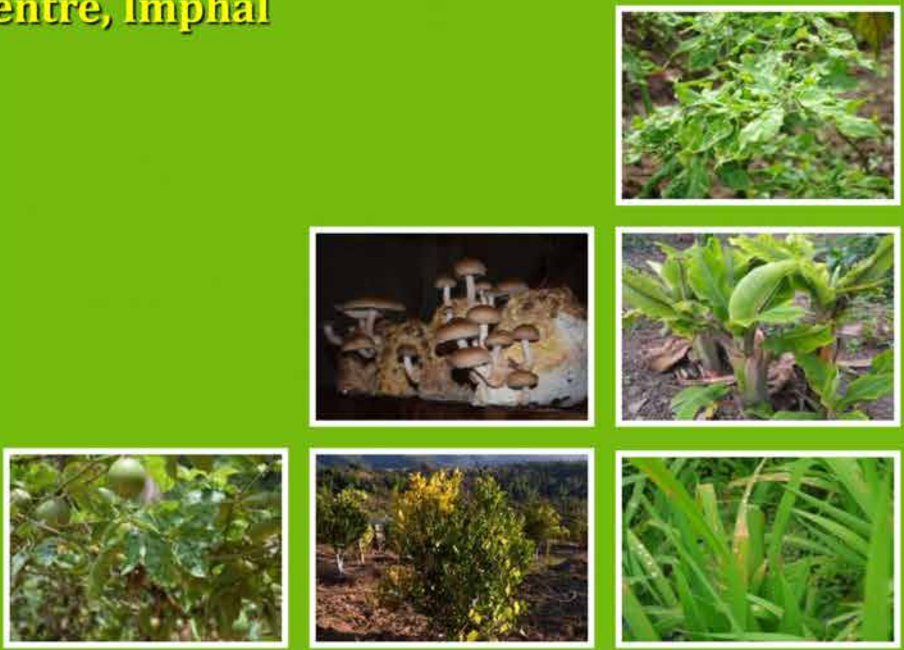
EMERGING AND RE-EMERGING PLANT DISEASES IN NORTH EAST INDIA : CHALLENGES AND STRATEGIES

SOUVENIR & ABSTRACTS

October 10-11, 2017

Venue

ICAR Research Complex for NEH Region
Manipur Centre, Imphal



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NATIONAL SYMPOSIUM

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SOUVENIR & ABSTRACTS

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October 10-11, 2017
ICAR Research Complex for NEH Region, Manipur Centre, Imphal

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Citation : Ngachan SV, Prakash N, Sharma SK, Singh IM, Roy SS, Ningombam A, Punitha P, Ansari MA, Singh RK, Sailo B, Singh TB, Sonia Ch, Anand YR, Singh TS and Singh YH (Eds.) 2017. Souvenir and Abstracts of National Symposium on Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies. 10-11 October, 2017, Imphal, Manipur, India. pp. 144.

Published by:
Director
ICAR Research Complex for NEH Region
Umroi Road, Umiam, Meghalaya – 793103

Printed at:
R. B. Printing House, Nagamapal, Imphal

Messages

सत्यमेव जयते

CHIEF MINISTER
MANIPUR

Imphal,
September 29, 2017

Message

I am extremely happy to learn that ICAR Research Complex for NEH Region, Manipur Centre and Zonal Chapter, Indian Phytopathological Society (North-Eastern Zone) are jointly organizing National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" at Imphal, Manipur. The society has been regularly organizing many such events in the country and I am glad that Manipur is playing the host this time.

Manipur is a beautiful state with huge potential in many aspects, one of them being agricultural production in general and organic cultivation in particular. To realize this immense potential might take time but scientific principles, reasoning and logic carving the way forward will eventually lead us to our destination sooner than later. Plant diseases and their occurrence in the North Eastern region of India are significantly different than the other parts of country. Hence, concerted efforts are needed to tackle them and make agri-horticultural production economically viable. In order to meet the goals of doubling farmers’ income by 2022, Science of Plant Protection in general and Plant Pathology in particular has to play a pivotal role.

I hope the Symposium will have many discussions and interactions that focus on crop protection issues of the North East India and the scientific deliberations will serve as a guiding light in our endeavours towards realizing the agricultural potential of Manipur in a sustainable way.

I welcome all the participants, researchers, scientists, scholars and students from different parts of the country to Manipur and to the National Symposium.

I also extend my warm greetings and felicitations to the organizers and all the participants and wish the Symposium a grand success.

(N. Biren Singh)

Yumnam Joykumar Singh
Deputy Chief Minister
Government of Manipur

सत्यमेव जयते

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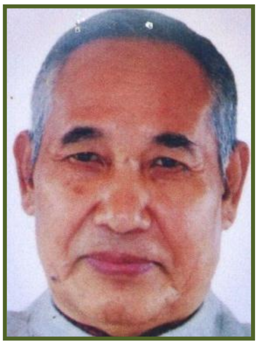
Imphal, the 3rd October, 2017



Message

I welcome the initiative of ICAR Research Complex for NEH Region, Manipur Centre and Indian Phytopathological Society (North-Eastern Zone) to organize a National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" at ICAR Research Complex for NEH Region, Manipur Centre, Lamphelpat during 10th-11th October, 2017.

Such seminars and Symposium particularly in the field of crop protection are very much needed and helpful in focusing on the plant protection issues of the NE Region. Disease and pest dynamics in the NE region are quite different and unique from those in the other parts of the country. The entire NE region has been considered as the potential Organic Hub for the country. Plant protection has a huge role to play for realization of this potentiality. With increasing temperature under climate change scenario, diseases and pests are expected to increase in abundance. Hence, the role of plant protection becomes vital and critical to the success of organic cultivation in the NE region.

I wish the Symposium and publication of the Souvenir a grand success.

Yumnam
(Yumnam Joykumar Singh)
3/10/2017

V. Hangkhanlian
Minister (Agri/Vety)
Manipur

सत्यमेव जयते
MESSAGE

Imphal, the 3rd Oct., 2017

Message

I am delighted to learn that ICAR Research Complex for North Eastern Hill Region, Manipur Centre and Zonal Chapter (NEZ), Indian Phytopathological Society are jointly organizing a National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies " at Imphal, Manipur during 10-11 October, 2017.

Agriculture is Manipur while being full of immense potential is also riddled with many challenges. Diseases and insect pests have always been the limiting factors in crop production. Being a sub-tropical region with high rainfall the losses due to diseases, insect pests and weeds both in field and in storage are huge. Scientists, researchers and farmers alike have put endless efforts towards reducing the damage caused by them. The targeted effort to reduce pest losses has unfortunately led to many harmful consequences such as pesticide resistance, pesticide residues in food, ecological imbalances in the agroecosytem and environmental pollution.

In this age of growing consumer consciousness about food quality as well as environmental cost in food production, we can no longer compromise environmental safety and sustainability for increasing crop productivity.

This National Symposium on the aspects of emerging and remerging diseases in North East region is the right forum to discuss about the present scenario of crop diseases and the appropriate strategies to be taken up to ensure sustainable crop cultivation.

I wish the Symposium a grand success and request the Society to host many more Seminars and symposia in the NE region to encourage such scientific interaction and discussion among agriculturists, researchers, extension functionaries and students.

V Hangkhanlian
(V. Hangkhanlian)

सत्यमेव जयते
त्रिलोचन महापात्र, पीएच.डी.
एफ एन ए, एफ एन ए एस सी, एफ एन ए ए एस
सचिव एवं महानिदेशक
TRILOCHAN MOHAPATRA, Ph.D.
FNA, FNASc, FNAAS
SECRETARY & DIRECTOR GENERAL

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Message

It is a pleasure to learn that, Zonal Chapter (North Eastern Zone), Indian Phytopathological Society and ICAR Research Complex for NEH Region, Manipur Centre, Imphal are jointly organizing a National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" during October 10-11, 2017.

North East region of India encompasses a biodiversity rich agro-ecosystems and varying agro climatic conditions, which provide vast opportunities for cultivation of diverse agri-horticultural crops. The unique agro-ecosystem of North East region of India coupled with large biodiversity makes conducive situations for various pests and diseases that account for losses in the farm produce to the tune of 30%. North East region also shares a large transboundary area with six neighbouring countries which makes it permeable to new pathogens and pests. Region has witnessed the emergence and re-emergence of various phytopathogens and their variants. If we could devise the strategies for combating these emerging and re-merging plant diseases, the losses can be reduced and region can become self-sufficient in terms of food and nutritional requirements. The thematic area and various sessions of the Symposium are very pertinent. It is hoped that learned delegates of the Symposium will deliberate and share their knowledge on the latest developments in different themes for formulating the strategies in combating plant diseases and developing durable management in a sustainable way.

I take this opportunity to compliment the participants on this occasion and convey my greetings and good wishes for a successful Symposium.

Dated the 22nd September, 2017
New Delhi

(T. Mohapatra)

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Prof. M. Premjit Singh,
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No. SVC/CAU/176/2017/
Imphal, the 3rd October, 2017

Message

I am happy to note that a National Symposium "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" is being organized at ICAR Research Complex for NEH Region, Manipur Centre, Imphal during 10-11 October, 2017 by the Indian Phytopathological Society (North-Eastern Zone). The Indian Phytopathological Society is one of the oldest societies related to crop protection in the country. It is heartening to note that after hosting many such events around the country, it is finally hosting an event in Manipur. I hope this is just the beginning of many more.

Being a crop protection professional myself, I am fully aware of the importance of crop protection in North East India. Here, various pathogens and pests are not only a threat to crop cultivation but also to the abundantly rich plant wealth including rare medicinal plants and orchids, in this biodiversity hotspot. The abundance of devastating pathogens and their emergence in the region has always been favoured by its humid and moderate climate and wide available host range. It is also a transboundary region with almost all the states sharing a porous international border with other countries. This also makes it open and vulnerable to the threat of introduction of new pathogens, their strains and insect-vectors carrying viral pathogens. NE India stands at the threshold of organic agriculture with the threat of climate change looming in the horizon. Our crop production systems can realize the full potential of organic farming only when scientific temper is involved.

Scientific discussions and events such as this National Symposium is the need of the hour and have come at this critical juncture. I congratulate the ICAR Research Complex for NEH Region, Manipur Centre and Indian Phytopathological Society (North-Eastern Zone) for organizing this Symposium in Imphal and wish it a grand success.

I hope many fruitful deliberations will be seen during the Symposium and will be a learning experience and eye-opening exposure to all the students and research scholars of the region.

3/10/2017

(M. Premjit Singh)

क. अलगुसुन्दरम
उप महानिदेशक (कृषि अभियांत्रिकी)
Dr. K. Alagusundaram,
Deputy Director General
(Agricultural Engineering)

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PUSA, NEW DELHI-110 012

04/10/2017

Message

It gives me immense pleasure to know that ICAR Research Complex for NEH Region, Manipur Centre and Indian Phytopathological Society (North Eastern Zone) are jointly organizing a National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" at Imphal, Manipur during 10-11 October, 2017.

Plant diseases are emerging as a major threat to national food and nutritional security. Several disease epidemics in India have called for the systematic research efforts to combat their emergence and re-emergence. North East region of India has tremendous potential to be the hub of second green revolution. Disease dynamics of the region is quite different compared to the other parts of India. The Symposium provides an excellent forum to the delegates to exchange scientific knowledge in different themes of plant disease research, thus devising strategies for the future research and developing sustainable disease management practices.

My heartiest greetings to the organizers and the participants for a great success of the Symposium.

4/10/17
(K. Alagusundaram)

Dr. P.K. Chakrabarty, PhD., FMASc
Adjunct Professor, UF (USA)
Assistant Director General
(Plant Protection & Biosafety)

भारतीय कृषि अनुसंधान परिषद
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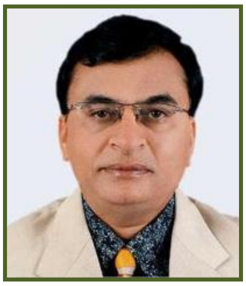

Message

I am happy to learn that ICAR Research Complex for North Eastern Hill Region, Manipur Centre and Zonal Chapter (NEZ), Indian Phytopathological Society are jointly organizing a National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" at Imphal, Manipur.

India is facing challenges to increase the food production and decrease the losses caused by diseases and insect pests. Science of Plant Protection has contributed significantly in the fields of diagnostics, epidemiology and integrated management. North East region of India is one of the potential areas which are expected to contribute significantly to the food and nutritional basket of country. Region has witnessed emergence and re-emergence of various pathogens which significantly reduced the production and productivity of agricultural and horticultural crops. Recent advances in the molecular biology and biotechnology has revolutionized the field of Plant Pathology particularly in terms of accurate identification of etiological agents and their identification at pathotype or strain level. The need to study the emergence of plant diseases and developing durable management strategies has largely been felt in the recent times. The theme of the Symposium is very relevant and expected to define the future road map for characterization of emerging and re-emerging plant diseases in North Eastern region and developing durable management strategies.

I sincerely hope, this Symposium will deliberate seriously on such issues paving way for integrated management of plant diseases. I wish all success to the Symposium and extend my good wishes to all participants.

(P.K. Chakrabarty)

डॉ. आनन्द कुमार सिंह
उप महानिदेशक (बाग. वि.)
बागवानी विज्ञानं संभाग

Dr. Anand Kumar Singh
Deputy Director General (Hort. Sci.)
Horticultural Science Division

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INDIAN COUNCIL OF AGRICULTURAL RESEARCH
KRISHI ANUSANDHAN BHAVAN-II
PUSA, NEW DELHI-110 012

Message

I take this opportunity to congratulate ICAR Research Complex for NEH Region, Manipur Centre and Indian Phytopathological Society (North Eastern Zone) for organizing the National Symposium on Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" during 10-11 October, 2017.

North East region of India is known for the unique agro-ecosystem and also the farming system practiced by the farmers. The kind of diseases and pathogen dynamics in this region is little different compared to the other parts of country. Climate change coupled with changing cropping patterns has been the major driving force for changing dynamics of diseases in common crops. It has necessitated researchers to reorient their research programmes through systematic multidisciplinary approaches which could help in deeper understanding of the subject and evolve improve and sustainable disease management strategies. Further, the North Eastern Region of India shares international border with five other countries which poses issues related to biosecurity.

Under this background the Indian Council of Agricultural Research, Research Complex for North Eastern Hill Region, Manipur Centre in collaboration with Indian Phytopathological Society (North Eastern Zone), is organizing a *National Symposium on Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies* on 10 & 11 October, 2017. I believe that the event will provide a forum to participants for discussing the various issues at length and making recommendations on way forward for future Research & Development on management of diseases of agri-horticultural crops of the North Eastern Region.

I take this opportunity to complement the organizers and wish the participants a fruitful Symposium.

5/10/17

(Anand Kumar Singh)

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Dr. S. V. Ngachan
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Message

With immense happiness I welcome the delegates to the National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" being organized jointly by Indian Phytopathological Society (North Eastern Zone) and ICAR Research Complex for NEH Region, Manipur Centre during 10-11 October, 2017 at Imphal, Manipur.

Agriculture in the entire North East region is complex, diverse and risk prone. Blessed by mother nature with abundant natural resources, its undulating topography and land locked geography has proved to be a challenge in crop management and protecting them from transboundary plant pathogens and insect vector carriers. Farmers have usually followed traditional methods of cultivation which is by default-organic in nature since time immemorial. Agricultural production in the region is also facing the pressures of increasing productivity to meet the demands of increasing population and industry. Climate change is expected to put more environmental stress, both biotic and abiotic on our cultivation systems. The usual norms of cultivation can no longer be relied upon to meet these challenges. The evolving plant pathogens have already demonstrated great adaptive capability over the years to different stressful stimuli. The challenge is to manage them without compromising our sustainability and preserving environmental health.

The National Symposium has come at the right time to deliberate upon the emerging issues facing us in our cultivation systems and bring forward the best management strategies to deal with them.

I wish the Symposium a grand success and welcome the participants and delegates to this corner of the North East.

(S.V. Ngachan)

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Prof. B.N. Chakraborty
FPSI, FISMPP, FNRS, FISPC,FMSI,FIMS,
FAScT, FRSC(London),FNAAS, FNABS
President, IPS

October 04, 2017

Message

Hosts and pathogens have evolved side by side. Host driven evolution of pathogens and their variants is well understood now. It is known that most of the pathogens have emerged and evolved in the areas where maximum genetic diversity of host plant exists. Thus, in order to have deep understanding of pathogen diversity, sampling from the area of maximum host diversity needs to be done. The region with maximum host diversity witnesses the emergence and re-emergence of distinct pathotypes thus representing a clear picture of pathogen diversity and evolution. North East region of India represent a geographically separated area with large transboundary area which is porous to the entry of new pathogens and their variants. Thus characterization of pathogens from this region is very important in order to design the durable management strategies.

The National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" being organized by Indian Phytopathological Society (North Eastern Zone) and ICAR Research Complex for NEH Region, Manipur Centre has its own relevance not only to the region but also to the country. The scientific knowledge which will be shared during the Symposium will provide a clear picture of research and extension in the area of Plant Pathology in the North Eastern region and thus guiding us to define the road maps for future.

I compliment the organizers for the initiative and extend my best wishes for the grand success of Symposium.

B. Chakraborty

(B.N. Chakraborty)

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Dr. Dinesh Singh
Secretary

October 04, 2017

Message

It gives me immense happiness to know that ICAR Research Complex for NEH Region, Manipur Centre in collaboration with Zonal Chapter (North Eastern Zone), Indian Phytopathological Society is organizing a National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" during October 10-11, 2017.

Plant diseases have always been a major constraint in the production and productivity of agri-horticultural crops. The vast diversity of cropping patterns, specific prevailing environmental conditions and evolving pathotypes leads to the occurrence of devastating diseases in different parts of India. North East region of India comprises a tremendous biodiversity in terms of cultivated crop species, their wild genotypes as well as races and strains of pathogens. Further the climate change and changes in the cropping patterns expose the plants to different spectrum of pathogens. The region has witnessed emergence of pathogens with distinct biological and genetic properties. These situations demand for the collaborative and systematic approaches for characterization and management of prevalent pathogens. The topic and different themes of Symposium are very pertinent and it is hoped that serious deliberations will be made which will lead to the concrete recommendations in management of emerging and re-emerging plant pathogens.

On the behalf of India Phytopathological Society and on my personal behalf I extend my greetings to the organizers and delegates for the successful Symposium.

(Dinesh Singh)

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From the Desk of Zonal President & Convener

With immense pleasure, I welcome all the delegates attending the National Symposium on "Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies" being organized by Zonal Chapter, Indian Phytopathological Society (North Eastern Zone) in collaboration with ICAR Research Complex for NEH Region, Manipur Centre. The North East region of India is endowed with vast diversity of plant species (both cultivated and their wild relatives) and also microbial diversity. Plant pathogens have long been recognized as one of the major constraint in successful production of crops in the region. The region shares geographical boundaries with neighbouring countries and is porous to the transboundary entry of new pathogens and their variants. Hence, the pathogen spectrum and their importance in the North East region is expected to be significantly different than from other parts of the country. This Symposium is therefore planned to bring Plant Pathologists from the region as well as across the country on a common forum to deliberate on the emerging and re-emerging plant pathogens, their threat to regional and national food and nutritional security and developing strategies to combat them.

On the behalf of Zonal Chapter, Indian Phytopathological Society (North-Eastern Zone) and my personal behalf, I extend my sincere thanks to the delegates for contributing Lead Talks, Oral Papers and Poster Papers covering all the themes of Plant Pathology starting from field and high throughput laboratory research to the extension Plant Pathology. This Symposium is a showcase of hard work and dedication of members of different committees and organizing committee. I take this opportunity to place on records my sincere thanks to Indian Phytopathological Society for providing the opportunity to organize this Symposium and Zonal Chapter meeting at Imphal. I profusely thank Dr. T. Mohapatra, Secretary DARE & DG, ICAR; Dr. K. Alagusundaram, DDG, ICAR; (Engineering and Natural Resource Management), ICAR; Dr. P.K. Chakrabarty , ADG (Plant Protection & Biosafety), ICAR; Dr. S.V. Ngachan, Director, ICAR RC NEH, Umiam; Dr. B.N. Chakraborty, President, Indian Phytopathological Society (IPS); Dr. Dinesh Singh, Principal Scientist, IARI and Secretary, Indian Phytopathological Society (IPS) and members of advisory committee for the continuous support and guidance in making this Symposium possible. I am confident that deliberations in this Symposium will help us to devise the strategies to combat the emerging and re-merging plant diseases and taking plant pathological research to the farmers' field.

Once again, I extend heartiest welcome to all the delegates and convey my good wishes for a happy and fruitful Symposium.

(N. Prakash)

Invited Talks

CONTENTS

Oral Presentations

Poster Presentations

LT (FP)-01

Rice blast: cross infectivity, virulence analysis and management in the Himalayan region

H Rajashekara, K K Mishra & A Pattanayak

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Rice (*Oryza sativa* L.) is a major staple food crop for half of the world's population. The International Rice Research Institute, Philippines, estimates that in order to feed the growing global population, rice production must increase by another one-third by the year 2020. Rice crop is affected by about 36 fungal, 21 viral and 6 bacterial diseases (Ou, 1985). Among fungal diseases, blast (*Pyricularia oryzae*), brown spot (*Helminthosporium oryzae*), sheath blight (*Rhizoctonia solani*), foot rot (*Fusarium moniliforme*), stem rot (*Sclerotium oryzae*) and false smut (*Ustilaginoidea virens*) are of major economic importance. The rice blast *Pyricularia oryzae* B. Couch [formerly *Magnaporthe grisea* (Hebert) Bar] is one of the important fungal diseases effecting considerable loss in rice production. It is a widespread and damaging disease of cultivated rice and around 50 per cent of production may be lost in a field moderately affected by blast infection. Each year the fungus affects rice enough to feed an estimated 60 million people (Zeigler *et al.,* 1994).

Historical perspective

The rice blast disease was first reported in china by Soong ying-shin in 1637 in his book utilization of natural resources (Manibhushan Rao, 1994) and it was first reported by Tsuchiya in Japan in 1704 (Goto, 1955). The causal organism, *Pyricularia oryzae*, was named by Cavara in Italy (Cavara, 1891) and subsequently in Japan (Shirai, 1896).

In India, it was first recorded in Thanjavur (Tanjore) delta of South India by Mc Rae in 1918. The disease has occurred from time to time in the country causing severe damage to rice production (Sundararaman, 1927; Thomas, 1930). However, it attracted the attention only when a devastating epidemic occurred in 1919 in the Tanjore delta of erstwhile Madras state (Padmanabhan, 1965). Seven epidemics of blast happened between 1980 and 1987 in the states of Himachal Pradesh, Andhra Pradesh, Tamil Nadu and Haryana resulting in huge yield losses (Sharma *et al.,* 2012).

Blast disease was first reported in Asia more than three centuries ago and is prevalent throughout the continents where rice is cultivated. The pathogen, *Pyricularia oryzae* is a complex species which is heterothallic and the races evolve continuously in the population with group of isolates that are diverse in phenotypic virulence (Tharreau *et al*., 2009). Wide geographic distribution, race evolution, high yield losses and additional costs of fungicides make this disease a serious threat to rice cultivation. This fungal disease is estimated to cause production losses of US$55 million each year in South and Southeast Asia. The losses are even higher in East Asia and other more temperate rice growing regions around the world (Herdt, 1991). The disease results in yield loss as high as 70-80 per cent (Ou, 1985) when predisposition factors (high mean temperature values, degree of relative humidity higher than 85-89%, presence of dew, drought stress and excessive nitrogen fertilization) favour epidemic development (Piotti *et al.,* 2005). Understanding the biology of rice blast disease is therefore of particular significance, because it offers the promise of developing new and durable disease control strategies (Skamnioti and Gurr, 2009).

Isolation and multiplication of pathogen

Although *P. oryzae* has been extensively studied for several decades worldwide, most of the workers face difficulties in isolation of the pathogen from diseased leaf and neck blast samples and their purification to monoconidial isolates (Jia, 2009). Various pathological methods have been adopted by different workers to isolate blast pathogen from infected tissue. In commonly used slide moist chamber technique (Divya *et al*., 2013), blast lesions were surface sterilized with 0.1 per cent mercuric chloride solution followed by three rinses with sterile water and placed over clean glass slides kept inside sterile petridishes padded with moist cotton. Single conidia was identified from the sporulating lesions using a stereomicroscope and aseptically transferred to Potato Dextrose Agar (PDA) slants. Different media including synthetic medium like Richard's agar (Ramakrishnan, 1948) and natural media such as autoclaved leaves and grains of different hosts have been used for isolation and sporulation of the pathogen. Good growth of *P. oryzae* was obtained on rice leaf decoction (Nishikado, 1927). Among different culture media tested with three isolates of *P. grisea* from rice, finger millet and *Panicum* sp, prune agar and oat meal agar supported maximum mycelial growth and sporulation of the isolates both from rice and finger millet (Khadka *et al.,* 2012). The stem bits from maize, rice (20 days old crop) and *Panicum repens* have been used for mass multiplication of blast pathogen (Divya *et al.,* 2013). Recently, efficient method has been developed for isolation and mass multiplication of *P. oryzae* isolates (Rajashekara *et al.,* 2016)/

Host-range and cross-infectivity of pathogen

Rice blast, caused by *M. oryzae* (Ana. *Pyricularia oryzae*) is one of the most serious diseases of rice, which also infects small grains (Valent and Chumley, 1991; Talbot, 2003). *Pyricularia* blast disease on wheat was first identified in 1985 in the State of Parana, Brazil (Igarashi et al., 1986). In India, rice blast pathogen has been reported to infect several weeds (Singh, 1997). However, there is no information on the cross infectivity of rice blast pathogen on other economically important cereals. Limited outbreaks on wheat have been reported in South America (Valent and Chumley, 1994). Even it is known to infect *Arabidopsis* via a mechanism distinct from that in rice (Park *et al.,* 2009).

Virulence analysis pattern

In India, Thomas (1941) was the first to report the breakdown of blast resistance of the two selections 11348 and 10998. The existence of races of *P. oryzae* differing in pathogenicity was first noticed by Sasaki (1923) who ascertained that rice cultivars resistant to strain A were severely infected by strain B. By about 1960, 12 cultivars were selected as differentials, two tropical, four Chinese and six Japanese in origin. Thirteen pathogenic races were identified and classified into these groups called T, C and N. (Goto, 1960, 1965).

Rathour *et al*. (2004, 2009, 2011) analysed population Structure of *P. oryzae* from North-western Himalayas through the use of international monogenic blast differentials (LTH background) developed in a IRRI-Japan collaborative program (Fukuta *et al.* 2004). Variar (2006), characterized the pathogen population of *P. oryzae* from Eastern India by using the monogenic differential set. The first international differential system of rice was established in 1960 to determine the pathogenicity of *P. oryzae* (Ling and Ou, 1969) and is still being used (Ling *et al.,* 2004; Dai *et al.,* 2010). The system was modified in China into the following China National Differentiating Varieties (CCNDV): Tetep, Zhenlong 13, Sifeng43, Hejiang 18, Dongnong363, Guandong51 and Lijiangxintuanheigu (LTH) (Lei *et al.,* 2002; Wang, 2005). These host-pathogen characterization systems have been effective in rice breeding; however, they were not designed to guide the deployment of any particular blast resistance genes. A set of monogenic lines containing 24 major R genes (*Pia, Pib, Pii, Pik, Pik-h, Pik-m, Pik-p, Pik-s, Pish, Pit, Pita, Pita-2, Piz, Piz-t, Pi1, Piz-5, Pi3, Pi5(t), Pi7(t), Pi9, Pil2(t), Pi11(t), Pi19*, and *Pi20*) in the blast-susceptible recurrent Japonica variety LTH (Ling *et al.* 2000; Telebanco-Yanoria *et al.,* 2008), developed by the International Rice Research Institute, are excellent materials for determining plant-specific resistance in rice breeding (Tsunematsu *et al.,* 2000; Telebanco-Yanoria *et al.,* 2010; Koide *et al.,* 2011). Pathogenicity of 331 blast isolates collected from different rice growing regions of Bangladesh were performed on 23 monogenic blast differentials and it was observed that wide variation in virulence was found among isolates (Khan *et al*., 2016).

Race designation system in *P. oryzae*

The occurrence of physiologic races in *P. oryzae* in India was first reported by Latterell *et al.,* 1960, who used the US blast differentials and adopted three categories of host-reaction: resistant, moderate, and susceptible. Padmanabhan reported the occurrence of physiologic races of the pathogen from India (Padmanabhan, 1965) after studying isolates of *P. oryzae* representing the different regions of the country. Chakrabarti *et al.,* (1966) and Padmanabhan *et al.,* (1967) reported the occurrence of 12 and 13 races after analyzing 17 and 19 isolates of *P. oryzae*, respectively, using US blast differentials and adopting resistance and susceptibility as criteria for distinguishing physiologic races. Most of the isolates reported by those two communications were the same.

Venkatarao and Apparao (1976) reported the occurrence of 17 races in Andhra Pradesh. Sharma *et al.* (2002) characterized the pathogen population consisting of 119 isolates from north-western Himalayan region and grouped them into 52 pathotypes on the basis of disease reaction on international differential rice lines. Highest frequency of virulence was trapped on the rice line Caloro (*Pi−ks*) followed by NP125 (*Pi−*? and K-60 (*Pi−kp*) while it was lowest on Tadukan (*Pi−ta* and/or *Pi−ta*^{2}) and BL-1(*Pi−b* and *Pi−sh*). Virulence was rare on Fukunishiki (*Pi−zs*). Rice line Tetep (*Pi−kh*+?) was found to be highly effective in north-western Himalayan region as none of the isolate could infect this line.

Hayashi and Fukuta (2009) developed a new systematic, expandable method that allows easy understanding of the relationships between races and resistance genes for building up an international standard designation and classification of blast races. Blast races were characterized by reactions to 26 Lijian-xintuan-heigu (LTH) monogenic lines for targeting 23 resistance genes, which were divided into five groups, (1) LTH, IRBLa-A, IRBLsh-S, IRBLb-B, and IRBLt-K59, (2) 3 lines of *Pii* locus region, (3) 7 lines of *Pik* region, (4) 4 lines of *Piz* region, and (5) 7 lines of *Pita* region. Each group consists of 1 to 3 variety unit (s), which were allocated with 3 differential lines (genes) in each and applied codes, 1, 2, and 4, for compatible reactions of blast isolates, respectively.

Use of germplasm for blast resistance

The use of resistance (R) genes in rice improvement breeding programme for disease management has been considered as one of the best options (Hulbert *et al*., 2001). However, host resistance is short-lived in disease-prone environments because of high level of variability in the pathogen population. The frequent variation of race in pathogen population has been proposed as principal mechanism involved in loss of inheritance (Ou, 1980). A number of studies have been reported for appearance of new races at extremely high rates (Giatgong and Frederiksen, 1968; Ou and Ayad, 1968). Development of durable blast resistance rice varieties, isolation of more resistance genes with varying specificities is required, as this helps in the gene stacking into elite cultivars through marker-aided breeding. Alternatively, broad spectrum disease resistance genes can also be used for blast management. Wild germplasm of rice are treasure trove, as they harbour many useful traits for tolerance to biotic and abiotic stresses, particularly disease resistance (Barclay, 2004). So far, more than 100 blast resistance genes from japonica (45%), indica (51%) and other (4%) genotypes have been identified and 22 R-genes have been cloned and functionally validated (Sharma *et al*., 2012; Imam *et al.,* 2013). It is roughly estimated that during the past, more than 30,000 rice cultivars were grown in North East and Eastern parts of India (Ngachan *et al*., 2011). The presence six to seven blast resistant genes in rice accessions from the North Eastern state of Manipur was related to high level of resistance in the accessions (Mahender *et al.,* 2012). Identification of new donors for blast resistance is a pre-requisite for effective utilization of diverse germplasm for marker assisted incorporation of blast resistance into improved varieties (Shikari *et al.,* 2014).

Staking of R-genes for blast resistance

Conventional breeding augmented with marker assisted selection (MAS) has demonstrated a discernible progression in developing crop varieties with improvement towards the desired traits (Vogel, 2014). Several successful examples can be displayed across crops of using molecular markers for incorporating genes governing resistance against multiple biotic and abiotic stresses (Jeena & Mackill, 2008).The utility of MAS in pyramiding genes for resistance to blast from different donors into a common recurrent parent has been successfully demonstrated in various studies for introgressing blast resistance genes in developing resistant cultivars (Khanna *et al*., 2015; Singh *et al*., 2012). In basmati rice, pyramiding of two dominant blast R-genes namely, Pi2 and Pi54 and two bacterial blight R-genes, including one recessive (xa13) and one dominant (Xa21) gene in two widely grown Basmati rice varieties PB1121 and PB6 through MABB has been reported (Ranjith *et al*., 2016). Stacking of two R-genes Pi54 and Pi54rh having broad spectrum resistance against multiple isolates of *P. oryzae* has been reported (Mandeep *et al*., 2017). Both Pi54 and Pi54rh expressed under independent promoters were transferred into a blast susceptible japonica rice, Taipei 309 (TP309).

Management of blast disease

Management of blast disease involves the selection of suitable variety possessing field resistance to disease through host plant resistance, which is economically viable and eco-friendly. Emergence of highly virulent races of *P. oryzae,* which makes management of pathogen more difficult and even with use of one selective management practice bringing disease below threshold level is meagerly achieved some time. Occurrence of new races of the pathogen in Japan has resulted in frequent breakdown of resistance causing 20-100% of crop losses despite utilization of effective blast resistance genes in local varieties (Khush and Jena, 2009). Use of integrated approach in managing disease with available options like selection of resistant genotype, use of combination or single bioagents (fungal or bacterial formulation) and chemical fungicides are suitable. Due to emergence of highly virulent races, adoption of single management practice becomes unfeasible resulting in yield loss. Use of multiple management practices will help in curtailing the disease under threshold level. Induction of systemic resistance by *Pseudomonas syringae* pv. *syringae* in rice against *P. oryzae* was also reported by Smith and Matraux (1991), Kumawat *et al.,* (2008).The efficacy of biocontrol agents, botanicals and organically approved fungicides in the management of blast disease in rice was conducted and it was found that copper fungicides, *Pseudomonas fluorescens*, botanicals like garlic and neem oil can be used in an integrated manner for the management of blast in rice under organic conditions (Gopi, *et al*., 2016).

Future prospects

Rice blast is a major menace in all rice growing ecosystems of country, managing rice blast involves identification of potential resistance sources from existing collection of rice genotypes and its effective utilization for MAS for blast resistance. Cross-infectivity, distribution and diversity of *Pyricularia* sp. in country with specific monogenic R-genes can lead to proper identification of resistance spectrum and integrated approach of managing blast disease with adoption of cultural, biological and chemical management practices.

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LT (FP)-02

Emerging and re-emerging fungal plant diseases in North East India: challenges and strategies

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Abstract

Plant diseases are a significant constraint to agricultural productivity. The extent of this threat has increased dramatically in the 1980s and 1990s due to the expansion of international trade in agricultural products and frequent movement of massive volume of people and goods across national boundaries. Introduction of new diseases has not only caused farm losses, but has also diminished export revenue since phytosanitary issues are linked to international commerce. Plant pathogens and their vectors have also moved across national boundaries, sometimes naturally and at other times influenced by the recent changes in trade practices.

The rise in emerging pathogens and strains has led to increased calls for more effective surveillance in plant health. The use of spatially explicit stochastic models to optimize targeting of surveillance and control resources so as to how modern detection and diagnostic technologies as well as information from passive surveillance networks (e.g., citizen science) can be integrated into surveillance and management strategies.

A rice trade crisis occurred at the beginning of 2008, which led to soaring retail prices on markets. This price spike affected foremost the poor, as rice is the staple of roughly half the poor in the world. Such events concern plant pathologists because plant diseases are major yield-reducers. A shortage of agricultural resources, in turn, causes unprecedented changes in rice production situations worldwide. The relationships between production situations and crop health are well documented in rice. Changes in cropping practices and systems will inevitably lead to new crop health problems, not only in terms of emerging or re-emerging diseases but also in terms of combinations of production and sustainability

Introduction

Modernization of agriculture, to increase efficiency and profitability and to meet the food needs of increasing population, has led to some profound changes in the way agriculture is practiced. Intensification of land use, modern cultivars, new land and crop management practices, changes in food preferences and associated food policy, dynamic trade policies, and frequent international movement of goods and people have all had effects on agriculture. These changes have varying effects on different components of the agricultural system.

The full potential of agriculture is rarely achieved due to the vagaries of nature, including losses caused by plant diseases. Plant diseases as a group cause substantial losses directly and indirectly by reducing the quantity and quality of food, feed, fiber, and industrial inputs. Notorious famines precipitated by plant disease include the Irish potato famine of the 1840s due to potato late blight, the Bengal famine of 1943 due to rice brown spot, and famines in Uganda in the 1990s due to cassava mosaic disease. Plant diseases have sometimes up- set national economies, changed food habits, caused poisoning, transformed landscapes, and caused hardships in other ways. Diseases are ubiquitous among plants, but some diseases are more damaging than others. Within a given agro-ecosystem, only a few diseases cause significant damage. The more damaging diseases are most often caused by infectious agents such as fungi, viruses, bacteria, and nematodes. Not all diseases of a plant occur everywhere the plant is grown. The causal agent of a disease must challenge a host cultivar at a stage when it is susceptible and at a time when environmental conditions are favourable to the pathogen. The relative importance of a particular disease on a crop is dynamic. In some cases, an important disease may become obscure when it is controlled with new disease management technologies. In other cases, an unimportant disease may re-emerge as damaging with changes in agricultural practices, and still in other cases a new disease may emerge as important in a geographic area. The spectrum of threatening diseases has changed dramatically in recent times. The concept of global movement of plant pathogens and the subsequent threat of exotic plant pathogens to agriculture is not new.

Threats of new and re-emerging diseases occur due to several factors. The major factors are: (1) movement of a new pathogen in a production system, (2) movement of one or more new virulent strains, or emergence of a new aggressive strain in an area where the pathogen existed, (3) introduction of new vectors that can transmit a pathogen efficiently, (4) changing agronomic practices that favour one or more components of epidemics of a specific disease, (5) increased pesticide use leading to development and proliferation of pesticide-resistant strains, (6) intensification of agriculture to maximize productivity and profit, (7) changes in cultivars, and (8) consistent change in climate in the short term. Some of these factors are intrinsic to crop husbandry, while others relate to extraneous, though important, forces such as trade, policy and international exchange.

In agricultural systems, plant breeders developing resistant crop varieties take the side of the crop species in the "arms race" with pathogens. Resistance strategies may include partial resistance, where the direct selection pressure for new pathogen types is lower. In cases where resistance genes are not available or not sufficient for disease management, strategies for the use of other cultural methods, such as changing planting times to avoid pathogens, or pesticides may be used. Plant pathologists work to optimize these systems by, for example, minimizing unnecessary pesticide use through weather- based disease forecasting to guide when pesticides would and would not be useful. But diseases that are new to a region are generally the most problematic, because neither plants nor plant pathologists have had sufficient opportunity to adapt to them.

Decisions about plant-disease management, just like decisions about medical treatment, consist of a series of compromises. Plant- disease risk is a complicated function of the characteristics of the host, pathogen, and environment. The fact is that decisions about how to manage plant diseases generally need to be made with a level of information that is unsatisfactory to scientists. For example, most plant pathologists would agree that having a homogeneous planting of a particular crop species could pose a risk if the genotypes deployed are unexpectedly susceptible to a disease, or if the acreage exerts selection pressure for new pathogen types to overcome resistance. It is clear that international trade in plant species provides many benefits but also an increased risk of introduction of a new pathogen. Because it is difficult to estimate the risk precisely, it is difficult to determine how much to restrict plant movement. The new science of characterizing ecosystem services and their economic value offers to help with such decision- making processes (Cheatham, *et al*. 2009). For example, if tillage can be used to reduce disease risk but it also increases the risk of soil loss, it would be useful to be able to compare these two risks from an economic standpoint.

Status of important rice diseases and their changing scenario in North East India

Major biotic factors that influence rice production in the north-eastern hills are diseases, insect pests, rodents and weeds. Rice blast is endemic and major disease of the region. Leaf and neck blast are common and both together cause yield loss ranging from 40 - 46%. Of late, sheath blight has emerged as an important disease and is well distributed in Manipur and Nagaland. Brown spot and bacterial leaf blight are other important diseases at low and mid altitude areas of Meghalaya and Nagaland, respectively. Sheath rot is assuming greater importance in high altitude areas. Leaf scald and grain discoloration are also widespread in the entire NEH region. Leaf scald generally appears at the maturity stage of the rice crop and, therefore, does not cause severe damage. Grain discoloration, which causes reduced germination, decay of seedlings and lowers quality, is a major problem in both upland and lowland rice.

In rice, several diseases, such as blast (*Pyricularia grisea)*, brown spot (*Helminthosporium oryzae*), sheath blight (*Rhizoctonia solani),* false smut (*Ustilaginoidea virens)*, sheath rot (*Sarocladium oryzae*), stem rot (*Sclerotium oryzae)*, bakanae (*Fusarium moniliformae)*, kernel smut (*Neovossia horrida*), bacterial blight (*Xanthomonas oryzae* pv. *oryzae*), bacterial grain and seedling rot (*Burkholderia glumae*), and tungro (rice tungro bacilliform virus and rice tungro spherical virus), do occur, resulting in significant damage to the grain and straw yield.

Disease management options, lies in the suitably tailored cultural practices *viz*., crop- rotation, intercropping regulating planting and harvesting dates, soil solarization and phytosanitation etc., quarantine and regulatory control measures, judicious manipulation of resistant genes including through transgenic approaches in rice cultivars, chemicals/ botanical products where host resistance is unsuitable or lacking can be deployed on the basis of surveillance. Thus IDM is an eco-friendly and economically feasible technology.

In India, with the introduction of high yielding rice varieties and high nitrogen application for about last four decades, there has a constant increase in the number of diseases, and also a concomitant shift in their intensity, diversity, and spread in rice. Assam is very rich in rice genetic diversity. Many traditional cultivars possess genes of resistance to most rice diseases. Many diseases infest rice plants in Assam, but the most important ones are sheath blight, bacterial blight, and blast in the *sali;* blast and sheath rot in the *ahu;* sheath rot and sheath blight and neck blast in the *boro*; and ufra and root knot in deep-water rice. The extent of average yield losses attributed to diseases is not known. However, it is assumed that 15-20% yield losses may occur in some infested fields, although average losses would be much less. Farmers seem to be not very much aware about diseases, unlike what they know of other pests. Although several cultural and chemical options are available for the management of each of the major diseases, it is not known what percentage of the farmers uses these technologies, if at all. Some fungicides are available at the grassroots level, but their use is very low. However, most of the popular modern rice varieties possess resistance to or tolerance for blast, and some degree of tolerance for sheath blight and bacterial blight.

Based on information derived from Production Oriented Survey (POS) in North Eastern states a shift in disease scenario is being noticed where in all the states of NE region blast disease emerged as common and most serious disease in any season in any parts of the rice plant but during 1980-1990 the region has witnessed major incidence of Sheath blight, BLB and RTV but gradually its intensity has come down due to resistant varieties, management schedule or other related factors, however earlier lesser known minor disease like False Smut, Bakane and Brown spot have re-emerged as dominant and major in terms of incidence and severity because of change of varieties, soil nutrient status degradation or climate change in most of the rice growing belt of NE States.

International and national rice pathologists of Africa were surprised to find symptoms of an important rice disease called bacterial leaf streak during their field visit. "The presence of bacterial leaf streak of rice was never reported before from East African country. Similarly the team of rice pathologists detected the symptoms of bacterial sheath rot of rice for the first time in Senegal in West Africa. "Farmers in northern Senegal were desperate as their rice crop was being devastated by this 'mysterious' disease and asked them for help. Plant diseases and pests are strongly influenced by changing weather patterns in the same way that many infectious diseases of humans and animals are climate-sensitive. Researchers are seeking to better understand the relationship between climate and disease occurrence and patterns to forecast disease outbreaks and develop control strategies.

With global warming occurring in some regions, experts think that changes in temperature, rainfall patterns, and extreme events could exacerbate the spread of some crop diseases and alter the pest-plant relationship. For example, symptoms of brown spot and narrow brown leaf spot are now increasingly seen in farmers' fields in West and East Africa. Unknown and unexpected crop disease occurrences, such as the ones mentioned above, are projected to increase and some minor diseases may become major problems in areas where they were previously insignificant. A case in point is sheath blight of rice, which had been a minor disease in Asia, but is now a serious problem. Such changes have potentially serious implications for food security. The negative impacts of climate change are also aggravated by poverty and population explosions still occurring in some developing countries.

What are plant pathogens and what causes them to "Emerge"?

Plant diseases can be caused by a combination of biotic and abiotic agents. Unfavourable environmental conditions, such as an excess or deficiency of nutrients, humidity, light, toxic chemicals, and so on, can damage plants. Infectious plant diseases can be caused by nematodes, viruses, bacteria, fungi, and protozoa (Agrios, 2005). The classic plant disease triangle of host, pathogen, and environment is often used to illustrate how the interaction of these components determines the occurrence and impact of plant disease in time and space (Madden, *et al*. 2007). There are many reasons why a plant disease may "emerge," or increase in importance: (1) The introduction of a new pathogen species or a new type within a species may be the most obvious source of emergent pathogens. An example of the latter is race Ug99 of the wheat stem rust pathogen, discovered in East Africa and moving north through important wheat- growing regions. Wheat stem rust has caused little yield loss in the United States in recent years because of effective resistance in common wheat varieties. But U.S. varieties do not generally have resistance to Ug99, so there is great urgency to develop effective resistance in U.S. cropping systems before Ug99 arrives through contaminated plant materials or even on the clothes of tourists. (2) An increase in the availability of susceptible crop acreage may lead to pathogen emergence. A classic example of a surprising emergent disease is southern corn leaf blight (SCLB). While the disease was known in the United States, it had typically not been a serious problem. When corn breeders switched to a particular form of male sterile cytoplasm for varieties grown throughout the United States in the 1970s, SCLB suddenly became much more important, and scientists realized that this cytoplasm conferred susceptibility to SCLB. Homogeneity of resistant plant varieties can also support disease emergence through the selection pressure for pathogen genotypes that can overcome that resistance. (3) New pathogens may arise through hybridization of existing pathogen species when they come into contact through changing geographic distributions; hybridization may have contributed to Dutch elm disease epidemics (Brasier, 2001); (4) In some cases, it is the introduction of an arthropod vector that makes a pathogen more important. For example, between 1927 and 1930, Citrus tristeza virus (CTV) was introduced into South America, but only in 1950 with the introduction of the aphid vector *Toxoptera citricidus* was this pathogen considered economically important (Anderson, *et al*. 2004). A similar situation was seen in California for *Xylella fastidiosa.* This bacterium caused Pierce's disease for a century in this state, but with the introduction of new insect vector species, Pierce's disease spread rapidly, causing significant losses (Anderson, *et al*. 2004).

What strategies can reduce the risk of disease emergence?

The potential use of plant population or community heterogeneity is an interesting and controversial option to reduce the risk of disease emergence. Margosian*, et al*. (2009) analysed the connectivity of the U.S. agricultural landscape and concluded that the large connected acreage of major crop species, such as maize or soybean, increases the risk of impact from introduced pathogens. Disease impact may be greater both because pathogens can more readily move throughout large areas of crop acreage and because attempts to limit or eradicate new pathogens are less likely to be successful. Thus, the risk imposed by large acreages of single plant species is difficult to quantify. If policy makers concluded that it would be important to reduce connectivity of major crop species acreage, implementation of plans to restrict planting in particular areas would likely be highly controversial. Another controversial approach to reducing disease risk would be implementation of stronger policies to reduce the movement of plant materials (food, fiber, genetic material, horticultural species, packing materials, etc.) between regions. While this would undoubtedly reduce the risk of disease spread, it would also impose a high "opportunity cost" in terms of reducing the benefits that might have been gained by making plant materials available across regions. Anthropogenic introductions of pathogens may be the primary route through which new infectious diseases emerge (Anderson*, et al*. 2004). In some cases, emerging plant pathogens can be excluded from a country by regulatory actions at the nation's borders. A number of regulatory strategies are in place in, for example, the European Union and the United States, with umbrella guidelines established by the World Trade Organization that oversees the international trade of plant materials. Although plant-health inspections and quarantine mechanisms continuously improve, some consider them ineffective or flawed. The main criticisms are that the regulatory mechanisms focus on visual inspections of the plant materials in both the exporting and importing countries. These inspections may, however, cover only a small proportion of the transported materials and therefore likely miss infrequent but viable disease agents. Furthermore, visibly symptomless plants may harbour disease agents in their tissues or in the substrates with which they are transported. This latter issue is further exacerbated by the fact that while many disease agents may be benign in their native environments and in association with their coevolved hosts, their behaviour in a new environment with new hosts is unpredictable. This issue may be best exemplified by a number of severe, introduced plant pathogens that apparently cause only little concern in the location of origin (e.g., *C. parasitica* causing extensive damage to native chestnuts when introduced to North America and Europe, in contrast to the more resistant Asian species). Whether the issue is the regulatory bodies' inability to detect the pathogens because of inadequate screening, the pathogens' un detectability during the inspections, or simply our inability to predict the risk of importing infectious agents that cause no severe threat in the location of their origin, the bottom line remains that the control of international borders may be inadequate to stop potential pathogens (Brasier, 2008). Natural phenomena, such as severe storms, can also introduce new agents across borders. Soybean rust (caused by *Phakopsora pachyrhizi*) is an example of the rapid long-distance dispersal of a plant pathogen. Originally identified in Asia in the early 1900s, soybean rust has spread through Africa and South America since the mid- 1990s and recently to the United States. The large potential economic losses caused by soybean rust and its rapid emergence in the new world motivated forecasting of soybean rust dispersal. The Integrated Aerobiology Modelling System (IAMS), a modelling tool to forecast pathogen dispersal from meteorological data was developed by Isard, *et al.* (2005). Simulations with IAMS suggested that a storm, Hurricane Ivan, could transport rust spores from Colombia to the United States. Subsequent analyses suggested that such severe weather events might be a common cause of long distance dispersal. Prevailing strong winds and favourable humidity allowed soybean- rust establishment more than 1,000 km from the closest known inoculum sources within the United States (Isard, *et al.* 2007). These data indicate that in our changing environment, in which severe weather events are predicted to increase, long distance possibly even cross oceanic pathogen dispersal may become more frequent.

Post- introduction strategies

The introduction of new plant pathogens is nearly inevitable. Now, if the control of these pathogens is possible once they have been introduced. Some diseases, such as Dutch elm disease (caused by *Ophiostoma ulmi* and its close relative *O. novoulmi*), may have spread across continents at a speed that has precluded any control. Diseases where environmental forecasting may allow pre-emptive action and where a detailed understanding of the organisms' biology may provide tools for (biological) control. Soybean rust (above) exemplifies predictive modelling combined with pre-emptive action. The IAMS predicts whether or not climatic conditions support the dispersal, germination, and establishment of the disease, which migrates annually from the southern United States to the north (Isard, *et al*. 2007). The ability to predict movement, combined with fungicide applications during the early colonization, can reduce crop losses as well as save in fungicide costs. Pathogen establishment can be costly as can be its control after establishment. Effective ecological forecasting tools, such as IAMS for soybean- rust establishment, help reduce the costs of subsequent pathogen control. Chestnut blight (caused by *C. parasitica)* provides an example of bio control, the use of a parasite or other natural enemy to manage an undesirable organism. In this severe fungal pathogen of U.S. native chestnut, a virus is passed between two strains of the pathogen. The virus infects the fungus and reduces its ability to cause disease (hypo virulence). The use of a pathogen of a fungus to control a disease in plants is appealing, as the establishment of a virus- bearing fungal population provides a long- term reduction in the disease symptoms. In the case of *C. parasitica*, the hypo virulent strains have established adequately well for chestnut recovery in tests in Europe and North America (Heiniger and Rigling, 1994). Unfortunately, the introduction of hypo virulence has not been universally successful (MacDonald and Fulbright, 1991). Although the potential bio control using the virus- bearing fungi has been well- documented and is worth consideration, it is only available because of a fortuitous well- studied system. Many introduced plant pathogens have not had similar research emphasis, and the basic research to develop bio control tools often requires decades of research. *P. ramorum*—the causal agent of sudden oak death (SOD)—is an example of a recent newcomer. This plant pathogen was identified in 1995 from German rhododendrons and was soon detected in the western United States, where its spread has been devastating to many native plants. The concern about the pathogen's impacts on forestry in California and Oregon led to a monitoring program and diligent quarantine regulations that included destruction of infected plants and their neighbours in nurseries and native stands (Goheen, *et al*. 2004; Rizzo, *et al*. 2005). Regardless of these aggressive measures, Prospero, *et al*. (2007) concluded that inoculum persisted after the eradication measures. The response to *P. ramorum* exemplifies the near-impossible task of controlling some plant pathogens. Furthermore, the success of regulatory actions and quarantine measures remains dependent on citizens' voluntary submission to restrictions. Several controversies persist for the development of strategies for managing new plant diseases. Increasing agricultural heterogeneity may decrease risk, as may decreasing the movement of plant materials. In both cases, it is difficult to quantify the costs and benefits of the actions so that the political will can be developed to implement needed policies. In the meantime, pathogens continue to spread to new areas with the potential for developing new pathogen types through hybridization and the potential to develop new vector associations through newly overlapping pathogen and vector ranges. As a result, threats to food security and to natural ecosystems increase. One certainty is that society would benefit from investing more effort in understanding these processes so that better strategies can be implemented.

Conclusion

Exotic plant diseases have caused appreciable losses in the agricultural sector during the 1990s. The threat from exotic plant diseases continues despite the recent spate of introduction of exotic plant diseases. Exotic pests remain exotic until they gain entry into a disease-free country. Not many diseases will remain exotic in the present climate of international trade and commerce. There is a need to stay prepared to combat the exotic diseases in case of their eventual entry into a new production system. Gaining knowledge to assess their risk and developing methods of control should receive priority at both the federal and state levels. However, ability to conduct research on these diseases before entry of exotic diseases is seriously hampered by the lack of funding and interest from administrators and policy makers. This is because these diseases are not taken seriously until they enter the country and threaten agricultural productivity and trade. By then, much valuable time is lost. Guarding agriculture against anticipated threat of emerging plant diseases would require preparedness and an action plan based on sound research and policy issues The strategy's four goals—surveillance and response, (applied) research, prevention and control, and strengthening infrastructure—apply to emerging diseases of plants too. Specific areas that need further research are the following:

- Improvements in basic identification of and discrimination between new pathogens
- Molecular and immunological detection methods, PCR, real time PCR, and molecular fingerprinting techniques
- Epidemiology and management of new and exotic plant diseases
- Development of disease resistant genotypes through classical breeding and genetic engineering
- Enhanced distance diagnostics, training, and communications regarding new and high-impact diseases

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LT (FP)-03

Effect of climate change on plant disease development

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Abstract

The effect of climate change is mainly impact on the growth and development of plants mean while the effect was also inflected on changes in pathogen host range, changes in plant-associated microflora and direct biological effects on rapidly evolving pathogens leading to outbreak and distribution pattern of plant disease in large area mainly affecting the world food production. The impact is mainly influenced by elevated levels of CO_2, temperature, ozone and ultraviolet (UV) radiation. The variation in all these factors in the environment, plants will subjected to biotic and abiotic stress, may lead to affect the crop growth. Because of biotic factors, most likely impact of climate change will be felt in the field of losses from plant diseases, in the efficacy of disease management strategies and in the geographical distribution of plant diseases. Pest and disease management played major role in doubling the food production, but mitigating the disease management due to climate change is very difficult task to manage and become another layer of complexity to meet the food requirement of the world. Intensified research on climate change-related issues could result in improved understanding and management of plant diseases in the face of current and future climate extremes.

Introduction

The earth's temperature has increased by 0.74^0C during 1906-2005 due to anthropogenic emissions of greenhouses gases (IPCC). It is also predicted that temperature increase is likely to be 1.8 – 4.0^0C by the end of this century. The carbon di-oxide, methane and nitrous oxide in the atmosphere have increased to 379 ppm, 1774 ppb and 379 ppm respectively in 2005 which were 280 ppm, 715 ppb and 270 ppb in 1750. The increases in carbon di -oxide concentration are mainly attributed to fossil-fuel use and land use change, while methane and nitrous oxide are primarily due to agriculture. Nitrous oxide has a global warming potential 296 times greater than CO_2. As per estimate, in India, 28 % of the GHG emissions are from agriculture, about 78 % of the methane and nitrous oxide emissions are also estimated to be from agriculture. The average global air temperature has already increased by 0.7^0C during the last century. For Indian region (south Asia) the IPCC has projected 0.5 – 1.2^0 C rise in temp by 2020, 0.88-3.16^0 C by 2050 and 1.56-5.44^0 C by 2080 depending on the scenario of future development (IPCC, 2007b). Such changes would lead to increase frequency of extreme events like flood, drought, extreme hot, cyclones etc. and will seriously affect the agriculture. Up to the 1990s, there was little information about climate change impacts on plant disease. The disease development may increase, decrease or remain stable depending on the particular pollutant and host-pathogen interaction. However, plant pathologists already realized in the 1990s that climate change was clearly set to pose a challenge to many pathosystems. It is now recognized that climate change will affect plant diseases together with other components of global change, *i.e.* anthropogenic processes such as air, water and soil pollution, long-distance introduction of exotic species and urbanization.

Impact of climate change on plants due to elevated CO_2

The atmospheric CO_2 concentration has increased to over 400 parts per million and continues to increase. An increase in CO_2 levels may encourage the production of plant biomass; however, productivity is regulated by water and nutrients availability, competition against weeds and damage by pests and diseases. Alternatively, a high concentration of carbohydrates in the host tissue promotes the development of biographic fungi such as rust (Chakraborty *et al.,* 2002). Thus, an increase in biomass can modify the microclimate and affect the risk of infection (Lambers *et al*., 2008). In general, increased plant density will tend to increase leaf surface wetness duration and regulate temperature, and so make infection by foliar pathogens more likely (Dalla Pria *et al.,* 2006). However, how abiotic stress factors interact to affect plants will be a key to understanding climate change effects on plants (Niinemets and Valladares, 2008); By the contrast low concentration of carbohydrates, in the host tissue also promotes development of diseases, this because the susceptibly of plants increase by stress (caused by climate or fertilization). Experimental research on the effects of high atmospheric CO_2 concentrations on plant–pathogen interactions has received little attention, and conflicting results have been published. Elevated levels of CO_2 can directly affect the growth of pathogens. For example, according to Chakraborty *et al*. (2002), the growth of the germ tube, appressorium and conidium of *C. gloeosporioides* fungi is slower at high concentrations of CO_2 (700 ppm). In another study Hibberd *et al*. (1996) evaluated powdery mildew in barley, and found that an acclimation of photosynthesis at elevated CO_2 and an infection-induced reduction in net photosynthesis caused larger reductions in plant growth at elevated CO_2; also, the percentage of conidia that progressed to produce colonies was lower in plants grown in high CO_2 (700 ppm) than in low CO_2 (350 ppm) and lower percentage of conidia producing hyphae in 700 ppm CO_2, it was due to a higher proportion of the spores being arrested at the appressorial stage. Some authors suggest that elevated CO_2 concentrations and climate change may accelerate plant pathogen evolution, which can affect virulence and plant-pathogen interactions.

Impact of climate change due to elevated temperature

Due to changes in temperature and precipitation regimes, climate change may alter the growth stage, development rate and pathogenicity of infectious agents, and the physiology and resistance of the host plant (Charkraborty and Datta, 2003). A change in temperature may favor the development of different inactive pathogens, which could induce an epidemic. Increase in temperatures with sufficient soil moisture may increase evapotranspiration resulting in humid microclimate in crop and may lead to incidence of diseases favored under these conditions (Mina and Sinha, 2008).

Temperature is one of the most important factors affecting the occurrence of bacterial diseases such as *Ralstonia solanacearum, Acidovorax avenae* and *Burkholderia glumea*. Thus, bacteria could proliferate in areas where temperature-dependent diseases have not been previously observed (Kudela, 2009). As the temperature increases, the duration of winter and the rate of growth and reproduction of pathogens may be modified (Ladanyi and Horvath, 2010). Similarly, the incidence of vector-borne diseases will be altered. Climate can substantially influence the development and distribution of vectors. Changes may result in geographical distribution, increased overwintering, changes in population growth rates, increases in the number of generations, extension of the development season, changes in crop-pest synchrony of phenology, changes in interspecific interactions and increased risk of invasion by migrant pests (Fabre *et al*., 2005; Mondor *et al*., 2005; Memmott *et al*., 2007). So thermal constant is the amount of heat or total effective temperature that each species requires to complete its life cycle. Considering this, studies has been carried out using thermal constant with the aimed to assess the potential impact of climate change on the spatial distribution of coffee nematodes.

Impact of climate change due to elevated ozone

The direct effects of elevated ozone on spring wheat infected with *Puccinia recondita* f. sp. *tritici*. Crop yield and growth were measured for plants exposed to two levels each of carbon dioxide and ozone and either inoculated with rust or left uninoculated. Results showed that ozone damage to leaves is largely dependent on both carbon dioxide concentrations as well as disease. Additionally, elevated carbon dioxide levels appeared to reduce and delay leaf damage caused by ozone. Tiedemann and Firsching (2000) were evaluated the effects of elevated O_3 on three soybean diseases: downy mildew (*Peronospora manshurica*), Septoria (*Septoria glycines*) and sudden death syndrome (*Fusarium virguliforme*) in combination with high concentrations of O_3, increased the severity of *Septoria glycines*. Alternatively the concentration of CO_2 and O_3 did not have an effect on sudden death syndrome. The authors concluded that high levels of CO_2 and O_3 induced changes in the soybean canopy density and leaf age, likely contributed to disease expression modification. Thus, the increase in both CO_2 and O_3 will alter disease expression for import fungal pathogens of soybean. Young plants are generally the most sensitive to ozone; but mature plants are relatively resistant. Symptoms include tissue collapse, interveinal necrosis depressed flowering and bud formation. Ozone-killed tissues are readily infected by certain fungi.

Pathogen and vector responses to climate change

The range of many pathogens is limited by climatic requirements for overwintering or over summering of the pathogen or vector. In the case of *Phytophthora infestans*, the introduction of multiple mating types, allowing sexual reproduction, increases the ability of the pathogen to overwinter. Temperature requirements for infection differ among pathogen species. For example, wheat rust fungi differ in their requirements from 2 to 15 °C for stripe rust, 10 to 30 °C for leaf rust, and 15 to 35 °C for stem rust the introduction of new vector species and changes in vector overwintering and over summering may have important effects on pathogen survival, movement, and reproduction. In many cases, temperature increases are predicted to lead to the geographic expansion of pathogen and vector distributions, bringing pathogens into contact with more potential hosts and providing new opportunities for pathogen hybridization. Increased transportation and human movement may act synergistically with temperature changes. In one of the most detailed analyses of a plant pathogen, Bergot *et al.* (2008) predicted the geographic range expansion of *Phytophthora cinnamomi* in Europe in response to increased temperatures that would allow for overwintering of this oomycete in new areas are being developed to identify large numbers of virus species simultaneously across plant species in agricultural and natural systems.

Quarantine and exclusion

Management of climate change will put additional pressure on agencies responsible for exclusion as a plant disease control strategy and prevention of movement of trans boundary diseases. In some regions, certain diseases of economic concern do not currently occur because the climate has precluded the causal agents from becoming established. Use of Geographical Information Systems (GIS) and climate matching tools may assist quarantine agencies in determining the threat posed by a given pathogen under current and future climates. This approach was used by Sansford and Baker (2008) to assess the risk of establishment of Karnal bunt in the cereal-growing regions of the European Union.

Plant disease management

Disease management strategies may require adjustment under climate change. Strategies such as delaying planting to avoid a pathogen may become less reliable. And one of the major problems with applications of biological control for plant disease management in the field has been the vulnerability of biocontrol agent populations to environmental variation and environmental extremes. If appropriate temperature and moisture are not consistently available, biocontrol agent populations may reach densities that are too small to have important effects, and may not recover as rapidly as pathogen populations when conducive conditions recur. Such risk models are of great economic importance when they bear on what trade restrictions may be applied against regions where a pathogen such as *Tilletia indica*, causal agent of Karnal bunt, is present. For many invasive pathogens, models of climatic conditions and requirements need to be supplemented by information about the availability of susceptible hosts and the likelihood of transport of pathogens by trade and other human networks Johnson defined durable resistance as resistance "that remains effective during its prolonged and widespread use in an environment favorable to the disease." If resistance is "inherently" durable, then climate change may have no influence on its continued efficacy. One conclusion about the effects of climate change for disease management is that changes, especially if they lead to greater variability in climate, will tend to add extra uncertainty to decision making. In tropical regions where food security is a particular concern, there may tend to be both greater climate variability and uncertainty and less investment in technologies supporting production of regionally important crops. For example, "orphan crops" of particular regional importance that have received less research attention than dominant temperate crops include plantain, cassava, sweet potato, millets, teff, and quinoa. Information about changing disease-management needs will be particularly important for such crops. In fact, incorporating climatic predictions based on El Ni no patterns were found useful for general decision making by subsistence farmers in Zimbabwe.

Conclusion

Climate change is an important phenomenon that affects agricultural production. By anticipating the future, we can prepare ourselves for problems caused by climate change, especially those related to agricultural activities, which generate the greatest amount of food consumed by humans. For several centuries, pests and plant diseases have played an important role in agricultural production. Because global warming may modify areas affected by pests and diseases, studies must be performed to assess pest and disease stages under the effects of climate change, determine the magnitude of disease and identify measures to minimize the risk of infection. The impact of climate change on disease for a given plant species will depend on the nature of the effects climate change has on both the host and its pathogens. Climate change could first affect disease directly by either decreasing or increasing the encounter rate between pathogens and host by changing ranges of the two species. Disease severity should be positively correlated with increases in virulence and aggressiveness of pathogens. However, both of these effects on disease will be mediated by host resistance and encounter rates, which in turn are potentially affected by climate change. Thus a positive effect of climate change on conduciveness to infection or pathogen aggressiveness or virulence could be offset by a concurrent increase in resistance, yielding no net change in disease impact. Species at highest risk for an increase in disease will be those with positive effects of climate change on encounter rates, environmental conduciveness to infection, aggressiveness, or virulence, but with neutral or negative effects on resistance.

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LT (FP)-04

Prevalence and organic management of emerging fungal diseases in some important horticultural crops of Manipur

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Chemical control measures of most of fungal diseases of plants have been developed and could extensively reduce the impact of these plant diseases to a great extent. The adverse effects of the chemical fungicides to our health and ecology are not always desirable. Further during the last few decades, there has been a global awareness that excessive and improper use of chemical fungicides had caused hazards to the health of humans, animals and the environment. Therefore, extensive research for environmentally safe and easily biodegradable bio-fungicides and other organics are being carried out. These compounds are natural in origin, have minimum adverse effects on the physiological processes of plants and are easily convertible into common eco-friendly organic materials. Plant extracts, essential oils, gums, resin, *etc*. have shown to exert biological activity against plant fungal pathogens *in vitro* and *in vivo* and can be used as bio-fungicidal products (Jalili *et al.,* 2009). These products are generally assumed to be more acceptable and less hazardous for the ecosystems and could be used as alternative remedies for treatment of plant diseases (Chuang *et al*., 2007).

Natural plant products are mostly nontoxic for antagonistic microorganisms, show limited field persistence and have a shorter shelf life and no residual threads. They often constitute a part of Integrated Pest Management (IPM) programs, generally safe to humans and environment in comparison to conventional synthetic chemical pesticides. They can easily be adopted by farmers in developing countries who traditionally use plants for the treatment of human diseases (Nuzhat and Vidyasagar, 2013). It is estimated that there are more than 250,000 higher plant species on the earth offering a vast virtually untapped reservoir of bioactive chemical compounds with many potential uses. Many reports approve the efficacy of natural products of plants in controlling fungal growth and mycotoxin production, *e.g*.: cinnamon, clove, oregano, palmarosa and lemongrass oils (Marin *et al*., 2004), tea tree oil (Burgiel and Smaglowski, 2008), common thyme, cinnamon leaf and aniseed oils (Cosic *et al*., 2010), sweet basil, neem, eucalyptus, datura, garlic and oleander extracts (Nashwa and Abo-Elyousr, 2012).

Biocontrol agents also played important role in management of plant diseases and some *Trichoderma* species possess good antagonistic abilities against plant pathogenic fungi, *e.g*. *Fusarium, Pythium*, *Rhizoctonia* and *Sclerotinia* species. Antagonism is based on different mechanisms, like the production of antifungal metabolites by *Trichoderma,* competition for space and nutrients and mycoparasitism. Mycoparasitic *Trichoderma* strains are able to recognise the host hyphae, to coil around them, develop haustoria, penetrate the cell wall of the host with cell-wall degrading enzymes like chitinases, glucanases and proteases, and utilise the contents of the host hyphae as nutrient source. *Trichoderma* strains with effective antagonistic abilities are potential candidates for the biological control of plant diseases. Abiotic and biotic environmental parameters may have negative influence on the biocontrol efficacy of

Trichoderma strains, therefore it is very important to collect information about the effects of environmental factors on the different activities of *Trichoderma* strains with biocontrol potential.

Because of wide variations in the agroclimatic conditions, many horticultural crops are grown in Manipur. However, many diseases occurred on these crops where some are found to be very severe and common that hampered the growth and yield of the plants. The effect of global warming has increased the number and seriousness of some of the diseases. Some common and serious diseases of important horticultural crops and their incidences are listed in table 1. Soil borne wilt disease is very serious on some crops, on chilli and pea the incidence ranged from 13.85 to 73.04 % and 33.00 to 77.00 %, respectively. Soft rot of ginger which is also soil borne disease ranged from 10.00 to 72.00 %. Leaf spot diseases are also very common where on ginger plant the incidence goes upto 67.42%, on turmeric upto 80.50%, on onion 66.67%, on mustard 56.36%, on tomato Alternaria leaf spot upto 76.67%, early and late blight of potato, 56.00% and 66.67%, respectively. Powdery mildew and rust diseases have become problem in many crop plants where on pea, powdery mildew incidence ranged from 1.13 to 61.87% and rust disease, 9.33 to 56.25%. In Manipur, white rust disease is found more serious on rapeseed than on leafy mustard and the incidence ranged from 2.30-56.48%. On brinjal, fruit rot and leaf mold diseases are common where the incidence ranged from 31.66-40.62% and 21.40-41.25% respectively.

Studies on organic management of important diseases of some horticultural crops in Manipur, has shown that different plant extracts and *Trichoderma* species were effective against horticultural crop diseases and are presented in table 2. Among the plant extracts, garlic extract was found to be the best in controlling foliar diseases like leaf spot, rust, powdery mildew, *etc*. and *Trichoderma* species for many soil borne diseases and also foliar diseases. Treatment of ginger rhizomes with 5% garlic extract was found very effective in controlling soft rot disease (19.09%) as compared to 57.14% in untreated control. *Trichoderma viride* and *T. harzianum* were also effective for soft rot disease of ginger with 20.72 % and 21.82 % infection respectively. Garlic extract was also found to be effective in management of leaf spot of ginger and turmeric with 25.76% and 24.50% infection as compared to 62.00 and 70.00% respectively in untreated control. Incidences of white rust and leaf blight of rapeseed and mustard, powdery mildew of pea, leaf spot of onion and leaf mold of brinjal were low in garlic extract sprayed plants in the field. There was only 0.33% white rust infection as compared to 16.33 % in control and 12.52 % leaf blight infection of mustard as compared to 41.96 % in untreated control. Incidences of powdery mildew of pea, leaf spot of onion and leaf mold of brinjal of garlic treatments were 7.70, 12.50 and 11.50 % respectively as compared to 36.61, 31.10 and 39.00 % respectively in untreated controlled plants. Trichoderma species were effective in controlling soil borne diseases. Among the different native *Trichoderma* species, CAUNCIPM-116 and CAUNCIPM-97A were found very effective for wire stem disease of rapeseed and mustard with 1.83 and 3.12% incidence respectively. There was 24.80 % incidence in controlled plots. *Trichoderma viride* and *T. harzianum* were found very effective for wilt of chilli and white rot of onion. Incidence of wilt of chilli in *T. viride* and *T. harzianum* were 23.33 and 30.00% respectively but found very high in control (76.50%). For white rot of onion, *T. harzianum* was more effective (15.50%) than *T. viride* (19.50%). Foliar spray of *T. harzianum* were also found effective for leaf spot of turmeric and white rust of mustard with 29.00 and 9.22% incidences as compared to 70.00 and 16.33 % respectively in untreated control.

Table 1. Incidence of some important fungal diseases on horticultural crops in Manipur

Crop	Disease/Causal pathogen	Incidence (%) (Range)
Ginger	Soft rot/*Fusarium oxysporum* Leaf spot/*Phyllosticta zingiberi*	10.00 -72.00 38.00-67.42
Turmeric	Leaf spot /*Colletotrichum capsici*	38.00-80.50
Chilli	Wilt / *Fusarium oxysporum*	13.85-73.04
Onion	Leaf spot / *Pestalotiopsis neglecta* White rot /*Sclerotium rolfsii* Purple blotch / *Alternaria porri*	21.12-24.37 37.00-67.42 17.78-66.67
Pea	Wilt / *F. oxysporum f.*sp.*pisi* Powdery mildew / *Erysiphe polygoni* Rust / *Uromyces pisi*	33.00-77.00 1.13-61.87 9.33-56.25
Rapeseed and mustard	White rust / *Albugo candida* Alternaria leaf spot / *Alternaria brassicae* Wire stem / *Rhizoctonia solani*	2.30-56.48 1.60-56.36 5.33-20.00
Potato	Early blight / *Alternaria solani* Late blight / *Phytophthora infestan*	21.12-56.00 37.00-66.67
Brinjal	Fruit rot / *Alternaria alternata* Leaf mold / *Cladosporium fulvum*	31.66-40.62 21.40-41.25
Tomato	Alternaria leaf spot / *Alternaria solani*	44.51-76.67

Table 2. Influence of Plant extracts and *Trichoderma* species on the control of plant diseases in Manipur

Diseases	Treatment	Incidence (%)
Soft rot of ginger	*Trichoderma viride* (5g/l) *T. harzianum* (5g/l) Garlic extract (5%) Copper oxychloride Control	20.72 21.82 19.09 17.75 57.14
Leaf spot of ginger	Garlic extract (3%) Sweet flag extract (10%) Carbendazim Control	25.76 32.00 15.80 62.00
Leaf spot of turmeric	Garlic extract (4%) *T.harzianum* Mancozeb Control	24.50 29.00 9.20 70.00
White rust of mustard	Garlic extract (2%) *T.harzianum* Ridomil MZ Control	0.33 9.22 0.11 16.33
Wire stem of rapeseed and mustard	*Trichoderma*(CAUNCIPM-116) *Trichoderma*(CAUNCIPM-97A) Copper oxychoride Control	1.83 3.12 1.41 24.80
Alternaria leaf blight of rapeseed and mustard	Garlic extract (5%) Eucalyptus extract (10%) Tricyclazole	12.52 22.48 12.49

	Control	41.96
Powdery mildew of pea	Garlic extract (5%)	7.79
	Ginger extract (10%)	9.47
	Sulfex (sulphur)	5.43
	Control	36.61
White rot of onion	*T.harzianum*	15.50
	T.viride	19.50
	Carbendazim	10.51
	Control	51.00
Leaf spot of onion	Garlic extract (5%)	12.50
	Ginger extract (10%)	14.69
	Mancozeb	5.24
	Control	31.10
Wilt of chilli	*T.viride*	23.33
	T.harzianum	30.00
	Carbendazim	15.00
	Control	76.50
Leaf mold of brinjal	Garlic extract (6%)	11.50
	Ginger extract (10%)	18.40
	Propiconazole	7.00
	Control	39.00

Conclusion

Due to hazardous impact of most of synthetic fungicides, in the near future the use of such chemicals may be regulated strictly by the governments which may lead to a growing demand for biological plant protection materials such as plant origin products. It would not only be safe for human health and animal health as well as for maintaining the environment from many adverse effects of chemical residues, but also could create opportunities to develop entrepreneurs with local resources for commercial production of more biopesticides and botanicals in the state.

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LT (FP)-05

PGR conservation in North Eastern hill region of India

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Agricultural biodiversity – or Agro-biodiversity, including plants, animals, insects, aquatic and microbial, is the foundation for sustainable agricultural development and is rather more crucial resource than even land, water and environment. Agro-biodiversity is the foundation of sustainable agricultural development and is an essential natural resource to ensure current and future food and nutrition security. It is high time we all realize the importance of utilization of agricultural biodiversity to overcome challenges posed by food insecurity and climate change. India is rich in agro-biodiversity in form of plants, animals, fish, microbes and insects, which are extremely important for livelihood security of farmers. India has robust and dynamic National Agricultural Research System including genetic resources management system for conservation and sustainable use of genetic resources in development of agriculture and to increase income of the farmers.

Crop or plant diversity is the foundation of agriculture or our food. The Plant Genetic Resources (PGR) comprise diversity among and within plant species that are of direct or indirect value to humans. PGRs are the heritage of humankind and the foundation for attaining food, nutritional and health security. Approximately 250,000 plant species have been identified and described to date. More than 30,000 are edible and 7000 have been used as food. More than 300 are cultivated for food and feed at present. PGR are the basic raw materials for current and future progress in crop improvement programmes. Globally, 7.4 million accessions are conserved in more than 1,750 genebanks (FAO, 2010). The PGR management activities include collection through exploration, characterization, evaluation, safe conservation using both conventional storage and biotechnological approaches for *in vitro* conservation and cryopreservation; generation and conservation of genomic resources. Besides, it is a nodal institute authorized by Government of India to facilitate international exchange of germplasm for research purposes and to undertake the quarantine.

The Indian subcontinent is one of the 12 mega-gene centers and represents three global biodiversity hotspots. This is evidenced through its rich diversity in domesticated plant species and crop wild relatives. The North-Eastern (NE) region of India comprising of eight states namely Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura, is extremely rich and diverse in terms of PGR. The geography of the NE states of India is unique having snowcapped peaks of the Himalayas, the ecological hot spots of the NE foothills and the Brahmaputra valley. High rainfall, humidity, varied topography and altitude, high natural selection pressures, environmental stresses have made the region rich both in floristic and crop diversities.

The NE India comprises about 8% (2, 62,179 Sq. Km) of India's total geographic area supporting around 50% of the flora (Ca. 8,000 species), of which about 32% (Ca. 2,526 species) is endemic. This region is described as 'Cradle of flowering plant' by Takhtajan in 1969, due to its angiosperm diversity. It is a part of the Vavilovian gene centre for many important cultivated plant species and it is well known for its richness in variety of landraces and primitive cultivars of several crops besides a huge floristic wealth of great economic importance. The region is also the home to more than 200 tribes in India who are the custodians of precious agro-biodiversity in this region. The various ethnic groups, practicing primitive agriculture, have preserved the local landraces and varieties of crop plants. These landraces are the product of many years of natural evolution and human selection and contain useful genes for resistance to biotic and abiotic stresses, as well as, adaptability to diverse climatic conditions. The traditional farming practices in the region encourage *in situ* conservation of precious agro-biodiversity. The NE India is the home to about 8,000 angiosperm species which belong to more than 200 families. Species richness is the highest in Arunachal Pradesh (62.5%) and the lowest in Tripura (20.0%). About 3,440 angiosperm species (43%) are endemic and 800 species are endangered.

The declared *in situ* conserved area is 5.53% of the total geographical area of the NEH region. *In situ* conservation is in the form of Biosphere reserve, National Park, Wild life sanctuary and Gene sanctuary. Sacred grove is also a novel method of *in situ* biodiversity conservation, also popular at community level especially in Meghalaya. The Nokrek, Manas, Dibru-Saikhowa, Dihang-Dibang and Kanchenjunga are the declared Biosphere reserve in the region. Besides this 17 National Parks and 55 Wild life sanctuaries are exist in this region. Maintenance and continuous cultivation over the generation of various crop landraces in farmer's field is another method of *in-situ* (on farm) conservation in NEH. Apatani plateau (Lower Subansiri district) and Khampti Valley (Lohit district) of Arunachal Pradesh is an example of *in-situ* conservation practice for rice landraces. Habitat preservation, another approach of *in-situ* conservation, is also popular in this region. *Nepenthes khasiana* (in Jaintia hills), *Lilium macklinae* and *Zizania latifolia* (in Manipur) *Coptis teeta* (in Dibang Valley) and *Gymnocladus assamicus* (in Tawang district of Arunachal Pradesh) are examples of such kind of conservation.

The NE region being one of the primary and secondary centers of many crops exhibits wide variability for several cultivated crops and other plant species. Varied altitude, climatic conditions and topography support the cultivation of a large number of domesticated plant species, and thus facilitating generation of a spectrum of genetic variability under natural or farmers' selection pressures. Agriculture and allied activities are the main source of livelihood for the people of NE region. The cultivation of crops is done in terraced fields, along steep hillsides as well as in plains. Net sown area is highest in Assam (35.1%) followed by Tripura (26.7%). Arunachal Pradesh has the lowest net sown area (3.7%) in this region. Cropping intensity is highest in Tripura (156.5%) followed by Manipur (152.1%), Mizoram (136.4%) and Assam (123.6%). Traditional farming system is *jhum* or shifting cultivation. About 1.6 m ha area is under *jhum* cultivation. Among the cultivated crops, vast diversity exist in rice, maize and beans. In Sikkim, the economically important crops are large cardamom and tea, however maize and rice are also cultivated in considerable area. In Arunachal Pradesh, rice, maize and oilseeds are the major crops. In Assam, rice is the main crop and cultivated widely in low land valleys. Jute is cultivated in inundated flood plains and hill slopes are utilized for tea cultivation. Other crops include wheat, oilseeds, pulses, etc. Meghalaya is an agricultural state where approximately 80% of population have agricultural livelihood. Common crop is rice, grows both in hill terraces and in the valleys. Alternate crops are maize, potato, vegetables, cotton and fruits. Besides the major food crops of rice and maize, several horticultural crops like citrus, pineapple, banana, guava, litchi, jackfruit, plum, pear, peach, etc. are also cultivated in this state. Potato, ginger, turmeric, black pepper, arecanut, cinnamon, betel vine, jute, short-staple cotton, mustard, etc are cultivated as cash crops. The major crops of Manipur, Mizoram, Nagaland and Tripura are rice, maize, millets, oilseeds (rapeseed, mustard and niger), potato, fibres, sugarcane, yams and taros. Farmers also cultivate different types of vegetables like brinjal, chilli, onion, tomato, carrots, melons, spinach, cucumber etc., and a variety of plantation crops such as pineapple, citrus, cashew-nut, jackfruit, tea, etc. The tribal dominated areas of these states are particularly rich in local variability of cereals (rice, maize, barley and wheat), pseudocereals (buckwheat, *Chenopodium*, amaranth and job’s tear), millets (finger millet and foxtail millet), legumes (rice bean, black gram, winged bean, adzuki bean, *Dolichos*, soybean, sword bean and peas), oilseeds (*Brassica* spp., perilla and sesame), vegetables (brinjal, cucurbits, lady’s finger and leafy vegetable such as amaranth, lai, lafa and spinach), fibres (*Corchorus* spp., tree cotton, kenaf and mesta), tuber and rhizomatous crops (taros, yam, ginger and turmeric), fruits (citrus, banana, mango, jackfruit and bael),spices (chilli and piper) and plantation crops (tea, arecanut, bamboo and canes). The diverse topography, altitude and climatic conditions of NE region offers a great scope for cultivation of a wide variety of horticultural crops like tropical, subtropical, temperate vegetables and fruits. Among economically important plants variability is found in bamboos (78 taxa; Hore, 1998) orchids and aroids (15 species; Hooker, 1893). A plenty of herbal wealth exists in this region extending from the dry alpine scrub zone and sub-tropical zone in Arunachal Pradesh and Sikkim to tropical moist deciduous forest and tropical wet evergreen forest in Assam and Tripura. About 138 herbaceous and 59 tree species of medicinal and aromatic plants are being exploited commercially and traditionally to cure several diseases such as cancer, tuberculosis, leprosy, malaria, paralysis, etc. Several other plant species of this category need proper exploitation. These include *Coptis teeta*, *Pyrethrum* sp. and lemon grass. Tremendous potential diversity exist in wild species under different crop usage categories such as fruits, tuber and rhizomatous crops, vegetables, legumes, etc., which warrant it future exploitation. It is estimated that among the total 326 species of CWR, at least 132 prevail in the NE region (Gautam *et al*., 1999). The occurrence of these species is primarily reported from secondary vegetation, open forest habitats of disturbed sites except for species like *Amomum*, *Musa,* etc., which also occur in dense forests. In this region, the compositions of dicotyledonous species are almost three times more than the monocotyledonous species. The dominant species belongs to the families are Orchidaceae, Poaceae, Cyperaceae, Rosaceae, Leguminosae, Asteraceae, Fagaceae, Magnoliaceae, Dipterocarpaceae, Urticaceae, Moraceae, Melastomataceae and Euphorbiaceae. NE India shares the maximum number of endemic and rare plant species showing discontinuous distribution. Many of them are threatened and need to be protected. Out of 1500 threatened forest species in India, about 650 species are from this region (Hore, 1998).

The management of such a vast wild as well as cultivated plant genetic diversity is a prodigious task. Wild and undisturbed forest areas are being maintained by the state forest departments. The tribal communities traditionally maintain the cultivated plants and their landraces. The

ICAR-National Bureau of Plant Genetic Resources (NBPGR) established in August 1976 under the auspices of Indian Council of Agricultural Research (ICAR) has the mandate to act as a nodal institute at national level for acquisition and management of indigenous and exotic plant genetic resources (PGR) for food and agriculture, and to carry out supportive research and capacity building through human resource development. The Bureau has its main campus at New Delhi with 10 Regional Stations located in different agro-ecological/ phyto-geographical regions of the country. The mandate of NBPGR is to act as a nodal institute at national level for acquisition and management of indigenous and exotic plant genetic resources (PGR) for food and agriculture. The mandate includes management and to promotes sustainable use of plant genetic and genomic resources of agri-horticultural crops and carry out related research; coordination of capacity building in PGR management and policy issues, governing access and benefit sharing of their use, and molecular profiling of varieties of agri-horticultural crops and GM detection technology research.

Since its inception, ICAR-NBPGR has played a pivotal role in crop improvement and diversification and management of PGR and related activities at national and international level. The ICAR-NBPGR has 10 Regional Stations covering all the agro-ecological zones of the country and a network of 59 National Active Germplasm Sites (NAGS). The component activities include, collection, characterization, evaluation, safe conservation using both conventional storage and biotechnological approaches for *in vitro* conservation and cryopreservation; DNA fingerprinting of agri-horticultural crops, generation and conservation and use of genomic resources and GM detection. The institute has so far undertaken 2,644 explorations and collected about 2.67 lakh accessions of crop species and their wild relatives. Mapping of collected diversity followed by gap analysis using GIS tools was undertaken in some crops. In rice, more than 35,000 accessions; in maize >8,000 accessions and in sesame over 2,500 accessions collected from different states of the country were georeferenced. Recognizing the importance of PGR with novel/unique traits, NBPGR plays a vital role in germplasm registration. About 1250 potentially valuable germplasm of over 204 species of various crops are registered so far.

The major activity in NE hill region is collection of germplasm, in addition to other PGR activities. Around 290 explorations trips were undertaken and over 30,000 collections have been made. Crop group-wise maximum accessions collected in cereal and millets (32%) with rice and maize being the major crops, followed by vegetables (20%), legumes (9%) and other crops comprising of wild relatives of crops, ornamentals, fibre crops, oilseeds, fruits, tuber and rhizomatous crops and spices. In last five years forty five explorations were carried out in all the eight states of NE Region namely Arunachal Pradesh (12), Assam (5), Manipur (6), Meghalaya (2), Mizoram (5), Nagaland (7), Sikkim (3) and Tripura (5). In total, 3,103 germplasm samples (190 taxa) were collected – cereals and millets (992), pseudocereals (104), pulses (265), oilseeds (107), fibres (61), vegetables (964), fruits (158), spices and Medicinal & Aromatic Plants (M&AP) (73), crop wild relatives (322) and minor economic species (57). The noticeable collections include: cold tolerant rice genotypes (Arunachal Pradesh), scented rice ('Chakhao') rice germplasm (Manipur), soft rice (Assam), tall and high tillering rice (Nagaland) Mishmi and 'Khamati rice (Arunachal Pradesh), maize landraces (Mizoram, Nagaland and Sikkim), frost tolerant type of banana (Arunachal Pradesh), tree cotton with long boll (Mizoram), natural coloured (brown-linted) cotton (Tripura), highly pungent bird's-eye chilli (Mizoram), brown-netted cold tolerant cucumber (Meghalaya), carotenoid-rich cucumber (Mizoram and Manipur), scented ash gourd (Mizoram, Arunachal Pradesh and Tripura), extra-long-fruited yard long beans (Nagaland), scented sponge gourd (Tripura), etc. Indigenous knowledge have been documented from Barak Valley (Assam), Manipur, Mizoram and Nagaland.

Many crop landraces have been collected for the first time, besides new species, distribution records, and uses. While genetic erosion has been apparently evident in two levels – loss of crop species (e.g. drastic reduction in cultivation of Job's-tears and buckwheat) and varietal erosion, its degree varies greatly with respect to topography (more in plains) and ethnic group (e.g. Nagaland tribal groups generally prefer to their own landraces). Conversely, exotic vegetables (e.g. *Abelmoschus caillei*, *Capsicum chinense* and *C. frutescens*, *Solanum aethiopicum* and *S. macrocarpon*) and semi-wild/semi-domesticated edible species contributing to diversity in food habits through supplementing/ substituting native crops was also noted. The collected landraces require rigorous characterization and evaluation using latest tools so as to unearth their potential for crop improvement, besides identifying probable duplicates as it is possible that the same material is being named differently by different tribal group. Explorers often faced challenges in collecting enough number of seeds in samples of crops cultivated at subsistence level (e.g. in kitchen garden), having big-sized seeds (e.g. cucurbits, beans), and also in crop wild relatives; which demanded the need for seed multiplication at isoclimatic conditions before conservation/ evaluation. Also constraints in germplasm collection had been experienced from some areas, particularly in Manipur, western Assam, and in some districts bordering Myanmar. Based on collected germplasm, gaps are identified for future exploration especially in a fine grid fashion in this region. Road connectivity to interior areas and in higher reaches in the recent years would serve as an opportunity to collect germplasm from unexplored areas in forthcoming years. Studies on ethno-botany of many tribals including domestication trends of wild economic plants from this area need an impetus. Information available in this report will help in the identification of crop diversity rich pockets, preparation of PGR maps, and establishment of *in situ* gene sanctuaries for important crop wild relatives and minor fruits.

Farmers have played a crucial role in the conservation of biodiversity including PGR. It is important that society recognizes and encourages this role through incentives, such as benefit sharing. The importance of utilization of PGR to overcome challenges posed by food insecurity and climate change needs to be more focussed. Efficient conservation and use of plant diversity is of immense importance in the current regime of climate change. There is an urgent need for managing genetic resources for food and agriculture in ways that promote the evolution and conservation of agro-biodiversity, and to ensure that they are available to all stakeholders for use to adapt to changing environment by developing new climate resilient genotypes to ensure the food and nutritional security. Climate change will also increase the importance of minor or under-utilized (potential or future) crops/species keeping in view the availability of vast genetic resources in NE hill region. Therefore, it is essential that all forms of agro-biodiversity are conserved through suitable characterization and evaluation, and to ensure their availability for improvement programmes of food and agriculture. Many farmers and tribal communities do conserve useful germplasm of different varieties and crops as well as traditional knowledge. Therefore, enhanced efforts are obviously needed to develop community level seed gene banks and establishing link them with national/international gene bank networks. In addition to that, efforts should be needed for conservation and protection of land races and farmer's varieties by suitable instruments (PPVFRA/GI/ NBPGR) and value addition to these resources. Awareness generation at various levels through formal and informal education needs to be emphasized in conservation of plant diversity. These approaches in PGR management will definitely help in doubling the farmer's income and sustainable development of agriculture.

Following are the thrust area for effective agro-biodiversity management in NE hill region:

1. Accessions from widely distributed habitats are required to be augmented and conserved. Special missions are needed to be undertaken in the area of occurrence of rich diversity to collect and conserve the germplasm using *ex-situ* and *in-situ* approaches.
2. Emphasis needs to be given on targeted collection, conservation and sustainable management of economic germplasm and their wild relatives.
3. Efforts are needed in conservation of some of the hot spot and critical habitats such as *Citrus* Gene Century of Meghalaya.
4. Gaps identified in the management of the PGR should be bridged through appropriate research and development (R & D). Different organizations / institutes engaged in the R & D work should come together and work jointly to conserve the diversity.
5. There is a need of systematic documentation and updating the scientific data base.
6. Development of core sets for agro-climatic regions and/or agro-biodiversity centres
7. Prioritizing *in situ* conservation and linking with protected area network
8. Enrichment of germplasm holdings both in seed banks and FGB in view of future needs
9. Characterization and evaluation of germplasm for identification of trait-specific germplasm
10. Awareness generation at various levels through formal and informal education need to be emphasized in conservation of biodiversity.
11. Farmers have played a crucial role in the conservation of biodiversity. It is important that society recognizes and encourages this role through incentives, such as benefit sharing.

LT (FP)-06

Trichoderma- effective biocontrol agent against soil borne diseases

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Introduction

Phytopathogenic microorganisms affecting plants and post-harvested vegetables have led to considerable losses in crop production and storage worldwide. Chemical pesticides have been used to protect the plants from diseases, but abuse in their employment has resulted in the development of resistant pathogen strains, environmental contamination and presence of pesticide residues on food. *Trichoderma* sp. is considered to be the most important ones among the biocontrol agents (Abada, 1994) due to its biological control ability against several plant pathogens (Kubicek & Harman, 1998).

Classification of *Trichoderma* sp.

Bissett (1991) and Rifai (1969) stated that identification of the Trichoderma at species level is not reliable on morphology based techniques and further declared the use of light microscope the most common approach to determine individual species by studying their morphological characters such as the branching pattern of conidiophore, the conidiophore apex elongation and shape (coiled, straight or undulate), the phialides shape, structure and size and the conidial shape. Since the boundaries of the *Trichoderma* genus are ill defined and the existence of both anamorph and teleomorph stages increase the complexity of *Trichoderma* species identification there is a drawback of the use of light microscope. Trichoderma pers. Ex. Fr., is a genus under Deuteromycotina, Hyphomycetes, Phialasporace, Hyphales, Dematiaceae is characterized "as rapidly growing colonies bearing tufted or pustulate, mostly bright green conidia borne in slimy heads, repeatedly branched conidiophores with lageniform phialides".

Molecular characterization of *Trichoderma*

Only morphology in Trichoderma was not enough for a satisfactory taxonomy. Frustrated users of the existing taxonomy made their first efforts for macromolecular characterization of Trichoderma strains and species. Compared to the traditionally observed and analyzed data, characters derived from nucleic acids and enzymes proposed a greater objectivity. Wuczkowski *et al*., 2003 investigated the occurrence and genetic diversity of *Trichoderma*, forty-six strains at the species level by analysis of morphological characters, by sequence analysis of their internal transcribed pacer regions 1 and 2 (ITS1 and 2) of the rDNA cluster and in some cases, a fragment of the translation elongation factor 1alpha (tef1) gene, and RAPD-analysis. A representative 64 isolates were confirmed at the species level using sequence of the ITS1 and 2 region of the rRNA cluster from longest intron of tef1 gene and by oligonucleotide barcode program TrichoKey v.1.0 and the custom BLAST server TrichoBLAST. Genetic and metabolic diversity of endemic species of *Trichoderma* were assess by using *Trichoderma* spp. (Kubicek *et al*., 2003).

Mode of action

Trichoderma is a ubiquitous genus present in any habitat and at high population densities (Chet *et al.*, 1997). Ascomycetous, deuteromycetous and basidiomycetous fungi, which are mainly soil-borne but also air-borne pathogens are control by Trichoderma BCAs (Monte, 2001). Trichoderma is more efficient in acidic than alkaline soils. Since Weindling (1932) recognized the antagonistic effect of Trichoderma species against plant pathogens, several species of Trichoderma have been extensively studied as biological control agents against fungal pathogens. Production of antibiotic, volatile and non-volatile chemicals influence the permeability of cell membranes and result in an efflux of the cytoplasm (Howell, 1998).

For over 70 years *Trichoderma* species have been investigated as biological control agents (BCAs) (Hjeljord and Tronsmo, 1998), but lately this strains have become commercially available. Trichoderma strains can exert control against fungal phytopathogens either by direct or indirect mechanism. Competing for nutrients and space, modifying the environmental condition, promoting plant growth, plant defensive mechanisms and antibiosis are the indirect mechanism that is used to control against fungal phytopathogens or directly by mechanisms such as mycoparasitism. Specific metabolites production, such as plant growth factors, hydrolytic enzymes, siderophores, antibiotics, and permeases is required for activation of each mechanism. A series of morphological and biochemical changes in the plant is initiated by specific strains of fungi in the genus Trichoderma by colonizing and penetrating plant root tissues and is considered to be part of the plant defense response, subsequently leading to induced systemic resistance (Bailey and Lumsden, 1998). Mycoparasitism is one of the most important mechanisms of biocontrol wherein Trichoderma utilize the contents of the host hyphae as nutrient source. They will coil around the host hyphae, then develop haustoria and penetrate the cell wall of the host with cell-wall degrading enzymes like chitinases, glucanases and proteases (Kredics *et al.*, 2003). A proposed mechanism although not proved to be a main activity was competition. Scanning electron microscopy and fluorescence microscopy showed that *T. harzianum* and *T. hamatum* were mycoparasites of both *Sclerotium rolfsii* and *Rhizoctonia solani*.

In 1983, Howell and Stipanovic isolated and described a new antibiotic, gliovirin, from *Gliocladium* (*Trichoderma*) *virens* (GV-P) that was strongly inhibitory to *Pythium ultimum* and a *Phytophthora* species. Two unusual pyridones, trichodin A (1) and trichodin B (2), together with the known compound, pyridoxatin (3), were extracted from mycelia and culture broth of the marine fungus, *Trichoderma* sp. strain MF106 (Wu *et al.*, 2014). Gliotoxin produced by *Trichoderma virens* is used for controlling of *Rhizoctonia solani* (Wilhite *et al.*, 1994).

Trichoderma is completely safe there has never been a recorded adverse reaction on humans and livestock. *T. harzianum* has been shown to be bioactive against *Armillaria mellea*. Growth of the fungus *Gaeumanmyces graminis* var *tritici* is inhibited by 6-pentyl-pyrone and other-pyrone analogues. There is also report of inhibition of growth of *Rhizoctonia solani* by 6- pentyl-pyrone thereby reducing the rate of damping-off in lettuce (Tarus *et al.*, 2003). Chitinases and ß-1,3-glucanases are the best-studied antifungal proteins. Chitinase encoding genes are the most used to improve plant defence against fungal pathogens. Linear homopolymer of ß-1,4-Nacetyl- D-glucosamine, the main component of the cell wall of most phytopathogenic fungi is degraded by chitinase enzymes and in vitro it also show a strong inhibitory activity on germination and hyphal growth (Lorito*et al*., 1996). Strategies include biological control, breeding of resistant varieties, improvement in cultural practices, storage conditions to those less favorable for pathogen attack and survival, application of chemical fungicides and using integrated pest management (IPM).

Benefits of *Trichoderma*

1. **Disease Control:** *Trichoderma* is a potent biocontrol agent and used extensively for post-harvest disease control.
2. **Plant growth promoter:** *Trichoderma* strains solubilize phosphates and micronutrients. The application of *Trichoderma* strains with plants such as grasses increases the number of deep roots, thereby increasing the plant's ability to resist drought.
3. **Biochemical elicitors of disease resistance:** *Trichoderma* strains are known to induce resistance in plants. Three classes of compounds that are produced by *Trichoderma* and induce resistance in plants are now known. These compounds induce ethylene production, hypersensitive responses and other defence related reactions in plant cultivates.
4. **Transgenic plants:** Introduction of endochitinase gene from *Trichoderma* into plants such as tobacco and potato plants have increased their resistance to fungal growth. Selected transgenic lines are highly tolerant to foliar pathogens such as *Alternaria alternata, A. solani,* and *Botrytis cirerea* as well as to the soil-borne pathogen, *Rhizoctonia* spp.
5. **Bioremediation:** *Trichoderma* strains play an important role in the bioremediation of soil that are contaminated with pesticides and herbicides. They have the ability to degrade a wide range of insecticides: organochlorines, organophosphates and carbonates.

Method of application

1. **Seed treatment:** Seed treatment with bio-control agents either in dry or wet conditions is highly effective in controlling soil borne diseases which cause pre and post emergence mortality. Many soil borne diseases have successfully been managed through seed treatment with antagonist. Mix 6 - 10 g of *Trichoderma* powder per Kg of seed before sowing.
2. **Nursery treatment:** Apply 10 - 25 g of *Trichoderma* powder per 100 ml of nursery bed. Application of neem cake and FYM before treatment increases the efficacy.
3. **Cutting and seedling root dip:** Mix 10g of *Trichoderma* powder along with 100g of well rotten FYM per liter of water and dip the cuttings and seedlings for 10 minutes before planting.
4. **Soil treatment:** Apply 5 Kg of *Trichoderma* powder per hectare after turning of sun hemp or dhaincha into the soil for green manuring or Mix 1kg of *Trichoderma* formulation in 100 kg of farmyard manure and cover it for 7 days with polythene. Sprinkle the heap with water intermittently. Turn the mixture in every 3-4 days interval and then broadcast in the field.
5. **Plant treatment:** Drench the soil near stem region with 10g *Trichoderma* powder mixed in a liter of water.
6. **Spraying:** Spraying suspension of propagules at high concentration (generally 10^6-10^8 spore/cell/ml) continues to be the chief method used for applying biocontrol agents to foliage and flowers.

7. **Contact application:** It is more efficient than spraying and dusting for treating tree and plants.
8. ***Trichoderma* formulations:** Important commercial formulations are available in the name of Sanjibani, Guard, Niprot and Bioderma. These formulations contain 3x10^6 cfu per 1 g of carrier material. Talc is used as carrier for making powder formulation.

Recommended for *Trichoderma* is most useful for all types of Plants and Vegetables such as cauliflower, cotton, tobacco, soybean, sugarcane, sugarbeet, eggplant, red gram, Bengal gram, banana, tomato, chillies, potato, citrus, onion, groundnut, peas, sunflower, brinjal, coffee, tea, ginger, turmeric, pepper, betel vine, cardamom etc.

Compatibility: *Trichoderma* is compatible with organic manure *Trichoderma* is compatible with biofertilizers like *Rhizobium, Azospirillum, Bacillus Subtilis* and *Phosphobacteria*. *Trichoderma* can be applied to seeds treated with metalaxyl or thiram but not mercurials. It can be mixed with chemical fungicides as tank mix.

Precautions

- Don't use chemical fungicide after application of *Trichoderma* for 4-5 days.
- Don't use *Trichoderma* in dry soil. Moisture is an essential factor for its growth and survivability.
- Don't put the treated seeds in direct sun rays.
- Don't keep the treated FYM for longer duration.

Contribution of Department of Plant Pathology, COA, CAU, Imphal

Altogether 200 numbers of *Trichoderma* spp. isolated and screen against soil borne pathogens. Morphological and molecular identification of the potent isolates were carried out. The mass production of the native potent *Trichoderma* spp. standardize with locally available agriculturally substrates. Now the technology is given to the farmers and some of the farmers are started producing own *Trichoderma* as per their requirement.

Conclusion

Biological control is one of the best alternative methods for controlling plant pathogens. Scarce knowledge on the ecology of rhizosphere and use of *in vitro* antagonism for selection of biological control agents limit its use. However, it is more advantageous compared to chemical pesticides. *Trichoderma* species are efficient biological agents against plant pathogens and simultaneously it increases the growth of plants proving as opportunistic symbionts in rhizosphere of plants. It reduces the use of chemical pesticides which pollutes the environment. Their ability to reduce the incidence of disease caused by plant pathogenic fungi has made *Trichoderma* spp., a potential biocontrol agent. Therefore, there is a need for mass movement or awareness campaign for use of eco-friendly *Trichoderma* based biocontrol agents for sustainable agriculture.

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LT (FP)-07

An age old problem of citrus decline in North East India: elucidation of factors responsible for it and management

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The genus "*Citrus*" belongs to family rutaceae and subfamily Aurantioidae. It comprises of a large number of species and varieties. Some of the closely related wild genera of Citrus are Atalantia, Severinia, Poncijus and Fortunella. Citrus fruits are rich in carbohydrates, minerals, vitamins, alkaline salts and fibres. The fruit type is berry called hesperidium. It is highly juicy with almost 80-90 % water in its pulp. Citrus is grown in 114 countries in the entire globe and out of which 53 countries grow citrus commercially with a total production of more than 121 million tonnes. China ranks first in production with 29.56 million tonnes followed by Brazil with 22.7 million tonnes and USA with 10.4 million tonnes. India ranks 4th position with a production of 11.14 million tonnes (Lakshman chandra de, 2017). Commercial citrus fruits of the trade include sweet orange (*Citrus sinensis* Osbeck), mandarin (*Citrus reticulata* Blanco), lime (*Citrus aurantifolia* Swingle), lemon (*Citrus limon* (L) Burm.f), grapefruit (*Citrus paradisi* Macf.) and pummelo (*Citrus grandis* (L.) Osbeck). In the world, citrus is dominated by sweet orange with 64% contribution followed by mandarins with 20%, limes and lemons 10% and rest of the 6% contributed by grapefruit and other citrus fruits. In India, the area under citrus is 1.78 million ha with a production of 11.14 million tonnes and average productivity of 10.3 tonnes/ha. Total mandarin production in India is 3.43 million tonnes with 0.33 million ha area and 10.4 tonnes/ha as productivity while limes/lemons have occupied an area of 0.28 million ha with 2.83 million tonnes production and 9.9 tonnes/ha productivity (HNB-2014).

The North Eastern Hill (NEH) Region of India is one of the richest reservoirs of genetic variability with almost 136 horticultural species growing in the region. The region has been described as one of the major centre of diversity for citrus, banana and mango. The total area and production of citrus in North East India is 73.2 thousand hectare and 270.30 MT with the average productivity of 3.84 t/ha which is very low as compared to national productivity (10.3t/ha). Among the North Eastern states, Arunachal Pradesh covers the highest area of 19.6 thousand hectares and Assam is top in productivity with 8.2 t/ha (NHB, 2014). This region is the natural home of *Citrus indica, C. assamensis, C. latipes, C. ichagensis, C. macroptera, C. aurantium, C. reticulata, C. megaloxycarpa, C. jambhiri, C. aurantifolia, C. grandis, C. limon and C. karna* (Ghosh, 1984). Even though citrus is cultivated in large scale, it is threatened by dearly decline complex this region as well as other parts of India. Citrus trees harbour a large number of biotic and abiotic factors leading to citrus decline. Average annual yield losses caused by HLB in Asia are estimated about 40-60%.

Genetic resources of citrus in North East India

It is believed that most of the species under the genus *Citrus* are native to tropical and subtropical regions of South East Asia, particularly, India, China and in the region between the two countries. The North Eastern (NE) region of India stretches from 21° 57' N to 29° 28' N and from 89° 40' E to 97° 25' E is considered as one of the natural home of citrus. Out of total Asian *Citrus,* 17 species are found in North Eastern region of India (Bhattacharya and Dutta, 1949). Of which, only 8 species are indigenous to this region. They are *Citrus aurantium* L., *Citrus karna* RafL, *Citrus limonia* Osbeck, *Citrus indica* Tanaka, *Citrus limon* (L.) Burm, *Citrus megaloxycarpa* Lush., *Citrus assamensis* (Bhattacharya and Dutta, 1949) and *Citrus ichangensis* Swingle. In lemon alone, as many as 32 strains are available. The species *C. limon, C. medica, C. jambhiri, C. ichangensis, C. latipes, C. macroptera*, *C. assamensis*, *C. indica* and *C. aurantium* are considered indigenous to the NE region. The Indian wild orange *C. india* is found in the Naga Hills and Meghalaya. (Source: Various publications of ICAR Research Complex for NEH Region, Umiam, Meghalaya). Though production of citrus in Indian plains is high, it is comparatively very less in North Eastern region due to lack of quality planting materials and poor orchard management, which necessitates to explore for advance techniques that can manage higher demand of this crop (Rabha *et al*., 2013). North-Eastern region, one of the biodiversity hot spot, has a good genetic diversity of citrus species (Hazarika, 2012). The state of Arunachal Pradesh is one of the major centres of diversity of citrus in the North Eastern region of India (Singh, 2010)

In Manipur, one of the typical lemon types citrus called Kachai lemon named after the Village called “Kachai” in Urkhrul district is cultivated. Kachai Lemon (*Citrus jamibhirri* Lush.) is one of the most important fruit crops of Manipur and one of the potential underutilized fruit crops of North Eastern India. The crop was first introduced in Kachai village, Ukhrul district of Manipur by Late S. Paisho during 1944-45 and only three plants started bearing fruits in 1950. That was the beginning of today's Kachai lemon in a village known as Kachai which is located in between $25^{o}14'$ N latitude and $94^{o}16'$ E longitude at an elevation of 1376 m above MSL. The climate of Kachai village is subtropical, characterized by coolness and extreme humidity. In the year 2012-13, Kachai village authority was awarded prestigious ‘Plant Genome Saviour Community Award’ by Protection of Farmers’ Varieties and Farmers Right Authority (PPV & FRA) in recognition of long track record for conserving plant agro-biodiversity.

Threats to citriculture with special context to NE Region

Citrus Industry in India is facing a major challenge from the devastating decline complex. The decline complex is caused by pathogens, insect-pests, abiotic factors (nutritional deficiencies etc.) and management related issues. The traditional mandarin orange cultivation of North East India is seedling origin and no rootstock is being used. The quality of fruits is excellent but the prevailing varieties being highly susceptible to many diseases (*Phytophthora*, *Citrus tristiza virus* (CTV), huanglongbing (HLB) diseases etc.) leading to serious decline in the region. The famous coorg mandarin in Karnataka is under threat of extinction due to severe infection of huanglongbing (previously known as greening disease). Similarly, the sweet orange in Punjab, mosambi in Western Maharashtra and Sathgudi cultivar in Andhra Pradesh were also reported to be seriously infected with CTV and HLB disease. Various surveys conducted in different parts of North East India showed widespread occurrence of CTV and HLB in citrus plantations.

Citrus decline and its symptoms

Citrus decline is a syndrome, not a specific disease, but merely a term that denotes the wasting away the growth and fruit production and may involve in the ultimate death of the tree (Knorr, 1957). It is also known as frenching, chlorosis, neglectosis etc. in India, blight in Florida, *declinio* in Brazil and *declinamiento* in Argentina. The symptoms of the affected citrus trees have been attributed to die back disease at first and later the symptom was called “decline”. Citrus decline was first reported in Madhya Pradesh as early as eighteen century. Its occurrence was reported in the Assam during 1888 by Bonavia. Later, its occurrence was reported in 1912 in western India (Cheema and Bhat, 1929). Symptoms of decline syndrome vary with the cause of the malady. All the citrus species are susceptible, however sweet and mandarin are worst affected. In early stages, symptoms are restricted to a few limbs, but eventually the whole tree shows decline. Trees show sparse mottling leaves, stunted growth, and sickly appearance. Midrib and lateral veins of old mature leaves turns yellow with interveinal areas along the veins show diffuse yellowing. Yellowing, shedding of leaves and the die-back of twigs starts with the passage of time. The shoots of the tree continuously die from top to downwards. The feeder root system gets depleted, turns black and covered with rotting bark leading to decline.

Types of citrus decline

There are mainly three types of citrus decline viz., quick decline, slow decline and spreading decline. The *Citrus tristeza virus* and huangloNgbing are usually responsible for quick decline, minerals deficiency for slow decline and nematode (*Tylenchulus semipenetrans*) for spreading decline. Among these, quick decline is the worst.

Factors responsible for citrus decline

Citrus decline is caused by various biotic and abiotic factors. Some of the important abiotic factors are Soil factors (Soil Texture, Soil salinity, Soil drainage, Compactness/ hardness of soil surface, Soil organic matter), Nutritional factors (Mainly Zinc deficiency), rootstocks, hormonal imbalance and cultural practices. Among the biotic factors, pathological (Fungus, Bacteria and virus and virus like organisms), entomological and nematogogical factors can be mentioned.

Emerging pathogens responsible citrus decline in North East Region

***Citrus tristeza virus* (CTV):** The word “*Tristeza*” means sadness in the Spanish language. It is a destructive disease of citrus worldwide and has destroyed millions of citrus tree worldwide. Disease is caused by a longest known flexuous RNA virus under of the genus *Closterovirus* and family *Closteroviridae*. CTV caused serious decline symptoms on sour orange root stocks, due to the phloem necrosis. The virus is limited to phloem tissues and transmitted by brown citrus aphid (*Toxoptera citricida*) in a semi-persistent manner. The virus is also transmitted by grafting and budding. Molecular detection techniques have been developed for routine indexing of CTV in India. An RT-PCR assay using CTV genome specific primers (CP region of viral genome) amplifying an amplicon of 672 bp was employed for detection of CTV from Darjeeling hills (Biswas, 2008). Primers from CP region (672 bp), variable partial ORF1a region (404 bp) and other regions of viral genome were also used in RT-PCR assays for CTV detection in India (Biswas, 2010, Tarafdar *et al*., 2013; Sharma *et al*., 2012; Singh *et al*., 2013). Using overlapping primers covering entire CTV genome, complete genome sequence of decline inducing CTV isolate was reported from India (Biswas *et al*., 2012a). Citrus samples collected from different citrus growing regions of India were detected using primers from CP region and partial ORF1a region and high genetic diversity was reported among the CTV isolates (Biswas *et al*., 2012b; Biswas *et al*., 2014). Studies conducted at ICAR Research Complex for NEH Region, Manipur Centre showed widespread occurrence of CTV in different citrus groves of North East India (covering surveyed locations of Manipur, Meghalaya and Sikkim)

Huanglongbing (HLB): Among different factors associated with citrus decline and reduced production and productivity, huanglongbing (HLB) previously known as greening is the most destructive which has been the major causes of wiping out of citrus industry in different parts of the world including India. HLB has emerged as one of the most important disease in citrus plantation of different parts including NE India. It is known as yellow dragon shoot because of the appearance yellow patches in the newly flushes coming out. The disease is caused by a true bacterium (Jagouex *et al*, 1995) which is gram negative, phloem limited (Gannier *et al.* 1984), alpha protobacterium. There are three types of huanglongbing viz. Asian type; *Candidatus* Liberibacter asiaticus (CLas), African type; *Candidatus* Liberibacter africanus (CLaf) and American type; *Candidatus* Liberibacter americanus (CLam). The Asiatic and American types are transmitted by citrus psylla (*Diaphorina citri*) and African type by *Tryoza erytreae*. The Asiatic type is heat tolerant and most destructive in nature while African and American types are heat sensitive. In comparison to viruses (CTV; *Indian citrus ringspot virus*: ICRSV; and *Citrus yellow mosaic virus*: CYMV) HLB bacterial load accumulates fast in the infected tree and also spread at a relatively faster rate in orchards. CLas bacteria multiply in phloem sieve cells of citrus host plant and its infection result in die-back, yellowing, blotchy mottle of leaves (typical symptom of HLB), off tasting and malformed fruits and decline. Its symptoms are often confused with symptoms of nutrient deficiency and viral infection. Most interestingly in North East India, citrus plants showing zinc deficiency symptoms were detected positive for HLB in PCR based detection procedures. This might be due to use of Zn in the form of zinc chelate by the CLas bacterium thus leading Zn deficiency like symptoms. HLB infection also causes noticeable symptoms on fruits and reduces the quality of fruits (Gottwald, 2010). Occurrence of CLas has been reported from citrus orchards in different parts of India including NE (Das *et al*., 2007; Adkar-Purushothama *et al*., 2009; Ghosh *et al*., 2015). Average annual yield losses caused by HLB in Asia are often estimated as 40-60% and occasionally as much as 70-95%. Results of the surveys conducted during 2005-06 showed an incidence of 5-30% in Sikkim (Das *et al*. 2007). Incidence of 5-8.3% was detected on Khasi mandarin. Ghosh et al. (2015) reported a HLB incidence 32% in different areas surveyed. A few samples of CLas collected from different states of NE India were characterized at molecular level except for Manipur (Ghosh *et al*., 2015). Recently we have surveyed different locations of NE India (Noney, Nungba, Tamenglong, Kachai area of Manipur and Pashighat and Bodak areas of Arunachal Pradesh) where an incidence of 37-64% was recorded. 58% of the citrus samples collected from different locations of Manipur were positive for HLB. On average, the disease can cause yield losses up to 30-100% depending on the severity of the disease (Iftikar *et al*., 2014). Our findings have indicated that HLB and CTV are two major pathogens responsible for citrus decline in NE India.

Citrus gummosis/foot rot: *Phytophthora* spp. produces symptoms of decline through rotting of the rootlets (foot rot), gummosis and dropping of the blight leaves. Foot rot results from an infection of the scion near the ground level, producing lesions which extend down to the bud union on resistant rootstocks. Infected bark remains firm with small cracks through which abundant gum exudation occurs. Citrus gum disappears after heavy rains but remain persistent on the trunk under dry conditions. Lesions spread around the circumference of the trunk, slowly girdling the tree. Large trees may be killed likewise, but typically the trunks are partially girdled and the tree canopy undergoes defoliation, twig dieback, and short growth flushes. The disease is transmitted from soil. Surveyed at different locations of Manipur (Noney, Tamenglong, Kachai area of Manipur) conducted by researcher of ICAR Research Complex for NEH Region, Manipur where an incidence of 15-25% was recorded.

In addition to these, canker, trunk borer and psyllids are other associated biotic factors for citrus decline complex in different locations of NE India. However, location specific identification of factors associated with citrus decline is required to be investigated

Management of citrus decline

Since citrus decline is a syndrome caused by biotic and abiotic factors, every aspect should be considered while going for management practices. Management strategies must include preventive measures like proper site selection, use of disease free planting materials, orchard care including integrated nutrient and water management, use of plant growth regulators, use of resistant rootstocks and plant protection measures consisting of integrated disease management, nematode management and integrated pest management.

Rejuvenation of declined citrus orchard

The words rejuvenation means to make young. The practice is widely used in declined citrus orchard for getting good yield for 2-3 further. This practice is very useful for farmer to get income from the declined orchards as well as they can wait newly planted seedlings till fruiting. Rejuvenation of severely declined mandarin in Manipur was successfully demonstrated in Manipur by ICAR Research Complex for NEH Region, Manipur Centre. It was observed that fruit yield of 10-12 t/ha was recorded in the third year of treatments. The measures adopted are removal of vegetation other than citrus, removal of parasitic plants and pruned twigs, tree bases levelled through soil working and making of half-moon terraces. Bordeaux pasting up to one metre tree trunk, borer holes plugged after injecting insecticide and soil application of NPK (400:250:400g/tree) and foliar spray of Mg, Zn and B in April- May.

Future line of work

Future line of work has to be on location specific identification of major factors causing decline in different citrus growing grooves of North East India and thus devising management modules. Bud wood certification programme has to be strictly followed in the region. Citrus germplasm of the region need to be screened for important pathogens (*Phytophthora*, HLB, CTV etc.) for identification of resistant or tolerant varieties which can then be used as rootstock. This in turn will help developing integrated management modules for citrus decline in NE region of India.

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LT (FP)-08

Management of biotic and abiotic stress for food and nutritional security under changing environment conditions

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Introduction

Agriculture is one of the most vulnerable sector to climate change. Increased incidences of abiotic and biotic stresses impacting productivity in principal crops are being witnessed all over the world. A plant disease is the result of interaction between a susceptible host plant, virulent pathogen, and the environment. Human activities and the presence of microbial antagonists to the pathogen may also play role in the development of a disease. The reason behind is the environment significantly, directly or indirectly, influences plants, pathogens, and their antagonists, changes in environmental conditions are strongly associated with differences in the level of losses caused by a disease, and environmental changes are often implicated in the emergence of new diseases (Anderson *et al*. 2004). Climate change is the most complex, global environment issue these days. The effect of greenhouse gases and climate changes are already evident from raising ambient temperature, recurrent drought, erratic rains, flooding /submergence etc. Over the past hundred years, the global temperature has increased by 0.8^0C and expected to reach 1.1-5.4^0C by the end of next century. On the other hand, CO_2 concentration in the atmosphere has increased drastically from 280 ppm to 370 ppm and is likely to be doubled in 2100. This change is attributed mainly to the over exploitation and misuse of natural resources for various anthropogenic developmental activities such as increased urbanization, deforestation and industrialization resulting in aberrant weather events like changes in rainfall patterns, frequent droughts and floods, increased intensity and frequency of heat and cold waves and outbreaks of diseases. The impact of climate change are global but Indian subcontinent is more vulnerable due to dependence of its large population on agriculture. These climatic changes have direct effect on growth and multiplication of plant pathogens.

Climate variability is adding a new dimension to managing plant diseases by altering the equilibrium of host-pathogen interactions resulting in increased epidemic outbreaks or new pathogens surfacing as threats or less known pathogens causing severe yield losses. Climate change will be a major impediment in achieving food security in the 21 Century. With changing weather parameters plant pathogens may attribute tendencies to evolve new variants at higher rate, multiplication behaviour and parasitic fitness ability thus shifting prevalence and occurrence of disease spectrum. Hence there is need to relook development and application of new technologies, including curbing losses due to abiotic and biotic stresses to achieve food security under fast changing climate. This chapter describes the major effects of climate change on the occurrence of plant diseases and possible strategies of biotic and abiotic stresses to combat with the changing climatic situations.

Effect of climate change on plant diseases

Plant diseases alone contribute to 20% reduction in the yields of food and cash crops (Thind, 2012). Plant diseases have direct impact on the production and productivity of agricultural crops and the changes in the climatic variables are predicted to have significant effects on the plant pathogens and the diseases they cause. The shift in the geographical range of insect pests as well as plant pathogens in response to the changing climate has been well documented. Although, there could be the direct effects of changing climatic situations on individual plants or plant communities in the absence of pathogens, but this also have significant effect on the ways in which pathogens interact with their hosts. Climate change has the ability to influence the plant architecture, thus affecting the microclimate and risks of pathogen infection. The increased concentration of atmospheric CO_2 will increase the production of plant biomass (Gautam *et al.*, 2013; Pautasso *et al.*, 2012). This increased biomass will modify the microclimate and in turn encourage the infection and severity of biotrophic fungal pathogens (Chakraborty *et al.*, 2002). Due to the enhanced photosynthesis, increased water use efficiency, and reduced damage from ozone under elevated CO_2, there will be changes in the plant structure and architecture. Since many foliar pathogens benefit from denser plant growth and the resulting humid microclimate, there is the potential for these changes in plant architecture to increase the infection rates. Due to changes in the precipitation patterns, the duration of leaf wetness, ambient relative humidity and temperature will change which will attract the infection of various foliar pathogens. A study has indicated that different changes associated with the high CO_2 concentration such as reduced stomata density and accumulation of silicon at appressorial penetration sites has increased the host resistance to powdery mildew (*Blumeria graminis*) fungus in cereals (Hibberd *et al.*, 1996).

Effect of changes in the environmental temperature regimes can be visualized in terms of spread of diseases and their survival during off seasons. It has been predicted that at higher temperature the aggressiveness and severity of yellow rust (*Puccinia striiformis*) will be more (Mboup *et al.*, 2012). Under Indian situations, dry root rot (*Rhizoctonia bataticola*) of chickpea and *Phytophthora* blight (*Phytophthora drechsleri* f. sp. *cajani*) of pigeon pea have emerged as the major diseases during the last two decades possibly due to the effect of changing climatic conditions particularly temperature (Gautam *et al.*, 2013). In addition to the fungal diseases, the occurrence of bacterial diseases has also been influenced by the changes in temperature regimes. The effect of changed temperature on occurrence of bacterial pathogens like *Ralstonia solanacearum* and *Burkholderia glumea* has been studied in terms of changed virulence patterns and severity (Kudela, 2009).

Changes in the precipitation patterns and atmospheric relative humidity also have significant consequences on the disease patterns. Favorable air temperature and rainfall conditions were predicted to increase the severity of downy mildew on grapevine (*Plasmopara viticola*) (Salinari *et al.*, 2006). Various other models have predicted influence of weather variables on the incidence and severity of black sigatoka (*Mycosphaerella fijiensi*) of banana and downy mildew of grapevine (Gautam et *al*., 2013). Excess moisture favours the soil-borne pathogens like *Phytophthora*, *Pythium*, *Rhizoctonia solani* and *Sclerotium rolfsii*. It has been predicted that in North west India, the changes in the temperature and humidity will tend to reduce the incidence of yellow rust (*Puccinia striiformis*) and Karnal bunt (*Tilletia indica*), whereas leaf rust, foliar blights and stem rust will increase (Kaur *et al*., 2008). Temperature, moisture and other weather parameters affect the reproduction rate of pathogens and also influence their evolution by having the effect on the population size and overwintering or over summering rates. Periods of drought were also observed in many situations. Drought conditions will lead to increased severity of tree pathogens through the effect on the host physiology (Desprez-Loustau *et al*., 2006). In case of vector-borne viruses, warmer periods may lead to more number of insect generations, thus increasing the transmission rate of viruses (Robinet *et al*., 2011). Further, it has also been speculated that under changing climate change scenario, there could be a remarkable changes on the genetic and physiological structure of plant species. Due to the climate change, there could be effects on the abundance of a particular plant species and different population may evolve during the co-evolution process of host and pathogen.

Direct impact of climate change on plant pathosystems

Increasing climate variability with the change in climate is recognized unequivocally. With the changing climate patterns and cropping systems, host, pathogen and favourable environment interactions are leading to disease epidemic in a range of crops. Three essential components are required simultaneously for a disease to occur: a virulent pathogens, a susceptible host and favourable environment and effect over times of the evolutionary forces on living populations leading to new disease epidemics often referred as "Disease Tetrahedron". Even with minor deviations from the normal weather, the efficiency of applied inputs and food production is seriously impaired (Rotter *et. al*., 1999). Agriculture production of rainfed regions, which constitute about 65% of the area under cultivation and account for about 40-45% of total production in India, is expected to suffer severe as a result of climate change (Agrawal, 2003). A plant disease is the result of interaction between a susceptible host plant, virulent pathogen, and the favorable environment conditions for suitable time period. Because the environment significantly influences plants, pathogens, and their antagonists either directly or indirectly, the changes in environmental conditions are strongly associated with differences in the level of losses caused by a disease. The changes in the environmental conditions are often implicated in the emergence of new diseases or previously minor diseases (Anderson *et al*. 2004). For these reasons, the changes associated with global warming (i.e. increased temperatures, changes in the quantity and pattern of precipitation, increased CO_2 and ozone levels, drought, etc.) may affect the incidence and severity of plant disease and influence the further co-evolution of plants and their pathogens (Chakraborty, 2005; Burdon *et al*., 2006; Garrett *et al*., 2006; Eastburn *et al*., 2011).

Plant health is predicted to generally suffer under climate change through a variety of mechanisms, from accelerated pathogen evolution and shorter incubation periods to enhanced abiotic stress due to mismatches between ecosystems and their climate and the more frequent occurrence of extreme weather events (Sutherst *et al*., 2011).Drought is expected to lead to increased frequency of tree pathogens, mainly through indirect effects on host physiology

(Desprez- Loustau *et al*., 2006). The Biotic plant diseases are caused by organisms such as fungi, bacteria, viruses, nematodes, phytoplasma and/or parasitic plants. On the other hand, abiotic diseases are always associated with chemical and physical factors such as temperature, moisture extremes, nutrient deficiencies, mineral toxicities and pollution as well (Fig. 1). There are many examples how a pathogen of less economic importance which is associated with a minor disease has emerged as a major pathogen under the influence of climatic change. However, the exact effect and correlation of changing climatic factors on the simultaneous co-evolution of host and pathogens need to study in detail.

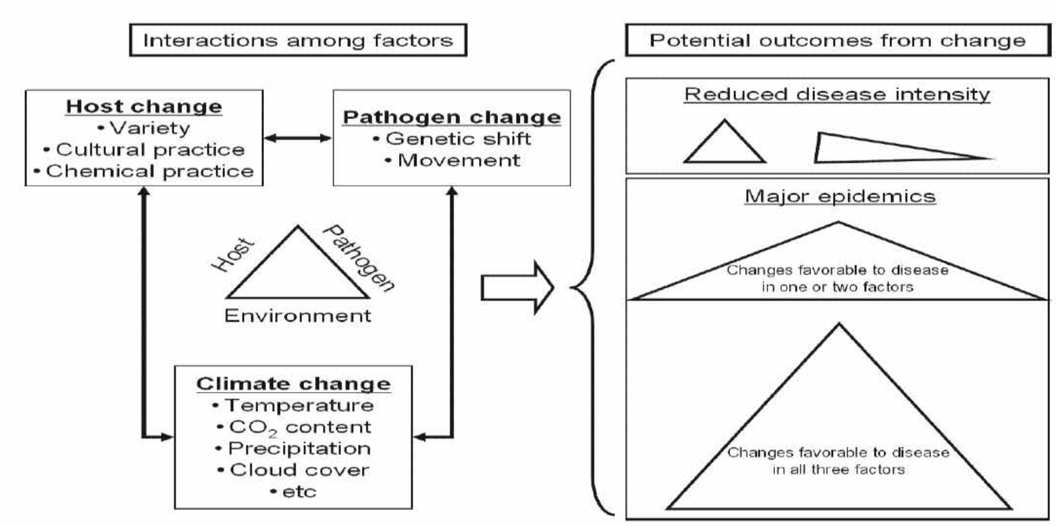

Fig. 1. Climate change and the disease triangle
(Source:Available online www.scholarsresearchlibrary.com)

Climatic changes may affect plant pathosystems at various levels viz. from genes to population, from ecosystem to distributional ranges from environmental conditions to host vigour/susceptibility and from pathogen virulence to infection rates. In general climate variability has shown positive and negative impact on host-pathogen interaction. However, in general climatic changes could result in following changes in diseases/pathogens

A. Extension of geographical range
B. Increased over-wintering and over summering.
C. Changes in population growth rates.
D. Increased number of generations.
E. Loss of resistance in cultivars containing temperature-sensitive genes.
F. Extension of crop development season.
G. Changes in crop diseases synchrony.
H. Changes in inter-specific interaction.
I. Potential impact of climate change on plant diseases
J. Changes in geographical distribution of pathogens
K. Changes in the physiology of the host-pathogen interaction

The losses of marketable yield in crops and the reduction in growth and productivity of tree species caused by exposure to high levels of O_3, pollutants can influence plant pathogens, and foliar pathogens can affect the leaf responses to O_3. Generally, ozone exposure tends to decrease the incidence of disease caused by obligate parasites, increasing the disease incidence caused by facultative parasites (Table 1).

Table 1. Effect of ozone (O_3) on some fungal plant diseases

Fungi	Host plant	Effect on disease
		Obligate biotrophs
Puccinia graminis f. sp. tritici	Wheat	Decreased hyphal growth and urediospore production on O_3 injured leaves
Erysiphe graminis f. sp. hordei	Barley	Reduce rate of infection if exposed to sufficient O_3 during incubation
		Necrotrophs
Botrytis cinerea	Potato	Infection only in O3 injured leaves
Lophodermium sp.	Pine	Increased severity of needle blight

Commonly, necrotrophic and biotrophic pathogens show a different behaviour as regards their nutrition. The first obtain nutrients from dead tissues, while the second derive nutrients from living cells and maintain a prolonged and deep interaction with their host. Therefore, all climatic factors that cause or accelerate tissue death (high temperatures or O_3 levels) could favour necrotrophic pathogens. In addition, climatic factors that stimulate plant growth such as elevated levels of CO_2 or increased temperature will change the physiology of the plant, altering host colonization by biotrophic pathogens (Kudela, 2009). In particular, the decomposition of high- CO_2 litter occurs at a slow rate, increasing the biomass availability which combined with higher winter temperatures, might increase pathogen survival on crop residues accumulating the amount of initial inoculum to infect subsequent crops (Coakley *et al*., 1999).

Some aspects associated with climate change, such as the increase in temperature and changes in precipitation and moisture, can directly affect pathogens, enhancing their fitness in terms of number of generations and sexual reproduction (influencing the evolutionary potential of individual populations), extending the amount of time available for reproduction and dissemination. This is the case with *Phytophthora* species which increased the incidence of root rot in central Europe forest trees as a result of the rise in mean winter temperatures, the shift in precipitation from summer to winter and the tendency toward heavier rains (Elad and Pertot, 2014). In the last decades, a northward shift was observed in *Cercospora beticola* causing leaf spot in sugar beet in southern Germany, probably due to an annual mean temperature increase by approximately 0.8°C-1°C in the last century (Richerzhagen *et al*., 2011). In addition, strong effects of temperature on pathogen fitness traits as well as genotype x temperature interactions were found for *Puccinia striiformis f.sp. tritici,* the agent of wheat yellow/stripe rust. There are indications of increased aggressiveness of stripe rust isolates adapted to higher temperatures, suggesting that rust fungi can adapt and benefit from warmer climate conditions (Mboup *et al*., 2012).The increase of temperature contributes to the spread of pathogens in new geographic areas, where they can encounter potential hosts. Until 2002, *Monilinia laxa* and *M. fructigena* were the only pathogens responsible for brown rot in stone and pome fruits in

Europe, when another species, *M. fructicola*, causing brown rot on stone fruits, was detected in France (Lichou *et al.*, 2002).

Most of the available data indicated that increased CO_2 would affect the physiology, morphology and biomass of crops (Challinor *et. al.,* 2009). Elevated CO_2 and associated climate change have the potential to accelerate plant pathogen fecundity due to altered canopy environment that resulted in conducive microclimate for pathogen multiplication (Pangga *et.al.*, 2004).Increased CO_2 levels can impact both the host and the pathogen in multiple ways. New races may evolve rapidly under elevated temperature and CO_2, as evolutionary forces act on massive pathogen populations boosted by a combination of increased fecundity and infection cycles under favourable microclimate within enlarged canopy (Chakraborty, 2005). Foliar diseases like Ascochyta blights, Stemphylium blights and Botrytis gray mold can becomes a serious threat in pulses under the higher canopy density, increased CO_2 will lead to less decomposition of crop residues and as a result soil borne pathogens would multiply faster on the crop residue. Pathogen growth can be affected by higher CO_2 concentrations resulting in greater fungal spore production. However, increased CO_2 can result in physiological changes to the host plant that can increase host resistance to pathogens (Coakley *et al.*, 1999).

Plant pathogens have varying ranges of temperature requirements that affects the various steps in disease infection cycle such as penetration, pathogen survival, survival dispersal, epidemic development, survival and sexual reproduction. A change in temperature may favour the development of different inactive pathogens, which could induce an epidemic. Due to changes in temperature and precipitation regimes, climate change may alter the physiology and resistance of the host plant (Charkraborty and Datta, 2003). Few studies have shown that wheat and oats become more susceptible to rust diseases with increased temperature and more frequent moisture stress (drought) are predicted to increase in many regions and is likely to influence plant disease epidemics. For example, dry root rot of chickpea (caused by *Rhizoctonia bataticola*) is becoming more severe in rainfed environments as the host plant is predisposed by moisture stress and higher temperatures during the flowering to pod filling stage (Pande *et.al.*, 2010). Weather and dry root rot disease data collected in India for one decade showed higher incidence of dry root rot in chickpea varieties that resist Fusarium wilt in years when temperatures exceed 33^{O}C **(**Pande *et.al.*, 2010). On the country, cooler temperature and wetter conditions are associated with increased incidence of stem rot on soyabean (*Sclerotinia sclerotiorum*); blights (*Ascochyta* spp.) in chickpea, lentil, pea and anthracnose in chickpea and lentil (Pande *et al.*, 2010; Pangga *et al.*, 2004). Many models that have been useful for forecasting plant disease epidemics are based on increases in pathogen growth and infection with in specified temperature. Climate change is also reported to cause a shift in the geographical distribution of host pathogens (Mina and Sinha, 2008). A change in temperature may favour the development of different dormant pathogens, which could induce an epidemic. Increase in temperature with sufficient soil moisture may increase evapotranspiration resulting in humid microclimate in crops and may lead to incidence of diseases favoured under these conditions (McElrone *et al.*, 2005). Diseases such as common bunt (*Tilletia caries*) and Karnal bunt (*Tilletia indica)* in wheat can be importance under changing climatic conditions in regions with low productivity if proper seed treatment is not followed in this crop (Oerke , 2006).

Temperature is one of the most important factors affecting the occurrence of bacterial diseases such as *Ralstonia solanacearum, Acidovorax avenae* and *Burkholderia glumea* that indicated that bacteria could proliferate in areas where temperature-dependent diseases have not been previously observed (Kudela, 2009). Similarly, the incidence of most of the virus and other vector-borne diseases will be altered due to climate that can substantially influence the development and distribution of vectors. Genetic changes in the virus through mutation and recombination, changes in the vector populations and long-distance transportation of plant material or vector insects due to trade of vegetables and ornamental plants have resulted in the emergence of tomato yellow leaf curl disease (Navas-Castillo *et al.*, 2011). Research has shown that host plants such as wheat and oats become more susceptible to rust diseases with increased temperature; but some forage species become more resistant to fungi with increased temperature (Coakley *et al.*, 1999).

Many mathematical models that have been useful for forecasting plant disease epidemics are based on increases in pathogen growth and infection within specified temperature ranges. Generally, fungi that cause plant disease at cold average temperatures are likely to experience longer periods of temperatures suitable for pathogen growth and reproduction if climate is warm. Earlier onset of warm temperatures could result in an earlier threat from late blight with the potential for more severe epidemics and increases in the number of fungicide applications needed for control. The effects of elevated temperature on plants will tend to vary greatly throughout the year. During colder parts of the year, warming may relieve plant stress, whereas during hotter parts of the year it may increase stress. A striking example of the potential effect on the yield of crop plants in response to elevated temperature, rice yield in the Philippines was estimated to decline 10% for each 1^0C increase in the minimum temperature during the dry season (Peng *et al*., 2004).

Another climate variable, moisture can impact both the host plant and pathogens in various ways. For example high moisture (rainfall) favors most of the foliar diseases and some soil borne pathogens such as *Phythophthora, Pythium, Rhizoctonia solani* and *Sclerotium rolfsii* etc. Forecast models for these pathogens are based on leaf wetness and relative humidity and precipitation measurements. An outbreak of Phytophthora blight of Pigeonpea (*Phythophthora drechsleri f.sp. cajani*) in Deccan Plateau of India is attributed to erratic and heavy rainfall (>300mm in 6-7 days) leading to temporary flooding (Sharma *et al*., 2006; Pande *et. al*., 2011). Alternaria blight of Pigeonpea is being seen more frequently in recent years in semi-arid tropic regions due to the untimely rainfall. However in areas where moisture is decreasing due to climate change, Fusarium wilt, dry root rot etc. will becomes problematic for the cool season pulses.

Plant disease management strategies under climate change

Agriculture is one of the most vulnerable sectors to climate change. Increased incidences of abiotic and biotic stresses impacting productivity in the principal crops are being witnessed all over the world. Climate change adds an extra layer of complexity to management of plant diseases. Unfortunately, there are almost no studies on how climate change may affect chemical control (Coakley *et al*. 1999). There are few discussions on how chemical control will be affected by climate change, despite the importance of this subject. Changes in temperature and precipitation can alter fungicide residue dynamics in the foliage and the degradation of products can be modified. Alterations in plant morphology or physiology resulting from growth in a CO2-enriched atmosphere or from different temperature and precipitation conditions, can affect the penetration, translocation and mode of action of systemic fungicides. Besides that changes in plant growth can alter the period of higher susceptibility to pathogens which can determine a new fungicide application calendar (Coakley *et al.*, 1999; Chakraborty & Pangga, 2004; Pritchard & Amthor, 2005).

Under worst-case scenarios, several crops may require more fungicide spray treatments or higher application rates, thus increasing costs for farmers, prices for consumers, and the likelihood of development of fungicide resistance (Juroszek and von Tiedemann 2011). Annual crops will have an advantage over perennials, as they provide more flexibility when it comes to adopting new cultivars and cultural practices. Potential adaptation strategies must be accompanied by cost–benefit analyses. Evaluating the efficacy of current physical, chemical, and biological control methods under changing climatic conditions and research concerning new tools and strategies (including plant breeding) for coping with the predicted changes will be of great strategic importance.

Agronomic practices, such as crop rotation, tillage, fertilization, irrigation, selection of the production site, use of resistant/tolerant varieties, and sanitation to reduce the amount of overwintering inoculum, can be used to prevent or reduce the increased disease risks associated with the predicted climate change (Juroszek and von Tiedemann 2011). Fungicides are an effective method of controlling plant diseases, despite negative public perceptions. Fungicides may continue to serve as common disease suppression agents, although alternative measures, such as cultural methods and biological control, should be developed. The persistence of plant protection chemicals in the phyllosphere is highly dependent on weather conditions. Changes in duration, intensity, and frequency of precipitation events will affect the efficacy of chemical pesticides and how quickly the active molecules are washed away. There is almost no information on the effects of climate change on biological control of plant disease (Ghini *et al*. 2011a).

The impact of climate change on plant diseases will be more, disease management strategies will require adjustments. Although physiological changes in host plants may result in higher disease resistance under climate change scenarios, the durability of resistance may be threatened and many lead to more rapid evolution of aggressive pathogens races (Hibberd *et al.*, 1996). The population dynamics of beneficial microorganism such as rhizobia, biocontrol agents and mycorrhizal fungi may get affected due to increase temperature, moisture and CO_2. Under elevated CO_2 conditions, mobilization of resources into host resistance through various mechanism such as reduced stomata density and conductance (Hibberd *et al.*, 1996); greater accumulation of carbohydrates in leaves; more waxes, extra layers of epidermal cells and increased fiber content and increased biosynthesis of phenols (Hartley *et al.*, 2000).The efficacy of fungicides may change with change in climate variables. For examples more frequent rainfall event could make it difficult for farmers to use the fungicides on plant leading to more frequent application.

Some microorganisms have been developed for use as biocontrol agents of plant diseases (Elad and Freeman 2002). Biocontrol agents can serve as alternatives to chemical fungicides when applied alone or in combination with other control methods. Because they are living organisms, these biocontrol agents are also affected by the abiotic environment. For example, the biocontrol of the fungal foliar disease gray mold (*Botrytis cinerea*) in greenhouse cucumber crops is affected by climate. Suppression of gray mold by the biocontrol agent *Trichoderma harzianum* T39 is more pronounced at higher temperatures and lower RH levels (Elad *et al.* 1993). More recent research into the effects of climate change on pathogens and their biocontrol is reported here.

- Climate change impacts on plant health are likely to be ubiquitous, both in terms of direct and indirect ones. Maintaining plant health across the planet, in turn, is a key requirement for climate change mitigation, as well as the conservation of biodiversity and provision of ecosystem services under global change as disease management strategies depend on climate conditions (Fig. 2)

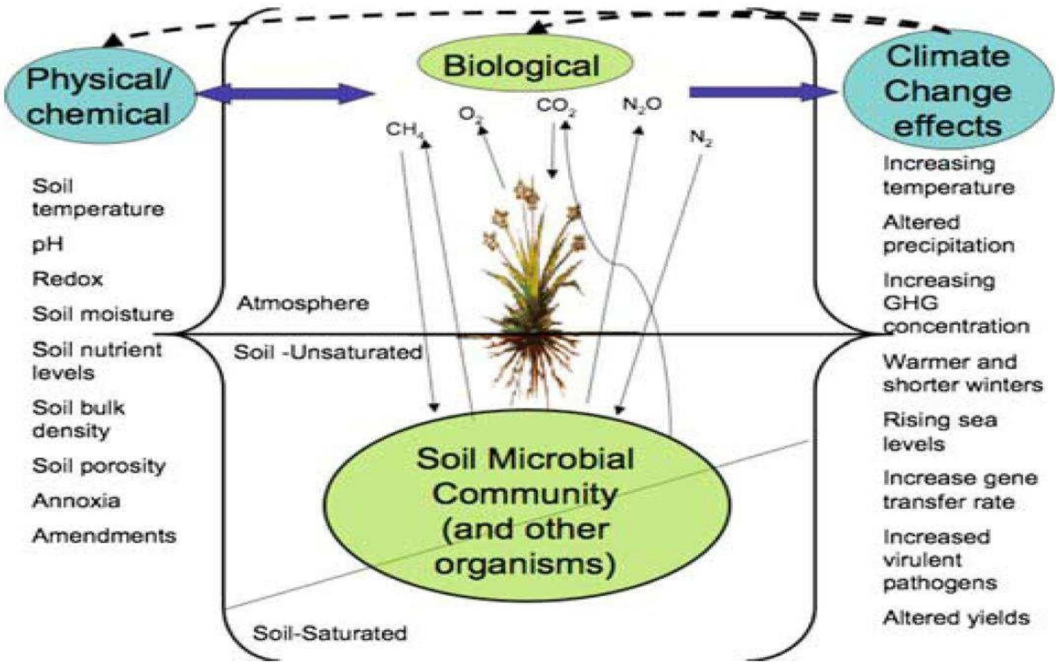

Fig. 2. Climate change, soil microbes and plant health

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Use of microbes for biotic and abiotic stresses management

Microbes are an integral component of agricultural ecosystems. Microbes colonizing the roots, rhizosphere, phyllosphere and spermophere to organic relationships with plants and are capable of influencing their physiological process, including tolerance to biotic and abiotic stresses. Besides influencing the physio-chemical properties of rhizospheric soil through production of exopolysaccharides and formation of biofilm, microorganism can also influence higher plants response to abiotic stresses like drought, chilling injury, salinity, metal toxicity and high temperature through different mechanisms like induction of osmoprotectants and heat shock protein etc. in plant cells. A good amount of information is available on the use of microbes (Fungi and bacteria) for the management of biotic stresses such as disease and pest (Harman, 2004; Singh *et al*., 2004). Trichoderma species are known to alter the response of plants to abiotic stress. To alter the drought response includes drought avoidance through morphological adaptation, drought tolerance through physiological and biochemical adaptations and enhanced drought recovery. The root colonization by *Trichoderma* increase the growth of roots and the entire plants, thereby increasing plant productivity and the yield of reproductive organs.

Feedback received from several farmers, who have used Trichoderma for wheat seed treatment, indicated that wheat crops raised from *Trichoderma* treated seeds tolerate drought better than crops raised from non -treated or chemically treated seeds. This could be due to better root growth and/ or better availability of nutrients (Singh *et al*., 2004). Clearly plants are induced to operate more efficiently and to be better able to resist biotic and abiotic stresses if their roots are colonized by effective Trichoderma strains. *Brassica juncea* plants raised from *Trichoderma harzianum* isolates PB 9 or PB 23 treated seed tolerated water stress better than untreated plants or those treated with other isolates of *T. harzianum.*

It is well documented that *T. harzianum* enhances root growth and helps in water absorption and nutrient uptake under osmotic stress (Harmann *et al*., 2004). When plants are under stress, the contents of reactive oxygen species may increase to toxic concentrations. Several studies have shown that root colonization by *T. harzianum* results in increased level of plant enzymes, including various peroxidases, chitinases, a-1-3-glucanases, lipoxygenase-pathway hydroperoxide lyase and such changes in plant metabolism can lead to accumulation of compounds like phytoalexins and phenols (Harman, 2006). These compounds act as scavengers of ROS. Almost similar mechanism was involved in better germination of *T. harzianum* strain T-22 treated seeds of tomato exposed to biotic (osmotic, salinity, chilling or heat stress) or physiological (poor seed quality introduced by seed aging) stress (Mastouri *et al*., 2010). The consistent response to varying stresses suggests a common mechanism through which the plant-fungal association enhance tolerance to a wide range of abiotic and biotic stresses. A common factors that adversely affects plant under these stress conditions is the accumulation of toxic ROS resulting in increased concentration of lipid peroxidase. Treatment of seeds reduced accumulation of lipid peroxides in seedling to stress by scavenging ROS. *Trichoderma* strains enhance the activity of these pathways in part by enhanced expression of genes encoding the component enzymes (Mastouri, 2010; Mastouri *et al*., 2010). Enhancement of theses pathways in chloroplasts would increase photosynthetic efficiency by reducing damage by the superoxide anion and other reactive species involved in photosynthesis. At least part of the resistance and probably the increased photosynthetic efficiency is because the fungi improve the redox status of the plant.

Biotic and abiotic stress management through symbiotic fungi

Numerous studies supported the fact that plant colonized by mycorrhizal fungi is better nourished and better adopted to its environment. Its gains increased protection against environmental stresses such as drought, cold, salinity, heavy metal toxicity and micronutrient imbalances and pathogens (Siddiqui and Singh, 2005). On the whole the growth health of colonized plants is improved and at same time, obtain increased protection against biotic and abiotic stresses detrimental to their survival. Mycorrhizal plants may avoid drought to some extent through enhanced water uptake at low soil moisture level by increasing host growth rates during drought by affecting nutrient acquisition and possibility hydration and water use efficiency (Auge, 2001). AM fungal hyphae contributed extensively in terms of improving soil structure and its water holding capacity (Miller, 2002).

Arbuscular Mycorrhizal (AM) symbiosis also increase the flexibility of host plants against salinity stress, perhaps with greater consistency than to drought stress and occurs widely in salt stressed environment (Wang and Liu, 2011). They help in alleviating the effect of salinity (Al Karaki *et al*, 2001) by compensating nutritional imbalances imposed by salinization through improved nutrient acquisition, enhancing the ability of the plants to cope with salt stress, ion balance and improving plant nutrient uptake (Asghari *et al.*, 2005). Symbiotic stress tolerance involves activation of host stress response systems as soon as the plant is exposed to stress. This helps the plant in avoiding or adjusting the stress impact and synthesis of antistress chemicals by endophytic microbes (Miller, 2002).

Management of biotic and abiotic stress through tolerant varieties

A lot of work is in progress to develop the crop varieties which can tolerate abiotic stresses. A good progress has already been made in rice. During recent years the International Rice Research Institute has made considerable progress in developing rice varieties with increased tolerance to submergence, drought and salt stress. The submergence tolerance gene SUB1 was identified from an Indian land race from Orissa FR13A. It was fine mapped and transferred into several mega rice varieties, five of them are from Indian subcontinent, using marker assisted backcross (MABC) approaches to conventional plant breeding. These mega varieties are Swarna (MTU7029), Sambha Mahsuri (BPT5204), IR64, CR1009 and BR 11. In 2003, IRRI started a programme to introduce the SUB1 gene into mega-varieties popular in Asia. The objectives was to introduce only a small segments of the chromosomes of SUB1gene. All the evaluation initial indicated that these mega varieties were phenotypically identical to the original varieties in nearly all traits.

Mega varieties with SUB1 gene varieties are being widely evaluated both at farmers' field and on research station through the research institutions. They have shown excellent promise at farmer's field in India, Bangladesh and Nepal under flash flood condition even up to 17 days of complete submergence (Singh *et al.*, 2010). In one such trial in Orissa, India, conducted by state agriculture department, minimum yield of Swarna Sub-1 after 13 days of submergence was 2.9 tons/ha, whereas under similar condition no other rice variety could be harvested. On an average they offer yield advantage of 1 to 3t/ha following submergence for variable duration as compared to other varieties, importantly, these tolerant varieties reduce farmer's risk. One of these lines Swarna Sub-1 is already released in India; two (Swarna Sub-1 and BR11-Sub-1) in

Bangladesh and two (Swarna-sub1 and Sambha Mahsuri Sub-1) in Nepal for commercial cultivation. These Sub1 varieties provide a significant yield advantage even under short submergence of 2-4 days, which may happens anywhere in wet season in rice growing areas. Mega varieties with Sub-1 gene are capable of enhancing rice productivity in flood prone areas by 1-2 tones per ha in sustainable manner. These varieties also offer opportunity for limited rice area expansion during the wet season, these varieties can be promoted in highly flash flood prone fields where no rice is cultivated presently during the wet season. The Sub-1 varieties can tolerate flash floods up to 17 days but they are not effective in case where water stagnates above 25 cm usually for few weeks to months. IARI has developed new lines which can tolerate both flash and stagnant flood.

A few short duration drought tolerant lines (IR 7437-46-1-1, IR 74371-54-1-1 and IR 74371-70-1-1), developed through conventional breeding by IARI have shown excellent promises in India. Under severe drought (when yield of control variety like IR64 is nil) these lines yield approx. 1 to 1.5 tons/ha, when there is no drought these lines are as good as or better than the current popular rice varieties being grown in these areas. On an average they offer yield advantage of 1ton/ha as compared to existing popular rice varieties. One such lines is already released in India as Sahbhagi Dhan,in Nepal as Sookha dhan 3 and in Bangladesh in the name of BRRI dhan 56. Rice varieties recently released in India including CSR-36 and Narendra Usar Dhan 3have shown great promise for cultivation in sodic /saline (Usar) soil of Uttar Pradesh and Bihar in India. One IRRI lines (CSR-89-IR8) has shown very good performance in Usar soil and is likely to be released soon for the commercial use. Similarly some salt tolerant lines developed at IRRI have shown excellent promise for costal saline areas in India. These varieties are evaluated in farmer's field, these salt tolerant varieties provide greater opportunity for increasing and stabilizing productivity in salt affected areas.

A good progress has been made in developing rice varieties with multiple stress tolerance like submergence + salinity, submergence + drought, Flash flood + stagnant flood etc. These varieties should be very useful in managing abiotic stresses in field as quite often more than one stress in involved.

Conclusion

Understanding the potential effects of climate change on agriculture in terms of its impacts on severity and incidence of diseases is an important issue. Climate changes will affect diseases, yield and quality of agricultural and horticultural crops. Our knowledge is limited on how multifactor climate changes may affect plant health. The prediction is that climate change may alter rates of pathogen development, modify host resistance and lead to changes in the physiology of host-pathogen interactions, which may influence the pattern as well as severity of plant diseases. Climate change can have positive, negative, or neutral impact on individual pathosystems because of the specific nature of the interactions of host and pathogen. Climate change operates at a global scale; therefore a systematic understanding of epidemic processes at relevant environmental and spatial scales is required. From a disease management need to refinement of existing management practices, there is a need for simulation models to assess the potential of emerging pathogens for given crop production system and also shift in pathogen population and fitness that may demand modification in current production systems. There is a need for a greater understanding of the effect of climate variables on the efficacy of synthetic fungicides, their persistence in the environment and development of resistance in pathogens population to the fungicides. Recently national and international network is also actively anticipating and responding to biological complexity in the effect of climate change on agriculture and crop diseases. The primary benefit of such studies to growers will be their ability to control the diseases that become severe as result of climate change, select the varieties that are less vulnerable for diseases and reduce fungicide application. Abiotic stress tolerant plant varieties particularly in rice are proving to be boon for the farmers, however only host gene is not enough under high stress severity or where crop is exposed to multiple stresses like flooding, drought and diseases. Similarly microbes alone may not be enough to provide proper protection against abiotic stresses. Therefore evoking crop-microbes interactions within and around the roots of abiotic stress tolerant varieties may further enhance tolerance of these varieties to not only multiple abiotic stresses but also biotic stresses. Therefore need to evaluate these microbes along with tolerance under field condition to manage multiple stresses for food security under climate change.

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LT (FP)-09

Pigeonpea stem rot caused by *Sclerotinia sclerotiorum*: a new biotic stress of pigeonpea in India under climate change scenario

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Pigeonpea is one of the most important pulse crops of India. It is known as red gram, arhar and tur in the country. It is an important source of proteins (22%) along with carbohydrates, fibre, certain minerals viz., iron, calcium, magnesium, zinc, iodine, potassium and Phosphorous and ‘B’ complex vitamins. Pigeonpea stalks are also a major source of firewood and livestock feed. India is the world’s largest producer and consumer of pulses including pigeonpea. About 90% of the global pigeonpea area is in India contributing to 93% of the global production. It occupies 4.9 m ha area with 3.1 mt production which accounts for a productivity of 1145 kg/ha; ranking ninth in the world (GOI, 2015). *Kharif* is the main growing season of pigeonpea in India and major pigeonpea growing states are Maharashtra, Uttar Pradesh, Madhya Pradesh, Karnataka, Gujarat, Andhra Pradesh, Tamil Nadu, Bihar and Chhattisgarh. Cultivation of pigeonpea on bunds in low land areas is becoming popular and profitable among the farmers. Traditional varieties of pigeonpea need about 6 to 9 months to mature, while the improved varieties developed can be harvested in 3-4 months. Both long duration (180 days) and medium duration (130-140 days) genotypes are grown in India under various cropping systems. This pulse crop is grown mostly as an intercrop between cereals crops and plays a unique role in enriching the soil, by adding 40-90 kilogram nitrogen per hectare over a given season. It has the ability to resist drought and to add large quantities of biomass to the soil in addition to nitrogen fixation makes it a good choice for rainfed as well irrigated production systems. The deep root system of the crop helps to recycle plant nutrients from deeper layers, and the acid secretions from its roots increase the availability of phosphorus in the soil. Limitation to the increasing productivity of pigeonpea is also due to abiotic and biotic stresses prevalent across the pulse growing regions. The crop is affected by more than 100 pathogens, including fungi, bacteria, viruses, phytoplasmas and nematodes (Nene, 1996). Among biotic stresses diseases viz., *Fusarium* wilt, *Phytophthora* Blight, Sclerotinia stem rot, sterility mosaic and foliar diseases and, insect pests feeding on pods lead to significant yield losses. Management of these stresses can contribute to a yield recovery of 300-350 Kg/ha.

Study detail

Field studies were conducted at the experimental farm of ICAR-IARI Regional Station, Pusa, Bihar (India) during the years, 2012-13 and 2013-14. The farm site (25^0 59’ N, 85^0 40’ E and 52 m above mean sea level) is located in Samastipur district of Bihar (India) on southern bank of Budhi Gandak River. The soil type at the experimental site was calcareous clay in texture, pH (8.1), low in organic carbon, nitrogen, zinc, boron, sulphur and intermediate in phosphorus and potash content. The pigeonpea crop was sown in the month of August in RBD with three replicates in plots of size 6.0 x 4.0 m spaced at 75.0 x 25.0 cm.

Symptoms

The symptoms of the disease first appeared as light brown water-soaked lesions on stem and branches. These lesions girdled the entire stem or branches and enlarged in both directions and became notably covered with white fluffy mycelium (Fig. 1). Ultimately, the leaves, inflorescence and pods were covered with white mycelial growth of the pathogen. Affected leaves lost turgidity and ultimately were blighted on the stem (Gupta, et al., 2015).

Fig 1. Pigeonpea branches showing the critical symptoms of the stem rot disease under field condition

The pathogen

S*clerotinia* rot of pigeonpea caused by *Sclerotinia sclerotiorum* (Lib.) de Bary in India (Gupta et al., 2015). *Sclerotinia sclerotiorum* (Lib.) de Bary is a necrotrophic pathogen with a broad host range worldwide. It is a simple interest plant pathogen using ascospores as primary source of inoculum and spreads horizontally through contact of infected plant to nearby healthy plants. The pathogen causes root, stem, twig and head rots in oilseeds, pulses, vegetables, ornamentals, medicinal and fodder crops, leading to crop failures with 60 - 80% disease incidence and up to 100% yield loss worldwide (Mehta, 2009). Isolation studies from diseased tissues and sclerotia consistently produced white fluffy mycelial colonies and abundant large black sclerotia on PDA. Sclerotial formation started after 72 h of incubation and appeared fully on the surface of mycelial growth in the form of a ring at the periphery of the plate after 6 days (Gupta, et al., 2015).

Cultural, morphological molecular characteristics

Fungal colony colour creamy white to light brown with sparse, fluffy type of growth was observed. Hyphae was hyaline in colour, colour of sclerotia whitish to blackish and appeared in form of ring at the periphery or scattered in the centre of the plate. The internal transcribed spacer (ITS) regions 1 and 2, including the 5.8S ribosomal DNA (rDNA) region, were amplified by polymerase chain reaction (PCR) using universal primers ITS1 (TCCGTAGGTGAACCTGCGG) and ITS4 (TCCTCCGCTTATTGATATGC) (white, et al., 1990) synthesized by Sigma Aldrich House, Suffolk, UK. The PCR amplification reaction was carried out in a final volume of 25 µL, which consisted of 1X PCR assay buffer, 200 mM dNTPs mixture, 2.0 mM $MgCl_2$, 0.1 µM primer, 1.5 U Taq DNA Polymerase and 50 ng template DNA. PCR reactions were carried out in an Icycler, Bio-rad (96 well system) under initial denaturation at 94 ^{0}C for 4 min, annealing at 57 ^{0}C for 1 min, 72 ^{0}C for 1 min, and final extension at 72 ^{0}C for 7 min. The PCR fragments were sequenced and the sequences were aligned using the multiple sequence alignment program, Clustal W (white, *et al.,* 1990). The phylogenetic analysis was performed using MEGA 4.0 (Tamura et al. 2007) with a bootstrap of 1000 replicates. *Fusarium oxysporum* strain ATCC-MYA 3931 was used as the outgroup taxon. The internal transcribed spacer (ITS) region of the pathogen was amplified using the primers ITS1 and ITS4 and sequenced. The BLAST searches in NCBI database revealed 100% query coverage and 99% identity with *S. sclerotiorum* (Mehta, 2009).

Host range

The fungus infects more than 500 plant species belonging to 278 genera and 75 plant families spread over gymnosperms and angiosperms including monocots and dicots (Mehta, 2009). *Bidens pilosa*, *Capsella bursa pastoris* and *Vernonia cinerea* new weed hosts were also recorded for this pathogen. These weed hosts were not observed earlier in this area for the same pathogen. These weed hosts may act as source of primary inoculum for the disease development (Gupta, et al., 2016).

Predisposition factor

The experimental location, Pusa (Bihar) is characterized by a humid sub-tropical climate under irrigated and no`n-limiting soil moisture conditions in NEPZ of India. Cool humid weather along with heavy dew occurred during the months of November to February. Relative humidity is usually higher than elsewhere due to its specific location on southern and western bank of Budhi Gandak river. During December and January of 2012-13 and 2013-14, average minimum air temperatures were 10.1 and 8.4 ^{0}C, whereas average maximum air temperatures were 22.2 and 19.3 ^{0}C, respectively. The average minimum RH (%) during December and January was 62.3 and 67.2, whereas maximum RH (%) was 93.0 and 92.3, respectively, for both the years. December and January are the coldest months of the year, and above 93% relative humidity accompanied by 9.5-12.2 mm rainfall (2-3 rainy days) upholds ideal conditions for sclerotial germination and apothecial development (Gupta et al., 2016). Pigeonpea crop was planted in the month of August and developed a closed canopy till November and December. However, flowering occurs in December which coincides with cool, wet and humid weather conditions along with dead flowers providing favourable conditions for disease initiation and spread. Pathogen infection, development and spread is being highly affected by high temperature during the months of December and January. The cool sub-humid climate with average minimum (9.2 ^{0}C) and maximum temperatures (21.0 ^{0}C) along with more than 93% relative humidity play an decisive role for stem rot disease development and spread in pigeonpea crop (Gupta, et al., 2016). The disease was found to appear on pigeonpea crop during 2012-13 and 2013-14, while in 2014-15 crop season no disease incidence was recorded due to high temperature in winter season (Fig. 2). The three months' i.e., November, December and January of 2014-15, minimum temperature (15.2, 9.36, 7.1^{0}C), maximum temperature (29.6, 24.1, 22.2^{0}C), minimum relative humidity (53.8, 56.5, 56.5%) and (89, 88.7, 91%) has vast effect on appearance of disease on crop (Fig. 2 and 3). Maximum rainy days were observed in the month of August during 2012-13, 2013-14 and 2014-15. However, during 2012-13 and 2013-14, November and December months were completely dry, while rainfall occurred again in January month of both the years. Surprisingly, during 2014-15, no rainfall was occurred after October month till February which is very sensitive months for spreading of this pathogen (Fig. 4). Sunshine hours were also lowest in the months of December and January during 2012-13, 2013-

14 and 2014-15 (Fig. 5, 6). Probably higher maximum temperature and low relative humidity checked the infection and occurrence of the disease on pigeonpea crop in the NEPZ region of India. This is a critical example of climate change mediated non-occurrence of plant disease in pigeonpea crop.

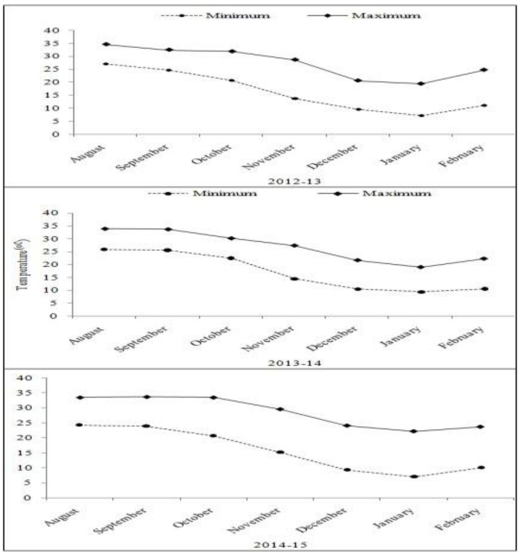

Fig. 2. Average maximum and minimum monthly temperature (°C) during the years, 2012-2015

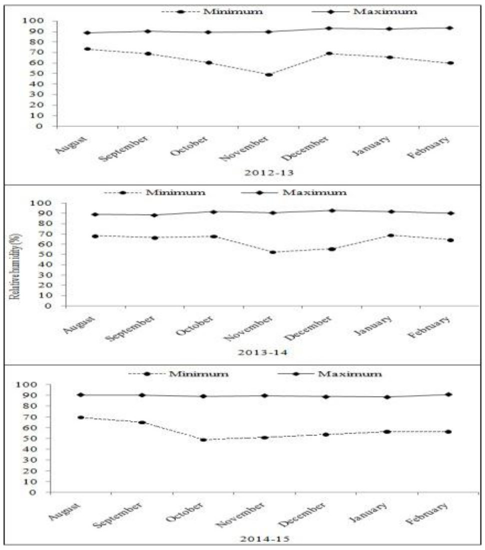

Fig. 3. Average relative humidity (%) during the years, 2012-2015

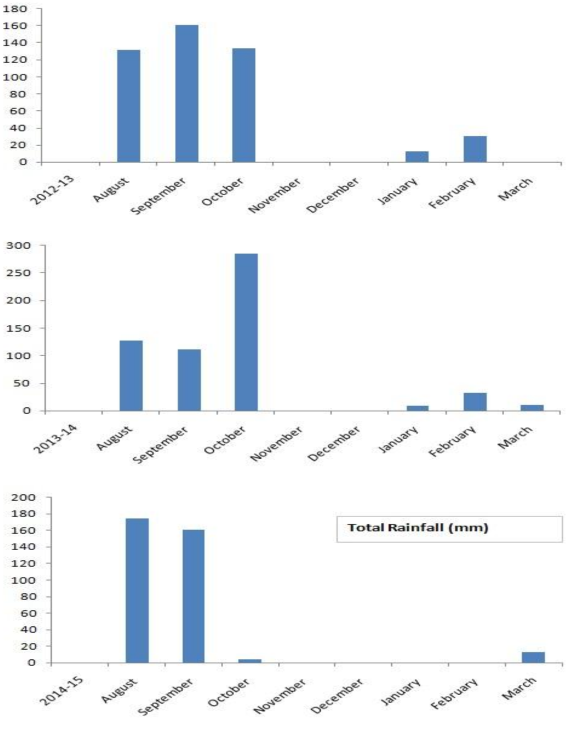

Fig. 6. Total monthly rainfall (mm) during the years, 2012-2015

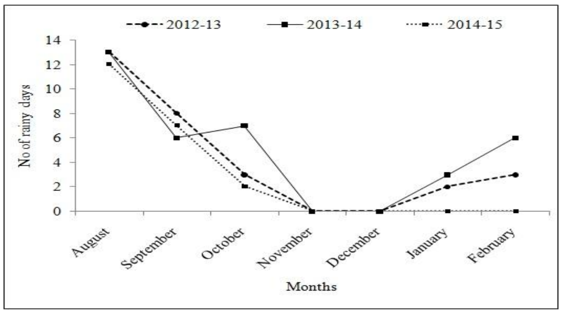

Fig 4. No of Rainy days

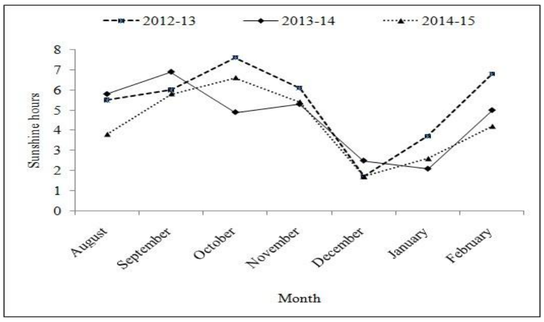

Fig 5. Sunshine hours during wheat growing season 2012-13 and 2013-14 at Pusa, Bihar (India)

Conclusion

The disease and pathogen highly affected by high temperature during the months of December and January. The cool sub-humid climate with average minimum (9.2^0C) and maximum temperatures (21.0^0C) along with more than 93% relative humidity plays a decisive role for stem rot disease development and spread in pigeonpea crop. However, the disease has been found to appear on crop during 2012-14, while in 2014-15 crop season no disease incidence was recorded due to high temperature, low relative humidity and no rainfall in winter season resulting checked the infection and occurrence of the disease on pigeonpea crop. This is a typical menace to the pigeonpea crop production under climate change scenario occurred in North Eastern Plain Zone of India.

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LT (FP)-10

Deciphering the viruses associated with viral complex of king chilli in North East India and an ecological engineering based viral disease management module

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The North East region of India is one of the biodiversity 'hot spot' having the unique agro-ecological environment with high relative humidity acting as the centre of speciation for an array of plant species. This region has given rise to one of the hottest naturally occurring chillies (King chilli, Umrok, Naga chilli or Bhut jolokia) of the world. King chilli (*Capsicum chinense* Jacq) is widely grown in North Eastern region and consumed in many preparations, both as spice and medicines. It is one of the hottest chillies grown worldwide, being grown in the states of Manipur, Nagaland, Mizoram and Assam. It is used as a spice in food or can be eaten in raw along with the staple food. King chilli is known for its refreshing aroma, palatability and medicinal properties. This chilli is native to the North Eastern Region of India and subsequently, the geographical indication (GI) of goods tag for this chilli has been obtained.

The king chilli in North East is being infected by a viral disease complex showing varying symptoms ranging from leaf mottling, vein banding, leaf distortion, narrowing of leaf lamina, severe curling, necrosis and stunted growth. The initial survey in different king chilli growing pockets has indicated the wide spread occurrence of viral disease complex in North Eastern Hill region particularly in the states of Manipur, Nagaland, Meghalaya etc. King chilli is grown both as annual as well as ratoon crop by the farmers of the region, and due to initial infection by the viral complex, production and productivity are reduced to a greater extent. Recently association of a *Potyvirus*, *Chilli veinal mottle virus* (ChiVMV) has been reported from Meghalaya (Banerjee *et al.*, 2014), and our studies have confirmed the association of mixed infection of ChiVMV and *Cucumber mosaic virus* (CMV) with the king chilli from Manipur. The survey and symptoms based analysis has indicated the probable infection of begomoviruses and *Tospovirus*. Association of begomoviruses (Shih *et al.*, 2006; Senanayake *et al.*, 2006; Krishnareddy *et al.*, 2008) with the chilli have been reported from other parts of India, however, there is no detailed information available on the viral disease complex of king chilli being grown in the North Eastern region. We therefore undertook in-depth analysis of viral complex of king chilli to decipher the associated viruses and finally developing an ecological engineering based disease management module.

Survey and characterization of viral complex of king chilli from Manipur

A high incidence of viral disease complex on king chilli was recorded in Manipur during last three years (2014-2017). Surveys in different pockets of Manipur were conducted for the viral complex of king chilli and an incidence of 48-64% was recorded based on symptoms. To identify the associated virus (es) with the viral complex symptoms, collected symptomatic samples were screened using primers specific to genomic regions of *Chilli veinal mottle virus* (ChiVMV), *Cucumber mosaic virus* (CMV) and *Begomovirus* in reverse transcription PCR (RT-PCR) and PCR respectively. Out of 113 symptomatic samples showing symptoms of leaf puckering, shoestring, veinal mottling, yellowing, small leaf lamina etc. collected from different districts of Manipur, 50.44% were tested positive for CMV and 21% for ChiVMV. None of the samples were found positive for *Begomovirus* infection. Mixed infection of CMV and ChiVMV was very common in field samples. Out of the tested samples, 17% were having mixed infection of CMV and ChiVMV. Selected isolates of CMV and ChiVMV originating from different pockets of Manipur were also characterized at molecular level. Present study indicated that CMV and ChiVMV are the most commonly associated viruses with viral complex of king chilli in Manipur.

Ecological engineering based integrated disease management module

An ecological engineering integrated viral disease management module was developed for the field management of viral disease complex of king chilli. Seed treated with carbendazim were sown under insect-free poly house covered with insect-proof net for raising the virus-free healthy seedlings of king chilli. Initial experiment was carried out with seedling dip treatment of bare rooted king chilli seedlings with (i) chlorpyriphos, (ii) Crusier (thiamethoxam 5S), (iii) Actara (thiamethoxam 25WP) and (iv) imidacloprid for 6 hours to overnight. Treated seedlings were transplanted in different plots where barrier crops (maize, sunflower, buck wheat, foxtail millet and barnyard millet) around 20-25 days earlier to transplanting. Mulching with silver plastic mulch or paddy straw was done separately in different plots. Whole experiment was undertaken in split plot design for three consecutive seasons. After 20-25 days post-transplanting, one foliar spray of respective insecticide and micronutrient mixture was given to the transplanted king chilli. Weekly vector population and infected plants were recorded in each plot. In treated plots significantly lower viral disease incidence (0-4% after 30 days of transplanting and 9-10% after 60 days of transplanting) was observed as compared to untreated (78% after 30 days of transplanting and 95% after 60 days of transplanting). Based on the combined results of three seasons, treatment with Crusier (thiamethoxam 5S) or Actara (thiamethoxam 25WP), followed by transplanting in plots having 20-25 days old maize plants as barrier crop and silver plastic mulch or paddy straw mulch protected the king chilli plants from any secondary viral infection carried through vectors for at least for 60 days post-transplanting and gave significantly higher yield (63% higher yield) over the untreated control. This module was successfully demonstrated in farmer's field during 2015-16 and farmers who adopted this module witnessed 58% increase in income compared to those who had not adopted it

Conclusion

Viral complex of king chilli is the major constraint in the production and productivity with an incidence of 48-64%. Viral complex is caused by association of two aphid-transmitted viruses (CMV and ChiVMV). To manage the menace of viral complex, an ecological engineering based module was developed. In future large number of king chilli samples from different groves of North East India are required to be indexed to elucidate the possible occurrence of other viruses like begomoviruses, tospovirues, potyviruses and *Tobamovirus*. This will help in developing multiple detection assays in on-site format.

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October 10-11, 2017
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Citation : Ngachan SV, Prakash N, Sharma SK, Singh IM, Roy SS, Ningombam A, Punitha P, Ansari MA, Singh RK, Sailo B, Singh TB, Sonia Ch, Anand YR, Singh TS and Singh YH (Eds.) 2017. Souvenir and Abstracts of National Symposium on Emerging and Re-emerging Plant Diseases in North East India: Challenges and Strategies. 10-11 October, 2017, Imphal, Manipur, India. pp. 144.

Published by:
Director
ICAR Research Complex for NEH Region
Umroi Road, Umiam, Meghalaya – 793103

Printed at:
R. B. Printing House, Nagamapal, Imphal

LT (A)-01

Diagnosis and management of bacterial wilt disease of solanaceous crops- a report

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Ralstonia solanacearum (Smith) Yabuuchi *et al.,* 1995 causes wilt disease in solanaceous crops and reduces the production of crops. The loss due to this disease is very high from 2 to 100% depending on environmental conditions and crop genotypes and virulence of the pathogen. The affected plants show a typical wilt symptoms and browning of vascular tissue in roots stems and tubers. The pathogen is a gram -ve, rod shaped, frequently occurs in pairs, motile with 1 to 4 polar flagella, aerobic, non-fluorescent, positive in catalase and oxidase tests and forms nitrites from nitrates and negative in levan production and starch hydrolysis. Virulent isolates on 2,3,5-TriphenylTetrazoliumChloride (TTC) medium develop fluidal, irregular colonies having peripheral white and pinkish in centre. In India, race 1 and bvs 3 & 4 are prevalent in tomato chilli capsicum and brinjal. However, race 1 and 3 infect the potato. Presently, *R. solanacearum* strains are categorized into four genetic groups called phylotypes which reflect the geographical origin and also ancestral relationships between the strains. Besides cultural, morphological and biochemical tests, sero-diagnostic like ELISA (Enzyme-linked immunosorbent assay), immunofluorescent cell staining, lateral flow devices, serological kits are applied for detecting *R. solanacearum* from infected plant, tubers and soil. To improve the sensitivity, various modifications have been made like enrichment in SMSA broth, nutrient broth or CPG broth to allow bacteria to multiply prior to do conventional PCR, called as BIO-PCR and two round PCR as nested- PCR. Multiplex -PCR protocols have been developed to simultaneously detect either *R. solanacearum* or *E. carotovora* subsp. *carotovora*. Management of bacterial wilt disease of solanaceous crops is very difficult due to its soil borne nature. Different workers throughout the world have made efforts to control this disease by using cultural, chemical, biological and host resistance methods, either alone or in combination of these methods.

LT (A)-02

Fungal disease scenario inorganic agriculture: threats, challenges and strategies

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Organic agriculture, being an age-old farming system with great potential in India is emerging as a potential alternative to the environment & health hazard chemo-centric agriculture marked by the green revolution for meeting healthy food demand while maintaining the ecology of the agro-biodiversity of the system. However, the question of its sustainability in terms of productivity and food security ensuring availability of organic compliant alternative resources amidst abiotic and biotic constraints of the system including the emergence and re-emergence of pest pathogens is a great challenge to answer for all of us. Northeast India rich in traditional knowledge-based farming and bio-resources with negligible use of chemicals in the agro-biodiversity system has a great potential and hub of organic agriculture being in practice using traditional wisdom. However, the occurrence of insect, pest and pathogen on varieties of organic crops almost at par with the conventional system is a major constraint and threats to the sustainability of the system that posed a great challenge to the plant protection scientists. Further, with the enforcement of several agriculture-related International Treaties under WTO and climate change, the disease scenario of agrobiodiversity crops is being altered resulting in the emergence of new pathogens, resurgence of existing pathogens, minor disease becoming major ones, are a matter of concern. Weed pest reinforced by Invasive Alien Species aggravated the problem of host-pathogen complexities under organic farming system as they provide alternate host to several pathogens. In addition, unrestricted flow of plant materials from the international borderland areas contribute to the severity of fungal diseases.

Having known some of these problems of pest pathogens, current organic crop management practice include traditional cultural practices, augmentation of agronomic practices, judicious selection of seed materials along with soil health management practices, formulation and application of micro-organisms based bio-pesticides & fungicides, medicinal plant extracts, etc. No doubt these practices mitigate the occurrence of diseases in certain organic crops of subsistence farming, credibility and validity of the practices is being scanned for their fluctuating effect. As such, disease scenario under organic farming system continued to be more or less at par with the conventional system. Here lies the challenges in overcoming the fungal diseases menace beyond traditional practices keeping in mind the ecology of the system. Therefore, molecular approaches for the management of fungal diseases of organic crops could be one of the strategies. However, without a clean diagnosis and highly accurate prognosis, the idea cannot be put in practice. PCR- based molecular diagnostics, development and use of molecular markers for pathogen detection, identification of numerous genes involved in the defence response of host plants, if developed successfully, at least for certain standard crop, could serve for long-term crop management strategy. Although the negative impact of fungal diseases are well known, their quantification is still fragmented and incomplete. Assessing and modelling crop losses to fungal diseases may inform long-term strategic decisions and avoid the wrong decision in the application of control measures which otherwise impose unnecessary strains on the agricultural ecosystem.

LT (A)-03

National agriculturally important microbial culture collection – an overview

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India has been blessed with massive microbial diversity and is one of the acclaimed hotspots for mega biodiversity among different countries of world. In the past few years, many projects have been funded by the Department of Biotechnology for discovery of vast microbial diversity which could be used in agriculture, medicine and industry. The ICAR-National Bureau of Agriculturally Important Microorganisms (ICAR-NBAIM) was established by the Department of Agricultural Research and Education (DARE) and ICAR, Ministry of Agriculture, Government of India under the IX Five Year Plan in 2001. The Bureau started functioning at Old Building of NBPGR, New Delhi. The ICAR-NBAIM was shifted to the campus earlier occupied by the National Institute of Sugarcane and Sugar Technology (NISST) at Kushmaur, Mau Nath Bhanjan, Uttar Pradesh on June 1, 2004. The DARE and ICAR jointly laid the foundation of ICAR-NBAIM with underlying objectives to explore, collect, maintain and conserve microbial wealth of the country and to ease the availability of agriculturally and industrially important microorganisms to researchers, farmers, industry and others stakeholders. A landmark development of ICAR-NBAIM was the establishment of NAIMCC in the year 2004. Currently, India has 30 microbial culture collections including a few microbial resource centres (MRCs) that are registered with the WDCM. The storage capacity of NAIMCC currently is nearly 10,000 agriculturally important microorganisms (AIMs). The NAIMCC was registered as an affiliate member of WFCC in 2014 (www.wfcc.info/ccinfo/collection/by-id/1060) and is working as per the guidelines and principles laid down by the WFCC/OECD/NBA. The ICAR-NBAIM has been recognized as a Designated Repository (DR) by the National Biodiversity Authority, MoEF&CC, Govt. of India (www.nbaindia.org) for management of agriculturally important microbial genetic resources of the country. Currently, NAIMCC holds 6322 accessioned microbial strains comprising of 3801 fungal strains, followed by 2293 bacterial strains and 228 cyanobacterial accessions. Microbes belonging to 50 bacterial genera, 33 fungal genera and 18 cyanobacterial genera constitute the total microbial holdings in NAIMCC. Amongst the microbial cultures deposited in NAIMCC; *Bacillus*, *Pseudomonas*, *Streptomyces*, *Lactobacillus* and *Paenibacillus* represents the prominent bacterial genera; *Fusarium*, *Trichoderma*, *Pleurotus*, *Aspergillus*, *Alternaria*, *Agaricus*, *Colletotrichum*, *Chaetomium* represent main fungal genera and *Nostoc*, *Anabaena* and *Calothrix* represent predominant cyanobacterial genera. NAIMCC's accessioned bacterial species belong mainly to the phylum Firmicutes followed by γ-Proteobacteria, Actinobacteria, α-Proteobacteria. NAIMCC has 475 cultures of mushroom from ICAR-Directorate of Mushroom Research (ICAR-DMR), Solan. Some of the cultures have also been received from ATCC (American Type Culture Collection), USA, NCL, Pune, CCUBGA, New Delhi and MTCC, India. At present in India, NAIMCC represents the only culture collection with an exclusive focus on preservation of microorganisms possessing agriculturally and industrially important traits such as phosphate solubilization, production of siderophore, cellulase, ligninase and antibiotic production and mitigation of biotic and abiotic stresses such as drought, cold, high temperature, salt etc. NAIMCC is developing a core-collection of potential microorganisms with reference to traits, crops, soil types and agro-climatic zone so that it would be widely utilized. NAIMCC accepts microbial cultures under general and safe deposit. With a view to safeguarding these microbial resources, a duplicate set of collections in the form of lyophilized ampoules and glycerol stock are preserved in culture storage facility developed at NBPGR, New Delhi. The microbial germplasm registration facility is also available at NAIMCC for registering elite microbial germplasm which is distinct, unique and stable (DUS) and has potentially proven attributes of academic, scientific, agricultural and industrial importance. The Microbial Germplasm Registration Committee (MGRC) is the advisory committee which approves the registration of the microbial germplasm. The details of submission of microbes for accession number and supply of cultures to users are available at Microbial Genetic Resource Portal (www.mgrportal.org.in). With a view to harmonize data of biopesticide of already registered strains in the country and for future registration of biopesticides, the CIB & RC has accredited ICAR-NBAIM for DNA finger printing of biopesticides as well as to accession under safe or general deposit in the country. In addition, the Bureau is also extending support to the Department of Plant Protection, Quarantine and Storage (DPPQS), Faridabad in importing cultures from abroad and NBA to enforce BD Act 2002 for access and utilization of microbial genetic resources and access benefit sharing under Nagoya Protocol.

LT (A)-04

Molecular characterization and diversity analysis of some important viral diseases of crop plants of North Eastern region of India

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The North Eastern region of India is endowed with rich crop diversity including cereals, pulses, oilseeds, fruits, vegetables, spices and tuber crops. Many of these crops are under constant threat from viral diseases causing huge loss in production and productivity. Existence of most of the insect and mite vectors in high population density further aggravates the problem in the region. Here we are documenting the molecular detection, characterization and phylogenetic analysis of some important virus and virus like diseases of crops grown in the region. The presence of these viruses and virus like diseases were confirmed by polymerase chain reaction (PCR) and reverse transcriptase polymerase chain reaction (RT-PCR) assays. The partial genome of the respective viruses and virus like organisms were sequenced and analyzed. PCR assays could successfully detected Citrus greening disease (CGD, 703bp), Tomato leaf curl virus (ToLCV, 348 bp) and Chilli leaf curl virus (ChLCV, 550 bp), Banana bunchy top virus (BBTV, 1018 to 1111 bp), Sesamumphyllody (SP, 1.2 kb) and Sugarcane grassy shoot (SCGS, 1.2 kb). However, RT-PCR resulted amplification of Citrus tristeza virus (CTV, 672 bp), Potato virus Y (PVY, 328 bp), Potato leaf roll virus (PLRV, 629 bp) diseases from the fields of North Eastern region of India. Recently a new virus disease, Konjac mosaic virus (KoMV, 328 bp) in the genus Potyvirus and family Potyviridae has been detected using RT-PCR assay from the elephant foot yam from the experimental field of Assam Agricultural University, Jorhat, Assam. Genome analysis and phylogenetic tree configuration of CTV, CGD, ToLCV, ChLCV, BBTV, PVY, PLRV, SP, SCGS and KoMV have revealed some distinctive isolates and diverse genome characters to the extent of 99-100 per cent similarities and as low as 71 per cent dissimilarities within and across India.

LT (A)-05

Biologically mediated and chemically synthesized nanoparticle can give better control of plant pathogens and has positive effect on plant growth parameter and defence metabolite

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Rapid developments in the field of nanotechnologies in the past decade have opened up a systematic way of controlling and 'fine-tuning' material properties to suit a wide range of new industrial and consumer applications. The fundamental drivers behind most nanotechnology applications include the potential for reducing the use of chemical substances and the

development of improved or novel functionalities for different products and applications. For example, nano-sizing of water-insoluble substances can enable better dispersion in aqueous media, thus enabling a reduction in the use of organic solvents (e.g. in cosmetics, paints, pesticides, agrochemicals), and fat or surfactants (e.g. in food products). Nano-sized medicines, nutrients and food supplements are also claimed to have better absorption and bioavailability in the body compared to bulk equivalents. This aspect alone has opened up a vast area of new applications in the supplement, nutraceutical and health-food sectors.

At Department of Plant Pathology, Assam Agricultural University, Jorhat nanoparticles like Gold (Au), Silver (Ag), Copper (Cu), Zinc oxide (ZnO), Chitosan etc with novel properties of suppressing the plant pathogen, insect pests, nematode with enhanced plant growth, seed invigoration and resistance to biotic and abiotic stress has been synthesize by biological and chemical approaches. The nanoparticles were characterized for morphology, size, crystallinity, shape, charge, concentration, functional group etc by UV Vis spectroscopy, SEM, TEM, Diffraction light scattering, Zeta potential, FTIR etc.

Trichoderma asperallum mediated silver nanoparticle (AgNP) with 27.63 nm size and charge of -1.34 zeta potential and fairly stable at a pH above 7 and cubic shape has the ability to suppress the growth of four soil-borne plant pathogens at four different dosages (10, 30, 50 and 100 ppm). Similarly, plant-mediated AgNP found effective against *Leucinodes orbonalis*, and *Spodoptera litura*. We also synthesized zinc oxide (ZnO) nanoparticle by wet chemical approach and found effective against plant pathogens at 100 and 225 ppm with enhanced plant growth, increased plant biomass, leaf area, chlorophyll content with higher nodulation of french bean when ZnO NP was applied as seed treating agents. The microscopic data revealed that AgNP and ZnO NP- treated hyphae were seriously damaged on hyphal walls, resulting in the plasmolysis of hyphae. Both the nanoparticles were also found effective for causing mortality of J2 larvae of *Meloidogyne incognita* with reduced number of galls and eggs in the treated plant. Study on biochemical defense mechanism of AgNP and ZnO NP treated host plant showed enhancement of secondary metabolite, which may help in acquiring resistance in the crop plants.

LT (A)-06

Molecular and morphological approaches for identification of powdery mildew pathogens

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Chasmothecial (teleomorph) characters like type of appendages were used for identification of powdery mildew pathogens but in tropical climate absence of chasmothecia makes identification very difficult. Now a day's typical anamorph characters and molecular approaches which have been developed by several research workers have made identification possible even in absence of Chasmothecia. Anamorph characters like wrinkling pattern on surface of conidia which can be clearly observed using scanning electron microscope are now considered very important for establishing link with teleomorph genera. By using molecular evidence it is possible to establish anamorph - teleomorph relationship. We have identified several powdery mildew pathogens (anamorphs) using scanning electron microscopy and molecular approaches (ITS region) like *Erysiphepisi* on pea, *Podosphaera xanthii* on several cucurbits and pulses, *E. quercicola* on citrus. These findings will help the breeders and plant pathologist for accurate identification of resistance sources against specific pathogens.

LT (A)-07

Progress of phytoplasma disease research in India

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Phytoplasmas have been found associated with 129 plant species in India including vegetables, legumes, spices, medicinal plants and ornamental plants, cash and oil crops, palms, fruit trees and weeds, where ten 16Sr groups of phytoplasmas have been identified so far. Sesame phyllody, brinjal little leaf, sugarcane grassy shoot, sandal spike, coconut root wilt, areca nut yellow leaf and many diseases in ornamental plants are causing the most severe economic losses in the country. Identified Phytoplasmas are related to *‘Candidatus Phytoplasma* asteris’, ‘*Ca*. P. *pruni’*, ‘*Ca*. P. *ziziphi’*, ‘*Ca*. P. *trifolii’*, ‘*Ca*. P. *solani’*, ‘*Ca*. P. *cynodontis’*, ‘*Ca*. P. *oryzae’*, ‘*Ca*. P. *phoenicium’*, ‘*Ca*. P. *australasia’* and ‘*Ca*. P. *pini’*. Among them ‘*Ca*. P. *asteris’*-related strains (aster yellows, 16SrI group) are the prevalent phytoplasmas identified associated with 62 diseases followed by phytoplasmas classified in 16SrII, 16SrVI, 16SrXIV and 16SrXI groups. The majority of the reported phytoplasmas have been classified up to subgroup levels on the basis of RFLP analysis. Moreover, some phytoplasma diseases which were confirmed only by symptoms or transmission electron microscopy observation remains to be identified at molecular levels. Complete phytoplasma genome sequencing has not been done so far and thus would be a major thrust area of research in coming years. At least seven insect vectors, belonging to leafhoppers and planthoppers species, have been reported as putative or natural vectors for important phytoplasma diseases. The majority of phytoplasma disease reports are from north and south part of India. Little attempt has been made to genomics, epidemiology, host phytoplasma interaction and management aspects of these diseases. Moreover, for understanding host phytoplasma interactions, it is important to identify the function of membrane proteins or secreted proteins and effectors encoded in the phytoplasma genome. Presently the suggested effective management practices in India are growing resistant varieties, application of tetracycline, control of insect vectors, weed species as alternative hosts and use of healthy planting materials. The management approaches of widespread phytoplasma disease on major economic crops in India also need attention towards developing resistant genotypes, RNA interference and checking the natural spread of other alternative sources of weed hosts and potential insect vectors are also important information to be achieved. Numerous new phytoplasma strains have been identified in the last decades, and a preliminary classification of known and new phytoplasma strains has revealed that phytoplasmas are more diverse than the previously thought. Epidemiologic studies should also be carried out to prevent further epidemic spreading.

LT (A)-08

Extension approaches to plant protection: an analysis from secondary sources

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The plant protection is an important segment of agriculture. It encompasses pests, diseases and weeds. The objective of the paper is to look into the different extension approaches suitable for plant protection as highlighted from secondary sources. The secondary sources include both national and international literature which explains the extension approaches in the context of plant protection. The secondary sources highlights that the crop protection research mainly focussed on curative control of pests, diseases and weeds which has significantly contributed to increased agricultural production. However, it has created other negative effects on food-safety, public health and the environment. The literature emphasises to add preventive control along with curative control of pests, diseases and weeds. The different approaches to plant protection include technology oriented approach and system oriented approaches. The Farming System approach, Agriculture Knowledge and Information Systems and Agricultural Innovation Systems are part of system oriented approaches. The system oriented approaches highlights farmers as experimenters, experts, partners, entrepreneurs and part of innovation network. The review also highlights that among the crop protection publications studied from 1945-2012, the transfer of technology approach dominates the publications. The researchers highlighted that there is a need to shift from technology oriented approaches to system oriented approaches which emphasis on farmer participatory research, learning based approaches which bring together different stakeholders for enriching farmers knowledge and multi actor collaborations in research and extension activities. Further, the national and international experiences of participatory extension activities like Farmers Field School and their success stories, system approaches in research and extension activities highlight that the participatory approaches is the tool for plant protection which could be successfully deployed in North East Hill region.

MJN-01

Studies on antagonistic potential of *Beauveria* spp. against major soil borne pathogens

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Beauveria bassiana (Balsamo) Vuillemin is a soil dwelling necrotrophic fungus belonging to the order Hypocreales of the class Ascomycetes having a broad host range against both insect pests and plant pathogens. The antagonistic activity of *Beauveria* is associated with antibiosis, mycoparasitism, endophytism, production of lytic enzymes and secondary metabolites. A total of 22 isolates were obtained from different parts of Meghalaya of which morphological and microscopic studies were conducted. The isolates were screened for their production of extracellular hydrolytic enzymes *viz.,* amylase, caseinase, cellulase, chitinase, lipase and protease. The screened isolates were further evaluated for their antagonistic potential against major soil borne fungal pathogens of tomato *viz., Fusarium oxysporum, Rhizoctonia solani, Pythium myriotylum* and *Phytopthora infestans* by employing dual culture assay. Isolate BP1.1 showed significantly highest inhibition percentage of 68.30% (*F. oxysporum)*, 64.07% (*R. solani)*, 77.41% (*P. myriotylum)* and 69.46% (*P. infestans)* respectively. The endophytic potential of screened isolates was also tested in tomato by gnobiotic assay and highest per cent colonisation of 80.24% was observed in BP1.3. Eventually, BP1.1 was tested for its efficacy against soil borne fungal pathogens of tomato in pot culture condition of which plant growth factors were also studied. *B. bassiana* performed better against *P. myriotylum* in terms of per cent germination (75.41 %), shoot length (30.60 cm), root length (29.67 cm) and per cent disease incidence (37.78 %) as compared to control.

MJN-02

PGPM formulation mediated biochemical changes and defense response of tea (*Camellia sinensis* (L) O. Kuntze) against major diseases and insect pests

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The perennial tea plantation provides favourable conditions for a variety of pests and for management of these pests, chemointensive approach has been a regular practice today. As a result, the tea pests are showing higher level of resistance *vis-a -vis* accumulation of pesticide residues in made tea. In our study, four different microbial bioformulations (*Biosona*, *Biotime*, *Biogreen-5* and *Biogreen-L*) were evaluated for an environment friendly green approach of tea pests (Tea mosquito bug, Looper caterpillar, Red spider mites and Tea aphid) and disease (grey blight) management. All the bioformulations, applied as foliar spray at 15 days interval during 2016-17 were found significantly effective in reduction of different tea pests and diseases. Bioformulation *Biogreen-5* was found most effective, recording significantly highest reduction of tea mosquito bug (89.06%), red spider mite (92.04%), looper caterpillar (91.47%), aphid (92.53%) and grey blight (91.20%), along with increase in the green leaf yield (10.40q/ha).

Analytical assays done to evaluate biochemical changes in tea leaves due to application of the bioformulations revealed manifold increase in caffeine, total phenol, flavonoids, chlorophyll and total soluble sugar content in the tea plants treated with *Biogreen-5*. The study indicated direct correlation between application of PGPM formulation and tea quality and also updated the usefulness of current strategies based on biological control agents for effective management of tea pests and diseases.

MJN-03

Polyclonal antisera production, development of serodiagnostic assay, standardization of polymerase chain reaction technique and partial sequencing of PVY isolate from Jorhat district of Assam

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Potato virus Y (PVY) is recognized as one of the most economically important virus of potato causing severe mosaic disease. PVY pure culture was maintained on its host potato (*Solanum tuberosum*) and virus purification was done from the leaves following standard procedure to obtain purified viral protein. Purified viral protein (antigen) was used for raising rabbit polyclonal antibodies through immunizations. First injection with antigen plus Freund's complete adjuvant and subsequent two injections with Freund's incomplete adjuvant at alternate weeks and this followed by three booster doses at 6 weeks intervals in rabbit were done. Four batches of high quality antisera (AS4b, AS5b, AS6b, AS7b) were collected one week post boosters and the IgG fractions were separated through ammonium sulphate precipitation method. DAS-ELISA assay of all the IgG fractions from the booster doses with universal anti-rabbit enzyme conjugate as secondary antibody showed high specificity with the known PVY infected and healthy potato samples which was compared with the commercial ELISA kit (Bio Reba, AG, Switzerland). For further confirmation of PVY infection in potato, total RNA was isolated from infected potato sample from field and standardization of reverse-transcriptase polymerase chain reaction (RT-PCR) conditions were done using PVY specific primers for coat protein gene which gave the desired 328 bp RT-PCR product. Partial sequencing of the RT-PCR amplicons revealed that the virus is closely related to *Potato virus Y* and sequence analysis showed 99 per cent sequence homology with PVY isolates from different countries worldwide.

MJN-04

Isolation and characterization of bacteriophages of the olive knot causing pathogen *Pseudomonas savastanoi* pv. *savastanoi*

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The olive knot disease, caused by *Pseudomonas savastanoi* pv. *savastanoi* is considered as one of the most important bacterial diseases in all the olive growing countries of the world. The present study was undertaken to isolate and characterize the bacteriophages infecting *P. savastanoi* pv. *savastanoi* in order to use them as a potential bio- control agent (BCA). Eleven lytic bacteriophages of *P. savastanoi* pv. *savastanoi* were isolated from an olive knot infected field of Agria, Volos, Greece. Three rounds of purification were carried out to obtain phages having one genetic clone. During *in-vitro* plaque assay, the phage titers of the sample phages were found ranging from 1.7 x 10^8 pfu /ml to 2.9 x 10^{18} pfu /ml. Plaque morphology of the samples revealed that, in 9 out of 11 phages the plaques were surrounded by a halo. Morphological characterization by Transmission Electron Microscopy (TEM) have shown that all the phage samples had an icosahedral head along with a tail and base plate suggesting that they belong to the Order *Caudovirales*. Out of which 9 of the samples had a long, flexible and non-contractile tail with its breadth ranging from 9.43±1.19 nm to 12.75±2.83 nm suggesting that the sample phages belonged to the phage family *Siphoviridae*. The findings of the present study indicated the presence of bacteriophages that has the potential to effectively kill the host bacterium and hence could be used towards phage therapy in the near future.

MJN-05

Eco-friendly management of fruit rot of brinjal with botanicals

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Fruit rot is one of the most destructive disease of brinjal causing considerable losses to the fruits in field, storage, transit and marketing. The commercial cultivation of the crop is under serious threat in Assam due to the disease. The incitant pathogen was identified and confirmed as *Phoma exigua* (Id No. - 8221.16 of the National Centre of Fungal Taxonomy, New Delhi), which constitute a new host record from Assam. Antifungal potential of aqueous extracts of fifteen botanicals at 25% concentration were evaluated *in vitro* for their efficacy against *Phoma exigua* by “poisoned food technique”. Highest inhibition on mycelial growth of the pathogen was recorded in *Allium sativum* (90.24%) followed by *Allamanda cathertica* (87.80%), *Lawsonia inermis* (79.67%), *Laurus nobilis* (73.28%) and *Lasia spinosa* (70.15%) which were further tested at 5, 10 and 15% concentration. *A. sativum* at 15% showed highest inhibitory effect (88.03%) on mycelial growth of the pathogen, followed by 10 and 5% of *A. sativum* (78.51% and 74.33%). Next was *A. cathertica* (73.51%) and *L. inermis* (73.28%) at 15%, the effect of which were statistically *at par* with *A. sativum* at 5%. Least inhibition was recorded in 5% concentration of *L. spinosa* (57.14%). Phytochemical profiles of these five botanicals were also estimated and results revealed significantly higher alkaloid (g/100g) and phenol content (mg/g) in case of *A. cathertica* (2.764 ± 0.100; 55.50 ± 0.800) followed by *L. inermis* (2.550 ± 0.262; 49.68 ± 0.386), *A. sativum* (2.192 ± 0.034; 30.6 ± 0.165), *L. nobilis* (1.450 ± 0.042; 26.95 ± 1.001) and *L. spinosa* (0.086 ± 0.006; 3.71 ± 0.051)

MJN-06

Effect of Sugarcane grassy shoot disease (SCGS) on yield parameters and juice quality of sugarcane

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Sugarcane is one of the important cash crops grown in India and it is world’s 2nd largest producer producing nearly 15 and 25 per cent of global sugar and sugarcane, respectively. It is also an important cash crop in Assam and cultivated in an area of 28404 hectares. Sugarcane grassy shoot disease (SCGSD) caused by sugarcane grassy shoot phytoplasma, is becoming a serious problem in many sugarcane growing states in India and has been spreading rapidly to newer locations. Effect of SCGS disease on growth parameters of both infected and healthy plants were recorded on 10 months old canes of three sugarcane varieties *viz*., Co-997, Dhansiri and Nambor. It was recorded that SCGS infection also reduced the juice quality of sugarcane. Among the three sugarcane varieties under study, the reduction in cane height, cane weight, number of internodes, length of internodes and cane diameter were varied from 48.72-56.56 per cent, 49.28-54.46 per cent, 25.00-38.88 per cent, 55.63- 69.76 per cent and 59.66- 63.46 per cent, respectively. SCGS infection resulted in the reduction of Brix (%), sucrose (%), purity of juice (%) and juice weight (kg/lit) which varied from, 25.15 - 41.04 per cent, 40.45 - 53.35 per cent, 20.45 - 24.58 per cent and 44.75-47.60per cent, respectively over juice of healthy canes of Co-997, Dhansiri and Nambor under study.

MJN-07

Biosynthesized chitosan nanoparticle has the ability to enhance the biocontrol potentiality of *Trichoderma asperellum*

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Chitosan, a cationic polysaccharide (partly de-acetylated form of chitin) present in microorganisms can be used for synthesis of nanoparticles. In the present study, chitosan nanoparticle was synthesized from fungus belonging to four different genera. Synthesized nanoparticles were characterized by using UV-VIS Spectroscopy, Zetasizer, Dynamic Light Scattering (DLS) and Transmission electron microscope (TEM). Average size of the chitosan nanoparticles synthesized from *Fusarium oxysporum, Metarhizium anisopliae, Beauveria bassiana* and *Trichoderma harzianum* were found as 273.20 nm, 172.50 nm, 78.36 nm and 89.03 nm respectively. Compatibility of the nano chitosan with fungal biocontrol agent (*T. asperallum*) at different concentration when tested by poison food technique showed chitosan nano particle was found to be compatible with *T. asperallum* at 0.01, 0.02, 0.03 per cent. Combined effect of *T. asperallum* and chitosan nanoparticle was tested against three soil borne plant pathogens viz., *Fusarium oxysporum*, *Sclerotium rolfsii* and *Rhizoctonia solani* and found that the combined effect of *T. asperallum* and chitosan nanoparticle was superior in inhibiting the mycelial growth of the tested pathogens as compared to the recommended chemical at 0.1 per cent. Nanochitosan based liquid formulation of *T. asperellum* prepared by adding SDS @ 0.01 M showed significantly effective results against all the three pathogens alone with

increasing result of plant growth parameters. This study showed encouraging result of combined use of nanoparticle and biocontrol agent for the management of soil borne plant pathogens and it paves the way of possible way of reduced use of synthetic pesticides.

MJN-08

Evaluation of safety of different insecticides against *Chrysoperla carnea*, a promising predator for soft bodied insects

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The green lace wing, *Chrysoperla carnea* (Stephens) (Neuroptera: Chrysopidae) also known as golden eyes and aphid lions, is a cosmopolitan polyphagous and efficient predator with enhanced searching capacity and voracious feeding habits. As insecticides continued to be the preferred component of IPM in many crops, they have shown adverse impact on natural enemies which could be mitigated through choice of insecticides, dosage, or timing of insecticide application. Integrating biological control with selective insecticides also can minimize the likelihood of pest resurgence and possibly reduce the number of insecticide application and it is essential to assess their safety to natural enemies before recommending them. Bioassay studies on safety of six insecticides *viz.,* Chlorantraniliprole, Spinosad, Emamectin benzoate, Imidacloprid, Thiamethoxam and Diafenthiuron at recommended dose tested against egg hatchability, larval mortality, pupation, adult emergence and mortality of *C. carnea* revealed that among the insecticides, Imidacloprid was found less toxic recording maximum egg hatching of 86.67 per cent and least egg hatchability of 51.67 per cent was observed in Thiamethoxam. After 12 hours, none of the treatments caused mortality to larvae of *C. carnea* when fed with both insecticide sprayed *Corcyra* eggs and larvae. After 24 and 48 hours of treatment Chlorantraniliprole has recorded highest mortality both on treated eggs (26.67 and 46.67 %) and larvae (26.67 and 63.33 %) showing its toxic effects whereas lowest mortality (3.33 and 6.67 %) was exhibited by Spinosad after 24 hours in both the conditions. But, after 48 hours, Imidacloprid registered least mortality of 13.33 and 26.67 per cent to *C. carnea* larvae when fed on treated eggs and larvae of *Corcyra cephalonica* respectively. In case of adult mortality, Thiamethoxam registered complete mortality and Diafenthiuron caused least mortality of 3.33 per cent after 48 hours of treatment. From the study it can be concluded that Diafenthiuron and Imidacloprid are said to be least toxic to *C. carnea* at all stages with maximum pupation and adult emergence.

MJN-09

Race profiling, diversity analysis and development of molecular markers for detection of *Ascochyta rabiei* causing blight in chickpea

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Ascochyta blight caused by *Ascochyta rabiei* (Pass.) Labr. is a serious disease of chickpea worldwide. The present study was conducted to identify the races of the pathogen, analyse the morphological and genetic variabilities and also develop diagnostic marker for pathogen detection. For this twenty five isolates of *A. rabiei* collected from northern India were used. The

populations of *A. rabiei* showed variations in morphological characters like conidia size and density, colony colour and growth rate. Screening of 91 chickpea cultivars showed 33 cultivars resistant, 14 cultivars moderately resistant, 9 susceptible and 35 cultivars showed highly susceptible reactions. Ten genotypes were selected as differentials representing resistant, moderately resistant and susceptible reactions. Based on the reactions of the genotypes, the *A. rabiei* isolates were classified into 7 races. The genetic variability of *A. rabiei* isolates were also analysed using URP and SSR markers. The isolates showed 98.5-100% similarity amongst themselves in respect of their ITS sequences. The universal rice primers (URPs) gave 61.1% mean polymorphism while the simple sequence repeats (SSR) markers produced 71.8% mean polymorphism and grouped them into two major clusters. In general, the groups generated by URP and SSR analysis did not correspond to the geographic origin of the isolates. The molecular markers showed high polymorphism and revealed high genetic similarity. A SCAR marker specific and sensitive to *A. rabiei* was developed with a product of 196 bp amplicon size from *A. rabiei* isolates. This is the first SCAR marker developed against *A. rabiei* having high specificity and sensitivity towards the pathogen.

MJN-10

Mechanism of blast [*Magnaporthe grisea* (Hebert) Barr.] resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

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The mechanism of blast resistance in pearl millet genotypes to different pathotypes of *M. grisea* was studied by investigating the inheritance of and allelic relationships among the resistance genes, biochemical characterization of blast resistance in pearl millet genotypes and transcriptomic analysis of compatible and incompatible interaction of pearl millet with *M. grisea.* A set of nine pearl millet genotypes; seven resistant and two susceptible were crossed in half diallele fashion to make crosses and develop F_1, F_2 and backcross populations. The parents and derived populations were screened against Pg 45 and Pg 53 isolates of *M. grisea.* The behavior of screened progenies *viz.,* F_1, F_2 and backcross populations confirmed allelic dominant monogenic control of blast resistance against the two isolates in these genotypes. Fifteen genotypes of pearl millet were selected for biochemical characterization of blast resistance in pearl millet genotypes by studying the total phenol content, phenylalanine ammonia lyase, peroxidase and polyphenol oxidase activity in the host genotypes at different stages after inoculation of pathogen *M. grisea*. A greater activity of these enzymes was found in resistant genotypes than susceptible genotypes at all-time points of study. The transcriptomes of the compatible and incompatible interaction was captured by RNA-seq analysis of a pearl millet genotype (ICMB 93333) inoculated with two isolates Pg 45 and Pg 174 of *M. grisea* giving avirulent and virulent reaction on the genotype, respectively. The transcriptional changes in the incompatible interaction were observed predominantly for PR protein families encoding defense response genes, genes functional in reactive oxygen species, signal transduction, primary and secondary metabolic processes and cell wall alterations. The transcriptomic profiling was focused on functional classification and identification of novel genes or gene family members involved in plant–pathogen interactions the expression pattern of which could be of potential to assist in the development of new disease control strategies.

MJN-11

Inheritance of avirulence in *Sclerospora graminicola* and resistance in pearl millet to the pathogen

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Studies on development of simple sequence repeat markers and its validation, inheritance and molecular mapping of avirulence and inheritance and allelic study of resistance genes in pearl millet to the isolates of *S. graminicola* were undertaken at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Telangana, India. A total of 14481 sequences spanning 215561828 bp were screened using a microsatellite search tool, MISA, that identified 7453 SSRs from 3912 SSR containing sequences, of which 235 (3.3%) SSRs were of compound type and remaining 7218 (96.7%) were of perfect type. The overall relative abundance and density of SSRs in whole genome were 34.57 /Mb and 459.67 bp/Mb, respectively. A total of 2702SSR primers were developed, 106 were custom synthesized and screened for diversity analysis on 60 isolates of *S. graminicola*. The gel electrophoresis result showed 22 scorable polymorphic markers. Allele frequencies i.e 57 alleles with an average of 2.59 alleles per locus were detected. Dendrogram developed through neighbour joining (NJ) method across 60 *S. graminicola* populations revealed five major clusters. Analysis of molecular variance (AMOVA) revealed 56.21% of the variance over 22 SSRs loci due to the differences among the isolates within states, 35.28 % due to within isolates and 8.51% was due to differences among the states. Besides, *S. graminicola* primer pairs also amplified the fragments from other oomycetes *P. sorghi* (67.9%) and *Phytophthora* species (52.7%). To conduct avirulence mapping, two distinct mating types Sg 019 (*Mat 2/*A_2) and Sg 445-1/Sg 018 (*Mat 1/*A_1) were selected and 120 F_1 progenieswere established separately from oospores on the susceptible line 7042S. Parents and 120 F_1 progenies were screened on five differential lines along with susceptible check 7042 S. Avirulence in Sg 019 was segregated in F_1 progenies on IP 18292 and 852 B in the ratio of 3:1 (avirulence: virulence) that implied the heterozygous nature of avirulence gene and involvement of two loci for avirulence in Sg 019. Segregation of F_1 progenies on ICMB 01333 and ICML 22appeared in the ratio of 1:1 indicated the monogenic control of avirulent gene in Sg 019. The complete loss of avirulence in F_1 progenies against 81B-P6 suggested complex inheritance. Tagging of avirulence gene was carried out by modified bulk segregants analysis (BSA). Out of 106, only three primers Sg_SSR 49, Sg_SSR 68 and Sg_SSR 99 revealed polymorphisms between two parents and four bulks. Genetic linkage among three markers revealed two markers Sg_SSR 49 and Sg_SSR 68 to be linked. The association of markers with avirulence trait showed tight linkage (0 cM) of Sg_SSR 49 to the avirulence trait on IP 18292 and ICMB 01333 with LOD value of 6.96 and 7.43 respectively. In order to determine the diagnostic value of avirulence linked microsatellite marker, a set of 60 isolates of *S. graminicola* were phenotyped on pearl millet lines IP 18292 and genotyped by linked SSR marker Sg_SSR 49. Isolates expected to carry avirulence gene showed high level of avirulence to the cultivar IP 18292. Genotyping also confirms the presence of avirulent gene in 44 isolates. Inheritance and allelism of resistant genes was deciphered through three resistant 834 B, IP18294 and IP18298 and one susceptible line 81 B. Crosses (Three S × R and three R × R) were generated, F_{1s} were selfed for F_2, back crosses $BC_1F_1P_1$ (S x F_{1s}) and $BC_1F_1P_2$ (R x F_{1s}) were generated and were screened with three selected diverse isolates of *S. graminicola* Sg 200, Sg 526 and Sg 542. The almost all resistant plants in F_1 generations to each isolate indicating that the resistance in these lines is governed by dominant gene(s). The R and S plants in F_2 generations of the cross 81B x 834B and 81B x IP 18294 showed 3R:1S to all three isolates, suggesting dominant monogenic control of DM resistance in 834B and IP 18294. The corresponding $BC_1P_{1s,}$81B x (81B x 834B) and 81B x (81B x IP 18294), had good fit to 1R:1S ratio. However, the F_2 populations from of the cross 81B x IP 18298 exhibited 15R:1S to all three isolates indicating the involvement of two dominant genes for resistance in IP 18298. The corresponding $BC_1P_{1,}$81B x (81B x IP 18298), showed 3R:1S. Allelism tests were conducted by crossing all three R parents with each other. Out of three crosses 834B xIP 18294 showed a good fit to the segregation ratio of 15R:1S to all the three isolates suggesting the involvement of two independent dominant resistance genes. This concluded that the resistance gene in 834B is different to the resistance gene present in IP18294. The lack of segregations in the F_2 populations of the cross 834B x IP18298 and IP18294 x IP18298 to all three isolates indicated allelic relationship between resistance gene of IP 18298 with both 834 B and IP 18294. Therefore, allelic relationship between resistance genes to three isolates of *S. graminicola* in this study suggested that 834 B and IP 18294 contain one non-allelic dominant gene designated as *RSg2* and *RSg3*, respectively. Two dominant resistance genes in IP 18298 to all three isolates in this study were symbolized as *RSg2* and *RSg3*.

APS-01

Purification, electron microscopy, antisera production, serodiagnostics and molecular characterization of *Potato virus Y* (PVY) causing severe mosaic of potato

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Purification was done from *Potato virus Y* (PVY) pure culture maintained on potato plants (*Solanum tuberosum*) following standard procedure to obtain purified viral protein from extracted leaves. Presence of viral protein was confirmed by transmission electron microscopy (TEM) of the purified material which showed flexuous filamentous particles. Rabbit immunization with purified viral antigen plus Freund’s complete adjuvant and subsequent injections with Freund’s incomplete adjuvant at alternate weeks followed by three booster doses after a rest period of 6 weeks was done to raise polyclonal antibodies. High quality antisera were collected one week post boosters (AS5b, AS6b and AS7b) and the IgG fractions were separated through ammonium sulphate precipitation method. The IgG fractions AS5b, AS6b and AS7b were tested for the detection of PVY by DAS-ELISA with universal anti- rabbit enzyme conjugate as secondary antibody which showed high specificity with the known PVY infected samples compared with the commercial DAS-ELISA kit (Bio Reba, AG, Switzerland). ELISA positive PVY samples were further confirmed by reverse-transcriptase polymerase chain reaction (RT-PCR) assay resulting a 328bp amplicon. Partial sequencing of RT-PCR product was done. Phylogenetic analysis revealed that the virus is closely related to *Potato virus Y* worldwide isolates.

APS-02

Study on Populations of *Candidatus* Liberibacter asiaticus from North East India based on genomic locus of short tandem repeat variability

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Citrus Huanglongbing (HLB) is the most devastating, destructive, threatening and dreadful disease of citrus worldwide as well in India. It is also known as yellow shoot disease due to the appearance of patchy yellow in the new flushes. HLB infection causes severe economic losses more than 100 million citrus trees were estimated to have wiped out due to its infection. Average annual yield losses due to HLB infection in Asia were to the tune of 40-60%. It is the most emerging citrus disease in different citrus growing pockets of India in general, North East India in particular. The disease is caused by a phloem-limited, non-cultured, gram-negative bacteria *Candidatus* Liberibacter asiaticus (CLas). Although, the disease has been reported from some parts of North East India except Manipur, there is no systematic study and knowledge on the molecular variability of the pathogen. Present study focus on identification of short tandem repeat numbers (TRNs) at the genomic locus CLIBASIA_01645 in order to elucidate the check variability of CLas isolates from North East India. The genomic locus was characterized and categorized into five classes based on the tandem repeat number (TRN) viz. Class I (TRN ≤ 4), Class II (TRN > 5 ≤10), Class III (TRN > 10 ≤15), Class IV (TRN > 15 ≤ 20) and Class V (TRN ≥ 20). The present study conclusively revealed that TRN CLas isolates from North East Region ranged from 4-21. The CLas population consisted predominately of strains with a TRN 9 at a frequency of 36.40 % followed by TRN 5 with 23.00 %. A few sample from Nagpur region were also characterised which showed TRN 9 with the samples from Arunachal Pradesh which had TRN ranging from 9-12. On the basis of cultivar analysis, it can be interpreted that CLas isolates infecting Khasi mandarin cultivar had TRN 9-12 with the highest frequency in TRN 12 and acid lime cultivar had TRN 4-6 dominated by TRN 4 and 5. Most interestingly a Citrus spp. from Manipur got highest TRN 21 which is the highest TRN reported till date. The present study conclusively revealed that Clas bacterium present in North East region is highly diverse at the genetic level compared to other parts of India.

TS1-O1

Preliminary investigations of *Parkia roxburghii* decline in North East India

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Parkia roxburghii commonly known as Zawngtah in Mizoram is a tree bean belongs to family Leguminosae. It is mostly grown in the homestead gardens, slash and burn or jhum lands and also found in the forests throughout the North Eastern states of India. The immature tender pods are consumed during its developmental stages and are one of the favourite foods among the people of North Eastern states for its unique taste and flavour. The mature seeds of the tree bean are also consumed as a vegetable. Unfortunately, the tree bean plants are under threat and there is a vast decline in its population in entire North Eastern states. The present investigation was carried out by ARCBR and RFRI and it is evident from the field studies carried out in Mizoram and Manipur, that the decline is due to a complex caused by the stem borer i.e. *Coptops aedificator Fabricius* and *Fusarium* species causing root infection; and when the trees become weak they are also infected by the shot hole borer in the later stages. *Fusarium, Colletotrichum* and *Botryodiplodia* species has also been isolated from the freshly infected galleries made by the stem borer and shot hole borer. Initially, the first instar of *Coptops aedificator* Fabricius feeds on the bark of the tree branch/trunk and symptoms appear as a scrapping of the bark. As the larvae shifts into the next metamorphic stages, it initially feeds on the pith of the branches and when there is no pith left it makes galleries in the main branch or trunk of the trees leaving an exit hole. An infected tree can be easily be identified by frass of the borer on the trunk at the point of infestation and in the basins of the tree if the infestation is very high. In marshy/waterlogged areas *Fusarium* species has been reported to cause the root decay and thus causing wilting of the tree. The infected/infested trees lose their vigour and leaves of the infected branches become yellow and later dry, gummosis has also been noticed in the infected/infested trees. Heavy infestation leads to the death of the tree, if not managed timely. There is an urgent need for confirmation of host-pathogen-insect interaction to develop an effective management strategy against this disease complex.

TS1-O2

Defective molecules associated with cotton leaf curl virus in North West Indian cotton growing areas

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Cotton leaf curl disease (CLCuD), caused by monopartite begomoviruses and its satellite molecules, is one of the serious constrains in cultivation of cotton in North West (NW) India. Surveys were made to study CLCuD incidence in the cotton growing areas of Haryana, Punjab and Rajasthan states of for three successive years from 2013 to 2015. The complete genome of 18 NW Indian CLCuD begomovirus isolates collected from different areas of NW India were cloned, sequenced and analyzed. They shared 80-100% nt identity among them. Along with betasatellites and alphasatellites, some defective interfering particles have also isolated and sequenced. Defective interfering particles (DI particles) are virus particles which contain genomes that are grossly altered genetically, generally by significant deletion of essential functions, but nevertheless retain critical replication origins and packaging signals, allowing for amplification and packaging in co-infections with complementing wild-type helper virus. DI molecules are also known as subgenomic DNA. Defective DNAs are associated with all families of DNA containing plant viruses. They are not restricted to a particular family and thus appear to be a natural by-product of virus infection. Defective forms of cotton leaf curl n virus DNA-A first reported by Liu *et al.* in 1998 from whiteflies transmitted tobacco plants. They reported that defective forms of cotton leaf curl virus DNA-A have different combinations of sequence deletion, duplication, inversion and rearrangement. Two defective DNA A molecules of S-9DI (KT228334) (1360nt) and Si-17DI (KT228335) (1372nt) were identified from the isolates S-9 and Si-17 respectively. They have characteristically deletion of some parts of nucleotides. In S-9DI (1-281nt and 1672-2753nt are intact), whereas in case of Si-17DI (1-276nt and 1672-2752nt are intact). Similarly one defective betasatellite molecule Ma-14-3BDI (KT228329) (672nt) (1-43,787-1433) was identified from the isolate Ma-14-3. Analysis of 1360 bp (isolate S-9) and 1372 (isolate Si-17) CLCuRV defective interfering DNA indicates the presence of small repeat sequences (iterons) (TTG) for (S-9) and (TTT and TTG) for Si-17 adjacent or close to the deletion points in the genomic DNA. They started and ended in intergenic region (IR), which contained nonanucleotide TAATATTAC sequence conserved in all begomoviruses.

TS1-O3

Occurrence, molecular characterization, physiological study and yield loss assessment of broad-leaved mustard (*Brassica juncea* var. *rugosa*) infected with *Turnip mosaic virus* in Arunachal Pradesh, India

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Turnip mosaic virus (TuMV), member of the genus *Potyvirus*, is the most important virus of commercially grown cole crops in many Asian countries. Cole crops are an important part of daily diet in India. The study revealed that the maximum mean disease incidence was in serrated leaf type (63.67%) of broad-leaved mustard. The maximum yield loss was recorded in green leaf type (19.46%). The occurrence of TuMV in broad-leaved mustard was confirmed by symptomatology, transmission electron microscopy (flexuous filamentous particles of 800 x 12 nm), DAS-ELISA, reverse transcription (RT)-PCR and partial characterization of cytoplasmic inclusion (CI) protein and coat protein (CP) domains. Phylogenetic analysis of the partial CP sequences of the new TuMV isolate (AR-BrLM; KP876503) revealed their closest relationship with the members of the World-B geno group of TuMV. The minimum amount of chlorophyll-a (1.06mg/g fresh tissue) was observed in mild to severe mottling type of symptom and the maximum (1.96mg/g fresh tissue) was recorded in healthy leaves. There was a significant increase in the total sugar and reducing sugar contents in light to mild mottling symptom (33.33% and 22.22% respectively) followed by significant decrease in severe puckering (33.33% and 66.67% respectively) type of symptoms. Similarly, total phenol content was found significantly increased in light to mild mottling symptom (42.86%) whereas significantly decreased in mild to severe mottling (14.29%) and severe puckering (42.86%) type of symptoms. Significant increase of 37.81% was also observed in total protein content of severe puckering followed by mild to severe mottling (5.04%) type of symptoms.

TS1-O4

Chilli veinal mottle virus in North East India: an insight to its biological and genetic diversity

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Unique ecological niche of the North East (NE) India is endowed with rich genetic resource of *Capsicum* species. The existing chilli diversity has led to the evolution of one of the hottest chilli '*Capsicum chinense* var. Oumorok' in the region. Popular for its high capsaicin content, this particular chilli resource has strong potential to uplift the economy of NE India. However, high incidence of virus-like diseases in chilli plantation has been a major bottleneck in the farmer's venture of large scale plantation. Prevalence of diverse vectors, wide host range and absence of resistant/tolerant varieties, makes *Chilli veinal mottle virus* (ChiVMV) to contribute significantly in decadence of the region's chilli plantations. With this view, the incidence of ChiVMV and its genetic insights has been studied incorporating symptomatic chilli plants from 40 sites covering nine districts of Manipur. Reverse transcription (RT)-PCR based indexing of ChiVMV using coat protein region revealed the viral presence in 31 sites (77.5%) of the total groves studied with 22.5% observed free from this virus. In the viral indexing of 127 samples, eighty one (81) samples tested positive for ChiVMV (63.78%). From the study, it has also confirmed that typical symptoms of mottling, curling, puckering, thinning of lamina, deformed leaves and shoestring were associated with ChiVMV infection in *Capsicum* sps., while rugosity along with rigidity in a few samples and white mottling on chilli leaf was not associated with this virus infection. Natural infection was recorded in four different *Capsicum* sps. viz; King chilli (*Capsicum chinense*), Chingpi morok (*Capsicum* sp.), Uchi morok (Bird eye chilli) and Morok atekpa (*Capsicum* sp.). Variation in degree of symptom expressed upon mechanical transmission to chilli host further reflected wide pathogenic diversity among the ChiVMV isolates collected in the present study. Phylogenetic analysis based on coat protein region of ChiVMV isolates from Manipur along with others revealed the distinctiveness of the isolates from Manipur. The present analyses concluded that ChiVMV has dominant presence in chilli plantations of NE India and require urgent intervention for its proper characterization so as to develop robust detection tools.

TS1-O5

Emergence of false smut (*Ustilaginoidea virens)* disease of rice in Manipur and development of a management module

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False smut caused by *Ustilaginoidea virens* is an emerging economically important grain disease of rice worldwide. Valley and hills of Manipur constitute major rice growing belt of North East Hill (NEH) region of India. However, systematic studies on prevalence, incidence and development of management modules for Manipur have not been undertaken, till the commencement of this study. The intensity of false smut disease on nine different varieties including two hybrids was studied under Manipur conditions during three consecutive seasons (*Kharif* 2014, 2015 and 2016). Percentage of false smut infected plants varied from 5-74% in different varieties surveyed. Maximum incidence of false smut disease was observed on hybrid cultivars (PRH series) and minimum in a local cultivar of rice (Phouoibi Phou). Among all the varieties surveyed and screened for false smut disease, RC Maniphou-10 had lowest percent infected tillers (9.50%) in infected hills. Among other cultivars grown in Manipur, Ginphou had the highest number of infected tillers (24%) among other varieties. Keeping the importance in view, a management module was developed for false smut disease. Efficacy of different fungicide molecules was tested at different crop stages (booting, 50% panicle emergence and 100% PE) for three consecutive seasons (2014-16). 11 chemicals: trifloxystrobin 25 % WP + tebuconazole 50% WP (Nativo), kresoxim-methyl (Ergon 44.3 SC), thifluzamide 24 SC (Spencer), tebuconazole, azoxystrobin 25 SC (Amister), hexaconazole + captan (taquat), carbendazim 50 WP (Bavistin), propiconazole 25 EC (Tilt), hexaconazole, carbendazim + mancozeb (SAAF 75 WP) and isoprothiolane (Fuzione) were tested for management of false smut disease using Ginphou as test variety. The natural disease pressure was augmented during flowering stage with spore suspension prepared from false smut balls. Based on the pooled results of three seasons, out of 11 chemicals tested, three sprays (at booting, 50% PE and 100% PE) of chemicals azoxystrobin 25 SC (Amister), hexaconazole + captan (Taquat), trifloxystrobin 25 % WP + tebuconazole 50% WP (Nativo), propiconazole 25 EC (Tilt), tebuconazole, hexaconazole and carbendazim + mancozeb (SAAF 75 WP) were effective in management of false smut (per cent infected panicles/m2 were 7.4 to 12.3% in treated plots). Spraying of all these chemicals significantly increased the yield (14.3 to 36.5%) over the untreated control. This management module was also validated in farmer's field during *Kharif* 2016. The present study, therefore, proved the high incidence of false smut disease on commonly grown varieties of rice under Manipur conditions and reports the development of an effective management module.

TS1-O6

Detection of endogenous banana streak viruses prevalent in banana genotypes of Manipur

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Banana streak viruses (BSV), a cryptic *Badnavirus* species complex are important pathogens of bananas and plantains (*Musa* spp.) worldwide. Due to the vegetative propagation of *Musa* crop, BSV has quarantine significance. BSV like sequences integrated to the banana genome which are known as banana endogenous viruses (BEVs) predicts the prehistoric distributions of badnaviruses. Diagnosis by symptomatology is unreliable because the symptoms are variable or absent. The genomic landscape of integrated BEVs and their allelic distribution is largely affected by host genotypes and prevailing environmental conditions. Hence, an attempt was made for diagnosis of endogenous BSV and to study their relationship with other episomal badnaviruses infecting banana. PCR using degenerate primer pairs (Badna FP and Badna RP) targeting RT/RNase H region of genome gave an amplicon of 580 bp indicating the presence of host integrated endogenous BSV sequences of variety Champa Kola (ABB), Meitei Hei (ABB) and Grandnaine (AAA) collected from Mana Ingkhol, Luwangsangbam, Leimatak, Noney (Manipur) and Leimaram. The PCR product was cloned and sequenced and found to have similarity to open reading frame III in the badnavirus genome, although exhibiting remarkable variation. The Cladogram depicted the relationships of the banana endogenous viruses (BEVs) to a range of badnaviruses and related pararetroviruses within the reverse transcriptase/RNase H gene.

TS1-O7

Characterization and management of gummosis disease of citrus in Manipur

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Citrus gummosis represents one of the most serious threats to citrus production leading to tree decline and yield losses. The present investigation on Citrus Gummosis was undertaken with regard to characterization and management of the pathogen causing gummosis disease. Surveys for the incidence of citrus gummosis were conducted in various locations in four districts *i.e.,* Imphal West, Imphal East, Tamenglong and Chandel district during the month of August to July 2016. The disease severity of different locations ranged between 2 per cent at Iroisemba in district Imphal West to 16 per cent at Lukhambi in Tamenglong district while disease incidence ranged between 10 per cent in a district Imphal West to 40 per cent at Lukhambi in Tamenglong district. The morphological characters revealed that the mycelium of

all isolates was sparse to densely aerial or partial to totally submerged in media with white or creamish white in colour. The ITS genome region of the four isolates were about 900 bp, and its identity was confirmed by sequencing. Efficacy of leaf extracts of Eucalyptus, Marigold, Lantana, Pogostemon and cow urine against *Phytophthora* spp. under in vitro conditions at 2, 10 and 20 per cent concentrations by poison food technique. It is evident from the data that all the extracts inhibited the mycelial growth of the pathogen in comparison to control. Cow urine was found most effective and significantly superior amongst all the treatments with 100 per cent inhibition in mycelial growth of the pathogen. They were followed by Lantana leaves and Pogostemon leaves extract with 85.42 and 84.58 per cent mycelial growth inhibition, respectively. Keeping in view the undesirable effect caused by the non-discriminate use of chemicals, developing environmentally safe, economic and effective alternatives is the only option for plant disease management in organic agriculture.

TS1-O8

Incidence and detection of episomal banana streak viruses in Manipur

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Banana streak viruses (BSV) infect banana and plantains worldwide. Integrated BSV-like sequences known as endogenous BSV (eBSV) are known to present in the genome of Musa, which interferes with the PCR based detection of cognate episomal BSV. The present study, therefore employed random-primed rolling circle amplification (RCA) for the detection of episomal BSV infection in banana samples collected from Manipur. Rouging surveys were conducted to cover major banana growing pockets of Manipur. During the surveys, symptomatic and asymptomatic leaf samples of different banana genotypes were collected. Surveys were conducted at Mana Ingkhol, Luwangsangbam, Mayang Imphal, Canchipur, Langthabal (Imphal West), Leimatak, Leimaram (Bishnupur District), Longmai, Noney (Tamenglong District), Machi Khun (Tengnoupal District) of Manipur. Under field conditions, typical streak symptoms were observed on different banana samples collected from Mana Ingkhol, Leimatak, Leimaram, and Noney. Champa Kola (AAB), Meitei Hei (ABB) and Grande Naine (AAA) cultivars of banana are most widely cultivated in different parts of Manipur. Banana streak viruses (BSV) infected symptoms were observed different places surveyed in the present study. The disease leaf samples were collected and the diseases corms were maintained at ICAR Langol Farm, Manipur. For testing the infection of episomal badnaviruses in collected leaf samples of banana, duplex-immunocapture-PCR (D-IC-PCR) and RCA were employed. D-IC-PCR was performed using specific antibodies against BSMYV. Hence results based on RCA were considered confirmatory. The RCA amplified products were digested by restriction enzymes (viz., *BamHI, KpnI, HindIII, XhoI, PstI, XbaI, SacI, SphI* and *EcoRI*). The infected leaf samples collected from Leimatak, (Bishnupur District) and Longmai, Noney

(Tamenglong District) of Manipur were detected positive for episomal BSVs. Some of the banana leaf samples which were found negative for episomal BSV infection were tested for the presence of integrated sequences using total DNA preparations as a template. The present study confirmed the association of episomal BSV with streak disease of banana in Manipur.

TS1-O9

Molecular evidence for association of *Cymbidium mosaic virus* with orchids from Manipur

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Cymbidium mosaic virus (CymMV) is one of the most prevalent and economically important viruses of orchids. CymMV displays severe disease symptoms that affect the quality of the flowers, significant ones being chlorotic mosaic, floral and foliar necrosis, colour-breaking of flowers causing variation in petal colour, size reduction, unpleasant leaf appearances, reduced vigour and stunted growth. This disease significantly reduces the economic value of orchids. Surveys were conducted in several regions for CymMV in Imphal West, Imphal East and Ukhrul districts of Manipur. Total RNA was extracted from symptomatic plants and RT-PCR was carried out by using a pair of coat protein (CP) gene primer of CymMV. The amplicon of expected size (348 bp) was obtained from symptomatic orchid plants. Sequence analysis of specific fragments revealed its identity as CymMV. To the best of our knowledge, this is the first molecular evidence for the association of CymMV with orchids from Manipur.

TS1-O10

Deciphering the prevalence and genetic diversity of virus and virus-like pathogens infecting different crops in North East India: a transboundary concern

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North East (NE) region of India is a unique agro-ecological niche for the evolution of genetically divergent plant species as well as their pathogens. The region shares its geographical boundary with other countries thus making it porous to the entry of new pathogens and their variants. Diseases caused by virus and virus-like pathogens have always been the most challenging threats to the cultivation of agri-horticultural crops. In order to decipher the prevalence of virus and virus-like pathogens in the region, systematic planned surveys were carried out. A biologically, serologically and genetically distinct potyvirus causing fruit deformation and yellow mottle disease of passion fruit in Manipur, Nagaland and Meghalaya was identified (37.4% samples tested positive). The virus had recombinant origin with passion fruit woodiness virus as minor parent. Phytologenetically passion fruit infecting potyvirus belonged to bean common mosaic virus cluster but did not share any serological reactivity. Occurrence of *Candidatus* liberibacter asiaticus (Clas) and citrus tristeza virus (CTV) was detected to be associated with citrus decline at different locations of the region. 38% of the citrus samples tested in present study were positive for both CLas and CTV. CLas isolates prevalent in Manipur and Arunachal Pradesh were genetically distinct and had tandem repeat numbers (TRN) up to 21. PCR and rolling circle amplification detected the infection of banana streak viruses (BSV) and banana bunchy top virus (BBTV) in the banana plants sampled from Manipur, Nagaland and Mizoram. In addition to the episomal BSVs, diverse endogenous BSV sequences were present in the banana genotypes. Recombinant origin of the BBTV isolates based on DNA-U3 and DNA-R genomic components was identified. We also detected a novel genogroup of papaya ringspot virus (PRSV) infecting papaya in Manipur. A genetic variability up to 14.7% for coat protein (CP) nucleotide sequences of PRSV isolates was identified. Cucumber mosaic virus (CMV) and *Chilli veinal mottle virus* (ChiVMV) were two widely prevalent viruses detected to infect chilli plantations in NE. 56.8% of the tested chilli samples were positive for either of the virus. CMV and ChiVMV isolates segregated to distinct phylogenetic cluster compared to the respective isolates reported from other parts of India. Genetically divergent zucchini yellow mosaic virus infecting cucurbits and turnip mosaic virus infecting broad leaved mustard were identified based on the sequences of CP coding region. The virus and virus-like isolates detected in the present study were very diverse at genetic level and showed more affinity to the genotypes reported form neighbouring countries indicating their distinct evolution and possible transboundary origin.

TS2-O1

Morphology and molecular variability study of *Pestalotiopsis mangiferae* in valley districts of Manipur

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A study was conducted to analyse the morphology and genetic variability of fifteen isolates of *P. mangiferae* collected from different districts of Manipur. The morphological characters under study consist of the colony and conidial characteristics such as colour, shape, size and appendages. The cultural growth colour of *P. mangiferae* on PDA varied from concolour to versicolour fuliginous. The conidial shape varied from oval and spherical to elliptical with prominent appendages. While the conidial length and width ranged from 22.4 to 24.9 µm and 5.7 to 6.6 µm respectively. All the conidia collected from different places consists of three septations. While the number of conidial appendages was found to be 2-3 numbers. The 15 isolates of *P. mangiferae* were also subjected to RAPD analysis using Jaccard's similarity matrix using UPGMA and resolved into three clusters. Cluster I consists 9 isolates, Cluster II comprised of 4 isolates and cluster III consists of 2 isolates respectively. The isolates collected from Andro KVK, Andro, Maringthel and Potsangbam were found to be most similar. While the isolates from Sekmaijing and Iroisemba were found to be diverse genetically from the rest of the isolates. The morphological and molecular diversity observed under the present investigation will be of immense help for further study on various management practices of *P. mangiferae* in valley districts of Manipur.

TS2-O2

Disease reaction of *Linum usitatissimum* L. germplasm towards *Melamspora lini*

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Linseed is an important oilseed crop of Himachal Pradesh. However, its cultivation is concentrated in the Palam area of Kangra and Mandi districts, accounting for almost the whole area and production in the state. Linseed rust is caused by a fungus, *Melamspora lini.* Rust is the main problem of linseed growers as it causes a reduction in seed yield and weakening/disfiguring of fibre in flax. Diseased plants become very conspicuous in the field because of the bright orange colour of the affected part. The leaves die prematurely; the brown-black telia appear as crust covered by the epidermis. With this view, disease reaction was studied under 4 locations including the disease hotspots in Himachal Pradesh *i.e.* Palampur, Malan, Kangra and Dhaulakuan. Thirty genotypes were scored for linseed rust at four locations *viz.*, Experimental farm of CRSKHPKV, Palampur, Rice and Wheat Research Centre (RWRC) Malan, Shivalik Agricultural Research and Extension Centre, (SAREC) Kangra and Hill Agricultural

Research and Extension Centre Dhaulakuan (HAREC) during 2013-14. Each experimental plot had a plot size of 1 X 1 m^2. The screening was done only under natural epiphytotic conditions in the field according to the scale devised by AICRP on linseed for linseed rust. Nineteen genotypes *viz.,*Himalini, Janaki, Jeewan, KL-241, KL-257, Nagarkot, Him Alsi-1, Him Alsi-2, Binwa, Surbhi, Baner, Bhagsu, Hearmies, Rajeena, Mariena, Giza-5, Giza-7, Giza-8 and Ariane were highly resistant (disease score 0 at all the locations); seven genotypes *viz.,*Nataja, Viking, Giza-6, Faking, Ayoyagi, Flak-1 and Canada were resistant (disease score 1 or < 1), while two genotypes i.e. KL-263 and B-509 were moderately resistant (disease score 2 or < 2), Belinka-60 was moderately susceptible (disease score 3 or < 3) and Himani was susceptible (disease score 4 or < 4). The genotypes categorized as highly resistance/resistant to rust need further evaluation under artificial conditions for their use as a source of resistance in the future breeding programmes.

TS2-O3

Molecular detection of *Chilli veinal mottle virus* (ChiVMV) & *Cucumber mosaic virus* (CMV) infecting chilli in Manipur and development of robust diagnostics

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Multiplex-RT-PCR developed for simultaneous detection of potyvirus *viz.,* ChiVMV and *Cucumo virus viz.,* CMV will be very helpful in finding the cause for the frequent decadence of chilli groves in the region and if there is an association between these two viruses. Impact of $MgCl_2$ concentration in routine molecular work using Taq Polymerase has been studied experimentally proven using $MgCl_2$ concentration gradient-PCR optimization. A simple semi-q-RT-PCR protocol developed in the present work can give impetus in performing large-scale analysis for their susceptibility or tolerance specific to ChiVMV. The present detection diagnostic techniques developed and semi-q-RT-PCR can give a huge impetus in further controlling through easy detection and identification and identification of tolerant varieties.

TS2-O4

Variability in blackgram genotypes with varying reaction to *Mungbean yellow mosaic virus* (*MYMV*) infection

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Reaction of sixteen genotypes of blackgram [*Vigna mungo* (L.) Hepper] *MYMV* infection were found highly variable ranged from 3.73 (DKU-87) to 96.15% (LBG-623). Of the 16 genotypes, nine genotypes were categorised as resistant, one as moderately resistant, four genotypes as susceptible and two as highly susceptible genotypes based on modified MULLaRP scale (0-9).

Significant variation was observed among the genotypes tested with respect to the morphological and biochemical characters. Leaves of *MYMV* resistant genotypes were thicker (126.31 to 160.41 µm) compared to highly susceptible genotypes (97.09 µm -101.51 µm). Amount of epicuticular wax was found high in resistant genotypes (0.45 to 0.58 mg dm^{-2}) than highly susceptible genotypes (0.20 to 0.24 mg dm^{-2}). Trichome density ranged between 12.25 (KPU-6) and 16.88 (DKU-87) in resistant genotypes and 6.13 (LBG-623) to 6.75 (Co5) in highly susceptible genotypes. However, the stomatal frequency was high in highly susceptible genotypes [150.15 (Co5) to 155.64 (LBG-623) per mm^2] compared to resistant genotypes [71.71 (DKU-87) to 102.10 per mm^2 (PU 12-11)]. The genotypes with purple petiole colouration or purple splash were with low disease severity, whitefly population and were resistant or moderately resistant in their reaction to *MYMV* infection while genotypes with green colour petiole were found to be either susceptible or highly susceptible. Total phenols were high in *MYMV* resistant genotypes (0.79 to 0.90 mg/100 mg) than highly susceptible genotypes (0.36 to 0.40 mg/100 mg). Total proteins content in resistant genotypes varied from 1.83 (PU 12-11) to 1.99 mg/100 mg (DKU-87) while in highly susceptible genotypes from 1.40 (LBG-623) to 1.48 mg/100 mg (Co5). Total chlorophyll was high in resistant genotypes and ranged from 0.113 (KPU-6) to 0.134 mg/100 mg (DKU-87) compared to highly susceptible genotypes, 0.036 mg/100 mg (LBG-623) to 0.043 mg/100 mg (Co5). High peroxidases activity was recorded in *MYMV* resistant genotypes (0.31-0.36 Δ Abs/min/g) compared to highly susceptible genotypes only 0.14 Δ Abs/min/g. Similarly, phenylalanine ammonia lyase activity was found to be high in *MYMV* resistant genotypes (124.61 and 147.98 η moles of transcinnamic acid/min/g) than highly susceptible genotypes (83.07 to 85.67 η moles of transcinnamic acid/min/g).

TS2-O5

Biochemical changes under induced resistance associated with the leaf blight diseases of wheat

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Leaf blight of wheat caused by *Bipolaris sorokiniana,* appears in all growth stages but susceptibility increase as plant mature. In order to study the biochemical changes by the chemical inducers a seed treatment with 11 non-conventional chemicals showed that all the chemicals reduced the disease severity significantly in comparison to untreated control and maximum reduction in disease (12.76%) and increased in yield (39.17 q/ha) was noticed on salicylic acid (10^{-4}M) for the management of leaf blight of wheat. It was also observed that with the increase in the age of the plant there was significant increase in total phenol content. Maximum phenol content was obtained on salicylic acid 10^{-4}M (4.59 mg/g) statistically at par with CuSO4 10^{-4}M (4.54 mg/g) followed by CuSO4 10^{-5}M (3.99 mg/g) irrespective of the age of the plant. Whereas in case of peroxidase activity was different, with increase in age of the plant there was decrease in peroxidase activity. The peroxidase activity was maximum on $ZnSO_4 10^{-5}$M

(10.54 µmol/g/min) statistically at par with isonicotinic acid 10^{-4}M (10.13 µmol/g/min), 2, 4 D 10^{-6}M (10.08 µmol/g/min) and untreated control (10.19 µmol/g/min) irrespective of different age of the plant. Minimum peroxidase activity was noticed on salicylic acid 10^{-4}M (8.19 µmol/g/min) treated plant followed by CuSO4 10^{-4}M (8.88 µmol/g/min). Therefore, the bio chemical studies indicated that the treated infected plants had higher post inflectional total phenol content as compared with untreated one. It seems that in treated plant there was rapid accumulation of more phenolic substances at the site of infection within a short period which cause reduction in peroxidase and polyphenol enzyme activity.

TS2-O6

Prevalence, detection, characterization and development of immuno captured based PCR for diagnostics of *Papaya ring spot virus* at different locations in Manipur

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Papaya (*Carica papaya* L.) also known as papaw or pawpaw is one of the most economically important fruit crops cultivated in the North East India since immemorable time. Papaya ringspot virus (PRSV) consists of a positive-sense, single-stranded, monopartite, RNA genome of around 10 kb. It is transmitted by aphid in a non-persistent manner. The survey was conducted at different papaya growing pockets of Manipur during 2016-17. During the survey, varies of symptoms like mottling, vein clearing, intense yellow mosaic, leaf distortion and shoe string leave were mostly observed. Different samples of both healthy and diseased of papaya from different areas of Manipur were collected. It was found that incidence of 80.13% was observed through double antibody-sandwich-ELISA (DAS-ELISA) and reverse-transcription-PCR (RT-PCR) detection. Four genomic regions (CP, NIb, NIa and Hc-Pro) were amplified from the symptomatic papaya plants and were cloned and sequenced. PRSV isolates for nucleotide sequences (PRSV-Mnp) had heterogeneity up to 14.7%. For amino acid sequences of CP had an identity of 88.8 to 99.6%. When compared to other PRSV isolates from India, Manipur isolates had an identity of 84 % (Uttar Pradesh PRSV isolate) to 93.2 (Assam PRSV isolate) for nucleotide sequences of CP. Phylogenetic analysis with 23 PRSV isolates reported earlier from India, Asia, America and Australia revealed high genotypic diversity among PRSV populations. The phylogenetic grouping thus obtained did not correlate with geographical origin. PRSV isolates from Manipur characterized in the present study segregated into two distinct groups (A and B). The Phylogenetic group A comprised of PRSV-Mnp-M3 etc. and group B consist of PRSV-Mnp-M4, PRSV-MnP-M1, PRSV-MnP-M2 etc. which was a new phylogroup to the world. The present study conclusively reported high pathogenic and genetic diversity of PRSV in North East region in general and Manipur in particular. A new simplified immunocapture-reverse transcription-PCR (IC-RT-PCR) assay was developed and standardized for detection of PRSV from crude plant sap. The IC-RT-PCR assay could have applications in routine indexing of PRSV and production of virus-free planting materials.

TS2-O7

Prevalence, detection and characterisation of viral disease complex in king Chilli (*Capsicum chinense* J.) from North East India

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King chilli (*Capsicum chinense* J.) known as "Umorok" or "Naga chilli" is the most important spice crop in North East India. The King chilli plant is a wonderful gift of nature as its fruit is one of the hottest chilli in the World and at the same time, it possesses a pleasant and palatable aroma. Although it is the main spice crop, its cultivation is limited by numbers of biotic and abiotic factors. Among the biotic factor, the viral complex has been considered to be the most significant, destructive and devastating factors. In this connection, surveys were conducted at different king chilli growing areas of Manipur and its neighbouring states (Nagaland, Mizoram, Meghalaya etc.) to record the incidence of the viral complex and characterise the associated viruses. Varying kind of symptoms ranging from leaf mottling, puckering, shoestring, vein banding, severe curling, mosaic and smaller leaf lamina were observed. Out of 170 samples tested for four viruses in RT-PCR using specific primers targeting CP regions of each viral genome, it was found that 56 samples were found positive for CMV (32.94 %) and 30 samples for ChiVMV (17.64 %) has shown positive. None of the above samples were found positive for begomoviruses and *Capsicum chlorosis virus* (CaCV). It was observed that four samples were found positive for mixed infection of CMV and ChiVMV. Further, four CMV isolates were analysed to infer genetic relationship by the Neighbour-joining phylogenetic analysis incorporating 19 CMV isolates from other parts of the globe using peanut stunt virus as outgroup. Based on nucleotide sequences of CP, all 23 CMV isolates segregated into 3 clusters (Group A, B, C and D). Manipur CMV isolates were in one cluster (Group B) with isolates from Iran and Serbia. Although Manipur isolates were in the same group with Iran and Serbia isolates, they formed separate cluster showing the high level of diversity of Manipur isolates. Sequence similarity of four CMV isolates from Manipur and 19 isolates of CP sequences originating from different parts of the world revealed that Manipur ChiVMV isolates were found to share an identity of 80 to 90% among them. ChiVMV-np1, 2 and 4 were more similar to nucleotide sequences of CP as compared to ChiVMV-np3. Similarly, nucleotide sequences of CP of Manipur CMV-MK isolates have an identity of 39-87% among them. It has been observed that Manipur isolates CMV-MK-1, 2 and 4 have shown more similarity (59-87%) as compared to CMV-MK-4 (39-44%) A comparison with CMV isolates from other countries showed that CMV-MK-1, 2, 3 and 4 had maximum sequence identities of 25-85% (Korea/Imphal). Those findings indicated that Manipur isolates are highly diverse at the genetic level. Further research work can be done on diversity analysis by covering large no. of chilli growing areas from North East India.

TS2-O8

Detection of citrus tristeza virus in different citrus groves of North East India

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Citrus tristeza virus (CTV) is a flexuous filamentous virus species of the genus *Closterovirus* (family *Closteroviridae*) having single stranded positive sense RNA genome. CTV has been reported to be associated with devastating 'Tristeza' disease of citrus all over the world. Extensive surveys were conducted in different citrus growing groves of Manipur to identify the prevalence and distribution of CTV. Extensive surveys were conducted in different citrus growing groves of Manipur (Churachandpur, Chandel, Tamenglong, Ukhrul and Imphal West) covering 36 locations and selected locations of Arunachal Pradesh, Sikkim and Nagaland to identify the prevalence and distribution *of Citrus tristeza virus* (CTV) on citrus species like mandarin, oranges, mosambi, *Citrus macroptera* and Kachai lemon. Based on the combined results of double antibody sandwich-ELISA (DAS-ELISA) and reverse transcription-PCR (RT-PCR), 42.7% of the indexed citrus samples (out of a total of 646 symptomatic and asymptomatic samples) were positive for CTV. Absorbance values ranging from 3.2 to 5.8 folds in infected samples compared to healthy control indicted the high concentration of CTV in field samples. Ten representative CTV isolates sampled from Manipur were characterized for coat protein (CP) gene sequences, which shared a sequence identity of 86-94% among them. Manipur CTV isolates had 89-98% sequence similarity with already reported Indian CTV genotype Kpg3 and segregated in to Kpg3 phylogroup. Out of the tested samples 26% were detected to have mixed infection of CTV and Huanglongbing (HLB), indicating these two pathogens to be responsible for citrus decline in NEH region.

TS3-O1

Marker assisted breeding through DNA based markers against pathogenic fungi and bacteria in wheat and rice crop

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Wheat and Rice are the two most important cereal crops for India and world which together covers a vast cropping area and provides the calorific requirement to millions of people. Both these crops are infected by a number of pathogenic fungi and bacteria which reproduce sexually to generate an enormous amount of genetic variability by their infective spores and strains on a real-time basis. DNA markers due to their abundance are ideal to counteract the astronomical menace of pathogens. Also, there is no need to dependent on single marker system but to choose from a variety of DNA marker systems like RFLP, AFLP, RAPD, SSR, ISSR, STS, CAPS etc. whichever works best to counteract the particular disease at a particular moment of time. Bacterial leaf blight, stripe rust, leaf rust, Fusarium head blight and powdery mildew are some of the major pathological diseases which are reported to be corrected by introgression of QTLs using SSR, RFLP, STS, CAPS etc. Hence, due to the evolution of pathogen it is needed to find associated DNA markers with pathogens on a timely basis. DNA markers also possess a lot of potential of improving and speeding up the conventional plant breeding process by marker-assisted selection. Marker-assisted selection can help in screening disease resistance lines. Some of the SSR markers like *Xpsp3000, CSLV34, Xbarc8* and *Xgwm582* in association with genes which are responsible for rust resistant in wheat. QTL mapping studies in different crops have provided DNA marker-trait association. This put forward the reason for the greater adoption of DNA markers in future. Due to the phenomenon of linkage a marker can be used to detect the presence allelic variation in genes associated with traits. Concerns for sustainable agriculture and greater production for feeding the growing population have put a lot of pressure on breeder for a release of new varieties with desirable traits. Marker-assisted selection can be a panacea in fulfilling this objective since it increases the efficiency and precision also. Marker-assisted selection along with conventional breeding is needed to maximize the probability of success of plant breeding *viz*. durable disease resistance. QTL mapping, marker-assisted backcrossing, gene pyramiding, early generation selection has been greatly assisted by molecular markers. This saves time and speeds up the process.

TS3-O2

Development of infectious clones of cotton leaf curl begomo virus components and agroinoculation for mass resistance screening infectivity test

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Cotton leaf curl disease (CLCuD) is a major viral disease causing constant epidemics in cotton-growing states of Northwest (NW) India. CLCuD is caused by a complex of whitefly (*Bemisia tabaci*) transmitted begomoviruses (monopartite, circular, ssDNA, genome (~2.7kb,) and it associated betasatellite (~1.35Kb) and satellite like alphasatellite molecules (~1.38Kb). Betasatellite involves in symptom modulation, suppression of host transcriptional (TGS) and post-transcriptional gene silencing (PTGS) and also help the helper virus in planta movement. Two begomovirus infectious clones, one IARI-45, a CLCuKoV-Burewala and another S-11, CLCuMuV-Faisalabad strains were constructed in binary vector pCAMBIA2301 consisting of 1.4 mer tandem repeat of the DNA-A (pCAMBIA+IARI-45-1.4 mer and pCAMBIA+S-11-1.4 mer). One infectious clones of betasatellite molecule, CLCuMB, associated with CLCuD-begomovirus isolate IARI-30 (a member of CLCuKoV-Burewala strain) was made in pCAMBIA2301 consisting dimer of DNA (pCAMBIA+IARI-30B 2 mer). Three cotton varieties RST-9, HS-6 and F 846 those are known to be highly susceptible to CLCuD-begomoviruses and experimental hosts, *Nicotiana benthamiana, N. tabaccum* and *N. glutinosa* were used to test infectivity of the infectious clones. No symptoms were observed in cotton and tobacco plants when DNA-A construct alone was inoculated but CLCuD-begomovirus DNA-A was detected in some agroinoculated plants. When DNA-A construct was co-inoculated with the betasatellite construct, inoculated plants produced symptoms on leaf yellowing and leaf curling on *N. benthamiana* but not on *N. tabaccum* and *N. glutinosa.* Slight leaf deformation with light green leaf-discolouration on all the inoculated cotton cultivars was observed and confirmed by PCR. The protocol of agroroinoculation of infectious clones made in the present study will be used for mass screening of resistance against CLCuD in cotton plants.

TS3-O3

Screening of certain rice varieties and its grain yield on the incidence of *Scirpophaga incertulas* (Walker) on rainfed rice crop-ecosystem of Manipur valley

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Rice is the most important staple food of Manipur. Among prevailing different insects associated with rice, the yellow stem borer, *Scirpophaga incertulas* (Walk.) is one of the most destructive pests and field losses are estimated as 5-8% depending on rice cultivar. Hence, a field experiment was conducted at Rice Research Farm, College of Agriculture, CAU, Imphal during the *Kharif* season, 2010 and 2011. Nineteen available rice varieties including one check were tested in the field for their resistance reaction against YSB. One-month-old seedlings were transplanted in RBD in the plot size of 5m x 4m at 15cm x 20 cm spacing with three replications. Results of the experiment revealed that during the two consecutive experimental years (based on two-year pooled mean data), among the entire test varieties, YSB infestation varied from 1.20 to 9.40 per cent dead heart (DH) and 1.31 to 7.70 per cent white ear head (WEH) which were observed at vegetative and reproductive stages of the crop, respectively. In which the highest incidence of YSB was recorded on 'TN-1' with 9.40% (DH) and 7.70% (WEH) whereas the lowest incidence was recorded from 'Phouoibiphou' with 1.02% (DH), 1.31% (WEH) while 3 varieties ' Leimaphou, Tamphaphou and KD-Awangba showed non-significant difference from 'Phouoibiphou' at vegetative stage. 'Phouoibiphou' showed resistance reaction against the borer at vegetative stage, but at reproductive stage, it was recorded with no damage reaction. However, 2 varieties 'Leimaphou (1.14% DH, 2.12% WEH) and Tamphaphou (1.33% DH, 2.27% WEH), 5 varieties 'RCM-9 (3.01% DH, 4.82% WEH), Matamphou (2.28% DH, 3.39% WEH), Sanapou (2.73% DH, 4.32% WEH), WR-1-9-17 (2.64% DH, 3.63% WEH) and WR-2-3-1(3.23% DH, 5.20% WEH), 3 varieties 'Punshiphou (4.43% DH, 6.48% WEH), Ereimaphou (5.44% DH, 6.18% WEH), CAUS-1 (4.04% DH, 5.94% WEH) and 1 variety 'KD-5-2-8' (7.20% DH, 6.82% WEH) reacted resistance, moderately resistance, moderately susceptible and susceptible in both the vegetative and reproductive stages, respectively. The 2 varieties 'IR-64 (3.44% DH, 5.27% WEH) and RCM-10 (3.65% DH, 5.53% WEH) were observed with moderately resistance reaction at vegetative stage which turned into moderately susceptible reaction at reproductive stage whereas 2 varieties 'Pariphou' (2.03% DH, 2.82% WEH) and KD- Awangba (1.73% DH and 2.67% WEH) were reacted moderately resistant at vegetative stage and turned resistant at heading stage. Similar, trends were also observed in case of 'TN-1 and WR-11-4-1' varieties which reacted highly susceptible at vegetative stage turned susceptible at reproductive stage. The grain yield data revealed that the highest grain yield (8.77 tha-1) was obtained from the plots of 'IR-64' as against (2.50 tha-1) in highly susceptible check variety 'TN-1'. It was closely followed by 'KD-Awangba' with 6.57 tha-1 and 'RCM-10' with 6.15 tha-1 whereas 'Punshiphou, Ereimaphou and WR-11-4' were recorded low yield with 2.91 tha-1, 2.86 tha-1 and 2.68 tha-1, respectively and showed the non-significant difference with the check variety 'TN-1'.

TS3-O4

Defense associated changes in taro (*Colocasia esculenta* L. Schott) leaves after challenging *Phytopthora colocasiae*

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When plant is invaded by a pathogen, there is an oxidative burst, characterized by increase in reactive oxygen species (ROS) production as reflected by sharp increase in H_2O_2 production. The ROS-scavenging system, include antioxidants and enzymatic antioxidative system to maintain ROS homeostasis in the plant cell. We have used Taro-*Phytopthora colocasiae* pathosystem to study the early defense responses in taro. About twenty taro genotypes collected from Manipur were investigated under *in vitro* conditions by using artificial spore inoculation technique. Various early defense associated biochemical changes *viz*., *in situ* ROS detection, H_2O_2 content, lipid peroxidation, total antioxidant activity by DPPH scavenging assay and phenol content were studied. The consequences of ROS production and its effect on antioxidative system were also investigated. In our studies of *P. colocasiae*-taro interaction, oxidative burst was characterized by increase in ROS production and higher concentrations of H_2O_2 accumulation (23.2-42.5%) in resistant cultivars (RCMC-5 and Kasamkhullen) than susceptible ones (12.2-21.0%); which could be one of the strategies of defense against the fungal pathogen. Lipid peroxidation in leaves of all studied genotypes of taro increase significantly after *P. colocasiae* spore infection, however, the increase in MDA content was significantly higher (20.35-40.4%) in susceptible genotypes than in the resistant ones (RCMC-5 and RCMC-1). The results of DPPH scavenging assay revealed an increase in the total antioxidative activity (25.7-58.8%) of leaf extracts of resistant genotypes in response to fungal infection. As compared to susceptible, in the resistant genotypes (RCMC-5 and Kasamkhullen) a sharp increasing trend in antioxidative enzyme activities was also observed.

TS4-O1

Impact of climate change on plant-pathogen interaction

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Plant disease results from the interaction of a pathogen with its host but the intensity and extent of this interaction is markedly affected by the environmental factors. Climate change is the main problem and biggest threat of the present century and is affecting plants in natural and agricultural ecosystem throughout the world. It is the result of enhanced acceleration in the increase in temperature and CO_2 concentration over the last 100 years. The impact of climate change has been observed in many dimensions such as effect on biodiversity, food grain production, insects and plant diseases etc. Changing weather can induce severe plant disease epidemics, which threaten food security if they affect staple crops and can damage landscapes if they affect amenity species. Impact of changes in temperature on plant pathogens and disease has been seen at higher temperature e.g. lignification of cell wall in forage species and enhanced resistance to fungal pathogen. Impact would therefore depend on the nature of the host-pathogen interactions and mechanism of resistance. The increase in ambient temperature, when the adequate soil moisture is present, may increase evapotranspiration from plant resulting in humid micro climate in crop canopy. This may further aggravate those disease favoured under warmed and humid condition. Some of the soil borne disease may increase at the rise of the soil temperature also. Impact of climate change on crop production has also seen in rice with rise in temperature, symptoms of brown spot (*Helminthosporium oryzae*) and narrow brown leaf spot (*Sphaerulina oryzina*) were seen in farmer's field of the North Eastern Region of India. Impact of changes in moisture has also seen in pathogen and disease emergences like potato and tomato late blight (caused by *Phytopthora infestan*) fungus infects and reproduces most successfully during periods of high moisture that occurs when temperatures are between 7.2°C and 26.8°C and other pathogen like the powdery mildew species tend to thrive in condition with lower moisture. Thus understanding the potential effects of climate change on agriculture in terms of its impacts on severity and incidence of pests and diseases is an important issue.

TS4-O2

Sclerotinia sclerotiorum causing pigeonpea stem rot in India under climate change scenario

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Symptoms of *Sclerotinia* rot including formation of cottony white mycelium and numerous large sclerotia on diseased parts were observed first time on pigeonpea in India during 2012-14. The incidence of *Sclerotinia* rot disease was recorded from early flowering to pod setting stage on different cultivars of pigeonpea at the Experimental Farm, Indian Agricultural Research Institute

Regional Station, Pusa, Bihar (India) during winter season of 2012-13 and 2013-14. The fungus was identified on the basis of cultural, morphological, pathological and molecular characteristics. The internal transcribed spacer (ITS) region of the pathogen was amplified using the primers ITS1 and ITS4 for the molecular identification of the pathogen and sequenced. BLAST search of NCBI database revealed 99% identity with *S. sclerotiorum* of different hosts (60 records). The cool sub-humid climate with average minimum (9.2°C) and maximum temperatures (21.0°C) along with more than 93% relative humidity plays a decisive role for stem rot disease development and spread in pigeonpea crop. The pigeonpea cultivar, ‘ICPL-151’ showed the highest disease incidence, twig infection and yield loss, while ‘Kudrat’ and ‘MAL-13’ cultivars were found completely resistant to the disease. However, the disease has been found to appear on crop during 2012-14, while in 2014-15 crop season no disease incidence was recorded due to high temperature in winter season. This is a typical menace to the pigeonpea crop production under climate change scenario occurred in North Eastern Plain Zone of India.

TS4-O3

Study of bacterial leaf blight epidemiology of rice (*Oryza sativa*) incited by *Xanthomonas oryzae pv. oryzae* in relation with weather parameters

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The experiments were carried to study the influence of epidemiological factors on development of bacterial leaf blight in different rice varieties under field condition during *kharif* season of 2015-16 and 2016-17. The maximum percent disease index was observed in 40th and 39th standard week in 2015 and 2016 respectively. The correlation study under open field revealed that, development of bacterial leaf blight was positively correlated with relative humidity in all the varieties whereas temperature and rainfall were negative correlated in all the varieties during crop growth period during both the seasons. The maximum AUDPC of 103.6 and 90.74 were observed in 2015 and 2016 respectively.

TS5-O1

Effect of certain medicinal plants against *Alternaria* blight of rapeseed- mustard under organic farming system in Manipur

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The antifungal activity of aqueous extracts of locally available medicinal plants has been tested in vitro condition against *Alternaria brassicae,* the causal agent of Alternaria blight. Evaluation of plant extracts against mycelial growth of the pathogen at different concentrations *viz*., 5%, 10% and 15 % using poison food technique showed a higher percentage of inhibition in *Azadirachta indica, Michelia champaca, Adhatoda vasica* and *Eryngium foetidum* at 15% concentration. Among them, *Azadirachta indica* showed the highest percentage of inhibition (55.80%) over control. The remaining plants produced less inhibitory effect thereby *Zingiber officinale* manifested the lowest inhibition (24.20%). In field trial for two consecutive *rabi* seasons (2014 & 2015) *Azadirachta indica* resulted in the highest percentage of disease control.

TS5-O2

Fungal diseases of maize under organic farming system in Manipur

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Maize (*Zea mays*) is cultivated both in hills and plains. In the hills, maize is cultivated purely under organic condition whereas, in plains, certain amounts of chemical fertilizers are applied for better crop yield. Maize cultivation in hills includes different traditional varieties whereas in plains recommended varieties of maize such as Vivek QPM-9, Prakash, PMH-4, HQPM 1, HQPM 2, etc are cultivated mostly as kitchen garden crop for human consumption, animal feeds, etc. Commercial cultivation of maize is found in certain patches under jhum cultivation in the hills under Kangpokpi, Senapati, Chandel and Ukhrul districts that too in jhum sites. In both the hill and valley, cultivars of maize are prone to fungal diseases like turcicum leaf blight, common rust, brown spot, smut, etc. Initial investigation on fungal diseases of maize both in the hills and plains reveals that turcicum leaf blight is the most commonly found fungal disease of maize. However, sufficient application of organic manure restricts the current diseases under traditional maize farming in the hills. Details of maize cultivation, different maize cultivars, types of organic manure applied for the cultivation of maize, disease parameters of maize on certain varieties *viz*. yellow maize, white maize, HQPM 2 and *chakhaochujak* are presented in the full length of the paper.

TS5-O3

Identification of powdery mildew disease resistant recombinant inbred lines (RILs) in green gram (*Vigna radiata* (L.) Wilczek)

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Green gram, [*Vigna radiata* (L.) Wilczek], the third important pulse crop of the country is affected by various biotic stresses. Powdery mildew caused by *Erysiphe polygoni* D. C., is resulting in losses up to 100% if attacked at seedling stage. Considering this, the present investigation was formulated involving F4 and F5 generations of RILs of two crosses viz., Chinamung × BL-849 and Chinamung × LM-1668 which has contrasting features for powdery mildew resistance with 146 and 155 lines respectively. Out of 146 F4 RILs screened in cross Chinamung × BL-849, one of them was found to be highly resistant *viz*., C1-34-23. When screened in Rabi season (F5) showed fourteen RILs to be highly resistant. Whereas in cross Chinamung × LM-1668, 155 F4 RILs screened, thirty-nine RILs were found to be moderately resistant whereas in Rabi season (F5) showed one hundred and four lines to be moderately resistant. Some of the lines in two populations are showing a similar response in both the seasons. The RIL ‘C1-34-23’ is showing a highly resistant response in cross Chinamung × BL-849 whereas C2-14-11, C2-16-13 RILs are showing a moderately resistant response in cross Chinamung × LM-1668 in both seasons. This clearly indicates that these lines have become stable for the disease response. Such lines can be screened for yield-related traits to develop highly resistant breeding lines with high yielding ability in green gram which has ample scope in regions suitable for organic agriculture. Further, the two populations studied have significant variability present between lines which can be utilized for QTL mapping for dissecting the nature of gene action controlling the disease.

TS5-O4

Effect of different *Pseudomonas* based bioformulations against bacterial wilt pathogen (*Ralstonia solanacearum*) of Bhut jolokia under Assam condition

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Four aggressive strains of *Pseudomonas* spp. isolated from different parts of North Eastern states of India were evaluated for management of bacterial wilt (*Ralstonia solanacearum*) of Bhut jolokia (*Capsicum chinense* Jacq.) under Assam condition. Their Talc based bioformulations were prepared for pot evaluation and applied in *planta* as combination of seed treatment, root treatment and soil application for management of bacterial wilt of Bhut jolokia. Strain Biofor-*Pf* (T_5) collected from Bacteriology Laboratory of Department of Plant Pathology, AAU was used as positive control and treatment with *R. solanacearum* alone was used as negative control. Among the four *Pseudomonas* strains; the percent disease incidence was significantly reduced in Bhut jolokia plants treated with bioformulation of *Pf* stain T_4 (Assam) treated seeds (4%). Corresponding to the decrease in bacterial wilt incidence there was increase in plant yield (160 g/plant) in the *Pf* stain T_4 treated plants. Plant organic carbon content (21.07%) and soil organic content (4.34%) also significantly increased when the plant and soil were treated with *Pf* stain T_4 as compared to control. The population dynamics of *Pseudomonas* spp. in rhizospheric soil of Bhut jolokia at 90 days after transplantation significantly increased in all treatments as compared to control. Correlation studies recorded negative correlation between population dynamic of *Pseudomonas* spp. and percent wilt incidence.

TS6-O1

Trichoderma species as biocontrol agents

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Plant diseases play a direct role in the destruction of natural resources in agriculture. In particular, soil-borne pathogens cause important losses, fungi being the most aggressive. The distribution of several phytopathogenic fungi, such as *Pythium, Phytophthora, Botrytis, Rhizoctonia* and *Fusarium,* has spread during the last few years due to changes introduced in farming, with detrimental effects on crops of economic importance. The breeding of resistant crops is time-consuming and difficult as often new races of pathogens evolve and crops become susceptible. The use of agrochemicals in controlling the disease has been ineffective and cause environmental hazards. By contrast, the use of microorganisms that antagonize plant pathogens (biological control) is risk-free when it results in enhancement of resident antagonists. Antagonists of phytopathogenic fungi have been used to control plant diseases, and 90% of such applications have been carried out with different strains of the fungus Trichoderma. Most of these strains are classified as imperfect fungi since they have no known sexual stage. Strains of Trichoderma are increasingly being used to control soilborne plant pathogens. The most frequently suggested mechanisms of biocontrol by Trichoderma include mycoparasitism, antibiosis, competition for nutrients, or all of the above. Trichoderma can inhibit the pathogen by means of antibiotics or cell wall-degrading enzymes (CWDEs) such as chitinases, β-1, 3-glucanases, proteases, mannanases, and other hydrolases. The relative importance of these two mechanisms in the antagonistic process depends on specific pathogen-host interactions. Several genes encoding to hydrolytic enzymes (chitinases, β-1, 3-glucanases) have been isolated and characterized from *Trichoderma spp*. The genes from Trichoderma species have been transferred and expressed in plants for improving biotic and abiotic stress tolerance. Endochitinase and endoglucanase genes can serve as a useful source for resistance in case of some important diseases like sheath blight of rice, where resistant germplasm is not available in the wild relatives. Crops can be transformed with endochitinase and endoglucanase genes to develop resistance against various plant pathogens.

TS6-O2

Association of *Agaricales* spp. in chickpea wilt complex and its management by native *Trichoderma* spp. in Manipur

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Chickpea (*Cicer arietinum* L.) locally known as gram or chana is an important pulse crop widely grown in the world and as well as in India. It is a rich source of high-quality protein. The present study was undertaken to characterize chickpea pathogen isolated from the infected plant of chickpea using both morphological, molecular approaches and effect against native *Trichoderma* spp. in vitro in Manipur. The isolated pathogen was identified based on the type of fungal mycelium and mustard shaped of sclerotia and confirmed by molecular identification as *Agaricales* spp. PCR amplification of the pathogen followed by 1.2% agarose gel electrophoresis of internal transcribed spacer (ITS1 and ITS2) found approximately 262 bp for *Agaricales* species (KX242159). In vitro effect of *Trichoderma* isolates on the growth of *Agaricales* species showed that maximum inhibition by CAUNCIPM-4 of 83.13 % and CAUNCIPM-45 showed minimum inhibition of 58.80 %. Effect of the volatile compound produced by *Trichoderma* spp. against *Agaricales* species showed inhibition ranged from 14.27 to 39.67 % where the highest inhibition was recorded with isolate CAUNCIPM-4 (39.67 %) and for non-volatile compound it was ranged from 14.07 to 49.07 % at 7.5 % v/v concentrations and from 20.00 to 56.83 % at 15 % v/v. The highest percent inhibition at 7.5% and 15 % v/v concentration was recorded with the isolate CAUNCIPM-4. For the competitive parasitic ability, percent colonization of the two *Trichoderma* isolates to the sclerotia of *Agaricales* species were found to be more in sterilized soil. The biopriming of chickpea seed showed an increase in vigour index over control.

TS6-O3

Understanding the potentiality of native phosphate solubilizing bacteria (PSB) from the rhizospheric soil of rice (*Oryza sativa*) in Manipur

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Phosphate solubilizing micro-organism plays an important role in plant nutrition through increase in phosphate uptake by plants and used as biofertilizers for agricultural crops. A large number of micro-organisms present in the rhizosphere of rice are known to solubilize and make available the insoluble phosphorous in the available form. The present investigation was carried out to isolate, identify and characterize the phosphate solubilizing bacteria from the rhizospheric soil of rice. With the aim to evaluate the potential of Phosphate Solubilizing Bacteria (PSB) and to develop biofertilizer, soil samples from different districts (60 places) *viz.,* Imphal West, Imphal East, Bishnupur and Thoubal district were collected randomly to isolate PSB by using plate assay method. A novel defined microbiological growth medium, National Botanical Research Institute's Phosphate growth medium (NBRIP) was used for screening phosphate solubilizing microorganisms. A total of 14 Phosphate Solubilizing Microbial colonies were isolated on the NBRIP agar medium, the colonies showing clear halo zones around the microbial growth were considered as phosphate solubilization. Among the 14 isolate tested, highest Phosphate Solubilization Index (PSI) ranges from 1.04-3.42 and the highest was found in *Bacillus megaterium*. Through molecular characterization, 11 isolates were identified as *Burkholderia contaminans* (MF536127), *Burkholderia* sp (MF536128), *Burkholderia* sp (MF536129), *Burkholderia* sp (MF536130), *Burkholderia* sp (MF536131), *Burkholderia anthina* (MF536132), *Burkholderia vietnamiensis* (MF536133), *Bacillus megaterium* (MF536134), *Burkholderia cenocepacia* (MF536135), *Burkholderia cenocepacia* (MF536136) and *Burkholderia* *gladioli* (MF536137). Best isolates could be considered as an appropriate substitute for chemical phosphorous fertilizer in organic and sustainable agricultural systems as PSB is one of the alternative components of sustainable agriculture.

TS6-O4

Screening of native actinobacteria of Manipur for phytostimulating activity, production of agroactive compounds and biocontrol potential

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Crop losses are creating a major threat to the food production with about 27 to 42% loss in global food production caused by plant pathogens. Many measures have been used in the management of plant pathogens like resistant varieties especially GM crops or use of agrochemicals, but all of them have some limitations or harmful effects. Biological control is, thus, being considered as an eco-friendly way to control plant pathogens. Hence, the screening and selection of superior, naturally occurring native bacteria as biocontrol agent has emerged as a new subject of interest. In this present study, twelve actinobacterial strains were isolated on starch casein nitrate agar medium. All the strains were screened for plant growth promoting and biocontrol activity against three major phytopathogens. Of these, nine isolates exhibiting plant growth promoting (PGP) or biocontrol activity or both were identified as *Streptomyces spp*. by partial 16S rRNA gene sequencing. Eight strains *viz*., RCM-SSR-1, -2, -5, -6, -8, -11, -12 and -14 were found to be positive for phosphate solubilization. All the strains could produce ammonia; whereas, ten strains namely RCM-SSR-1, -2, -3, -4, -5, -6, -8, -9, -11 and -12 could produce siderophore. Maximum IAA production was observed with RCM-SSR-6 (36.3±2.1 µg mL-1) followed by RCM-SSR-11 (25±0.2 µg mL-1), SSR-RCM-8 (22.0±2.0 µg mL-1) and RCM-SSR-5 (21.5±0.8 µg mL-1). RCM-SSR-1, -2, -5, -6, -9 and -11 showed antagonistic activity against the three fungal pathogens. Maximum colony growth inhibition (67%) of *Fusarium oxysporum* was shown by RCM-SSR-5; followed by RCM-SSR-6 and -11 (62%). Up to 60% inhibition of colony growth of *Pyricularia oryzae* was noticed in RCM-SSR-5, -9 and -11; whereas, RCM-SSR-9 inhibited colony growth of *Rhizoctonia solani* to the tune of 61%, followed by RCM-SSR-2 (60%). The study revealed that actinobacteria isolated from tomato rhizosphere in North East Indian Himalayan Region are potential microbial inoculants because of their intensified plant growth promoting traits such as phosphate solubilization, ammonia production, IAA production and siderophore production as well as biocontrol potential. Four isolates *viz.,* RCM-SSR-1, -2, -5 and -6 reported in this study were identified as multi-traits plant growth promoting rhizobacteria and can be considered as promising candidates for the development of phytostimulators and biocontrol agents or can also be exploited for the production of agroactive compounds like Indole-3-acetic acid.

TS6-O5

An easy and economic technology on mass production of native *Trichoderma* for the farmers in Manipur

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Sustainable food production for the rapidly increasing population may be greatest challenging things. Conventional practices by using chemical fungicides might overcome for a while but in the long term, it affects the environment. *Trichoderma* is soil borne; free-living, easily present in almost all the agricultural soils, which play a major role in controlling soil-borne diseases of plants. Highly effective against diseases like root rot, collar rot, stem rot, wilt, blight, damping off etc. Mass production of *Trichoderma* spp. from agriculturally available waste or substrates was developed by Department of Plant Pathology, College of Agriculture, CAU, Imphal based on different combinations of rice bran, dextrose, sugar, sawdust, mustard cake, etc. The Farmers were trained on mass production of *Trichoderma* spp. for their own production with the locally available substrate, field application in place of chemical fungicides. As a result of the training, farmers from the Leimaram and Thoubal produces their own Trichoderma substrate according to their requirements. The present technique is slowly adopting by the literate and progressive farmers.

TS6-O6

Evaluation of *Trichoderma* isolates for their potential of biosorption of cadmium stress

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Trichoderma species are imperfect filamentous fungi with teleomorphs and belong to the order Hypocreales in the Ascomycete division. They play an important role in ecology by taking part in the decomposition of plant residues, as well as in biodegradation of man-made chemicals and bioaccumulation of high amounts of various metals from wastewater and soil. Metal-containing pollutants are increasingly released into soil from industrial wastewater, as well as from wastes derived from chemical fertilizers and pesticides used in agriculture. Some metal-containing pollutants are not biodegradable; they enter the food chain and lead to bioaccumulation. Evidence has suggested that *Trichoderma* spp. exhibit considerable tolerance for metals and accumulates high amounts of metals from polluted habitats. Therefore, metal-tolerant *Trichoderma* spp. may become dominant organisms in some polluted environments and may play an important role in eco-friendly metal removal technology. Fourteen Trichoderma isolates were evaluated for their tolerance to cadmium stress. Three isolates MT-4, UBT-18 and IBT-II showed better tolerance to cadmium stress than other isolates. Among the cadmium-tolerant isolates, IBT-II showed both maximum biomass production and a maximum MIC50 value in cadmium stress. The increase in cadmium concentrations resulted in a decrease in biomass

production and positively correlated with an increase in residual cadmium in the culture broth. Cadmium stress influenced the sensitivity of the Trichoderma isolates to soil fungistasis. Isolate UBT-18 was recorded to be most tolerant to fungistasis under cadmium stress.

TS6-O7

Identification of native *Trichoderma* spp. and phosphate solubilizing bacteria (PSB) from the rhizospheric soil of *Oryza sativa* in the valley districts of Manipur

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Investigation on the occurrence of native *Trichoderma* spp. and Phosphate Solubilizing Bacteria (PSB) from the rhizospheric soil of rice from different regions of the valley districts of Manipur were carried out during the year 2015-2016. Evaluation of the potential of native *Trichoderma* spp. and PSB were tested under in vitro condition. Fifteen soil samples each from the four districts were collected randomly to isolate native *Trichoderma* spp. and PSB by using agar plate method. Isolates of native *Trichoderma* spp. were screened by dual culture method and phosphate solubilizing microorganisms were screened by evaluating phosphate solubilization index using Edi Premono method in National Botanical Research Institute's Phosphate growth medium (NBRIP). Six isolates, three isolates, two isolates and four isolates of Trichoderma spp. were isolated from different regions of Thoubal, Imphal East, Imphal West and Bishnupur district respectively. Thirteen isolates, one isolate and another one isolate of PSB were isolated from Bishnupur district, Imphal East and Thoubal district respectively. All the Trichoderma isolates tested showed a considerable level of antagonistic activity against two isolated rice soil-borne pathogenic fungi namely *Sclerotium oryzae* (stem rot causal pathogen) and *Rhizoctonia oryzae* (Sheath blight causal pathogen). Isolates of PSB also showed varying levels of solubilizing activity on the NBRIP medium.

TS6-O8

Management of anthracnose disease of chilli through fungicide tolerant PGPR strains

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Chilli is an important commercial spice and condiments crop of Indian home as it adds pungency, taste, flavour and colour to the dishes. Commercial cultivation of chilli resulted in the outbreak of anthracnose disease leading to quantitative and qualitative losses as reflected by the survey conducted in chilli growing area. The organisms associated with this disease were isolated and identified as *Colletotrichum gloeosporioides* (Penz.), *C. capsici* (Syd.) and *C. acutatum* (Simmonds) based on ITS sequencing and species-specific primers. An attempt was made to isolate the fungicide tolerant PGPR strains from rhizosphere soil of chilli and to test their fitness potential in managing anthracnose disease in single and in combination, both under glasshouse and field conditions. The result indicated that 0.1 per cent of Propiconazole was highly effective with minimum disease incidence and was statistically on par with

Propiconazole (0.05 %) + *B. subtilis* (0.2 %) and Propiconazole (0.05 %) + *P. fluorescens* (0.2 %) under glasshouse as well as field conditions indicating possibility of reducing dosages of fungicides by supplementation with PGPR strains. Further, the combined application also enhanced the defense enzyme activity in chilli seedlings.

TS6-O9

Development of a biocontrol based management module for *Fusarium oxysporum* f.sp. *zingiberi* causing soft rot of ginger

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Soft rot disease caused by *Fusarium oxysporum* f.sp. *zingiberi* is one of the major diseases of ginger in North East region of India causing significant yield losses. During the surveys carried out in different districts of Manipur, soft rot incidence ranging from 19 to 56% was recorded. The highest incidence of 56% was recorded in Makhan area of Senapati district and lowest of 19% at Litan area of Ukhrul district. In order to develop a biocontrol based management strategy, native *Trichoderma* isolates collected from Manipur were evaluated against by *Fusarium oxysporum* f.sp. *zingiberi* under in vitro conditions. Under in vitro conditions in dual culture technique, *Trichoderma harzianum*–CAUNCIPM-61 isolate showed best results (88.21% inhibition) after the two most effective cultures of *T. viride* and *T. harzianum* obtained from Bangalore. Effect of the volatile compound produced by *Trichoderma* spp. against *F. oxysporum* ranged from 26.27 to 46.27% where the highest inhibition was recorded with *T. viride* (46.27%) whereas for non-volatile compound it ranged from 7.06 to 12.94% at 7.5% (v/v) concentration. Under in vivo conditions, the efficacy of ten potent *Trichoderma* isolates and one fungicide (copper oxychloride) against *Fusarium oxysporum* f.sp. *zingiberi* tested at two different locations, showed significant disease reduction as compared with the control. Besides chemical fungicide, *T. viride* treated plots showed lowest incidences (20.72% at Langol area and 35.66% at Sawombung area). Among the *Trichoderma spp.*, maximum yield was obtained with *T. harzianum* (18.60 tonnes/ha at Langol and 17.75 tonnes/ha at Sawombung). Higher yield was also observed in all other *Trichoderma* isolates treated plots and found to be better than the untreated plot. The present study clearly indicated that native *Trichoderma* isolates and their formulations can be effectively used in soft rot management under Manipur conditions for organic ginger production.

TS10-O1

Pheromone traps: a win-win technology for the farmer and environment in Manipur

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Around the globe, the use of pheromone traps has proven itself to be an efficient and effective technology for both monitoring pest density as well as managing their population by mass trapping. It is a clean technology that does not cause any environmental pollution while managing pests and can be used under organic farming too. In North East India, the use of pheromone traps for pest management is very low. Farmers are lacking in awareness about the use and advantages of pheromone traps. Most agricultural input shops do not stock any kind of pheromone traps/lures for sale. Further farmers are not aware of the decision support systems such as EIL (Economic Injury Level) and ETL (Economic Threshold Level) of IPM which enables timely intervention of insecticidal application. Excessive reliance on chemical control leads to an overload of pesticides on the environment, the killing of beneficial insects and harmful pesticide residues. With these existing lacunae in mind, an initiative was first undertaken to demonstrate the use of pheromone traps and gauge the response to the technology among the farmers in participatory mode. Pheromone traps were installed at five locations *viz.* Sangaithel, Khabi Bamdiar, Heigrujam, Khumbong and Lamphel during *Kharif* season in rice crop in 2016. Traps for Yellow Stem borer, *Scirpophaga incertulas,* which is one of the major pest in rice were installed in 30 days old crop in the main field. To monitor pest population to know the ETL of a known pest, five traps are required per hectare at a distance of at least 20 m^2 from each other. The farmers were taught how to monitor the pest population in the field using these traps and the concept of ETL was explained. They were told to give insecticidal application only when ETL (eight adult moths per trap) was reached. Weekly observations and surveillance of all the trap installations were done in all the locations however, none of them reached ETL except for one week (last week of August 2016) in Khabi Bamdiar after which insecticidal sprays were advised. The regular observations and monitoring with the use of pheromone traps revealed the less incidence of the pest during 2016 *Kharif* season in rice. Farmers who were introduced to this technology expressed satisfaction at the relative ease of monitoring insect pests in their field. After the success of this intervention, this technology was then demonstrated and tried in Ukhrul district of Manipur (Sihai village) in early 2017 among the by-default organic cabbage farmers. Here, the pheromone traps were used for mass trapping instead of monitoring. Since Diamondback moth (*Plutella xylostella*) was the major pest of cole crops, this pest was targeted for management. For mass trapping, ten traps were installed per hectare and the farmers were taught how to install and monitor the trap themselves. The organic farmers of Sihai village expressed great satisfaction and amazement to the workings of pheromone traps and wanted to adopt this technology in future. Neighboring farmers who had seen the effectiveness of the technology through such demonstrations also wanted to adopt this technology in their own field in future.

TS10-O2

Farmer club approach for technology dissemination on plant protection and improved production techniques

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The present study was conducted on three Farmer's Club *viz*. Sangaithel Farmer's Club, Khabam Bamdiar Farmer's Club and Khumbong Farmer's club. Primary data were collected from 75 numbers of farmer's club members and another 75 farmers who are non-members of farmers club. Various training and demonstration were conducted at farmer's club during year 2015-16 with a major focus on pest and disease free and low cost cultivation of kharif paddy. Trainings were also given on control and management of pest and diseases of rice through IPM approaches. Through this participatory approach monitoring and visit to farmer's field have been made to examine the performance of crop growth and occurrence of pest and diseases. For the first time pheromone trap have been introduced and installed at each demonstration plot of the Farmer's club and regular recording of insect trap were done. Use of natural methods to control pest and disease right from selection of disease free seeds, cultural methods, timely sowing, scientific spacing, judicious use of fertilizers, use of right plant protection chemicals with the right dose, etc were taught to the farmers. It has been found that adoption of high yielding disease resistant paddy varieties were more in case of member farmers compared to non-members. The average cost of rice cultivation was Rs. 46,650 per hectare for member's compared to Rs. 48,492 for non-members respectively. The B: C ratio was 1.84 for member compare to 1.61 for non-members. As per the knowledge gained by the farmers through farmers club, it has been found that 15 percent of the member's farmers know about pheromone trap and can use it by them. Regarding organic pest control measures maximum of the farmers express that they have no knowledge or just heard about it.

TS10-O3

Indigenous Traditional knowledge for plant protection of Ukhrul

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Indigenous Knowledge (ITK) is the unique, traditional, local knowledge existing among and developed around the specific conditions of society indigenous to a particular geographic area. North East (NE) region of India is blessed with strong cultural, social and tradition knowledge base which is the most invaluable resource of this region. Farmers of NE India in general and Manipur in particular have long been practicing a plethora of ITK practices which has been transferred from generation to generation. In last few years we have recorded and validated a few ITKs in context to plant protection practiced by the farmers of Manipur (Tribal in hills). *Artemesiu parviflora* a plant species commonly grown in Manipur is being used by the people of Tangkhul community in Ukhrul district of Manipur to protect the crops from insect pests in field and storage. Its fresh leave branches whole plant is put in and around the paddy field to reduce the insect pest incidence. Dried branches leaves of *Artemesia parviflora* are mixed - with potato tuber seeds, which effectively controls the storage insect pests and post-harvest diseases. Other ITK’s is in plant extracts were documented which are used to manage pest and diseases. The documented ITK’s need to be validated and refined. After validation, the ITK’s will be disseminated based on location specificity by the KVK Ukhrul.

TS11-O1

Mushroom as a potential supplemental food in the dietary habits: a review

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Since many decades mushrooms have been long used as food supplements and for medicinal purposes. Though it is neither a vegetable nor a meat yet it is commonly called as the ‘meat of the vegetable world’. Out of the reported 14,000 to 22,000 species, only 2,000 species are edible. Among the edible mushroom species just around a dozen are commercially cultivated and a few are even poisonous. China dominates the international mushroom market as the major producer of edible mushroom. About half of the cultivated mushroom comes from China alone where 2.7 kg mushrooms are consumed per person annually. In the present scenario, mushrooms are gaining popularity in the culinary dishes as a functional food around the world owing to their high-quality vitamins, proteins, fibers and many other medicinal properties and hence is rightly called as ‘nutraceuticals’. They are favoured because of their flavour, aroma and high nutritive values along with medicinal properties. Also, many researchers have reported that most of the edible mushrooms contain bio-active metabolites like polysaccharides, lipopolysaccharides, proteins, peptides, glycoproteins, nucleosides, triterpenoids, lectins, lipids and their derivatives so, if taken in the correct proportions in diet it can control and modulate many functions of the human body and help maintain a good health by reducing risks of many diseases. Thus there is a promising scope for the future mushroom market in the coming years. Hence its cultivation and production should be encouraged as they have antifungal, antibacterial, antiviral and antioxidant properties and can fulfill all the criteria of a healthy diet food.

TS11-O2

Mushroom cultivation transforms the livelihood of the farmer: a success story of Mrs. SR. Shanghnu

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In Chandel district, cultivation of mushroom was not popular until establishment of Krishi Vigyan Kendra, which popularizes its cultivation and production technology through training and demonstration programmes. The demonstration programme on mushroom production was organized by KVK Chandel in October 2008 with the collaboration of ICAR Research Complex for NEH Region, Manipur Centre under the TSP to different farmers of Chandel district, where Mrs. SR. Shanghnu, 50 years of age from Abungnikhu Village, Chandel, was one of the trainee. Being an active and hardworking farmer started her own mushroom cultivation right after attending the training. While observing her dedicated and keen interest, KVK Chandel conducted front line demonstrations on mushroom production var. *Pleurotus* spp sponsored by TMN-I at her unit in the Year 2010. She could produce 100 kg mushroom from 200 kg straw in 3 months in her unit. She could harvest 4 times with the net income of Rs.24, 000 per year and raised her income significantly in meeting the needs of the family. Further, she continued the same enterprise and found more interested for growing mushroom when she became normal from her diabetic and high blood pressure after consuming of mushroom. Through her success story, she became a role model not only to farmers but also to diabetic patients in growing and eating mushroom in and around Chandel. She is thankful and grateful to KVK Chandel for providing logistics supports to her.

TS11-O3

Improvement of nutritional status with value added mushroom products

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Mushroom is a fleshy spore-bearing fruiting body of fungus typically produced above the ground on soil and decay wood during the rainy season. Some of the mushrooms are grown in nature and some are cultivated. Mushrooms have been providing the natural way to good health since ages. Mushrooms are rich in high-quality protein, vitamins and fibre. Thus they are called as white vegetables or vegetarian meat. Nowadays people are more concerned about health. Therefore, being cholesterol free, mushrooms are now accepted as an ideal food item suitable for all age group and it occupies a place between meat and vegetables. The superior quality protein of mushrooms supplements the carbohydrate-rich, protein deficit primarily cereal based Indian diet. Mushroom is an excellent source of vitamins and minerals. It is a very rich source of vitamin B complex and vitamin C. It also contains folic acid and vitamin B12 which are not found in any green vegetables. The vitamin present in mushroom are not lost during cooking. Besides the mineral like potassium, sodium and phosphorous are also abundantly found in food bodies along with the traces of copper, zinc and magnesium which have proved as a perfect food for the young and old by providing nutritious and health benefits. Mushroom has been an important and major component of the folk medicine as well as modern medicine. The absence of cholesterol with the higher proportion of unsaturated fatty acid makes them a good diet for a heart patient. The calorific value of mushroom is low in starch, less sugar and low fat which makes it ideally suitable for a diabetic and obese patient. It also helps to prevent prostate and breast cancer. The different antioxidants present in different species of mushroom help to reduce the ageing process as well as to maintain healthy eye, kidney, bone marrow, liver and skin. In this study, a survey was conducted in order to assess the types of mushrooms consumed and assess the technology used for the differentiation of edible from non-edible mushroom as it is wildly available during the rainy season. Some old people were also interviewed in order to know the traditional use of mushroom for the prevention and treatment of many diseases. Nutrient contents of the traditional mushroom items consumed by the people were also calculated. Some of the nutrient-rich value-added mushroom recipes were also developed and popularized by KVK, Chandel in order to supplement the nutrient-rich food in the daily diet and to improve the livelihood of farm women by making value-added mushroom product.

TS11-O4

Nutritional characterisation of *Pleurotus florida* produced using wild banana leaves as substrate

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Unavailability of paddy straw in the hill of Mizoram is a major constraint for the cultivation of mushroom. Evaluating and promoting the use of easily available lignocellulose rich plant waste for conversion to nutritious food and safer environment is an urgent need. Therefore, the objective of this work to evaluate the effects of different lingo rich agro-wastes on the yield, and nutritional composition of oyster mushrooms *Pleurotus florida* (Pf). Three substrate formulas including wild banana (WB), oil palm (OP), paddy straw (PS) as control and in the combination of 75 : 25, 50 : 50 and 25: 75 ratio between WB and PS, WB and PS were investigated. The results indicated that WB substrate formulas gave a significant difference in the yield parameters like total colonization period, characteristics of fruiting bodies, yield, and biological efficiency as compared to PS. The nutritional properties of the control sample (PS) were similar to values reported in the literature, while the nutritional composition (moisture, fat, protein, Nitrogen) and mineral contents (Mn, Zn, Cu, and Ca) of the samples obtained using WB, and its combination was highly satisfactory. Based on the mushroom yield, nutritional factors and biological efficiency of the substrates tested, wild banana (WB) leaves appeared to be the best alternative material for growing *P. florida* which can be either substitute or mixed with paddy straw (PS) in the hill of Mizoram in the North Eastern region of India.

TS12-O1

Field efficacy of bio-control agents and seed dressing fungicides for management of false smut disease of rice caused by [(*Ustilaginoidea virens* (Cooke.)Tak.] and their impact on yield attributes under submergence prone ecology.

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The false smut disease of rice caused by *Ustilaginoidea virens* has gained worldwide importance and its affects both quantitatively and qualitatively. Yield losses ranging from 0.2-49% reported from India (Ansari *et.al.,* 1988). KVK Sitamarhi conducted on farm testing trails from 2014 and 2015, under the project entitled "Improved Rice Based Rainfed Agricultural System" funded by International Rice Research Institute Philippines, Manila, to find out the effect of different chemicals and microbes alone or in combination on growth and yield of rice and cost effective method of false smut management in rice under flood prone ecology. The observation on different growth parameters of transplanted rice such as, disease severity (%), plant height at maturity stage, days after 50% flowering, days to maturity, tillers/m^2, grain yield(kg/ha), straw yield(kg/ha), harvest index(%) and B:C ratio were undertaken. The plant height measured at maturity stages of the crop, varied significantly among the treatments. However, the highest plant height (82.7 cm) was recorded in treatment T_4 (Trichoderma seed treatment @12g/kg seed + one spray of Copper oxychloride @ 2g/lt of at 50% panicle emergence) and treatment T_7 [Chemical seed treatment (Tricyclazole @0.4g/kg seed) + one spray of Copper oxychloride (@ 2g/lt of water at 50% PE)]. Days to fifty percent flowering and days to maturity showed non-significant difference. The highest number of tillers per m^2 was measured in the treatments T_4 and it varied significantly among the treatments. The minimum disease severity (22.40%), maximum grain (34.50 q ha^{-1}), straw yield (36.05 q ha^{-1}) and harvest index (%) were observed under treatment T_4. It might be due to lower unfilled grain per panicles and lower infected spikelet per panicle in the treatment of Trichoderma seed treatment (@12g/kg seed) + one spray of copper oxychloride (@ 2g/lt) at 50% panicle emergence.

TS12-O2

Integrated management of Ganoderma wilt of arecanut in Goalpara district of Assam

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Assam has emerged as the third largest producer of arecanut after southern states Karnataka and Kerela. During 2014-15 Assam produces 60,000 tons arecanut from a cultivated area of 74,000 ha. From last few decades, Ganoderma wilt disease became a limiting factor for the cultivation of arecanut in Assam. This disease is also known as Anabe / Foot rot or Basal stem rot. It has not only affected the productivity but has also wiped out areca plantations in certain localities. In India, the disease has also been reported from Karnataka, Tamil Nadu, Kerala, Bengal and Nicobar Islands. Symptoms include yellowing of leaves followed by droop down, brownish patches at the base of the trunk, central tissue of the affected portion of the stem base become dark brown and secretion of brownish gummy exudates resulting musty smell, 'Anabe' or fruiting body of the fungus develops just above the soil level prior to the wilting or just after the death of the palm. The family Ganodermataceae Donk was erected for polypore mushrooms having a double-walled basidiospore. The type species of the family is *Ganoderma lucidum* (W. Curt.:Fr.) *P. Karsten*, is the causal organism of the Ganoderma wilt disease of arecanut. It is more or less prevalent in the lower Assam districts namely Goalpara, Kamrup, Barpeta, Bongaigaon, Kokrajhar, Dubhri, Nalbari and Darrang. It has been reported highest Ganoderma disease incidence in Assam recorded up to 77 per cent in Goalpara. But in our recent survey, we found disease incidence of 12-55 per cent in different localities of the district. In the last few years, disease incidence have found to come down. In Goalpara district many arecanut plantations have shifted to rubber plantation due to Ganoderma havoc. Farmers adopted integrated management practices includes maintaining the spacing of 2.7m. X 2.7m.; growing of banana as intercrop in arecanut plantation; application of recommended dose of organic manures; application of neem cake containing Trichoderma @ 5kg /palm/year; drenching the basin with 25 litres of 0.1% Calixin; drenching the soil with 1 per cent Bordeaux mixture for management of the disease.

TS12-O3

Enhancement of production and productivity in jhum farming through seed treatment

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In Chandel district, Jhum cultivation is still the most viable agricultural practices with over 1250 sq.km of the district land mass coming under this ancient form of farming. A flagship Jhum Improvement Programme was implemented by ICAR RC for NEH Region Manipur centre during Kharif season in 2014, 2015 and 2016 in Chandel district in collaboration with KVK Chandel under Tribal Sub-Plan (TSP). The technology intervention before sowing *i.e.,* seed treatment by Carbendazim@ 2 gm/kg seeds for Groundnut, Maize, Soybean, Ginger and Turmeric were done. Before implementation of this programme, the farmers have no knowledge about the seed treatment and its importance. No seed treatment was done and also not much of plant protection chemicals were used by the farmers. Through the intervention of seed/rhizome treatment the farmers could get a Groundnut yield production of 17.50 q/ha as compared to 10.25 q/ha of farmer practice, Soybean 19.01 q/ha as compared to 11.25 q/ha of farmers practice, Maize 35.75 q/ha as compared to 27.30 q/ha of farmer practice, Ginger 137.42 q/ha as compared to 125.55 q/ha of farmer practice and Turmeric 233.22 q/ha as compared to 192.35 q/ha of farmer practice. The farmers were so delighted to know about the seed treatment done before sowing of the crops which decreases the incidence of diseases during the crop growth thereby increasing the yield production and productivity. This intervention made a positive impact in sustaining agriculture in Jhum Improvement for food security of tribal farmers.

TS12-O4

Standardization of surface sterilization technique for *in-vitro* propagation of *Anthurium* (*Anthurium andraeanum Lind*.) cv. Jewel

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Surface sterilization is the most important step in explant preparation for micropropagation as it controls the fungal and bacterial contamination from field sources. An experiment was conducted to standardize the surface sterilization technique of *Anthurium andraeanum* cv. Jewel using immature bronze coloured leaves as explants for callus induction. Explants were collected, cleaned repeatedly using Tween–20 in fresh running water and then treated with 12 different combinations of Sodium hypochlorite (1.5%), Mercuric chloride (0.1%) and ethyl alcohol (70%) with varying exposure durations. Surface-sterilized explants were then inoculated in MS medium supplemented with various concentrations and combinations of 2,4-D, BAP and TDZ. Leaf explants when treated with mercuric chloride (0.1%) (3 minutes) + ethyl alcohol (70%) (30 seconds) resulted in lowest percentage (3.67) of contaminated cultures, lowest explant mortality (11.33%) as well as highest survivability (85.67%). Sodium hypochlorite (1.5%) (15 minutes) resulted in highest explant mortality (49.33%) while 5 minutes treatment resulted in lowest survivability (30.33%). Mercuric chloride (0.1%) (3 minutes) + ethyl alcohol (70%) (30 seconds) may be recommended for micropropagation of *Anthurium* through leaf explants.

TS12-O5

Combating pests under climate changes regime at the threshold of organic agriculture

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In the present century, climate change possesses the biggest threat to mankind and his environment. The impact has been witnessed in many sectors such as effects on biodiversity, food grain production, insects and plant diseases. Impact of climate change is more likely in developing countries due to high dependency on climate-sensitive livelihoods like rain-fed agriculture, water, and forestry. The most significant factor involved in global climate changes are increase in temperature, the rise in the concentration of atmospheric CO_2 and the shifts in precipitation pattern leading to the changes in the distribution of plant disease and pests, which have unfavourable effects on agriculture. Majority of the North East India’s population depends on agriculture for food and livelihood. As temperature increases, the robustness of the pathogens enhanced in terms of a number of generations and sexual reproduction, extending the amount of time available for reproduction and dissemination. Higher CO_2 concentration favours pathogen growth resulting in fungal spore formation, higher photosynthesis rate, reduction in transpiration and stomatal conductance and improved water-use efficiency. Climate change can also influence the development and distribution of arthropod vectors. It can

also affect the insect pests’ rate of reproduction, development, and adaptation. It will increase the overwintering of insects making it vulnerable to parasitoids and predators. The interaction between insect pests and their host plant is affected. Climate change also affects the relationships between pests, their environment and other species like natural enemies and competitors. There is a potential shift in the pests’ species distribution due to the climate change, as they expand to higher latitude and altitude and disappear from areas that have become climatically unfavourable for survival. Studies have illustrated that organic farming can be the good option for battling the climate change by reducing the amount of carbon in the atmosphere and decreasing greenhouse gas emissions thereby strengthening the food security. Organic agriculture contributes management practices that can help farmers adapt to climate change through strengthening agro-ecosystems, diversifying crop and livestock production, and building farmers’ knowledge base to best prevent and confront changes in climate.

TS12-O6

Management of leaf curl disease in king chilli

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In Tamenglong district of Manipur, King chilli (*Capsicum chinense* Jacq) is often attacked by leaf curl disease during the month of August to October. Leaf curl disease is a plant viral disease caused by tobacco leaf curl virus (TLCV). On-farm testing were conducted on farmers’ fields at Tupul and Noney villages of Tamenglong district during *Kharif* season of 2014-15 and 2015-16 to study the effect of different management practices like foliar spraying of Imidacloprid 17.8 SL @ 0.5 ml/L plus roguing of the infected plants and installing yellow sticky traps, foliar spraying of neem products (Achook @ 2 ml/L) on leaf curl disease of King chilli (local cultivar) and compared with farmers’ practice (Local check). Results from on-farm trials(2014-15) showed that leaf curl disease incidence was observed to be 6% and the average fruit yield was 9.62 q/ha and BCR was 2.95 in plots where treatment was given while in farmer’s practice, the disease incidence was found to be 35% and the average yield was 6.00q/ha and the BCR was 2.1 Similarly, results from On-farm testings (2015-16) showed that both the treatments (Treatment 1 and Treatment 2) were effective in managing the disease thereby resulting in higher yield and proved better than farmer’s practice. However, Treatment 2, where the foliar application of Imidacloprid 17.8 SL @ 0.5ml/L was given, was found to be more effective than Treatment 1 (foliar spraying of neem products + installing yellow sticky traps@10 traps/ha) in managing the disease. In Treatment 2 the average fruit yield was 8.83q/ha and the leaf curl disease incidence level was 6% whereas in Treatment 1, the average yield was 7.6 q/ha and disease incidence level recorded was 15%.

TS12-O7

Integrated disease and insect pest management of king chilli (U-morok)

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King chilli is an economically important crop of North East India in general and Manipur in particular. Diseases and insect pests are the major constraint in the production and productivity. An integrated disease and insect-pest management module was validated and standardized for king chilli under Manipur conditions. Soil application of *Trichoderma harzanium* (@ 50g m/10 litre water in 2 sqm area) was done 3-4 days ahead of sowing. Seeds were treated with *T. harzanium* @ 10 gm/1k g seed before sowing. To manage the incidence of sucking insect pests and the viral diseases (thrips, aphids, whiteflies etc.) they transmit, imidaclorprid 70 WS @ 2gm or Thiamethoxam 25 ws @ 5 gm per 10 litre water was sprayed twice at 15 days interval in the nursery stage. Spray was again repeated twice to thrice (based on the prevalence of insect pests) at vegetative, flower and fruit initiation stages along with immune booster Green guard @ 50 ml per 10 litre water. In the plots where king chilli was transplanted, yellow sticky traps (10-15 strips per 500 sq ft.) were installed and a spray of broad spectrum fungicide- Azostrobin 23 SC @ 10 ml per 10 litre water was given as and when fungal diseases appear. Further in demonstration plots, spray of alkaloids based plant extract (Rakhawala) @ 15-20 ml per 15 litre water twice at 15 days interval was also useful. A micro nutrient mixture i.e. agromin gold @ 10 ml per 10 litre water at least 2-3 times at vegetative, flowering and fruiting initiation was also found very effective for increasing the growth and yield of the fruits. This module was successfully demonstrated in farmers’ field (Kh. Nimaichand Singh) at Imphal, Manipur.

TS1-P1

False smut is emerging threat for rice production in Odisha

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False smut of rice is becoming an emerging threat to many rice growing regions of the world. The disease appearance and severity have been reported in different parts of India too. Therefore, to understand the disease status, we undertook a survey to assess the disease for incidence and severity levels in the paddy fields of Kishan nagar and National Rice Research Institute, Cuttack for 15 paddy varieties following standard procedures during *Kharif* 2016. The highest disease incidence was observed on Pooja showing 55.61% followed by CR Dhan 1014 and Swarna sub1 both showing 33.33% but Geetanjali was free from infection. The remaining varieties were intermediate in the levels of disease incidence. Similarly, the highest disease severity was observed on Pooja showing 359.82 followed by Naveen (76.95) and CR Dhan 1014 (50.16). The mean disease incidence and severity of the varieties were 17.64 and 43.79% respectively. The per cent infected tillers were observed to vary between 4.82% and 55.61%. The smutted ball per panicle ranged from 0.53 to 6.47. The mean weights of 100 healthy and smutted seeds were 2.33 gm and 7.94 gm respectively. The present data suggested that rice false smut is becoming a regular occurrence in Odisha with moderate level of severity but has the potential to increase its severity in the near future.

TS1-P2

First report of rust caused by *Uromyces vicea-faba* on fababean (*Vicia faba* L.) in North East India

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The occurrence of rust disease on faba bean was observed during January-February of 2016 in ICAR Research Farm, Dimapur district of Nagaland as a first report of rust disease on faba bean in North East India. The rust pustules were initially light brown colour which later turns into dark brown in colour. After aging, rust pustules become corky encrustation on leaves. Under microscope, the rust spores were observed and confirmed with the presence of uredospores and teliospores. Uredia are yellowish- brown colour, round with double layers, whereas the telia were elongated dark brown in colour with elongated stalk. Under field condition, 59 faba bean lines were screened and severity of disease was computed by using 0-9 scale and calculated the PDI (Per cent Disease Index). Among them, the occurrence of disease incidence ranges from 0-90% was noticed. The maximum disease incidence of 90% was reported in EC-628957.

TS1-P3

Survey, detection and characterization of huanglongbing in different citrus growing groves of Manipur and adjoining areas

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Citrus is an important fruit crop of North Eastern region of India. The production of citrus is limited by a number of biotic and abiotic factors leading to decline. Virus and virus-like pathogens have been one of the major causes of citrus decline and are most difficult to manage. In the present study, systematic surveys were conducted in different citrus growing pockets/grooves of North East India including Burma and Nagpur (Manipur, Tripura, Arunachal Pradesh, Nagaland and Burma) for detection of Huanglongbing (HLB) previously known as citrus greening. A typical symptom of Huanglongbing (HLB) fluctuating from yellowing of leaves, branches, Zn deficiency like appearance, irregular blotching called mottling were observed under field conditions. Among the above-mentioned symptoms, mottling is the typical one. Most remarkably, those samples showing Zn deficiency like symptoms were found positive in North Eastern region. During the survey, *Diaphorina citri,* a vector responsible for transmission of HLB also collected from Pasighat and Bodak regions of Arunachal Pradesh to check the prevalence of HLB bacterium. Out of total 70 samples tested from different parts of North Eastern Region including Burma and Nagpur by normal PCR using specific primer targeting 16srRNA 48 samples were confirmed positive *i.e.* 68.57 % infection indicating a high occurrence of HLB in North Eastern India. The highest incidence of HLB was observed in Bodak and Pasighat, Arunachal Pradesh exhibiting 76.47% followed by Manipur (58.33 %). It was found from the analysis of sequence identity that 99-100 % identity was found among the isolates of Manipur showing a high level of resemblance and there is 90-100 % identity was found with others isolates of HLB reported all over the globe. Further, 12 samples (HLB) were analyzed to infer genetic relationship by Neighbor joining phylogenetic analysis incorporating 20 HLB isolates from other parts of the globe using *Halomonas sp*. HS215 as out-group. Manipur Isolate HLB_Mnp28 was different as compared with remaining Manipur isolates and isolates from other parts of the World.

TS1-P4

Present scenario of sheath blight of rice in India

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Sheath blight caused by *Rhizoctonia solani* is a persistent problem in rice cultivation. The pathogen is polyphagous competitive saprophyte which has a wide range of hosts. The crop planted with high density and closed canopy accompanied by high nitrogen doses favours the development of disease from the time of panicle initiation. The incurred yield losses by this particular pathogen may range from 1.2 - 69%. Disease infection increases peroxidase, chitinase and polyphenol oxidase activities and decreases the activity of catalase. Infected tissues contain higher levels of phenols compared to healthy ones. Initial symptoms of the disease appear in the form of circular, oblong or ellipsoid, greenish, grey and water-soaked spots of about 1cm long on the leaf sheath just about the water line. A Recent survey in different districts of Manipur showed a variation on the occurrence of sheath blight. Reports suggested that till date only partial resistance has been noticed as revealed by the survey of 6000 rice cultivars from 40 countries, from which no single cultivar with a major gene for sheath blight resistance. The initial study on the variation of the isolates available isolates of *R. solani* is in progress.

TS1-P5

Present scenario of brown spot of rice in India

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Brown spot disease is caused by the fungal pathogen *Helminthosporium oryzae* (Syn: *Drechslera oryzae*; sexual stage: *C. miyabeanus*), which causes significant yield loss in rice production (up to 90%). The fungus attacks the crop from seedling in the nursery to milk stage in the main field. The disease appears first as minute brown dots, later becoming cylindrical or oval or circular. A Recent survey in Manipur showed an increase in the incidence of brown spot of rice in Bishnupur and Imphal West. Some resistant varieties like Co4, Cauvery are under in commercial cultivation. Research during the previous two decades has led to the possibility of biological control as an increasingly realistic option for rice disease management, *Trichoderma* spp. has been shown to be effective for the control of brown spot disease and the increase of plant growth on rice. Biotechnological approaches like Real-time quantitative PCR (RT-qPCR) reports the quantitative expression of known defence genes in rice leaves upon *B. oryzae* infection. Effective control measures carrying by using the phenolic antioxidants substances on rice diseases. Mitogen-activated protein kinases (MAPKs) are ubiquitous and evolutionarily conserved enzymes connecting cell surface to intracellular regulatory targets activating various morphogenetic changes. The variability study of the pathogen in Manipur is in progress.

TS2-P1

Morphological and cultural characterization of *Alternaria solani* (Ellis and Mart.) Jones and Grout causing fruit rot of tomato

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Fruit rot of tomato caused by *Alternaria solani* is most destructive and causes fruit rot in storage, transportation, and marketing. *A. solani* produced dark or olivaceous brown mycelium and conidiophore, Conidiophores arose singly or in groups with regular septations. The conidia were pale to olivaceous-brown in colour produced singly or seldom in short chains, elongate-obclavate and muriform in shaped. The mycelial diameter was around 11.25 µm and Conidia length measured about 237.5 µm and 30µm in breadth with 1-4 longitudinal septa and 5-7 transverse septa. Maximum fungal growth was found in Oatmeal agar (83.67 mm) followed by Potato dextrose agar (58.33 mm) and Czapeck's dox agar (57.33 mm), whereas least growth was recorded in Elliott's agar (28.00 mm). The maximum sporulation was found in Potato dextrose agar (40 X 103 spores/ml) which was followed by Czapeck'sdox agar (28 X 103 spores/ml) and host extract agar (24 X 103 spore/ml).There was no sporulation in Elliott's Agar medium. The growth characteristics such as the colour of colony, margin of colony and zonation along with the sporulation of the test fungus were studied on these solid media. All the culture media under test supported the linear mycelial growth of *A. solani*. The fungal growth in liquid culture media was found to be maximum in Potato dextrose broth (433.13 mg) followed by Richard's broth medium (311.7 mg) and Malt extract broth (297.00 mg). Morphology and cultural characteristics of *Alternaria solani* were investigated for identification and physiological studies.

TS2-P2

Understanding mycelial compatibility of S*clerotium rolfsii* in Manipur

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Sclerotium rolfsii is a soil inhabitant, non-target, polyphagous, and a ubiquitous facultative parasite. It is widely distributed in tropics, subtropics and also in warmer part of the temperate zone of the world. It has wide host range infecting more than 500 plant species. The present study was undertaken to investigate the mycelial compatibility groups of *S. rolfsii* by following methods of Punja and Grogan (1983). A total eleven isolates of *S. rolfsii* are isolated or collected for these studies and among them, six are isolated from Manipur, two from Andhra Pradesh and one from Tripura, whereas one each collection was done from Orissa and Chhattisgarh. The isolates were assigned as SR1, SR2, SR3, SR4, SR5, SR6, SR7, SR8, SR9, SR10 and SR11. Pairings of isolates were examined macroscopically after 5 and 10 days of incubation for the presence of an antagonism zone in the region of mycelial contact. Altogether there were sixty-six numbers of the combination were done among *S. rolfsii* isolates. The results of mycelial compatibility showed that a total of 35 numbers under 0 scale, 8 numbers under 1 scale, 11 number under 2 scale, 2 numbers under 3 scale and 10 numbers under 4 scale respectively. The present finding shows there is the presence of compatible as well as non-compatible isolates of the *S. rolfsii* in Manipur with respect to other isolates.

TS2-P3

Morphological and pathogenic variations in the isolates of *Rhizoctonia solani* of different hosts

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Rhizoctonia solani (Teleomorph: *Thanatephorus* spp.) is a plant pathogenic fungus with a wide host range and worldwide distribution causes severe damages in crops all around the world. *R. solani* is best known to cause various plant diseases such as collar rot, root rot, damping off, sheath blight, hypocotyls, stem canker, web blight, and wire stem throughout the world. Morphological variability was studied in 11 isolates of *R. solani* having different hosts from 2 different places *viz.*, Tripura and Assam. Colony size, colony growth, colour and sclerotia formation (central, peripheral, or scattered), location (aerial or surface) and texture (smooth or rough) varied in these isolates. A number of nuclei per cell were examined by staining the hyphae with safranin-0, KOH and lactophenol blue where lactophenol blue gave the best result. A number of nuclei per cell were variable (7 to 37, n=20), providing evidence that the isolates belonged to *R. solani.* Mycelial compatibility was studied between the isolates of different hosts. Isolates, when combined with the same host, gave compatible (+) reaction whereas isolates when combined with different host gave an incompatible (-) reaction. Pathogenicity test was conducted on hypocotyl by mixing the soil with culture having *R. solani* and seeds were sown for germination. Fifteen days after the germination of seeds, seedlings showed symptoms, whereas controlled seedlings remained healthy. Pathogenicity test was conducted on leaves by inoculating mycelial disc on healthy plants of different hosts, with non-inoculated plants serving as a control. Few inoculated plants developed symptoms, whereas controlled plants remained healthy.

TS2-P4

Molecular detection of banana bunchy top virus from North East India

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Typical symptoms of the narrower leaf with wavy-yellow margins, stunted growth and deformed fruit are of common appearance in certain cultivated banana varieties in Manipur. Such symptoms of the banana disease are commonly associated with Banana bunchy top disease caused by Banana bunchy top virus (BBTV). To know the exact identity of the associated virus, PCR based tool was employed. Symptomatic leaf samples were collected from 20 plantation sites covering 6 districts of Manipur and subjected to PCR amplification using primers to 'DNA R and DNA U3' of BBTV genome. Amplification of 1,110 bp fragment revealed the association of BBTV. In all together, ten (10) samples showed the amplification of the DNA R region while the remaining samples were not able to give the expected amplicon. Isolates of BBTV have also undergone PCR amplification for U3 region of BBTV (1,050 bp). In the present analysis, banana varieties 'Meitei Hei' and 'Korbot' samples did not give respective PCR amplicon of both the fragments (DNA R and DNA U3) of BBTV. BBTV specific amplicons were amplified from symptomatic banana cultivars *viz*; Jehaji, Granaine, Amrita kola and Champa kola. Partial sequence analysis of four isolates for both DNA R (467 bp) and DNA U3 (441 bp) of BBTV virus using MEGA 6 software revealed the close affinity with BBTV reported from Pacific-Indian Oceans (PIO) group through DNA R sequence analysis. DNA R based analysis reflects four isolates of Manipur has sequence similarity between 66-95% among them. Manipur isolates show close proximity with those reported from Arunachal Pradesh, Congo, Chennai, Sri Lanka and China. While DNA U3 sequence analysis from four samples revealed a sequence similarity of 90-97% among them. The present analyses, therefore, revealed the presence of BBTV in certain banana cultivars and require further study of its genetic insights so as to achieve an easier way of detection and diagnostic tools.

TS2-P5

The biotic causes associated with no-podding syndrome of soybean in Vidarbha region, Maharashtra

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Soybean (*Glycine max* L.) is a species of legume native to East Asia, which serves as a principal dietary food and oil source. It is the major cash crop of the Central zone of India. It has been facing a serious setback due to the occurrence of no-podding syndrome since the past decade causing more than 80% yield losses and the average no-podding syndrome incidence ranged from 8.0 to 14.6% in different parts of the states where soybean is cultivated. The symptomatic plants produced either no or deformed pods and distorted flowers and they remained green after maturity. Also, infected plants showed thicker stem and shorter internodes as compared to the asymptomatic plants. Soybean samples with no-podding syndrome were analyzed by PCR and serologically by DAC-ELISA showed a positive reaction and confirmed the presence of Phytoplasmas, Tobacco streak virus (TSV) and Groundnut bud necrosis virus (GBNV). It was also observed during the field survey that green stem syndrome and Soybean mosaic virus (SMV) was associated with soybean no-podding syndrome. The green stem does not have a clear effect on yield, but the green stems make harvesting more difficult. There is not an exact cause of green stem syndrome, but some factors that may influence the problem include environmental conditions, viruses and germplasm. The supportive and strong findings in this investigation on symptomological study, molecular detection and serodiagnosis will be helpful to find out suitable control measures of different biotic causes associated with no-podding syndrome of soybean in this region.

TS2-P6

Present status of chilli anthracnose in India

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Chilli (*Capsicum annuum* L.) is one of the important cash crop in India which belongs to the Solanaceae family. Indian chilli is considered to be world famous for two important commercial qualities, its colour and pungency levels. India ranks first in terms of chilli production. However, chilli anthracnose which is caused by *Colletotrichum* species is a major constraint in chilli production leading to huge economic losses worldwide resulting in high yield losses. Anthracnose disease is seen on mature fruits resulting in both pre-harvest and post-harvest fruit loss. The percentage incidence of anthracnose affected fruits under field conditions was more on green fruits which ranged from 55.53 % to 71.10 %. In India, a calculated yield loss of 10-54 per cent has been reported in yield due to chilli anthracnose disease. The disease is found to be prevalent in almost all the chilli growing states with disease incidence ranging from 51.75% to 66.70% in Rajasthan (Jaipur), 47.8% in Uttar Pradesh, 37% in Punjab followed by 11.56 to 31.49% in Maharashtra. In Manipur, a severe anthracnose occurrence of chilli was observed at an experimental farm causing 80% seedling mortality. Developing resistance against the pathogen in the host is seeking to be the most important and sustainable approach for managing the disease. Recently, nine varieties have been reported *viz*., BS-35, BS-20, BS-28, Punjab Lal, Bhut-Jolokia, Taiwan-2, IC-383072, Pant C-1 and Lankamura Collection. These strategies not only eliminate the losses caused due to the disease but also remove the chemical and mechanical expense of the disease control. The use of resistant cultivars is the cheapest, easiest, safest, and most effective means of controlling crop diseases.

TS2-P7

Study on the occurrence of white rust of rapeseed and mustard caused by *Albugo candida* in Manipur

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Rapeseed and Mustard are the second most important oilseed crop in India after soybean. It is a rich source of oil (31-48%) and protein (40%). The white rust caused by *Albugo candida* affects a number of Brassica plants of economic importance causing yield loss up to 23 to 54.50%. Therefore the present work was undertaken to study the occurrence of white rust caused by *A. candida* in Rapeseed and Mustard growing areas of Manipur. The survey was taken up during Rabi season 2016-17 at seven *viz*., Mayang Imphal, Wangoi, Wangjing, Kakching, Iroisemba, Lilong and Vajing valley areas of Manipur and its incidence were ranged from 2.22-16.70 %. Maximum disease incidence was found in Vajing (16.70%) of Churachandpur district, and minimum at Kakching (2.22%) of Thoubal district. Morphological studies of sporangia of seven isolates of *A. candida* revealed slightly spherical in shape and size of sporangium varied from 13.22×11.69-18.50×12.96µm. Sporangial germination of different isolates was ranged from 58-

80 %. Pathogenic variability of all *A. candida* isolates showed creamy white pustules, however, size of pustules in all isolates ranged from 1-5mm in diameter. The shape of rust pustules were also varied in *A. candida* isolates *viz*., pinhead, raised, circular, surrounded by pure white was observed in Vajing, while pinhead, raised, circular, depressed at center was observed in Mayang Imphal, Wangoi, Kakching, Lilong and pinhead, raised, circular, scattered was observed in Iroisemba, Wangjing isolates. The present study showed the prevalence and presence of variability of *A. candida* in Manipur.

TS2-P8

Tree Bean (*Parkia roxbhurghii*) decline in perspective of Plant Pathological point of view in Manipur

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The issue of tree bean quick decline or sudden death disease is an unsolved prolong problem to mankind. This disease has been becoming an increasing threat for tree bean production in the North-Eastern region of India. Plant protection is the most important aspect for management of tree bean. In entire North Eastern region in general and Manipur in particular, a large scale of dieback has been observed during the last 6-7 years. Tree bean decline has emerged a major threat to its cultivation in the last decade. A large number of trees have been wiped out due to the problem of decline in Manipur and other NE states. Decline of the tree bean plants can be observed in one – two year old plant as well as older plants. The symptoms include withering from the tip on words, gradually proceedings top to bottom (in one-two year old plants). The discolorations of the roots as well as infected stems are observed in wilted plants. The associated pathogen is isolated from the vascular discoloured area of infected plants and isolated fungus does not produce any spore in PDA media. Further identification and molecular study is being in progress.

TS2-P9

Stem rot of rice present scenario in India

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Rice (*Oryza sativa* L.) is the most extensively grown staple food crop in India. India is the second leading rice producers in the world. Rice crop is attacked by several bacterial, fungal and viral pathogens and caused devastating damage every year. Among all the diseases, stem rot comes under minor disease, but in Manipur, it is one of the major disease causing severe loses. Stem rot of Rice is caused by *Sclerotium oryzae* in general, but in Manipur, there is an association of other pathogens such as *Fusarium* spp. The symptoms can be seen in the early stages of the crop and early infection causes more losses to rice yield. In a recent survey by the State Agriculture Department, Manipur, it was found that the incidence of the disease is increasing year after year. The disease is favoured by low soil potassium and high nitrogen levels. Stem rot is more serious in fields where rice is grown continuously for several years. In rice-growing

valley areas, stem rot first appears during the tillering stage as small, black lesions on leaf sheaths at the water line. As the disease progresses, infected sheaths die and slough-off. Stem rot leads to the production of chaffy grains and unfilled panicles. The details research on the incidence of this disease and variability of the pathogen is in progress.

TS2-P10

Detection of seed borne fungi of black gram [*Vigna mungo* (L.) Hepper]

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A total of twenty seed borne fungi belonging to 13 genera *viz.*, *Acremonium stictum, Aspergillus flavus, A. fumigatus, A. niger, Botryodiplodia theobrome, Chaetomium globosum, Cladosporium oxysporum, Epicoccum purpurascence, Fusarium Chlamydosporum, F. oxysporum, Mucor circinelloides, Nigrospora oryzae, Penicillium chrysosporium, P. glabrum, P. oxalicum, P. sclerotiorum, Phoma glomerata, Rhizoctonia bataticola, R. Solani* and *Syncephalastrum racemosum* were isolated from two black gram varieties *viz.,* Local and Uttara. Among the fungi isolated, *Aspergillus fumigatus, Aspergillus flavus* and *Aspergillus niger* were the common and dominant seed borne fungi associated with the black gram seeds. Agar plate method was found to be favourable for the maximum counts of seed borne fungi than the Blotter method.

TS2-P11

Survey for the incidence of soft rot of ginger caused by *Fusarium oxysporum* f. sp. *zingiberi* in different districts of Manipur

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Ginger (*Zingiber officinale* Rosc.) is an important crop grown for its aromatic rhizomes, used both as spice and medicine. It is an herbaceous tropical perennial belonging to the family Zingiberaceae. Rhizome rot disease caused by fungi (*Pythium* spp., and *Fusarium oxyporium* f. sp. *zingiberi*) is the major problem all over ginger growing areas of India. In Manipur, ginger plants are widely cultivated and soft rot disease are reported to be serious. A survey was undertaken during the year 2015 and 2016 in ginger growing districts of Manipur *viz*. Imphal-East (Nongpokheirok and Thayong), Imphal West (New Keithelmanbi and Keithelmanbi Namching), Bishnupur District (Yumnam Khunou and Oinam) and Churachandpur District (Vaging village and Khenjang village) to gather the basic information as well as to collect plant and soil samples from ginger fields for further study. During 2015, disease incidence ranged from 14.00 per cent to 47.00 per cent and during 2016, it ranged from 14.47 per cent to 53.30 per cent. There were variations of disease index in different locations and during 2016 disease indexes of all the locations were higher than that of 2015. The mean maximum per cent disease incidence (53.30 per cent) was observed in Keithelmanbi Namching of Imphal-West district, followed by Yumnam Khunou (51.0 per cent) of Bishnupur district whereas, the least per cent disease incidence (14.00 per cent) was observed in New Keithelmanbi of Imphal-West district.

TS6-P1

Trichoderma- a paramount tool for pathogenic fungi control

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Control a disease through biocontrol agent is an effective alternate nowadays. Soilborne pathogens, *viz*., *Rhizoctonia solani, Sclerotium rolfsii, Pythium debaryanum, Fusarium oxysporum* and *Fusarium solani* are the most destructive pathogens of many crops. These disease-causing pathogenic fungi cause considerable loss of crop productivity. To avoid the excessive and unnecessary use of chemical fertilizers these biocontrol agents were one of the effective alternatives to control the diseases causing by pathogenic fungi. Many natural biocontrol agents exist in the soil with their strong antagonistic activity against the incitant of diseases. Genus *Trichoderma* is one of the best antagonists in inhibiting the pathogenic fungi in the soil thereby promote the plant growth. Many species of Trichoderma *viz*., *Trichoderma harzianum, T. viride, T. reesei, T. Koeningii, T. atroviride* and *T. longibrachiatum* with the mechanism of competition for space and nutrients, mycoparasitism, rapid and profuse substrate colonization, cell wall degrading enzyme production, antibiotic production and induced resistance efficiently check the pathogens to develop diseases. Thus *Trichoderma* is a potential fungus for biological control activity and in inhibiting the growth of other pathogenic fungi.

TS6-P2

Piriformospora- an exertive fungus for plant growth promotion

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Piriformospora indica, an actively growing pear shaped mycorrhizal root-inhabiting fungus present in diversified tree species especially woody species as an important endophyte. In agriculture sector, *P. indica* used as a major bio-fertilizer for improving water absorption, mineral uptake, photosynthesis, plant growth by providing the phosphorous and make it available to the plant for vigorous development of plant and aid in crop fitness. Under favourable environmental conditions it will copiously colonizes the plant roots and in the rhizosphere zone, thereby promotes seed germination, early flowering, increased biomass production and crop productivity. *P. indica* is shown to have enormous bioprotective potential through fungistatic nature and by the production of lytic enzymes like chitinases and β-1,3-glucanases, antifungal metabolites, HCN, ammonia and the production of siderophores against plant pathogens *viz*., *Fusarium, Verticillium, Aspergillus* and *Rhizopu*s in agricultural and horticultural crops. Besides this, *P. indica* can induce both local and systemic resistance to fungal and viral plant diseases through signal transduction. In this perspective, despite of using of inorganic fertilizers, chemical fungicides and to enrich the soil *P. indica* application acts as a paramount tool for realizing the targeted improvement in the production of crop plants and sustainable agriculture

TS6-P3

Nanotechnology in plant disease management

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Nanotechnology is a rapidly advancing and extremely interesting science in the field of agriculture. Nanomaterials (1-100 nm) can be potentially used in the crop protection, especially in the plant disease management. This has led to the development of several types of nanomaterials, including the metallic nanoparticles Ag, Cu, CuO, ZnO and TiO_2 with carbon-based nanomaterials, such as carbon nanotubes (CNTs), as well as graphene oxide (GO) and metallic nanoparticles formed on silica nanoparticles. Among the different types of nanoparticles, AgNPs have been used as effective biocides against a variety of pathogens, fungi and viruses. Rapid detection technologies with high sensitivity and selectivity for plant pathogens are essential to prevent disease spread with minimal loss to crop production and food quality assurance. Nanomaterial synthesis by utilizing functionalized metal nanoparticles as a sensing component offer several desirable features required for pathogen detection. Nanoparticles may act upon the pathogens as same as chemical pesticides or carrier of active ingredients of pesticides. Because of the ultra-small size, it may target virus particles and thereby open a new field of virus control in plants.

TS6-P4

Effect of Volatile and Non-Volatile compounds of potent Native *Trichoderma* isolates against *Fusarium oxysporum* f.sp. *pisi* (Wilt of Pea)

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Pea is known to suffer from various diseases. Among the diseases affecting pea crop, wilt disease caused by *Fusarium oxysporum* f.sp. *pisi* was found to be the most serious. The disease spread through the infested soil and through affected seed and in severe cases the whole plant wilt and die. During recent years, wilt of pea has become very serious in many pea growing areas of Manipur. Fifteen potential isolates of native *Trichoderma* from different districts of Manipur namely Imphal East, Imphal West, Thoubal, Bishnupur, Ukhrul and Tamenglong were tested for their ability to produce volatile and non-volatile compounds (in two concentration *i.e* 7.5% and 15% v/v) against *F. oxysporum* f.sp. *pisi.* The effect of volatile compounds produced by different *Trichoderma* isolates against the causal pathogen ranged from 20.77 to 57.77% inhibition and highest was found in TTH-1 (Lilong of Thoubal district)with 57.77% and lowest was found in TUK-1 (Litan of Ukhrul district) with 20.77% inhibition. The inhibition effect of non-volatile compounds ranged from 6.66 to 37.77% at 7.5 % v/v concentration and 12.22 to 57.77% at 15% v/v concentration. Highest inhibition at 7.5 %v/v concentration was recorded in TTH-1 (Lilong of Thoubal district) (37.77%) and at 15%v/v concentration in TBI-2 (Toubul of Bishnupur district) (45.55%).

TS6-P5

Beauveria bassiana- an important beneficial microbe against important insect pests

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Entomopathogenic fungi constitute the largest single group of pathogens among its orders. *Beauveria bassiana* belongs to the order Hypocreales with an advantage of higher host specificity. They have a unique mode of action that caused infection by growing through insect cuticle by penetration. It was reported that multiple or single foliar applications of *B. bassiana* strain GHA (Bb-GHA) have been found effective for the management of Colorado Potato Beetle, *Leptinotarsa decemlineata.* Moreover, the physical and biochemical properties of conidia of *B. bassiana* and the hydrophobins layers covering conidia surface reduced *Ceratitis capitata* oviposition significantly on fruits by impairing the ability of cues detection by flies. Keeping a view on insecticides resistant, pest resurgence and concern over the environmental impact of agricultural inputs there is an urgency to search for the alternative, biologically based forms of pest control. The exotoxins Beauvericin, Beauverolides and Beauverolide of *B. bassiana* can be used against termites, silkworm, beetles and grasshopper. In recent studies on *B. bassiana* showed that they have potential to use in *Polyphylla fullo*. This review outlines the current state of knowledge of insect fungal pathogens as it relates to their present use and future potential as mycoinsecticides.

TS8-P1

Potential plant disease management using functional genomics

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With the advent of molecular biology, genomic manipulations are beginning to revolutionize our understanding of plant disease resistance. Large-scale sequencing combined with functional genomic analyses revealed the precise organization of resistance-gene complexes and the genetic mechanisms involved in generating new resistance and susceptibility specificities. Genomics could enable effective deployment of these genes in cropping systems, so providing better and more durable resistance against different pathogens. This includes the creation of plants with traits that confer resistance to various biotic stress and even, abiotic stress also. In the absence of genetic resistance, crop production relies heavily on chemical control of pathogens which has harmful effects on health and environment. The most renewable strategy to manage plant disease is to develop resistant plants, thereby obtaining environmental, economic, and social benefits. Recently new genome editing tools like zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindromic repeats/Cas9 (CRISPR/Cas9) have been developed. Progress towards new disease control strategies depends on obtaining additional genome sequences.

TS11-P1

Value addition of underutilised mushroom of Chandel district, Manipur

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Chandel, a hilly terrain is blessed with many underutilized mushrooms. A large portion of district's hill areas has been under jhum cultivation. In Chandel, there are many underutilized mushrooms which are yet to be exploited and some are already explored by the scientist. Mushroom is a nutritious natural vegetable which contains high-quality protein, vitamins, and fibers. The underutilized mushroom is available in plenty in the month of May to August every year; depending upon the rainfall in the hillock of Chandel district. It is highly perishable. Due to lack of storage and lack of knowledge for processing, preservation and value addition, a large amount of mushroom goes wasted every year. To tackle such problem KVK, Chandel took initiative for the promotion of processing and value addition of such underutilized mushroom. As a process, good quality mushrooms were selected for the preparation of different value-added products like pickles, dry preserves, pakaura for instant use and curry with different items. In the process of making mushroom pickles, fresh healthy mushrooms were selected and washed with clean water. For it, 20 kg mushroom, mustard oil 35 %, spices 0.4 %, salt 10 %, chilli powder 0.3 – 0.4, turmeric powder 0.1 %, acetic acid 0.5 % and make 100 bottles of pickle and labeling is done before marketing. In the process of making mushroom dry preserves, the fresh healthy mushrooms were selected and dried in the sunshine/sunlight without any treatment. For dry preserves, 30 kg are sundried and packed in 60 polyethylene polythene packet and levels are added before marketing. The processed product of mushroom could reduce post-harvest losses to 25% from 75%. The shelf life of the mushroom pickle has been extended up to 12 months by preventing the growth of micro-organism and fungus which creates serious problems in the pickle. The benefit-cost ration of mushroom pickle is estimated as 2.34 and for the dry preserve, it is estimated as 3.0. The processing and value addition of underutilized mushroom could improve the livelihood and nutritional security of many farm women of Chandel district by enhancing their income generation.

TS11-P2

Impact of front line demonstration on oyster mushroom yield in Churachandpur district, Manipur

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Wild mushroom collected from the jungles are one of the favourite food for the tribes of Churachandpur district since time immemorial. Very few people of the district have knowledge about cultivated mushroom. Oyster Mushroom cultivation is considered as an alternative source of income to uplift the living standards of poor farmers and also to add high quality protein in their daily diets to eradicate malnutrition problems. Oyster mushroom can easily be grown by the rural women with minimum efforts. One of the major constraints of traditional oyster mushroom cultivation is low productivity due to non-adoption of recommended package of practices. To replace this anomaly, KVK Churachandpur under ICAR Research Complex for NEH Region, Manipur conducted 14 frontline demonstrations (FLDs) on recommended production technology of oyster mushroom in six different villages of the district namely Talian, Henkot, Yaiphakol, Mata, Matiyang, L. Molvom during Rabi season for four years (2012-2013, 2013-2014, 2014-2015 and 2015-16). The present study was carried out with the objective of finding the yield gaps between improved package of practices and existing farmers practice of oyster mushroom and to educate the oyster mushroom growers about its scientific cultivation, right from substrate selection till harvesting, to increase the productivity of the crop. The average yield of oyster mushroom in FLD ranged from 550– 645gm /Kg dry substrate whereas in existing practice only 300 gm /Kg dry substrate was recorded. Per cent increase in yield after the adoption of the improved technology over existing practice was recorded in range of 83.00 – 115.00. The extension gap ranging between 250-345 gm /Kg dry substrate during the study period. The technology gap decrease from 150% to 55% which clearly indicated the farmer's cooperation, in carrying out such demonstrations with encouraging results in subsequent years. The decreasing trend of technology index i.e., from 27.27 to 8.53 clearly shows the feasibility of the new technology at the farmers' fields. The lower the value of technology index more is the feasibility of the technology.

TS12-P1

Incidence of various insects-pests of turmeric grown in Manipur

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Manipur is home to various food and cash crops, fruits and vegetables. Like any other cash crops, turmeric cultivation has also found a place in the soils of Manipur and the state is also becoming the safe breeding ground for it. Amongst the biotic stresses Leaf spot and leaf blotch of turmeric are the two important diseases that affect the aerial shoots, which lead to severe reduction in yield. Disease incidence of about 25.32 % of leaf blotch and 39.52% of leaf spot of turmeric were recorded in Mega-turmeric 1. While only 7.32% and 10.87% of leaf blotch and leaf spot were recorded respectively in local indigenous turmeric of Manipur which is black in colour. Amongst the insect pest shoot borer (*Conogethes punctiferalis*), leaf roller (*Udaspes folus*) and Bihar hairy caterpillar (*Spilosoma obliqua*) are the major constraints which reduce the yield drastically. In local indigenous turmeric of Manipur Shoot borer was predominant in early vegetative phase (45-60 days) and grand growth stage (100-120 days) of crop growth. Incidence of about 78.5% incidence of turmeric was recorded for shoot borer infection, 54.2% for leaf folder and 10.23% for Bihar hairy caterpillar in local indigenous turmeric of Manipur. Others minor pests of various species of leaf beetles, caterpillars and grasshoppers were also recorded. Mega- turmeric-1 was found to be more susceptible to leaf spot and leaf blotch of turmeric as compare to local indigenous turmeric of Manipur.

TS12-P2

Study on post-harvest diseases of mango in Manipur

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Post-harvest losses of mango is one of the important economic losses and among the factors of Post-harvest losses, the disease is one of the main reason. A detailed Survey to access the losses of Post-harvest diseases of Mango in Manipur was conducted in four different areas viz., markets of Tegnoupal, Imphal West, Bishnupur district and Orchard (Andro Research Farm) of Imphal East district in the month of June, July and August 2017 by using the severity scale of 1-5. Post-harvest disease assessment was done by observing disease appearance on Mango fruits. It was found that the disease incidence ranged from 15-30, 35-55 and 45-75 % in the month of June, July and August respectively. The percent disease index ranged from 16.67- 27, 20-25 and 20-30 % in the month of June, July and August respectively. It is also observed that the variety Amrapali showed highest disease incidence as compared to Dasheri, Mallika and the local variety of Mango. The present study showed the prevalence of post-harvest disease of Mango in Manipur and further sustainable disease management practices required from the losses due to Post-harvest diseases.

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