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Proceedings of National Symposium on Plant disease management for food security under climate change scenario and Annual meeting of Indian Phytopathological Society (North Zone) organised on January 9-10, 2020 at ICAR-Indian Institute of Wheat and Barley Research, Karnal

National Symposium on "Plant disease management for food security under climate change scenario" and annual meeting of Indian Phytopathological Society (North Zone chapter) were jointly organized by Indian Phytopathological Society (IPS), New Delhi, Society for Advancement of Wheat and Barley Research (SAWBAR), Karnal and CCS Haryana Agricultural University, Hisar at ICAR-Indian Institute of Wheat and Barley research (IIWBR), Karnal on January 9-10, 2020. Dr. P.C. Sharma, Director, ICAR-CSSRI, Karnal was the guest of honour in the inogural season of symposium. He stressed on the soil health aspects in relation to the influence of soil microbes on plant health. He also emphasized on the development of holistic approaches for the plant diseases management along with the need of tracking transboundary movement of pathogens. The chairman of the session, Dr. G.P. Singh, Director, ICAR-IIWBR, Karnal stressed on the integrations of efforts made by all the disciplines to make diseases management effective and profitable under changing climate scenario. He also appreciated the efforts made by organising committee for including very pertinent technical sessions on microbial diversity, pathogen variability, epidemiology, plant microbial interaction, resistance breeding and integrated plant diseases management under changing climate. At the outset, Dr. Rakesh Mehra, President, IPS (North Zone) welcomed the delegates and highlighted the relevance of the symposium and gave an overview of the programme and various deliberations made in different sessions of the symposium. Dr. Robin Gogoi, Joint Secretary, IPS, appraised the house about the activities of IPS. This session was attended by the IPS delegates, University and State Department personnel, invited scientists, teachers, students, and the corporate representatives and a total of 92 delegates across the country including North India participated in the symposium. The senior dignitaries gave the strong message for making collaborative efforts for channelizing the output of research conducted by scientists in the field of Plant Pathology to devise technology for sustainable agriculture, in view of drastic and unpredictable climate change scenario. The inaugural session was followed by nomination for Prof MJ Narishamn Academic Merit Award. In this contest, out of four contestants two students namely, Preeti Sharma and Annie Khanna were nominated to represent the zone for Prof. M.J. Narasimhan Academic Merit award competition at national level. A total three technical sessions were organised during the two day symposium. In these session, several lectures highlighting the plant disese problems of the North Zone under climate change scenario along with probable solutions were delivered by Drs. Naresh Mehta, Dr. Ashwani Basandrai, Dr. H.R. Gautam, Dr. Robin Gogoi, Dr. Kalyan K. Mondol, Dr. Sunita Chandel, Dr. Jasapl Kaur, Dr. Kushal Raj, Dr. Renu Munjal, Dr. OP Chaudhary, Dr. Rakesh Kumar, Dr. Puja Srivastava, Dr Gyandendra Singh and Dr. Vimla Singh. This two days symposium was concluded with plenary session followed by valedictory function. The function was presided by Dr. G.P. Singh, Director, ICAR-IIWBR, Karnal. Certificates to the award winners were distributed with the auspicious hands of the dignitaries on the Dias. The brief reports of each technical session were presented by Dr. Prem Lal Kashyap, organising secretary and Zonal Councillor, IPS (NZ) and following recommendations were evolved from the deliberations and discussion:

- With the changing climate, some of the diseases earlier known as of minor importance are now emerging as potential threat to the field and vegetable crops. The group recommended to work on epidemiological parameters and forewarning systems to redefine management strategies and innovate new technologies.
- For the integrated crop health management, cutting edge technologies (genomic, proteomics and nanotechnology) were recommended for accurate diagnosis and to monitor the changing trends in pathogenesis and the virulence spectrum in plant pathogens in climate change scenario.

- It was emphasised that the emergence of new races of lentil rust, chickpea Fusarium wilt and post flowering stalk rot disease of maize are becoming serious threat for successful crop cultivation and there is an acute need for developing strategies for their successful management.
- Research on the application of nanotechnology and biotechnological approaches such as gene silencing and genome editing techniques for the management of plant viruses should be intensified.
- Targeting spot blotch and yellow rust diseases of wheat and barley crops by identification of durable resistance was emphasized.
- To reduce the load of agrochemicals and related residue problems in field and vegetables crops, the emphasis was given on the field translation of various eco-friendly technologies based on microbial antagonists, botanicals and nanoproducts etc.
- Need was felt to motivate the younger generation to take up innovative research especially in the area of deciphering plant pathogen interactions under climate change.

The function concluded with the vote of thanks by Dr. Sudheer Kumar, co-organising secretary of the symposium.

PROF. M.J. NARASIMHAN ACADEMIC MERIT AWARD CONTEST

MJN-ABS1: Development of indigenous rhizobacterial based biofilm to promote growth and induction of defense against bacterial wilt of Chilli

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Biofilm is well organized, cooperating community of microorganisms. Microbial cells affix to the surfaces and develop a biofilm that represent commixed group of microorganisms in which cells stick to each other within a self-engendered matrix of extracellular polymeric substances (EPS); however, their utility as biofertilizers- cum-biocontrol agent has not been plenarily explored. The present investigation was geared towards *in vitro* development of biofilms utilizing fungal mycelia (*Trichoderma harzianum*) as matrices and *Bacillus subtilis* as partners. The Indigenous rhizobacterial isolates from different geographical regions were evaluated for the growth promotion and protection of *Capsicum annuum* L. (Chilli) against wilt disease caused by *Ralstonia solanacearum.* The total number of 56 rizobacterial strains were assessed of which 13 isolates were exhibited strong inhibition to R.solanacearum. The maximum antagonism was recorded upto 79% and GC-MS analysis reveled series of chemical compound involved in antagonistic behavior of these isolates. Growth promotion activities were assessed by screening siderophore (49% were found positive), HCN, ammonia, IAA and P solublization and it was recorded that eight isolates were able to produce IAA, ten isolates produces siderophore and able to solubilize phosphate. Few isolates were found to produce ammonia and HCN production. Out of the 56 isolates, 2 selected isolates were chosen to develop biofilm and is confirmed by using confocal microscopy. Rhizobacteria based biofilm treated seeds showed enhanced germination, shoot length, root length, dry weight, total chlorophyll, total biomass of chilli plants and reduced diseases incidence and had positive effect on biochemical parameters as compared to uninoculated control. The results indicated that the specific activity of defensive enzymes *viz.* peroxidase and polyphenol oxidase was significantly up-regulated from zero hours onwards after inoculation of *Ralstonia solanacearum.* Biofilm based biofertilizers obviate the desideratum of developing combi-formulation of fungal and bacterial biocontrol agents, which is cumbersome.

MJN-ABS2: Revisiting lentil rust disease: Molecular characterization of pathogen and mapping of host resistance gene

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Lentil (*Lens culinaris Medikus*) is an affordable source of good quality protein. All over the world, lentil production is under the continuous threat of rust disease caused by *Uromyces viciae-fabae*,which causes 25% yield losses to complete failure of the crop. The pathogen has overlapping host range and under the ongoing process of host specialization. The population structure of rust isolates infecting lentil and pea in different districts of Punjab was revisited on the basis of cross infectivity test and molecular characterization. Both lentil and pea rust isolates were found non-cross infective at different stages of plant growth. The ITS region of ~700 bp, amplified from DNA of these isolates showed more than 97% sequence homology with *Uromyces viciae-fabae* with over 90% query cover. Further, analysis showed less genetic variation among these isolates compared to the isolates from other geographical regions. Genetically diverse microsperma and macrosperma lentil lines could not differentiate the lentil rust populations prevalent at Gurdaspur and Ludhiana. Further, recombinant inbred lines (RILs) developed from cross between rust resistant (FLIP-2004-7L) and susceptible (L-9-12) cultivars were phenotyped against lentil rust for genetic analysis and molecular mapping. Genetic analysis indicated the role of major gene in resistance. The phenotypic data was also used to identify molecular markers associated with rust resistance. Out of 389 SSR markers, available in public domain, two markers, namely, LcSSR 440 and LcSSR 606 were found to be linked with rust resistance at 8.3 and 8.1cM, respectively. Availability of high-density linkage maps and genome sequence information in lentil can be helpful to extend the present study in identifying candidate resistance genes against *U.viciae-fabae.*

MJN- ABS3: Impact assessment of Arbuscular Mycorrhiza on chilli wilt caused by *Fusarium oxysporum* f.sp. *capsici*

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The present study was conducted to evaluate the impact of arbuscular mycorrhiza on chilli wilt caused by *Fusarium oxysporum* f. sp. *capsici.* Surveys in different district of Haryana were conducted during 2017- 2018 for mycorrhizal colonization (per cent), sporocarp number in soil and wilt intensity in the chilli and found that mycorrhizal colonization ranged from 1 - 17.3 per cent and sporocarp number in soil ranged from 9 - 130. Wilt intensity ranged from 0.5-7.9. The mycorrhizal per cent colonization and sporocarp number in soil were highest in Mahendragarh district (Ateli 17.3 per cent and 130, respectively), followed by Fatehabad district (Dani Binja Lamba 13.1 % and 91, respectively) and lowest in Hisar district (11.5 per cent and 69, respectively). The maximum wilt intensity was recorded from the Fatehabad district (Bhuna, 7.9), followed by Mahendragarh (Silarpur, 7.3) and minimum from Hisar (Kharar-Alipur, 5.2). Three *Glomus* species were tested on chilli. Plant growth parameters (plant height, root length, dry weight of root and shoot), SPAD chlorophyll content, per cent mycorrhizal colonization and sporocarp number was highest in *Glomus intraradices*, when 400 spores were inoculated followed by *Glomus mosseae* and *Glomus fasciculatum.* The maximum per cent disease control (57 per cent) was recorded when *F. oxysporium* + *G. intraradices* + *T. harzianum* were inoculated. For the management of chilli wilt *G. intraradices* and *T. harzianum* were used with different combination. For themanagement of chilli wilt G. intraradices and T. harzianum were used with different combination. Maximum plant growth parameters (Plant height, Root length, Dry weight of root and shoot), SPAD chlorophyll content and NPK content was in triple inoculation (*F. oxysporum* + *G. intraradices* + *T. harzianum*) and minimum in *F.oxysporum* at 90 DAT. Different mycorrhizal species may differ in their ability to control the disease. For the desirable effect on plant growth and inducing resistance to pathogens, suitable host symbiont combination has to be found. The use of mycorrhiza is an effective methods for disease control, mainly root and soil borne disease.

MJN-ABS4: Transmission studies on viruses associated with yellow mosaic disease of bitter gourd

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Bitter gourd yellow mosaic disease (BGYMD) is known to be caused by a wide range of viruses. In this, transmission of viruses associated with BGYMD causing typical blistering, yellowing and mosaic symptoms was studied. The viruses associated with BGYMD were sap and whitefly transmitted but failed to be transmitted by aphid and seed transmission methods. The test plant when inoculated with sap from BGYMD infected plant transmission exhibited blistering and mosaic type symptoms. Association of Cucumber mosaic virus (CMV) and Zucchini yellow mosaicvirus (ZYMV) was confirmed by Polymerase Chain Reaction (PCR) and EnzymeLinked Immunosorbent Assay (ELISA), whitefly transmitted ones developed blistering, curling and mosaic from the same source with confirmed presence of begomovirus by PCR. Sap and whitefly transmission took place in 8 and 20 days, respectively. The symptoms became severe and hundred per cent plants were infected on 12 and 22 days after sap and whitefly transmission, respectively. Intermittent transmission study was conducted to observe the difference in the development of symptoms by mechanical and whitefly transmission, wherein the infection was transmitted to the healthy bitter gourd plant using mechanical, mechanical followed by whitefly transmission, whitefly followed by mechanical transmission and whitefly transmission. The symptoms developed on whitefly transmission followed by mechanical and vice versa exhibited the symptoms resembling the symptoms of the source plant to some extent whereas the infection on mechanically and whitefly transmitted seedlings were different from the source plant.

MJN-ABS5: Genetic association of MLB disease with field screening of maydis leaf blight resistance by using SSR markers

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In maize, the major fungal foliar disease called Maydis leaf blight (MLB) or Southern corn leaf blight (SCLB) is a serious and widespread disease which causes substantial yield losses worldwide. The information on genetic nature of resistance of the diseases is scanty and aid of molecular markers may help in selection and adoption of breeding approaches suitable for improving yield, quality and disease resistance. Therefore, the present study has been planned with the objective to find the associated molecular markers with the resistant gene of Maydis leaf blight and to determine the genetic nature of MLB disease. The experimental material comprised of six generations (P1, P2, F1, F2, BC1 and BC2) was carried out at CCS Haryana Agricultural University, Regional Research Station, Karnal, during 2013 to 2016 harvesting season to study the infection caused by Maydis leaf blight on maize and detect the resistance parents and hybrids using artificial inoculation conditions using standard procedure of disease rating scale of 1-5. Eight inbred lines, out of which four inbred lines (HKI 209, HKI 1332, HKI 325-17AN and HKI 488-1RG) were susceptible and four inbred lines (HKI 1128, HKI 163, HKI 164D-4-(O) and HKI 193-2-2) resistant to maydis leaf blight on the basis of disease reaction in field were used to generate sixteen crosses *viz*., HKI 209 x HKI 1128, HKI 209 x HKI 163, HKI 209 x HKI 164D-4-(O) , HKI 209 x HKI 193-2-2, HKI 1332 x HKI 1128, HKI 1332 x HKI 163, HKI 1332 x HKI 164D-4-(O) , HKI 1332 x HKI 193-2-2 , HKI 325-17AN x HKI 1128 , HKI 325-17AN x HKI 163 , HKI 325-17AN x HKI 164D-4-(O), HKI 325-17AN x HKI 193-2-2, HKI 488-1RG x HKI 1128, HKI 488-1RG x HKI 163, HKI 488-1RG x HKI 164D-4-(O), HKI 488-1RG x HKI 193-2 during Kharif 2013 to obtain 16 F1s by using Line x Tester mating design. These F1s were advanced by part of seeds from each of the six parental inbred lines and their resultant F1 hybrids were planted in the field during rabi 2013-14 to produce F2, BC1 and BC2 generations. F2 generation of each cross was produced by selfing the F1 plants while BC1 and BC2 generations were developed by back crossing each F1 hybrid with its respective male and female parents. Futher after selfing and crossing the experimental material comprised of six generations (P1, P2, F1, F2, BC1 and BC2), 16 crosses were evaluated both for disease severity in the field and molecular studies were undertaken to find out the genetic nature of MLB disease, as well as to find associated markers to resistant genes. Frequency distributions of disease severity of F2 plants of the crosses in the field condition were found to be continous and thus indicated that inheritance of maydis leaf blight was governed by polygenes or by quantitative inheritance. Molecular markers (SSR) were also used to screen the plants of six generations for resistance and susceptibility, and to see the association of DNA marker with field studies. For this, fresh young leaves were collected and DNA of each parental line was isolated using CTAB procedure. PCR amplification conditions were optimized after qualitative and quantitative estimation of DNA. A total of 43 SSR primers were used to screen eight parental genotypes on the basis of their disease reaction for polymorphism and then analyzed F2 and backcrosses of each of the sixteen crosses, with the polymorphic primers to detect segregation pattern and association of DNA markers for maydis leaf blight resistance. Out of 43, 37 primers showed amplification in all parents under study, however, 5 were monomorphic *viz*., p-umc2253, p-umc1525, p-bnlg1732, p-bnlg2241and p-umc1159 and 32 were polymorphic. The six primers *viz*., p-umc1500, p-umc1250, p-umc1622, p-umc1641, p-umc1184, p-bnlg2248 did not show amplification. All F2 plants and 10 backcross plants were individually genotyped for these 32 SSR markers. The numbers of alleles confirm the wide genetic base of the maize varieties and the number of alleles at each locus ranged from 2 to 4. The overall size of PCR amplified products ranged from 105 (p-umc1380, p-bnlg1712, p-umc1020 and p-umc2158) to 230 bp (p-umc1086). The molecular size difference between the smallest and the largest allele at a SSR locus varied from 5 bp (p-bnlg1064) to 50 bp (p-bnlg1496). The polymorphic information content (PIC) value ranged from 0.36 (p-umc1812) to 0.84 (p-phi085). It has been observed that there was a strong association between field results for inheritance of maydis leaf blight and SSR marker studied due to high similarity between the two in all the crosses. The field results have shown that inheritance of maydis leaf blight is governed by more than two genes which was also confirmed by SSR marker analysis. The ratio obtained on the phenotypic and genotypic level was same i.e. which revealed that maydis leaf blight resistance is governed by quantitative inheritance or polygenes. However, the SSR markers which have been used for the study are validated for maydis leaf blight resistance but further needs to be validated whether or not these markers are responsible for maydis leaf blight resistance.

MJN-ABS 6: Antagonistic activity of endophytic bacteria against pathogenic fungi *Fusarium oxysporum* f. sp. *ciceris*, incitant of chickpea wilt

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

THEME-1 MICROBIAL DIVERSITY, PATHOGEN VARIABILITY AND EPIDEMIOLOGY

LEAD LECTURE

LL-1: Genome Assisted Plant Virus Classification and Diagnostics

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Viruses are simple and unique pathogens that are most difficult to manage. Though the history of plant viruses is >100 years old, presently there is greater emphasis on genomics which includes sequencing of viral genome, gene function, transgenic resistance, genome editing etc. More than 1500 plant virus species affecting field and horticultural crops have been documented globally (refer ICTV 2018 Master Species List MSL 34), while the Indian plant virus database developed in 2015 has listed 168 plant virus species. Based on the nature of the genome, plant viruses have been classified as viruses with : (i) ssDNA genome (586); (ii) retroid viruses (67); (iii) dsRNA genome (93); (iv) negative sense RNA genome (64) and (v) positive sense RNA genome (752). Further ICTV (2019) has approved the creation of a higher TaxonrealmRiboviria, which includes viruses with positive sense strand, negative sense strand and double strand genome RNA that use RdRp for replication and the number of Ranks has increased to 11 : Realm (1), Phylum (1), Subphylum (2), Class (6), Order (14), Suborder (7), Family (143), Subfamily (64), Genus (846), Subgenus (59) and Species (4958). Virus diagnostics has gained importance during the last 3-4 decades due to increased travel, traffic and trade. This has led to the development of immuno- and nucleo-based diagnostics ranging from ELISA to PCR, real time PCR, multiplex PCR, LAMP PCR, macro/micro-arrays and deep or next generation sequencing (NSG). More recently NSG coupled with high performance computing (HPC) has resulted in identification of newer viruses with the help of a public web interface such as VirFind (http://virfind.org/j) and VirusDetect (http://virusdetect.feilab.net).

INVITED LECTURES

IL-1: Scope of commercial cultivation of shiitake (*Lentinula edodes*) mushroom

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Edible, medicinal, and wild mushrooms are the three major components of the global mushroom industry. China is the main producer of cultivated, edible mushrooms. *Lentinula edodes* (Shiitake) is now the world's leading cultivated edible mushroom with about 22% of the world's supply. *Lentinula* and four other genera (*Pleurotus, Auricularia, Agaricus,* and *Flammulina*) account for 85% of the world's total supply of cultivated edible mushrooms.The worldwide mushroom industry has grown at a rapid rate since the late 1990s. World mushroom production has increased more than 30-fold during the last 35 years (from about 1 billion Kg in 1978 to about 34 billion Kg in 1913). At present, the total mushroom production in India is approximately 0.13 million tons. From 2010-2017, the mushroom industry in India has registered average growth rate of 4.3% per annum. Out of total mushroom produced, white button mushroom share is 73% followed by oyster mushroom (16%). Mushroom cultivation and the processing of mushroom products have been beneficial to millions of people in China, India, and other developing countries in terms of financial, social, and health benefits. In addition, cultivation and development of mushroom industry positively generate economic growth and have already had an impact at national and regional levels. This impact is expected to continue to increase and to expand in the future with sustainable research and development of mushroom production and mushroom products generating a nongreen revolution. The number of edible and medicinal wild mushrooms to be cultivated is expected to increase, because good research on cultivation of these mushrooms including strain breeding and selection has been undertaken.

Lentinula edodes (Shiitake mushroom) is an edible mushroom native to East Asia,which is cultivated and consumed in many Asian countries. Commercially, shiitake mushroom is grown on artificial substrate or hardwood logs. Shiitake is a prized mushroom with delicious taste and texture. The bioactive compound, lentinan extracted from the fruit bodies of shiitake is reported to have several anti-tumour properties and found with therapeutic applications in various cancer treatments In addition to their high-quality protein, mushrooms are a relatively good source of the following individual nutrients: fat, phosphorus, iron, and vitamins including thiamine, riboflavin, ascorbic acid, ergosterol, and niacin. Mushrooms not only can become nutritious protein-rich food, but also can provide nutriceuticals and pharmaceuticals products. Therefore, mushrooms, with their great variety of species, constitute a cost effective mean both of supplementing the food nutrition of humankind, through the production of edible mushrooms, and of alleviating the suffering caused by certain kind of illnesses, using medicinal mushrooms and their derivatives as nutriceuticals and pharmaceuticals. They can degrade, neutralize or accumulate pollutants of different kinds. Therefore, the significant impact of mushroom cultivation and mushroom derivatives on human welfare in the 21st century could be considered globally as “Non-green revolution.”

The emerging scenarios demand a paradigm shift and cutting edge initiatives in formulating and implementing the novel and innovative agricultural research programs. Integrating mushroom farming in the existing farming systems will not only supplement the income of the farmers but can contribute in achieving food nutritional and social security. Since the mushroom cultivation do not compete for land and have very high productivity per unit area and time, thus can occupy a prominent place to address the void of quality food requirements, health and environmental sustainability. Mushroom cultivation offers an added advantage to recycle agro-waste as carbon pool into good quality protein, much of which otherwise is burnt in the field. Mushroom being an indoor crop, utilizing vertical space offers solution to shrinking land and better waste utility.

IL-2: Emerging diseases of commercial ornamental crops

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Floriculture industry is flourishing worldwide and is growing at an alarming rate of around 6-10 per cent per annum. In spite of a long tradition of Agriculture and Floriculture, India's share in the international market for these flowers is negligible. However, the Government of India is taking initiatives and encouraging the trade of flower cultivation and number of schemes are operating in various states for increasing the state exchequer. Unfortunately due to the frequent large scale introduction of flowers from aboard and within the country has led to the outbreak of different kind of diseases which not only reduced the crop yield but also affects the quality of flowers. In addition the climatic change effect has aggravated few diseases, which were not known previously in Himachal Pradesh in commercial flowers. Diseases like chrysanthemum rust, Alternaria leaf spot and Verticillium wilt of chrysanthemum, Coleosporium leaf spot of marigold, Alstromeria leaf spot and Aster blight are few examples. Other diseases which were of minor importance are now becoming major concern and posing challenges in mitigating the losses. The powdery mildew of rose especially in polyhouses is of great concern. Grey mould of gladiolus and carnation wilt and stem rot are causing huge losses to the tune of 37 to 40 per cent. Thus the organic and integrated disease management strategies have been developed effectively to minimize the losses in the commercial flowers grown widely in the Himachal Pradesh to increase revenue and improve the livelihood of the farmers engaged in floriculture venture.

IL-3: Detection of mix infection of three viruses in sugarcane

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Many Viruses cause serious damage to sugarcane crop in India and worldwide. Three most important DNA and RNA viruses namely Sugarcane bacilliform virus (SCBV), Sugarcane yellow leaf virus (SCYLV) and Sugarcane Mosaic Virus (SCMV) cause quality and yield losses in India. Leaf samples of sixty sugarcane germplasm exhibiting mosaic, mid-rib yellowing and leaf fleck (Symptomatic and non-symptomatic) were collected from Sugarcane Research Institute, Shahjahanpur (UP) farm. Serological diagnosis of virus infected leaves was done by using Double antibody sandwich-ELISA (DAS-ELISA). PCR and RT-PCR assays were also used for virus detection by using specific primers during 2018-2019. Mixed infection of SCMV, SCYLV and SCBV were detected in seventeen accession of sugarcane germplasm such as CoS 09232, Co 05011, CoS 08276, Co 0238, CoS 88230, CoS 91230, CoSe 01434, CoS 07282, CoS 08279, CoS 12232, CoS 08272, UP 05125, CoS 03257, CoS 95422, CoS 7903, CoS 94270, CoS 6279. Two viruses namely SCMV and SCBV were also detected in twenty five samples of germplasm. Non-symptomatic sugarcane varieties also exhibited infection of SCMV and SCYLV. Mixed natural infection of two viruses SCMV and SCYLV was observed in Co 0238 during the visit in various sugar factories areas. SCBV was observed on various sugarcane varieties in Uttar Pradesh. This is the report of mix infection of three aforesaid viruses on same variety, which may cause serious damage to sugarcane crop.

IL-4: Indigenous bacteria antagonistic to root knot nematodes

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Vegetable crops show high susceptibility to infection by the root knot nematodes mainly of the genus *Meloidogyne* (*M. incognita* and *M. javanica*). These parasitic phyto-nematodes are microscopic round worms that feed on plants and cause damage to them. Nematode damage causes reduction in plant health and growth which results in decline in quality, yield and decreased resistance to biotic and abiotic stresses. Also the infected plant becomes susceptible to fungal and bacterial attack which causes additional yield reductions. Due to various harmful effects associated with the use of chemical nematicides, management of the root-knot nematodes through biological methods such as the plant growth promoting rhizospheric bacteria (PGPR) is a novel trend emerging for sustainable agriculture. Such bacteria are the safe, eco-friendly and most effective alternatives for the management of the disease and the pathogens associated with the disease. Twelve indigenous isolates *viz.* NAB-4, NAS-1, NAE-1, LBB-1, LBS-1, KMB-3, KMT-2, KMT-4, KMT-5, KMT-8, KMS-3 and KMS-6 when tested for nematicidal activities against *Meloidogyne javanica* showed minimum hatching in egg masses and higher mortality rate in juveniles of *M. javanica* (upto 92%). After all the screening tests, these were selected for experiment on brinjal crop under pot house conditions. There was an increase in rhizospheric microbial count in all treatments from 0 DAP to 45 DAP. Under pot house conditions, treatments like: T14 (RDF + KMT-4), T15 (RDF + KMT-5), T16 (RDF + KMT-8) and T17 (RDF + KMS-6) resulted in maximum plant growth, reduced no. of galls and eggs in roots, and also decline in final nematode population in the soil.

ORAL PRESENTATIONS

OP-1: Managing the disease triangle for effective colonization by Tilletia indica in wheat

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Karnal bunt caused by the *Tilletia indica* is a disease of quarantine importance. The disease has multiple modes of transmission and thus is difficult to control. The various methods available to control the disease works only partially and thus, does not eradicate the fungus from the area wherever it occurs. It is a well known fact that the initiation and development of Karnal bunt is highly dependent on suitable weather conditions during flowering which is most susceptible stage to infection. Germination of teliospores, production and multiplication of sporidia, their dissemination, lodging on the host surface at the vulnerable stage, infection and establishment depend upon suitable environmental conditions. Thus the correlations between different weather parameters (during the two months Feb and March) and incidence of KB over the last two decades were worked out. This analysis revealed a negative role of sunshine hours for the month of February and a positive role of rainfall, rainy days and relative humidity of the month of March for 20 years under consideration in the development and incidence of KB in Ludhiana, Punjab. By using these parameters, a multi-regression model was also developed for forecasting of this disease. The developed model was validated for four years. The regression analysis showed that these elements result in a coefficient of determination of 0.76 and D.W value of 1.88. The detailed analysis of historical data over 20 years showed that the total rainfall and evening relative humidity in the month of March along with SSH of February are the most critical factors for disease development.

OP-2: Morphological variability in *Verticillium fungicola* isolates collected from different mushroom farm of Haryana

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The dry bubble caused by *V. fungicola* is a serious disease of button mushroom. In the present work, to ascertain the morphological variability in the pathogen, 17 isolates of *V. fungicola* were collected from different parts of the state. From the collected isolates only eight were isolated and purified on PDA medium and coded as MHS (Hisar), BFT (Fatehabad), NJN (Jind), RHT (Rohtak), TPN (Panipat), BSN (Sonipat), FDB (Fridabad) and SKK (Kurukshetra), and morphological characters were recorded. The radial growth was fastest in isolate BSN (44.66 mm), followed by TPN (43.86 mm), FDB (43.33 mm), SKK (42.16 mm) and RHT (41.50 mm), while isolates MHS, BFT and NJN had slow growth i.e. 35.83, 34.50 and 38.00 mm, respectively after 12 days of incubation. The isolates MHS, BFT and NJN exhibited uneven and poor feathery colony growth, while rest of isolates had even, profuse feathery and raised colonies. The pigmentation of *V. fungicola* isolates was white and underside light yellow in MHS, BFT, NJN and RHT, whereas, isolates TPN, BSN, FDB and SKK had dark yellow colour. The size of conidia also varied among the isolates and it ranged from 2.4-5.1×1.2-2.1µm (BFT) to 3.0-7.9×1.1-2.5µm (BSN) the small size conidia was observed in case of isolates MHS (2.8-4.1×1.0-2.1 µm), BFT (2.4-5.1×1.2-2.1µm) and NJN (2.6-3.1×1.0-2.4 µm) and the others had i.e. RHT (2.9-5.5×1.0-2.1µm), TPN (2.9-6.5×1.1-2.3 µm), BSN (3.0-7.9×1.1-2.5 µm), FDB (3.0-6.5×1.0-2.2 µm) and SKK (2.8-4.1×1.0-2.1 µm) large sized conidia. A perusal of the data revealed morphological variability among the different isolates collected from various locations in the state.

OP-3: Mycelial compatibility studies among the isolates of *Sclerotiniasclerotiorum* (Lib.) de Bary causing stem rot in rapeseed-mustard

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Rapeseed-mustard is one of the major groups of edible oilseed crops in the world after soybean and palm oil. Several diseases pose a serious threat to successful cultivation of rapeseed-mustard. Amongst them, stem rot caused by *Sclerotiniasclerotiorum* (Lib.) de Bary, is now becoming very important fungal disease as it is soil borne, necrotroph and have wide host range. The most effective management strategy is resistant or tolerant cultivars. To identify and deploy host resistance, it is important to understand the diversity of this fungus. Mycelial incompatibility is an effective morphological marker to identify intra-specific heterogeneity within populations of *S. sclerotiorum.* A total of 48 isolates were collected from Punjab and adjacent states: which were paired in all possible combinations. These revealed high level of incompatibility amongst them as only 29 combinations out of 1128 were found to be compatible, 88 of intermediate type and rest were incompatible. The 25 isolates involved in compatible combinations were grouped into 19 Mycelial Compatibility Groups (MCGs) whereas the remaining 23 isolates singly represented a MCG as they were compatible only with themselves. It was observed that in general, isolates belonging to nearby areas were compatible and those from far away geographical areas were incompatible. This study revealed a considerable amount of variation as only 10.4 percent pairings were found compatible and thus it is very important to know the pathogen population structure for identifying reliable resistance sources.

OP-4: Taxonomic advances in lower fungi

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There are several kinds of microorganisms in this biosphere including fungi, bacteria, viruses, algae, diatoms, ciliates, dinoflagellates, protozoans, etc., where fungi constitute the third largest biomass composition of this biosphere after texa plant and bacteria. Fungi are showing great interactions with human, animal and plant populations with ubiquitous presence. One group of fungi differing in anatomy from true fungi, particularly cell wall compositions, is also termed as lower fungi, i.e. former Myxomycetes and Phycomycetes. Fungi as a whole was first discussed under plant kingdom, until 1969, when R.H. Whittaker mentioned Fungi as different kingdom among eukaryotes. On the other hands some systematists described them under Protozoa, Protista or Protoctista from the very beginning, but these were lumped for a long period of time. Recently based on molecular phylogeny the lower ones are described over kingdoms Protozoa and Chromista. Protozoa bearing animal like lower fungi is discussed under five separate lineages belonging to four phyla or of independent origin (Kirk et.al., 2008), but Ruggiero et al., 2015, purposes eight phyla under Kingdom Protozoa. Chromista comprising of ciliates, algae and few endoparasites probably in excess of 15, 00, 000 and fungi like chromistan are discussed over three classes, but Cavalier-Smith, 2018 has recently purposed eight different groups.

OP-5: Population variability and phylogenetic analysis of root knot nematodes infecting chilli and bitter gourd in punjab

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Root knot nematodes, *Meloidogyne* spp. are the most destructive plant parasitic nematode causing serious losses to vegetable crops worldwide. These nematodes attach to the tender roots of plants and form characteristic galls which hampers the nutritional uptake capacity of the crops affecting plant health, yield and quality. They have a wide host adaptability and are reported to parasitize over 3000 cultivated and wild plant species. More than hundred recognised species of genus *Meloidogyne* are documented worldwide. Knowledge on population diversity, prevalence and accurate diagnosis of the prevailing *Meloidogyne* species in an area is of paramount importance for designing management practices for sustainability of crop production. Survey of major chilli and bitter gourd growing areas of Punjab in districts of Patiala, Sangrur, Ferozepur Gurdaspur, Ludhiana and Tarn Taran were conducted for incidence and prevalence of root knot nematodes. In chilli growing areas, maximum prevalence of root-knot nematode (80%) was recorded in Sangrur and minimum in Ferozepur district (40%). In case of bittergourd an overall 55.93 per cent root knot nematode incidence was recorded in the districts surveyed. Maximum disease incidence (75%) was recorded in Ferozepur and minimum disease incidence was seen in Ludhiana (44.16%). Further, it was observed that root knot nematode infestation was higher in the fields where vegetable crops like brinjal, okra chilli and cucumber, etc. were grown in rotation with chilli or bittergourd as compared to the fields where rice, marigold, garlic and onion crops were included in the crop rotation. The soil and root samples were collected for population estimation and characterization in the laboratory. The protocol for DNA extraction from root knot nematode was standardised and species specific molecular were validated. The morphological and molecular characterization of the populations collected from farmer's field revealed *M. incognita* as the most prevalent species infecting chilli and bittergourd under Punjab conditions. In addition *M. javanica* sp. was also found to be prevalent in some chilli growing areas. The protocol standardised for DNA extraction and species specific markers validated in the present study can be used for quick detection of these nematodes.

OP-6: Pepper mottle virus a threat to chilli cultivation in Punjab

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In India occurrence of Pepper vein banding virus (PVBV), Pepper veinal mottle virus (PVMV), Potato virus Y (PVY), Cucumber mosaic virus (CMV), and Tobacco mosaic virus (TMV) has been reported (Ravi et al 1997, Verma et al 2004). In the year 1979 Sandhu and Chohan reported mottle disease infecting pepper in Indian Punjab. The same disease was also reported to infect peppers from USA (Zitter, 1972), Ethiopia (Agranovsky, 1993), Japan (Ogawa et. al., 2003), Korea (Kim et. al., 2009). Pepper mottle virus was first recognized as a new strain of Potato virus Y (PVY) infecting peppers in Arizona in 1969 (Nelson and Wheeler, 1972). In the early 1970s an "atypical" PVY isolate was also found in a survey of pepper fields in central Florida (Zitter, 1972) causing mottle disease and tentatively named Pepper mottle virus (PepMV). Pepper mottle virus (PepMoV) is a plant pathogenic virus in the genus *Potyvirus* belonging to family *Potyviridae.* Like other members of the *Potyvirus* genus, PepMoV is a flexous rod consisting of positive sense single stranded RNA (+ssRNA). Genomes have a VPg covalently linked to the 5 end and the 3 terminus is polyadenylated. Genomes encode a large polyprotein that is self-cleaved into a set of functional proteins. This virus infects many species of *Solanaceae* family, including several species of *Capsicum*(i.e. *C. annuum, C.frutescens*), *Datura* spp., *Lycopersicon* esculentum, Physalis floriana, tobacco(Nicotianaspp.) and nightshade (*Solanum* sp.). It was its reaction on *C.frutescens* (Tabasco pepper) that alerted researchers to the presence of a new virus in peppers. Survey conducted from 2015-2017, in the major pepper growing districts of Punjab namely Sangrur, Patiala, Ferozepur, SAS Nagar, Pathankot, Kapurthala, Jalandhar and Ludhiana showed the prevalence of vein-banding, mosaic, puckering and mottling type of symptoms are caused by Pepper mottle virus (PepMoV) during early crop season (March-June). Highest PepMoV incidence was recorded in Patiala (21%). Pepper mottle virus has a cross reactivity against the antisera of PVYn and PVYo/c. Among solanaceous hosts tested tomato showed association of PepMoV. NIb2F/ NIb3R primer pair was found promising for quick detection of poty viruses. The genome characterization of virus from chilli revealed that the prevalent virus shares up to 99% sequence homology with Pepper mottle virus reported from around the world. The virus has been proved to be of internal seed borne nature. It was observed that virus affect the seed formation in the suscptible germplasm. LAMP primers designed in this study could be further exploited for the quick and easy detection of Pepper mottle virus. One hundred forty genotypes of chilli were artificially screened of which four genotypes SL 472, NSS-2, S-343 and PP-9950-5197-0107-7058 were found to have potential for resistance against PepMoV and could be utilised further in the chilli breeding programmes.

POSTER PRESENTATIONS

PP-1: Effect of date of sowing and weather parameters on disease intensity and severity of powdery Mildew (*Erysiphe cruciferarum*) on rapeseed- mustard

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The oilseed crops, especially *Brassica* spp., belongs to the family *Cruciferae* play a pivotal role in the agricultural economy of India. The Powdery mildew disease *(E.cruciferarum)* is an important disease of rapeseed- mustard particularly in northern and north eastern states of India. Weather factors always play an important role in initiation and severity of disease in all host-pathogen interaction. The investigation was carried out on the field plots to determine the effect of weather parameters on the sowing dates with intensity and severity of powdery mildew of rapeseed-mustard and its impact on yield. In the Rabi season (2017-18), a periodical increase in the disease severity with the delay in sowing. The first appearance of Powdery mildew on leaves was in the form of small circular patches symptoms at 100 DAS whereas, the late symptoms at 110 DAS, 120 DAS and 130 DAS. The Percent Diseases Intensity (PDI) progression was higher during 3rd sowing (D3) in Giriraj with 11.93 %, 26.33 %, 8.43 % and 5.34 % after 100 DAS, 110 DAS, 120 DAS and 130 DAS respectively in *Brassica juncea* variety followed by *Brassica napus* and *Brassica carinata* varieties and the minimum (PDI) progression at 1stsowing (D1) in RLC-3with 8.98 %, 15.12 %, 9.87 % and 7.40 % after 100 DAS, 110 DAS,120 DAS and 130 DAS at the minimum temperature (11.4-14°C), minimum relative humidity (27-69%) and rainfall (1.9mm). The maximum seed yield (20.37 q/ha) was recorded on 1st sowing (D1) followed by 2nd sowing (D2) (12.59 q/ha) and the seed yield was lowest in case of 3rd sowing (D3) for all the four varieties. The variety PC-6 followed by GSC-7 showed least disease intensity under particular weather condition of the Punjab.

PP-2: Biology and effect of weather parameter on Karnal Bunt and Kernel Smut

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The present investigation was conducted to study biology of *Tilletia indica* (Mitra) and *Tilletia barclayana* Bref. under laboratory condition at Guru Kashi University,Talwandi Sabo, Bathinda. These pathogen cause diseases i.e. Karnal bunt in wheat and Kernel smut in rice. The results revealed that the symptoms of both diseases become evident only at the time of grain formation due to presence of black powdery mass called teliospores which germinate into primary sporidia in the whorl on the top of promycelium. These primary sporidia produce secondary sporidia (Allantoid and Filliform) and are responsible for floral infection under favourable conditions. Further effect of weather parameters studies revealed that hot climate accompanied with high relative humidity were highly conducive for the development of Karnal bunt of wheat and Kernel smut of rice during February-March and October crop season, respectively. Hence, these studies will helpful for finding successful management of these diseases to researchers.

PP-3: Screening of osmotolerant bacteria from Thar Desert, Rajasthan

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Due to harsher and extreme environmental conditions such as low moisture of sandy soils and high soil temperature, the Thar Desert contains a limited diversity of life forms. In present study, osmotolerant bacteria from the soil samples of Thar Desert were isolated and characterized. Bacteria were isolated from 100 g of 15 different soil samples, collected from sand dunes. Generic identification of bacteria was carried out by a total of 12 different biochemical and morphological characters. Isolates were also characterized based on 16S rRNA gene sequences and a phylogenetic analysis of isolates was carried out using these sequences. Osmotic tolerance potential of isolates was examined on glycerol, NaCI and alcohol. The soil suspended in water contained 2.4 x 10^5 bacteria/g of soil while alcohol suspended soil had 4.5 x 10^4 bacteria/g. A total of 29 bacterial isolates were found tolerant to 29% glycerol, 16% NaCI and 12% of alcohol. Among total 29 isolates, 32% bacteria belongs to *Corynebacterium* spp., 27% isolates belong to *Bacillus* spp. *Acinetobacter* spp. *Staphylococcus* spp. and *Enterobacter* spp. were in 21%, 14% and 7% ratio, respectively. All the isolates grew well up to 52 degrees C with gradual reduction on subsequent increment of temperature. Out of 29 isolates, 9 could survive at 67 degrees C while two isolates found able to grow at 65 degrees C. This study suggests that virgin sand dunes may be a rich source of bacteria, tolerant to osmotrophic solutes and high temperature, and can be examined for plant growth promotion activity in agriculture. Furthermore, this study also may help to resolve the desiccation in crop plants through their tactics adopted to defeat desiccation.

PP-4: Soil Metaphenome: An opportunity for the future

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Soil microbiome assemblages carried out all the important processes such as plant growth promotion, nutrient cycling, nitrogen fixation, bioremediationetc. But revealing of these microbial treasures as isolates is impossible and knowing their functions is quite difficult. Though, metagenomics reflects the identities and functional attributes of meta samples from varying physiological states microbial DNA sample. Here we aimed to reconnoiter the actual microbiome expressed function and their derived product encoded in metagenome in the varied environmental conditions by the “Metaphenome”. The soil metaphenome is driven by the combined genetic potential encoded by the soil community’s genome, their physiological status, resources access potential, socialism with other organisms and their capacity to respond with environmental alterations. Hence, metaphenome comprehends the entire ‘omics’ field, including the metagenome, metatranscriptome, metaproteome and the metabolome.

Soil structure is a major driven force for influencing the Metaphenome. It includes the soil respiration, mask details of the molecular reactions occurring by interacting members in discrete, spatially isolated soil consortia. Secondly, physiological status that is the physiological responses of individual microorganisms like genetic regulation and cell–cell interactions. Third are the microbial community interactions because combined metabolic outputs of the community members provide the metabolomic insight of sample.

Overall, the soil metaphenome is the best way to amidst the high diversity and complexity of soil microbiome that provides the mechanistic details of microbial communities to emergent properties of the given sample. This tool provides the important results for prediction of the impacts of environmental perturbations on key functions carried out by the soil microbiome and will enable development of new approaches for optimizing soil carbon cycling, managing nutrient transport, and sustaining crop production.

PP-5: The salinity stress in *Exigobacterium profundum* PHM11 reveals the global transcriptomic change towards osmotic, oxidative and antibiotic stress protection

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Salinity is one of the major issues which limit the production of agricultural crop. In this aspect the halotolerant bacteria *Exiguobacterium profundum* PHM11 was found to be tolerant in extreme salinity conditions. The growth kinetics supports that the 100-1500 mM salt concentration is the optimal and minimal for growth. To check the salt-induced fine-tuning *de novo* transcriptome assembly was performed of *Exigobacterium profundum* PHM11 wild type cells grown in 100 mM and 1500 mMNaCl condition, using the Illumina Hiseq platform in paired end module. An average of 7,619,425 row paired-end reads was obtained per sample and low quality mapped reads were evaluated and eliminated. The raw fastq files were processed before performing assembly. We performed base trimming, removal of adapters sequences and also filtered out reads with an average quality score less than 30 in any of the paired end reads. The cleaned reads were normalized and assembled using trinity with default settings and generated 2,320 transcripts. The assembled transcripts were compared with uniprot database using BLASTX program. Total 2320 transcripts were identified out of which only 2086 were identified with uniprot databases. The transcript analysis showed the increase in the expression of the genes related to the synthesis and transport of glycine betaine, ectoine and L-proline. Along with these the genes related to oxidative stress pathway like cytochrome oxidase, ferettine and hydroperoxide reductase were also increased. We also investigated the increase in the expression of the gene related to acriflavin resistance, penicillin binding,etc. The analysis suggest the shift of the global transcriptome changes towards the synthesis of the osmoprotectant, oxidative stress and antibody resistance.

PP-6: Microbial diversity analysis of wheat rhizosphere from Ballia region of Eastern Uttar Pradesh through metagenomics

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Wheat is the major crop in India and unlike other crops also subjected to influence by microbial communities of the rhizospheric region which are extremely diverse and definitely play a key role in plant growth promotion, productivity and health and nutrient cycling. In order to study how changes in the rhizospheric microbial community can make an impact on overall crop function, wheat rhizospheric soil samples from Ballia (25.778132 N 84.048146 E) regions of Eastern Indo Gangetic Plain,(EIGP), were collected and analyzed. Full length 16S rDNA gene amplification sequencing was performed to reveal the bacterial community in wheat rhizosphere. 50,072 read were analyzed, out of that only 44,537 reads are classified and 5,535 were unclassified using oxford nanopore sequencing and EPI2ME data analysis platform. Oxford nanopore sequencing results uncovered that dominant phyla were Proteobacteria(69%), followed by firmicutes (13%), bacteroidetes (3%), actinobacteria (3%) andacidobacteria (2%). The data is available at the NCBI

- Sequence Read Archive (SRA) with accession number: SRR8468314.

The abundance of proteobacteria demonstrates the dominance of most of the soil inhabitant.Gemmatimonadetes presence indicates soil with low moisture content is also in accordance with the soil analysis data, although the presence of aerobic thermophilic bacteria from chloroflexi reflects the presence of pesticides residues in soil, which can also be used as an indicator of the soil profile.

PP-7: Role of weather parameters in development of yellow vein mosaic virus disease of okra

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Okra (*Abelmoschus esculentus* L. Moench) is an important summer and rainy season vegetable crop of family *Malvaceae*, and grown extensively throughout the world for its immature nutritious fruits which are consumed as vegetable. Okra yellow vein mosaic virus (OYVMV) disease transmitted by whitefly is a devastating viral disease which has a wide occurrence and causes considerable yield losses quantitatively and qualitatively. The viral disease can appear at all stages of crop growth depending upon favorable conditions. The infection is more severe in rainy season crop as compared to spring or summer season crop with common appearance in all okra growing regions of Haryana. The OYVMV disease occurred throughout the growing season of okra crop. The disease initiated in the field at 20 days after sowing in the form of vein clearing of leaves on 2 to 3 young leaves. The higher percent disease index (PDI) was observed in Pusa Sawani cultivar as compared to Pusa A4 and Varsha Uphar. At the time of initiation of disease, the maximum temperature was 34±2 with more than 90 per cent morning relative humidity. As the crop growth advances, the PDI increased significantly. The highest PDI (73.00) was recorded on Pusa Sawani at 97 DAS during first week of October. Correlation coefficient between different weather parameters *viz.* maximum and minimum temperature (°C), morning and evening relative humidity (%), wind speed (km/hr), bright sunshine hours (hrs/day) total rainfall (mm) and disease severity were estimated for three cultivars of okra. The cultivar Pusa Sawani exhibited positive correlation with bright sunshine hours (0.529) and morning relative humidity (0.301). However, maximum temperature (0.256), evening relative humidity (0.363) wind speed (0.318) and rainfall (0.077) were negatively (non-significant) correlated while minimum temperature (0.844) was recorded negatively highly significant with PDI. Almost similar correlation matrix was found in case of Pusa A4 and Varsha Uphar.

PP-8: The rust genus *Puccinia:* A comprehensive account on diversity and distribution in Western Himalaya in India

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Puccinia is a rust parasite affecting healthy and vigorously growing plants all over the globe. It is an obligate plant pathogenic fungal genus which contains about 4,000 species.This group of rust fungi develop several unique morphological and microscopic features and appears as yellow orange or brown powder on a variety of host plants and plant parts. This rust genus is widespread in Western Himalayan region of India due to its irregular and disturbed topography as valleys and plateaus. The tropical climate at the base of the mountains to permanent ice and snow at the highest elevations leads to variable climatic conditions and diverse flora and fauna of this region of India. Additionally, the ideal conditions (average temperature up to 35°C along with 50–60 % relative humidity) required to initiate infection are also found in this Himalayan region which contribute to the vast diversity, distribution and host range of this fungal group. Therefore, this study is focused on comprehensive account on diversity and distribution of rust genus *Puccinia* in Western Himalaya in India. After analysis of results and information available in published literature, it was observed that about 167 species of the genus *Puccinia* were found distributed on about 204 plant hosts throughout the Western Himalaya. Further evaluation of the data collected revealed that maximum 94 Puccinia species were recorded from Uttarakhand followed by Himachal Pradesh (83 species) while lowest 67 species were reported from Jammu and Kashmir (Including Ladakh). It was also observed that molecular studies on these rust fungi found nearly negligible. As most of these rust fungi were characterized and identified only on morpho-taxonomic basis, molecular studies of these fungi are still required to classify them in their correct taxonomic position.

PP-9: Development of microsatellite markers for assessing molecular variability in *Ustilago segetum tritici* infesting wheat

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Loose smut is an important seed-borne disease of wheat caused by *U. segetum tritici*. It is prevalent in all wheat growing areas in the world. This seed-borne disease converts the wheat spikelets into a black powdery mass of spores. To understand the genetic and molecular variability of *U. segetum tritici* pathogen, there is paucity of molecular markers. However, simple sequence repeats (SSRs)have become a preferred choice due to their multi-allelic nature, co-dominant inheritance, high abundance, hyper-variance, extensive genome coverage, reproducibility and discriminatory nature. The available genome sequence of fungal pathogens is carrying various opportunities, which allows researchers to discover resistance genes, regulatory sequences, virulence genes and molecular markers. Genome-based microsatellite markers have proven to be useful for genetic characterization of fungal species. Non-availability of genomic sequences of *U.segetum tritici* creates hindrance in usage of SSRs for the molecular characterization of loose smut pathogen. Therefore, this study was carried out to explore the cross-transferability of genomic SSRs from the related species *Ustilago maydis* to loose smut pathogen of wheat. Using *in silico* analysis, 2703 SSRs were mined. These SSRs consisting of 44.5%, 29.77%, 2.7% and 6.5% of di-,tri-, tetra- and hexanucleotides, respectively. Around 100 UM SSRs were synthesized of which 65 yielded PCR apmlicons. Only 23 polymorphic markers were further utilized for molecular variability analysis. PIC for loose smut was 0.24 with a range of 0.63 for UM36 and UM49 markers. These newly developed microsatellite markers may have immediate applications for detection of genetic variability and in population studies in other seed - borne pathogens.

PP-10: Variability of *Rhizoctonia solani* Kuhn infecting small millets Varala

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Rhizoctonia solani Kuhn is a soil borne, polyphagous, necrotrophic plant pathogenic fungus with a wide host range. It became one of the emerging malady in successful cultivation of small millets. Hundred isolates of *R.solani* were obtained from four different small millets *viz.,* finger millet, little millet, foxtail and proso millet showing typical symptoms of the disease. Pathogenicity of all the isolates was proved by sheath inoculum method and agar method in susceptible varieties. Among them, only 53 isolates were selected and characterized. Studies on morphological characters revealed that the variation with respect to hyphal width(5-10µm), distance between the septation(19.31-541.85 µm) and mycelial weight(0.02-0.34 g). In foxtail millet isolates, distance between septation is more when compared to remaining isolates. Mycelial weight is maximum in finger millet isolates. In cultural variability, the colony diameter ranged from 41.33-90 mm at 72 hrs of incubation with varied colony colour white, light brown to brown. Majority of the isolates of foxtail millet and finger millet were slow growing. Concentric circle is completely absent in proso millet and little millet isolates. Dispersion of mycelium varied from subdued to aerial growth. Studies on sclerotial bodies revealed that, sclerotial formation is absent in 12 isolates. Foxtail millet isolates produced more number of sclerotia with minimum size and weight. Majority of the isolates have brown coloured sclerotia with round shape and smooth surface. In arrangement of sclerotia, foxtail millet and finger millet isolates showed greater variation with different patterns *viz*, peripheral, central, central+peripheral, concentric circle or uniformly/scattered. Pathogenic characterization, lesion shape is varied from elongated, oval to circular with variable lesion length (0.73 to 5.77 cm), incubation period (3-8 days) and among different isolates, all the proso millet isolates were highly pathogenic on foxtail millet.The diversity analysis showed considerable variation on morphological, cultural and pathological parameters of *R. solani*.

PP-11: Effect of epidemiological factors in development of Blue mould rot (*Penicillium islandicum*) in Indian Gooseberry

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Present investigations were undertaken at Chaudhary Charan Singh Haryana Agricultural University, Hisar. Aonla or Indian gooseberry, *Emblica officinalis* Garten, is an important horticulture crop of India. It is a rich source of vitamin C and used in various ayurvedic medicines. Blue mould rot caused by *Penicillium islandicum* was a minor disease earlier, but now it has becomea major disease of Indian gooseberry. The epidemiological studies revealed that the injury of the aonla fruits was found to be a pre-requisite for infection. Higher rate of pathogen entry in fruits was observed when fruits were injured by any method of injury and 100 per cent fruit infection was observed in pinprick injury, stem end removed and styler end punctured. Further studies indicate that a minimum number of 50 spores/ml was necessary for disease initiation which can be the inoculum threshold point of this fungus to cause infection. Maximum population build up of *Penicillium islandicum* was observed at the concentration of 500 spores/ml after 5 and 10 days of inoculation on the fruits. The most favourable temperature and relative humidity for the blue mould rot development was observed to be 30°C and 100 per cent, respectively. However, there was no diseases observed when the fruits were stored at 10°C temperature with 40 per cent relative humidity.

PP-12: Role of plant growth-promoting rhizobacteria (PGPR) in waste land management for sustainable agriculture development

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There is a thin layer of soil immediately surrounding plant roots that is an extremely important and active area for root activity and metabolism which is known as "rhizosphere". Metals like lead, arsenic, cadmium, copper, zinc, nickel, and mercury are continuously being added to our soils through various agricultural and industrial activities. All these sources cause accumulation of heavy metals in agricultural soils and pose threat to food safety issues and potential health risks due to soil-to-plant transfer of metals. The remediation of such soils is important because these usually cover large areas that are rendered unsuitable for agricultural and other human use.

Plant growth promoting bacteria were isolated from rice fields and further screened for PGPR traits. These isolates were tested against metal contaminated land area near kurukshetra, India for rice plants and further tested against heavy metal toxicity. when grown in soils supplemented with nickel, lead and zinc. It may be possible to inoculate plants with such rhizobial microbes in order to increase plant biomass and there by stabilizing, revegetating and remediating heavy metal polluted soils. Managing the microbial population in the rhizosphere by using an inoculums consisting of a consortium of PGPR, nitrogen-fixing rhizobacteria and biofertilizers, could provide benefits to plants and important for ecosystem restoration on contaminated heavy metal lands.

PP-13: Mobile app" Gehoon Doctor" on wheat crop diseases

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Gehoon Doctor is a mobile app developed by Indian Institute of Wheat & Barley Research (ICAR-IIWBR) in android version 3.0.1. Hindi language is used for information in this app, so that farmer community gets maximum benefit. This app has identifying features of diseases , their distribution, symptoms & management. It provides information about harmful insects (with their photos) so that farmer can easily identify them. Along with picture of insects complete information on distribution, development, nature of damage & insect Management is also provided on the screen.This app not only provides information on diseases and insects but also the integrated pest management practices of this crop along with post harvest safe storage and insect management during storage of wheat crop.

This app will help farmers to increase their crop productivity. Using this app information, farmers can look after their crop better and can identify the diseases /insects in it. Then they can adopt proper method to control that disease / insect.

The front end of the app has six options. User can decide the option by picture or the title and on single click the information is displayed.This app is developed using Android platform version 3.0.1 and is freely available on Google play store. It can be downloaded through following link: https://play.google.com/store/apps/details?id=com.Gehoon.GehoonDoctor

PP-14: Isolation and characterization of salt tolerant bacterial endophytes and their PGP traits from saline rhizosphere of Wheat (*Triticum aestivum*)

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Soil salinity is increasing day by day and it cast brutal effect on the productivity of crop plants, because most of the crop plants are sessile to salt stress. Bacterial endophytes have been shown to improve abiotic and biotic stress responses in plants. Plants growing under saline conditions along the

Haryana region could contain bacterial endophytes that improve persistence and growth of wheat in this environment. Four plants were collected along the Haryana region from six different saline stressed sites. Bacterial endophytes were isolated from root and shoot part ofthe plants. Results revealed that the population of bacterial endophytes is highly dynamic using different types of nutrients. The population of bacterial endophytes ranged from 2.6 x 10^{-2} to 2.9 x 10^{-3}, 0.8 x 10^{-2} to 1.8 x 10^{-3}, 1.8 x 10^{-2} to 0.5 x 10^{-3},0.4 x 10^{-2} to 0.56 x 10^{-3},and 2.8 x 10^{-2} to 1.35 x 10^{-3} on Nutrient Agar, 1/10 tryptone soy agar, Jensen's agar, Rojo-congo agar, and King's B agar respectively. Root harbours high number of bacterial morphotypes in comparison to shoot. Among six different regions, a total of 224 bacterial endophytes were obtained from root and shoot part of plants. Further, these isolates were screened at 0.5 – 2M salt concentration for their survivability in saline environment. Among them, 75 % (0.5 M), 64 % (1M), 44 % (1.5M) and 13 % (2M) showed tolerance ability. Moreover, these isolates also contribute in other plant growth promoting activities like P-solubilization, siderophore production, IAA production, ammonia production, etc. However, taxonomic characterization of the isolates would be carried out using 16S rRNA gene sequencing.

PP-15: Management and epidemiological studies on Sugarcane top rot caused by *Fusarium moniliforme*

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Top rot or Pokkah Boeng of sugarcane (*Fusarium moniliforme*) is an economically significant disease in Sugarcane growing areas of Andhra Pradesh during monsoon period. Field experiments were conducted at Regional Agricultural Research Station, Anakapalle during 2011-12 to 2017-18 to study the relation of weather factors with the incidence and spread of top rot disease. Data on weather parameters such as number of rainy days, rainfall, wind velocity, BSSH relative humidity (RH), evapotranspiration were recorded and comparisons were drawn with top rot severity. Our studies revealed that Per cent Disease Index (PDI) was influenced by rainfall and RH at 2 hours have shown significant positive correlation. However, evaporation has shown significant negative correlation. Other climatic factors were insignificant with positive values for minimum temperature and morning RH; whereas negative for maximum temperature. The disease initiation coincided with summer showers and progressed linearly through the season and gradually reduced towards the end of the growing season depicting a sigmoidal disease curve. Receipt of rains coupled with RH above 50% recorded at 2 hours favors the primary infection of the crop and progressed rapidly with increase in rainfall coupled with higher humidity levels. By employing step down linear regression models, based on preceding monthly averages, the incidence of top rot on sugarcane can be predicted with an accuracy of 85 %. Sett treatment + Foliar spray with carbendaizim @0.05% showed the highest per cent germination and low disease incidence (84.16% and 5.84%) respectively.

PP-16: Influence of different temperatures and pH on growth and sporulation of *Colletotrichum lindemuthianum* causing anthracnose of Mungbean

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Colletotrichum lindemuthianum, causal agent of anthracnose of Mungbean was tested at six various temperatures (10, 15, 20, 25, 30, 35°C) and 5 different pH of (5,6,7,8,9) to observe the growth and sporulation of test pathogen. Best temperature for maximum growth and sporulation was found at 25°C with maximum colony diameter of 78 mm at 168 hrs incubation, with mean diametric growth 11.1mm/ day. At 25°C temperature, sporulation was observed moderate to abundant, whereas maximum growth and sporulation was found at pH 6 with 77.6 mm radial growth.

PP-17: Antimicrobial activity of probiotic bacteria against human pathogens

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Probiotic are (bacteria and yeast) good for our digestive system. Probiotic compete with thousands of species already in the gut and help in digestion, improve the bowel movement and prevent the multiplication of harmful bacteria, that's by they are friendly bacteria or good bacteria. In the present study total six isolates were isolated from different food (dosa batter, chocolate and pickle) and milk products (curd, cheese and kaladi). These isolates were studied for their antimicrobial properties against human pathogens *viz. Eschericia coli* (MTCC1697), *Psudomonas aerugonisa* (MTCC741)and Salmonella typhimurium(MTCC98). The results revealed that out of six isolates, five isolates *viz.* L1, L2, L3, L4 and L5 had good antimicrobial potential against human pathogens and among them L1 with 41.00 mm, 39.00 mm and 45.00 mm zone of clearance respectively showed significant potential followed by L2 with 38.00 mm, 26.00 mm and 28.00 mm zone of clearance, respectively. Further all these isolates were evaluated for their probiotic potential *viz,* pH tolerance, bile salt tolerance, temperature sensitivity, lactose utilization and NaCl tolerance and the result showed that all the isolates from curd (L1), cheese (L2), kaladi (L3), and dosa batter (L4) showed good probiotic potential than that of the isolates from chocolate (L5) and pickle (L6). Morphological and biochemical studies revealed that all the isolates had characters similar to the genus Lactobacilli. This study concluded that the isolate L1 and L2 had best antimicrobialand probiotic potential and these isolates can be further studied for their identification at species level.

PP-18: Bioremediation of soil by microbes

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Bioremediation uses microbial metabolism in the presence of optimum environmental conditions and sufficient nutrients to breakdown contaminants notably petroleum hydrocarbons. We reviewed technologies for carrying out bioremediation and observed that biotechnological approaches that are designed to carry out remediation have received a great deal of attention in recent years. Biostimulation (meaning the addition of limiting nutrients to support microbial growth) and Bioaugmentation (meaning the addition of living cells capable of degradation) studies have enjoyed a heavy presence in literature and reviews of these technologies focusing on the technical aspects are very few if at all available. At times, nutrient application alone or augmenting with microbes is not sufficient enough for remediation leading to a simultaneous approach. Recent studies show that a combination of both approaches is equally feasible but not explicitly more beneficial. Evidently, selection of a technology hinges on site specific requirements such as availability of microorganisms capable of degradation in sufficient quantities, nutrient availability to support microbial growth and proliferation as well as environmental parameters such as temperature in combination with duration of exposure. This review focuses on these technologies and efforts are directed towards eventual manipulation of the processes of remediation all geared towards making bioremediation technically and economically viable for comprehensive treatment of petroleum hydrocarbon contaminated soils.

PP-19: Microbial diversity of rhizobia nodulating Sesbania cultivars from diverse agroecological zones of Indian soils

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The genus *Sesbania* contains about 70 species widespread over tropical and subtropical regions. The genus has attracted interest for its fast growth, high crop yield, flood tolerance, root as well as stem nodulation with high nitrogen (N2) fixation activity. Due to their importance and diversity within natural populations, identification and characterization of rhizobial strains imply a comprehensive and accurate approach. In present investigation 70 rhizobial isolates of different *Sesbania* species *viz.* 14 isolates of *S. sesban*, 20 of *S. grandiflora,* 10 of *S. aculeata*, 10 of *Sesbania rostrata* (root nodulating) and 16 of *S. rostrata* (stem nodulating) were isolated from 56 soil samples collected from different locations of India using trap plant method. The authenticity of these rhizobial isolates were tested on the basis of Gram's staining, Hofer's alkaline medium, Ketolactase and acid or alkaline production tests. On the basis of different PGP traits and nodulation efficiency under aseptic controlled conditions, 20 promising rhizobial isolates were selected. The Genomic DNA of selected rhizobial isolates for different *Sesbania* species was amplified for 16S rRNA gene using BAC27F and BAC1378R primers using standard PCR amplification conditions. ARDRA results showed enormous diversity among themselves and divergence among different Sesbania rhizobial isolates was initiated at approximately 54-65% levels of similarity coefficient. These isolates were distributed into two major groups and further into various sub and sub-sub groups. Five rhizobial isolates; SSKr(ii), SGKe(i), SAMa, SRKr(i)/r and SRTn/s were found to have more nodule number and nodule fresh weight as compared to control and remaining isolates both under sterilized as well as unsterilized conditions. These rhizobial isolates also showed significant increase in shoot and root dry weight along with shoot N and P uptake in their respective crop tested. These isolates have tremendous potential in near future to be used as biofertilizers in salt affected, alkaline and waterlogged field conditions, which will not only improve nitrogen availability and plant growth in *Sesbania* spp. but also act as nitrogen reserve for next crop. The promising *Sesbania* rhizobial isolates were identified as *Rhizobium* sp. on the basis of ribo-typing of partial 16S rRNA gene.

PP-20: Root trapping and bio-molecular characterization of plant growth promoting rhizobia of green gram found in central plateau of India

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Rhizobia are agriculturally important bacteria capable of forming root nodules on leguminous plants and fix atmospheric nitrogen. In the present study, fourty rhizobia were isolated from root nodules of green gram collected from different agro-climatic zones of Madhya Pradesh. Based on morphological characterization, 36 isolates were found gram negative with rod shaped morphology and four were gram positive. On the basis of biochemical characterization all the forty isolates were found efficient phosphate solubilizers, thirty eight isolates were IAA producers and thirty seven isolates were ammonia excretors. Similarly, all the fourty isolates were shown positive results in catalase test while thirty four isolates were positive with carbohydrate fermentation assay. Further, twenty superior isolates were selected with respect to their multifunctional properties and studied for molecular characterization. PCR amplification was done by using 27F and 1492R primer and amplicon of a size ~ 1500bp obtained. Based on 16S rRNA gene sequencing, these bacterial strains were identified under two genera: Rhizobium and *Bradyrhizobium.* Phylogenetic analysis divided 20 rhizobia isolates into two clusters and showed a broad genetic diversity among the studied rhizobia isolates. Thus, these isolates further may be used as PGPR for enhancing the agricultural productivity and reducing the load of chemical fertilizers.

PP-21: Isolation and screening of the Chitinase producing bacteria from soil

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Chitinases occupy a unique position in agricultural biotechnology because the lytic activity inhibits fungal development by degrading chitin and glucan components of cell wall, Chitinases therefore play vital role in agricultural industries and medical fields. Furthermore, fungal phytopathogens are one of the main reasons of concern as the diseases caused by them account for great loss of the crop yield. Chitin is the most versatile polymers lies next to cellulose and starch in copiousness and disseminate in marine and terrestrial environments. Microorganisms which secrete the chitinase enzymes are considered to be possible biological control agents of plant diseases caused by the phytopathological fungi. Soil samples were taken from different sites of GJUS&T, Hisar and near area of University and primarily screened for chitinase producing bacteria. In the study, a total of 12 bacterial isolates from the agricultural fields were screened for chitinolytic activity. Among these isolates only 8 isolates were found to have better potentials of chitinase production. All these 8 isolates showed good capability of growth on the agar media with producing transparent zones of hydrolysis and creamish coloured colonies. The antifungal activity against a common phytopathogen *Aspergillus niger* on the PDA plates indicated about the importance of chitinase as a biocontrol agent for the control of the plant fungal diseases. The percentage inhibition of mycelia growth by these isolates were recorded to ranged from 0-60% and bacterial colonies of different soil samples showed variation in antifungal activity against *Aspergillus niger.*

PP-22: Impact of different arbuscular mycorrhizal fungi on the growth of chilli

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Arbuscular Mycorrhizal Fungi (AMF) is popularly known as Vesicular Arbuscular Mycorrhizal fungi (VAM). Mycorrhiza is a symbiotic association between a fungus and the root system of vascular plants. A pot experiment was conducted in screen house of Plant Pathology, CCS HAU, Hisar, to see the effect of three mycorrhizal species i.e. *Glomus fasciculatum, Glomus mosseae* and *Glomus intraradices* with different doses (100, 150, 200 and 400) on plant height, root length, mycorrhizal per cent colonization and sporocarp numbers was calculated at 30, 45, 60 and 90 DAT (Days after transplanting). The maximum plant height was recorded, when 400 spores (chlamydospores/kg soil) were inoculated in pots (1 kg) viz., 35.43 cm (*Glomus intraradices)*, 32.47 cm (*Glomus mosseae*) and 29.23 cm (*Glomus fasciculatum*) at 90 DAT. The maximum root length was recorded, when 400 spores were inoculated inpots, *viz.,* 16.33cm (*Glomus intraradices*), 15.53 cm (*Glomus mosseae*) and 14.60 cm (*Glomus fasciculatum)* at 90 DAT. The maximum mycorrhizal per cent colonization was recorded, when 400 spores were inoculated in pots viz., 93.33 per cent (*Glomus intraradices*), 87.00 per cent (*Glomus mosseae*) and 77.33 per cent (*Glomus fasciculatum*) at 90 DAT. The maximum sporocarp numbers were recorded, when 400 spores were inoculated in pots 130, 120 and 89.67 sporocarps were in *Glomus intraradices, Glomus mosseae* and *Glomus fasciculatum,* respectively at 90 DAT.Within the three mycorrhizal species *Glomus intraradices* showed best effect. Among all the maximum plant growth parameters were observed, when 400 chlamydospores/kg soil were inoculated in all the three mycorrhizal fungi among the all the inoculum levels.

PP-23: Hyphomycete diversity of Himachal Pradesh

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Himachal Pradesh is situated between 30°22’40” to 33°12’40” along North latitudes and 75°45' 55" to 79°04' 20" along East longitudes. The altitude in the Pradesh, a wholly mountainous region in the lap of Himalayas, ranges from 350 metres to 6975 metres above mean sea level. Himachal Pradesh can be divided into three distinct regions, the Shivalik or outer Himalayas, middle Himalayas or inner Himalayas, and greater Himalayas or the alpine zone. 25.81% area of the total geographical area (55,673 Km^2 spread over 12 districts) is under forest cover and has vast variety of perennial plants. An account of seven hyphomycetous fungal taxa (*Cheiromycella microscopica, Monodictys nitens, Corynesporella indica, Helico madennessi, Ellisem biavaga and Dictyosporium subramanianii*) have been given.

PP-24: Genus *Uromyces* from Himachal Pradesh

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Genus *Uromyces* was established by (Link) Unger in 1833 with *U. appendiculatus* as type species. This genus belongs to family Pucciniaceae which includes rust fungi. A total of sixteen species have been reported from Himachal Pradesh on different hosts *viz. U. agropyri, U. ambiens, U. apluda, U. appendiculatus, U. caryophyllinus, U. ciceris-arietini, U. fabae, U. glycyrrhizae, U. mac-intirianus, U. polygoni-avicularis, U. rottboelliae, U. sommerfaltii, U. strobilanthus, U. valerianae, U. viciae* and *U. vossiae.*

PP-25: Diversity of Rust fungi from Himachal Pradesh

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Himachal Pradesh is a hilly state located in Northern part of India. Of the total geographical area (55.673 sq Km), 25.81% area is under forest cover and has vast variety of perennial plants. So far 23 rust genera *viz.Aecidium, Puccinia, Chrysomyxa, Coleosporium, Frommea, Gymnosporangium, Kuehneola, Kweilingia, Melampsora, Monosporidium, Ochrospora, Urocystis, Peridermium, Phakopsora, Phragmidium, Pileolaria, Pucciniastrum, Pucciniostele, Ravenelia, Skierka, Uredinopsis, Uredo,* and *Uromyces* have been reported from Himachal Pradesh.

PP-26: Hyphomycetous Genus *Dictyosporium* from India

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The genus *Dictyosporium,* erected by Corda (1836) with a single species *D.elegans*, is characterized by having micronematous conidiophores forming compact sporodochia or sometime effuse colonies. Conidia are holoblastic, cheiroid, with compact rows of cells, which may be either flattened in one plane (complanate) or non-flattened (not complanate) with or without hyaline appendages. Presently there are 65 species accepted in the genus (*Index fungorum*). Eight species *viz. Dictyosporium binatum, D. brahmaswaroopii, D. campaniforme, D. intermedium, D. solanii, D. subramanianii, D.polystichum, D. prolificum* have been reported from India.

PP-27: Variation in global climate and its impact on phyto-pathogens

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Climate change is expected to magnify food and feed problems for the global human population and animals. The change in global climate is due to increase in global surface temperature, CO_2 and other greenhouse gases concentration in the atmosphere. Research on impacts of climate change on plant diseases has been limited but these changes will not only have a great effect on growth, cultivation of different crops but also affect the survival, reproduction rate, spread and severity of many plant pathogens which ultimately leads to yield loss. Both plants and pathogens require specific environmental conditions to survive and flourish. Temperature, humidity and crop micro-climate affects the chain of events in diseases cycles. Generally high moisture and temperature favors and initiate disease development as well as germination and proliferation of fungal spores of diverse pathogens. Climate change could alter stages and rate of development of plant pathogens, modify host resistance and result in changes in the physiology of host – pathogen interaction. Change in the climate also impact the geographical distribution of host and pathogen and altered the crop losses. So for sustainable food and feed production, diseases management strategies should be reoriented as per changing climate scenario and intensified research on climate change and its impact on phyto-pathogens could results in improved understanding and management strategies of plant diseases.

THEME -II: PLANT MICROBE INTERACTIONS AND RESISTANCE BREEDING

LEAD LECTURES

LL-1: Research Development and Future Priorities of

Brassica Host-Pathosystem

Naresh Mehta

Former Assoc. Dean and Professor, Plant Pathology, CCS HAU, Hisar

Brassica encompasses large number of edible oil yielding crops (rapeseed-mustard), cruciferous vegetable crops, forage crops, and numerous weeds. These plants like all other living organisms do not live in isolation but are under the influence of interaction among themselves as well as environmental factors. Under natural conditions plants are always challenged simultaneously by biotic and abiotic stresses. The production and productivity of these crops is limited by a number of biotic and abiotic stresses. Cruciferous are known to be infected by more than forty diseases all over the world. However, diseases like Alternaria blight [*Alternaria brassicae* (Berk.) Sacc.], white rust [*Albugo candida* (Pers. ex. Lev.) Kuntze], downy mildew [*Hyaloperonospora parasitica (*Gaum.) Goker.], powdery mildew (*Erysiphe cruciferarum* Opiz. ex. Junell), and Sclerotinia rot [*Sclerotinia sclerotiorum* (Lib.) deBary] are of major consequences because of their widespread distribution, and devastating nature causing heavy yield losses. In future, the disease scenario in these groups of crops is bound to change from major to minor and vice-versa because of intensive cropping, large, and continuous area under same Brassica crop, and cultivar, heavy, and rapid irrigation, higher fertilization (Nitrogen), closer spacing, and rapid change in climatic conditions. Although lot of information have been generated on major diseases with respect to geographical distribution, losses incurred, symptomatology, disease cycle, epidemiology, host-parasite interaction, nature, and mechanisms of resistance, physiologic specialization, and integrated diseases management but still much more is required to overcome the annual losses caused through bridging the gaps in research, and comprehension with a holistic view. In the past research efforts have mostly been limited to individual stresses, but it is now quite apparent that a true picture would only emerge if these biotic, and abiotic stresses are studied holistically. Applications of modern science and techniques including omics data analysis, and functional characterization of individual's genes have revealed a convergence of signaling pathways for biotic and abiotic stress adaption. Multiple stress responses are coordinated by complex signaling network involving reactive oxygen species, and phyto-hormones (H_2O_2, and abscisic acid). Future research priority areas of Brassica host-pathosystem should be standardization of host differentials, and nomenclature of pathogenic races, identification of broad spectrum sources of resistance, resistant loci, and resistant genes in each locus, identification of slow blighting, slow mildewing, slow rusting, tolerant, partial resistant, strong, and weak genes, with suitable combinations, genetics of virulence, and virulence spectrum, mapping, cloning, characterization, and identification of genes for resistance, and virulence, biochemical basis, and genetics of *Albugo- Hyaloperonospora* association, comparative study of *Alternaria* spp. in relation to pathogenesis, transfer of detoxifying enzymes/genes from *B. alba* to *B. juncea,* induced resistance, role of phytotoxins in pathogenesis, and host resistance, identification, and use of hypo-virulent isolates of *Sclerotinia*, as well as identification of convergent points involved in the multiple stress signaling mechanism. There is need to percolate the technologies to the end user for the best use of IPM, and IDM technology for integrated Brassica crops management.

LL-2: Two decade with Lentil rust

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Lentil is an important component of farming systems in many countries. It enriches soil fertility through nitrogen fixation and green manuring, and serves as a source of dietary protein and other essential micronutrients in human nutrition. Among various diseases, rust caused by the fungus *Uromyces viciae-fabae,* is an important damaging disease of lentil and limits its production and productivity. It is prevalent in most of the lentil growing countries through out the world and emerged as an important disease in Bangladesh, Ethiopia, India, Morocco, Nepal, Pakistan and Turkey. In epidemiologically important countries like India and Ethiopia, crop losses up to 100% have been reported. In India, the disease is widely prevalent in low and foot hill areas in the states of Uttar Pardesh, Uttrakhand, Punjab, Haryana, Himachal Pradesh, Jammu and Kashmir, Bihar, West Bengal, Assam and other North Eastern states. My association with lentil rust dates back to 1996, when I joined at CSKHPKV, Hill Agricultural Research and Extension Centre, Dhaulakuan, an internationally known hot spot for lentil rust and this intimacy grew stronger when I was given the responsibility of National Principal Investigator of AICRP on MULLaRP Pathology in 2007. During this period, work was strengthened on identification and characterization of resistance sources among the cultivated and wild species of lentil, slow rusting resistant, pathogenic variation, fungicidal management and molecular characterization of lentil rust resistance genes. Durable and stable sources of resistance *viz.* EC 1, Vipasha, LL 931, PL 1, PL 4, PL 6, PL 024, PL 101, PL 151, PL 156, PL 168, PL 406, Precoz, LH 84-8, VL 507, IPL 237, IPL 316, IPL 326, IPL 533, LL 1122, 1112, 1221, 1273, 1279, L 4076, L 4146, L 4147, L 4149, PL 104, VL 507, VL 516, etc. were identified and many of which like EC 1, Vipasha, L 4149, LL 931, PL 1, PL 024, Precoz, LH 84-8, VL 507, L 4147, PL 4, PL 063, IPL 316, IPL 326, IPL 237, IPL 533, PL 6, etc. were used in national breeding program. Numerous rust resistant sources were identified among NBPGR germpalsm and advanced breeding material from ICARDA. High level of resistance has also been identified among the wild Lens species eg. accessions ILWL 6 & ILWL 9 (*L. nigricans)*; ILWL 430 (*L.lamottei*); ILWL 414, ILWL 418 & ILWL 441 (*L. ervoides*) showed combined resistance to rust, powdery mildew and Ascochyta blight. Accessions ILWL 117, ILWL 230 & ILWL 466 *(L. culinaris* f sp *orientalis*); ILWL 23, ILWL 34, ILWL 37 & IG 136639 (*L. nigricans)*; ILWL 90 & ILWL 198 (*L.C. tomentosus*), ILWL 35, ILWL 196, ILWL 409, ILWL 436 & ILWL 438 (*L culinaris* f spp *odemensis*) showed combined resistance to rust and powdery mildew. Slow rusting sources of resistance were identified among the cultivated and wild Lens spp. Resistance to rust in cultivated lentil has been observed to be simply inherited i.e. by single, two or three dominant genes. However, incomplete resistance and duplicate dominant genes and a recessive gene has also been reported for controlling resistance. Various molecular markers closely linked to rust resistance genes have been reported. Based on the segregating generations of cross PL 8 (susceptible) x L 4149 (resistant), a single dominant gene was controlling rust resistance in genotype L 4149 and SSR marker Gllc 527 was estimated to be linked to rust resistant locus at a distance of 5.9 cM. Such markers may be used for marker assisted selection for rust resistance. Pathogenic variation was studied in lentil rust populations using a differential set of 15-20 lentil genotypes with varying levels of resistance. It was observed that lentil rust populations were pathogenically variable at Dhaulakuan, Pant Nagar and Shillongani. Foliar sprays of fungicides propiconazole 25EC, hexaconazole 5EC, triademifon 25 EC @ 0.1% and difencozole 25EC and tebuconazole 25EC @ 0.05% were highly effective in reducing rust severity and increasing the yield. Though extensive work has been done on identification and characterization of resistance against rust in lentil, still there is need to develop near isogenic lines to study virulence dynamics of the pathogen and its pathogenic and molecular characterization. Precise mapping populations need to be developed for gentic characterization of resistance.

INVITED LECTURES

IL-1: Addressing shortfalls of post flowering stalk rot disease management in maize

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Maize (*Zea mays*) is the queen of cereals and regarded as the crop of the future for its high productivity achieving through hybrid maize venture. More than 60 maize diseases have been reported in India that cause decreased production. Location specific five different types stalk rot diseases appear in maize. Of these, post flowering stalk rot (PFSR) complex caused by *Macrophomina phaseolina* (Tassi) Goid and *Fusarium verticillioides* (Sacc) Nirenberg are most widespread and destructive one which can lead to total yield loss. In order to screen maize genotypes under field conditions for resistance to PFSR disease, toothpick method has been used for creating artificial epiphytotics. Under laboratory conditions, maize genotypes could be screened by two new methods of inoculation standardized in the present study. Cut and split stems were inoculated in the first method and un-split stems were inoculated by toothpick method in the other. Both the new techniques employed *in vitro* were faster in producing results as compared to the field screening of maize genotypes by the standard toothpick method. A new scale ranging from 1 to 16 cm was developed based on the existing 1-9 scale of PFSR for rating of the disease severity *in vitro*. Molecular characterization of maize inbreds was done for the resistance to PFSR disease using Simple Sequence Repeats (SSR) primers. Two SSR primers *viz.* SSRZ 135 and SSRZ 319 showed polymorphism for stalk rot resistance. The marker SSRZ 319 located on chromosome 1 clearly distinguished the resistant lines from the susceptible lines. Resistant genotypes identified in our study would serve as potential donors in the stalk rot resistance breeding programme. Further, a probable presence of QTL qRfg2 in the Indian maize inbred lines could be transferred to elite inbreds using marker-assisted selection. Integrated disease management (IDM) strategies are also addressed for successful management of PFSR in the context of future view points.

IL-2: Rice cyclophilin: a key target by *Xanthomonas oryzae* pv. oryzae T3SS effector XopF for bacterial blight induction Kalyan

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Xanthomonas oryzae pv. *oryzae* (Xoo), the causal bacterium of bacterial blight (BB), is amajor threat to rice production worldwide. The effective management of BB is mostly dependent on the use of antibiotic streptocycline and through use of pyramided resistant (Xa) verities. But recent years the resistance development against the antibiotic as well as short lived resistance in pyramided verities are the matter of concerns for the plant projectionists. This is mainly due to the re-emergence of new races in the Xoo population at a periodic interval. Therefore, it is important to understand the rice::Xoo interaction that leads to the disease development. Xoo interact with rice via secreting effector proteins directly into the rice cell through type 3 secretion system (T3SS). Thus, the effector helps Xoo for its successful proliferation into the rice plant. In this context, we studied Xoo race 4, one of the virulent races prevalent in North India, with reference to its interaction with basmati rice as mediated via T3SS effectors of Xoo. We elucidated the T3SS-effector's repertoire of race 4, that contains 21 Xop and 18 TAL effectors. Subsequent investigation revealed that XopF, identified as key effector, plays crucial role for bacterial virulence and in planta growth, and in the suppression of rice PTI. Recently, we identified rice cyclophilinas the cognate target for XopF effector. We employed Y2H system to search this target using rice cDNA library as prey (cloned into yeast vector pGADT7 in fusion with the GAL4 DNA-activation domain) and XopF as bait. The sequence analysis of the mated positive colonies led to the identification of cyclophilin II (Accession No. GQ848065) as one of the key interactors. Plant cyclophilin is a well-known target for bacterial pathogens to suppress plant immunity. Thus, XopF targets rice cyclophilin with the primary aim to subvert the immune responses of rice. This insight will be useful in exploring strategies for disease resistance.

IL-3: Confirmation of residual effect of defeated genes in RIL populations of PBW343 and HD2967 in the background of PBW621

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The predominance of a variety and in oust from farmers' field after breakdown of its resistance to stripe rust has been a regular feature of North West Plains Zone (NWPZ) of India. Mega cultivars like Kalyan Sona, WL711, HD2329 and PBW343 have gone out of cultivation once they became susceptible to the virulent race of the stripe rust pathogen. This necessitates the search for new and more durable resistance sources against stripe rust. The three bread wheat cultivars PBW 343, PBW 621 and HD 2967 once popular among the farmers have become fully susceptible to stripe rust at seedling as well as at adult plant stage. Initially, on release PBW 621 and HD 2967 were resistant to the pathogen race prevalent at that time. The cross of HD 2967were made with PBW 343 and PBW 621 for mapping and transfer of the resistance loci. The populations were evaluated up to F4, by then there was a shift in the virulence of stripe rust pathogen and both PBW 621 and HD 2967 turned susceptible to this new race. The RILs giving clean reaction became susceptible with varying degree of disease severity (100% to 10%). Nevertheless, F5 and F6 RIL population could still be categorized based on the disease severity on F1 (one leaf below flag leaf) and F (flag) leaf into three categories i.e. high, moderate and low level of APR (adult plant resistance) having 1-200, 200-400 and >400 values of AUDPC, respectively. The present study was conducted with the objective to assess the effect of loci which were once resistant but now still have some residual effect when combined with other unknown minor components. The various APR components (latent period, lesion growth rate, spore production and uredial density) were studied on one set from each category i.e. resistant, moderately resistant and susceptible. The values of APR parameters decreased as the level of resistance increased. This confirmed the presence of residual resistance in presence of Yr9, Yr17 and Yr27 genes in sets of cross PBW 621 × PBW 343. The molecular analysis revealed that additive effect of Yr9 and Yr17 provide the resistance. The major defeated gene Yr9 from susceptible parent PBW 343 contributed towards the resistance i.e. there is presence of ghost resistance. The surviving resistance components were also more durable than the ones that were overcome by the pathogen. Phenotyping and SNP data of the RIL population PBW621 X HD 2967 showed the presence of two QTLs responsible for the residual resistance and two markers BA 00402838 (AX-94454107) and BA 00503975 (AX-94918989) were found to be associated with the trait of interest on chromosome 5B.

IL-4: Gene pyramiding strategies for breeding resistance against wheat rusts

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Wheat being the flagship crop of Punjab, has a profound effect on both the culture and economics of Punjab. A total of 35.20 lakh hectare area is sown under wheat in Punjab, with the production touching a new high (182.1lakh tonnes) during the last crop season raising the productivity level to 51.73 q/ha. The production of wheat is affected by several factor including rising pest attack, rapidly changing climatic conditions and depletion of natural resources (water and nutrients). The scientific measures are directed towards increasing its yield under favourable conditions and stabilizing yield potential amidst any changes in the environment. Punjab lies in the invasion route of rust pathogens especially stripe rust, that originate from Africa, also the over wintering of the pathogen in the Himalayas, directly affect the sub mountainous regions of Punjab, creating stripe rust disease epicenters. Wheat breeding programme at PAU, has been trying to keep pace with the evolving pathogen and succumbing of varieties to rust pathotypes. Historically also, PAU has given the multilines (KSML) concept for managing disease. The conventional strategy of introgressing a known gene for resistance to rust has been augmented by simple MAS and advanced MABB strategy. Both of these have their merits and demerits depending upon number of genes and number of markers applied. At PAU, the advent of MAS started with introgressing leaf rust gene Lr24 and Lr28 into PBW 343. Secondly, gene from *Ae. ventricosa* and *Ae. umbelluata* were introgressed, these were pyramided following the marker assisted background recovery of PBW 343, the line got released as Unnat PBW 343 (PBW 723) for cultivation under NWPZ. The marker assisted selection capacity and the number of rust resistant gene have improved over years at PAU. It initially aimed at repairing the ruling, high yielding varieties. Presently, we are aiming at yield improvement in resistant backgrounds, three cultivars, PBW 752 (Yr10), PBW 757 (Yr15) and PBW771 (Yr40/Lr57) have been released through CVRC, based on yield superiority which carry a known gene for aresistance.

IL-5: Effects of double stranded RNA, mycoviruses, and plasmids on host pathogen interaction in plant pathogenic fungi

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The existence of mycoviruses and related double stranded RNA elements are of frequent occurrence in filamentous fungi genera Rhizoctonia sp. complex(*Thanatephorus* and *Ceratobasidium), Sclerotinia, Cyphonectria, Rosellinia necatrix, Agaricus, Fusarium, Gremmeniella, Helicobasidium, Ophiostoma, Thielaviopsis, Saccharomyces, Tuber fungi, Botrytis, Pleurotus, Helminthosporium, Magnaporthe, Diaporthe,* etc. In the last three decades fungal double stranded RNA elements (dsRNA) and plasmids have been considerably studied because of their adverse effects on pathogenicity of the fungus and the prospects of utilizing them in bio-control strategies against the host fungus, for example, association of dsRNAs enhance or diminish virulence in *Rhizoctonia* sp. These dsRNA occur in natural populations of *Rhizoctonia*. The different isolates of the fungus carry a unique combination of two or more dsRNAs. All the dsRNAs occur in the mitochondrion and cytoplasm of the fungus and none in the nucleus. The studies on transmission of specific dsRNAs to the cultures lacking them revealed that, the cultures possessing the same dsRNA genotype were found to have same degree of pathogenicity. Consistently, acquisition of a 6.1 kb dsRNA (M1 element) caused enhanced virulence, whereas, acquisition of a 3.3 kb dsRNA (M2 element) resulted in diminished virulence in the fungal isolates. The M2 dsRNAs found in filamentous plant pathogenic fungi is very distinct due to (i) apparent suppression of virulence in cultures and prolific replication forming a hypo virulent culture, (ii) its transmission via hyphal anastomosis and (iii) the direct proportion of reduced virulence to the titer of M2 related dsRNA. The transmission of dsRNA occurred between somatically compatible isolates only, however, repeated sub-culturing causes loss of dsRNA. The M2 dsRNA regulates the quinic acid-shikimic acid pathways in the fungus *Rhizoctonia* causing up-regulation of quinic acid pathway and down- regulation of shikimic acid pathway which are connected by two intermediate products, dihydroshikimic acid and dihydroquinic acid. The ORF A protein of M2 acts as a truncated inactive repressor, binds to the quinate pathway activator without affecting transcription of quinate pathway gene cluster thus diverting 3- dehydroquinate and dehydroshikimate from shikimate to quinate pathway. This leads to a significant decrease in phenylalanine acid (toxin) synthesis. The maintenance and spread of these dsRNAs in field population depends on their ability to move within and between the isolates. Occurrence of virus genomes *viz., Partitivirus, Totivirus,Mycorheovirus, Narnaviridae, unassigned Ourmiavirus, Levivirus, Allolevivirus Plant Bromovirus* and cytochrome c oxidase assembly factor in electron transport chain fungi, provides evidence of virus evolution from cellular genes of the fungus. The information on regulation of biochemical pathways by the fungal dsRNAs and plasmids may be used to devise strategies for management of the diseases caused by the fungus, and understanding the molecular genetics of hyper-virulence in plant pathogens, as well as characterizing genes involved in generation of virulence factors and hence, regulating inheritance virulence in fungi. These insights may help to understand how genomic events lead to pathogen development and open prospects to interrupt and prevent it. Use of dsRNA and plasmids based organic amendments, biorationals or microbial antagonists can be a potential alternative to agrochemicals for control of cosmopolitan fungal pathogen with a wide host range. Apart from dsRNA fungal plasmids are found in cultures isolated directly from natural populations. Plasmids represent a mysterious class of DNA which is parasitic or selfish DNA, which seems to exist only for the purpose of existing. Plasmids have been found in many fungi, including *Absidia glauca, Agaricus spp., Ascobolus immersus, Ascosphaeria apis, Alternaria alternata, Claviceps purpurea, Epichloe typhina, Erisyphe graminis, Fusarium solani, Fusarium oxysporum, Leptosphaeria maculans, Morchella conica, Nectria haematococca, Neurospora spp., Podospora anserina, Pythium spp., Rhizoctonia solani, Tilletia* spp., and *Trichoderma viride.*These plasmids may be used as potential markers for studying fungi at the population level and can uncover diverse molecular processes that are relevant not only to the plasmids themselves but also to the properties of DNA in general. The intimate association of plasmids with mitochondria can unveil molecular biology of mtDNA. Analysis of plasmids may lead to new insights into the evolution of dsRNA, viruses, introns and transposons.

ORAL PRESENTATIONS

OP-1: Tackling Yellow Mosaic Disease in Kharif pulses: Host resistance and characterization of associated viral and sub viral components

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Yellow mosaic disease (YMD), transmitted by whitefly is a major constraint in production of kharif pulses, causing heavy yield losses. Deployment of YMD resistance remained unsuccessful due to highly variable nature of the pathogen and mostly recessive genetic control of host resistance. In present research work, potential YMD resistant donors developed through intra and interspecific crosses and mutation breeding were identified by precise screening techniques. The stability of resistance in these donors was further confirmed over the years at multiple locations. For molecular mapping of YMD resistance, F2 population was developed from an interspecific cross between ML 267 (*Vigna radiata*) and Mash 114 (*Vigna mungo*)Whole genome sequence based SSR markers were developed and newly designed SSR primers were used to identify SSR markers linked withYMD resistance through bulk sergeant analysis. On the pathogen side, two species i.e. Mungbean yellow mosaic virus (MYMV) and Mungbean yellow mosaic India virus (MYMIV) were detected from all the samples. Mungbean yellow mosaic virus [Urdbean: New Delhi: 2011] accession no JQ398669 with variable DNA B component was found to be prevalent in Punjab during both summer and kharif season. Alpha satellite was not found in any of the samples.Cotton leaf curl Multan beta satellite was found to be associated with YMD infection on summer mungbean crop whereas Malachra yellow vein mosaic beta satellite was associated with YMD infection on kharif pulses. Similar strains of virus were also observed on different weed species, suggesting their role as green bridge for perpetuation of YMD.

OP-2: Identifying potential virulence factors and RNA silencing suppressors encoded by Geminivirus

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Geminiviruses are plant-infecting viruses characterized by a single-stranded DNA (ssDNA) genome. Geminivirus-derived proteins are multifunctional and effective regulators in modulating the host cellular processes resulting in successful infection. Virus-host interactions modulate host gene expression patterns, disruption of cellular metabolic signaling pathways, impair plant's defense system, and effectively evade RNA silencing response leading to host susceptibility. Plant viruses encode virulence factors or RNA silencing suppressors to reprogram plant cellular processes or to fine-tune host RNA silencing mediated defense responses. In previous study, Ageratum yellow vein mosaic disease (AYVMD) has been identified from a weed host showing yellow mosaic and dwarfing symptom, but the functions of its encoded proteins are unknown. In this study, all five proteins encoded by AYVMD were screened for potential virulence and RNA silencing suppressor activities. We found that V2, RepA, C1 affect the pathogenicity of a heterologous potato virus X. However, the results also showed weak suppression of gene silencing activities for C2 and C4 induced by GFP and mRNA associated with GFP was detected. In this study, we identified as many as four distinct suppressors of RNA silencing encoded by AYVV-ID [ID:Tom] and its cognate betasatellite in the family Geminiviridae, counteracting innate antiviral response.

OP-3: Mycelial compatibility studies among the isolates of *Sclerotiniasclerotiorum* (Lib.) de Bary causing stem rot in rapeseed-mustard

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Rapeseed-mustard is one of the major groups of edible oilseed crops in the world after soybean and palm oil. Several diseases pose a serious threat to successful cultivation of rapeseed-mustard. Amongst them, stem rot caused by *Sclerotinia sclerotiorum* (Lib.) de Bary, is now becoming very important fungal disease as it is soil borne, necrotroph and have wide host range. The most effective management strategy is resistant or tolerant cultivars. To identify and deploy host resistance, it is important to understand the diversity of this fungus. Mycelial incompatibility is an effective morphological marker to identify intra-specific heterogeneity within populations of *S. sclerotiorum*. A total of 48 isolates were collected from Punjab and adjacent states: which were paired in all possible combinations. These revealed high level of incompatibility amongst them as only 29 combinations out of 1128 were found to be compatible, 88 of intermediate type and rest were incompatible. The 25 isolates involved in compatible combinations were grouped into 19 Mycelial Compatibility Groups (MCGs) whereas the remaining 23 isolates singly represented a MCG as they were compatible only with themselves. It was observed that in general, isolates belonging to nearby areas were compatible and those from far away geographical areas were incompatible. This study revealed a considerable amount of variation as only 10.4 percent pairings were found compatible and thus it is very important to know the pathogen population structure for identifying reliable resistance sources.

OP-4: Population variability and phylogenetic analysis of root knot nematodes infecting chilli and bitter gourd in Punjab

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Root knot nematodes, *Meloidogyne* spp. are the most destructive plant parasitic nematode causing serious losses to vegetable crops worldwide. These nematodes attach the tender roots of plants and form characteristic galls which hampers the nutritional uptake capacity of the crops affecting plant health, yield and quality. They have a wide host adaptability and are reported to parasitize over 3000 cultivated and wild plant species. More than hundred recognised species of genus *Meloidogyne* are documented worldwide. Knowledge on population diversity, prevalence and accurate diagnosis of the prevailing *Meloidogyne* species in an area is of paramount importance for designing management practices for sustainability of crop production. Survey of major chilli and bitter gourd growing areas of Punjab in districts of Patiala, Sangrur, Ferozepur Gurdaspur, Ludhiana and Tarn Taran were conducted for incidence and prevalence of root knot nematodes. In chilli growing areas maximum prevalence of root-knot nematode (80%) was recorded in Sangrur and minimum in Ferozepur district (40%). In case of bittergourd an overall 55.93 percent root knot nematode incidence was recorded in the districts surveyed. Maximum disease incidence (75%) was recorded in Ferozepur and minimum disease incidence was seen in Ludhiana (44.16%). Further, it was observed that root knot nematode infestation was higher in the fields where vegetable crops like brinjal, okra, chilli and cucumber, etc. were grown in rotation with chilli or bittergourd as compared to the fields where rice, marigold, garlic and onion crops were included in the crop rotation. The soil and root samples were collected for population estimation and characterization in the laboratory. The protocol for DNA extraction from root knot nematode was standardised and species specific molecular were validated. The morphological and molecular characterization of the populations collected from farmers field revealed *M. incognita* as the most prevalent species infecting chilli and bittergourd under Punjab conditions. In addition *M. javanica* sp. was also found to be prevalent in some chilli growing areas. The protocol standardised for DNA extraction and species specific markers validated in the present study can be used for quick detection of these nematodes.

OP-5: Managing yellow rust disease in barley via resistance breeding

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Barley (*Hordeum vulgare L.*) an ancient crop, grown in more than 100 countries, is the fourth most important cereal crop in the world. Its productivity throughout the world is affected by different biotic stresses like rust, powdery mildew, net blotch, leaf blight, etc. Exposure to these biotic stresses induces disruption in plant metabolism leading to substantial decrease in fitness and productivity of a crop. Of the different biotic stresses, barley yellow rust disease is the most economically important because it causes significant yield losses worldwide. With the prevailing diversity of the yellow rust pathogens, concurrent evolution of new virulent strains and changing climatic conditions, the management of this disease is becoming ever challenging. The most effective and sustainable way of management of yellow rust is the enhancement of host resistance, which is an economical and environmental friendly approach. Identification of resistant sources, understanding genetics of resistance followed by hybridization and selection are important steps of breeding. Different barley breeding lines like BHS46, BHS366, BHS371, BHS383, BHS384, BHS447, BHS462, BBM760, BBM762, BBM777, BBM781, BBM782, BBM786 were found to be resistant to yellow rust pathotypes in seedling and adult plant stage. One lines BHS463 was found to be susceptible at seedling stage but resistant at adult plant stage. Forty-three SSR markers were used for diversity analysis. Screening of barley germplasm lines led to identification of resistant sources of following varieties: UPB1008, RD2668, VLB115, BHS169, BHS380 and BHS400 were found to be resistant to yellow rust pathotypes at seedling stage and genetics of resistance has also been studied in these genotypes.

OP-6: Spot blotch: Serious yield and malting quality limiting factor in Indian barley

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Barley is an important coarse cereal and is used for multiple purposes like food, feed and malting. During 2018-19, the crop occupied nearly 6.62 lakh ha area with the production of 1.75 mt grains, where the highest production was reported from Rajasthan (50 %) followed by Uttar Pradesh (23%) and Madhya Pradesh (17%). Spot blotch is an economically important disease in barley and is one of the serious impediments in productivity enhancement. Spot blotch is caused by the ascomycetous hemi-biotrophic filamentous fungus *Cochliobolus sativus* (Ito and Kurib.) Drechs.exDastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.].The disease is favoured by warm and humid climate and the north eastern Indo-Gangetic plains, eastern Uttar Pradesh, Bihar and west Bengal are highly prone for spot blotch incidences.With the changing climate and congenial weather parameters the disease is also one of the most important grain yield limiting factors in the states of Haryana, Punjab and Rajasthan. In the present study the breeder seed indent data (DAC&FW) of top ten breeder seed indented varieties (2019-20) were corroborated with the spot blotch reactions observed from national barley disease screening nursery (NBDSN)for rabi, 2017-18 and 2018-19. The six rowed barley variety RD 2786 showed the highest breeder seed indent (126.0 q) followed by RD2794 (103.05), DWRB137 (69.97), DWRB101 (60.0), etc. Based on consecutive two years disease data nearly all the varieties namely, BH946 (78), DWRB101 (67), DWRB137 (79), HUB 113 (79), K1055 (89), RD2786 (89), RD2794 (79) and RD2899 (79) were found susceptible to spot blotch. Therefore, it is immensely needed to develop spot blotch resistant varieties to check the yield losses and to get better malting quality in barley.

OP-7: Dual screening of elite chickpea (*Cicer arietinum* L.) genotypes to fusarium wilt and salinity under field conditions

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Chickpea (*Cicer arietinum* L.) is an important legume crop in many parts of the tropics and subtropics. It is one of the main source of quality protein among vegetarian population of the world. Various abiotic and biotic stresses affect the crop adversely thereby decreasing the quantity as well as quality of the produce. Among biotic stresses, wilt, dry root rot, and Ascochyta blight are of economic importance. On the other hand chickpea is also very sensitive to salinity. Review of literature indicates that no chickpea variety could grow at EC levels higher than 6 dS/m. On an estimate salinity causes 8–10% yield loss globally. Therefore, improved genotypes that are well adapted to salinity conditions along with resistance to Fusarium wilt are needed to sustain and enhance production in affected areas. Keeping in view, the importance of both the stresses, this study was aimed to identify resistant chickpea variety to Fusarium wilt and salinity in a wilt sick plot which has been maintained for last 43 years. A part of this wilt sick plot has saline soil and the salinity of the plot ranged from 2.81 to 8.94. This part of the plot was used for dual screening of chickpea genotypes. Wilt reaction from wilt sick plot without salinity was used as control as well as for recording percent wilt disease incidence. This study included 32 elite genotypes of chickpea, including 7 accessions from ICRISAT and released varieties *viz.,* C 235, H 208, HC 1, HC 3, HC 5 (from Hisar) and CSG-8962 (from Karnal). CSG-8962 from Karnal is known for its tolerance for salinity (up to 4 dS/m). All the tested genotypes showed a large variation for seed yield under salinity (0.0 to 11.90 g/plant). Under salinity conditions, all the genotypes germinated but in addition to their delayed germination, they showed variation for the plant growth stages, which were attained by them before they died. The critical perusal of the data clearly indicated that major trait related to salinity tolerance was the ability to maintain a large number of filled pods and the seed size. Seed size was smaller in sensitive genotypes. JG 62 was used as a susceptible check which showed 100 per cent disease incidence. HC 3 was the only genotype which was found tolerant to Fusarium wilt with fairly high level of salinity tolerance. It showed a reduction of 44.3% which was minimum among the tested genotypes followed by 62.5 % reduction shown by CSG-8962. But CSG-8962 was susceptible to Fusarium wilt. HC 3 was the only genotype showing minimum reduction in yield due to salinity along with MR reaction for Fusarium wilt. Its use in the breeding programmes is advocated for incorporating dual resistance/tolerance in future chickpea varieties.

OP-8: Phenotypic and molecular characterization of wheat germplasm for Spot blotch (*Bipolaris sorokiniana*) and adult plant rust resistance

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Wheat (*Triticumaestivum* L.) is one of the most important food crops worldwide, occupying largest cultivated area, and supplying 40% of food globally and 25% of calories for the developing world. Hence increase in its production and productivity is very much desired to meet the demand of ever increasing population. Climate change and global warming have profound effect on resurgence of new races/ pathotypes of different disease causing organism. Therefore, development of disease resistance varieties has been one of the important goals in crop improvement. Wheat is affected by several diseases, but rusts caused by *Puccinia* spp. are the most important. The impact of rust on yield reduction in wheat ranges from 10% under moderate and 65% under intense epidemics. Due to change in climate, the severity of spot blotch (*Bipolaris sorokiniana*) incidenceis increasing in North Western Plains Zone (NWPZ) of India where leaf and stripe rust, and powdery mildew were major diseases. Hence exotic germplasm obtained from CIMMYT, Mexico were screened under epiphytotic conditions and resistance lines were identified using gene linked markers.Two hundred germplasm accessions including four checks were evaluated in Augmented Block Design (ABD) at G. B. Pant. University of Agriculture & Technology, Pantnagar in 2013-14 and 2014-15. Screening of the germplasm accessions for spot blotch and adult plant rust resistance was done phenotypically.Area Under Disease Progress Curve (AUDPC) for spot blotch resistance was also measured and genotypes were grouped into different categories. Sufficient genetic variability was observed in the germplasm accessions for disease severity. Lines showing resistance for spot blotch were confirmed using specific SSR marker Xgwm148 and gene linked STS marker csLV34was used to confirm the presence of APR gene Lr34/ Yr18. Resistant accessions confirmed with molecular markers can be used in breeding programme for developing genotypes possessing spot blotch and adult plant rust resistance, and diverse germplasm accessions could be used for developing mapping populations for the detection of QTLs/genes for spot blotch resistance.

OP-9: Performance of elite sugarcane clones against smut disease in north-west zone under Punjab conditions

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Sugarcane (*Saccharum* sp. hybrid complex) is an important cash crop of India and served as source of sugar for hundreds of years. The crop is affected by several fungal, bacterial, phytoplasmal and viral diseases which contribute to low cane yield and quality. Of the various fungal diseases, smut caused by *Ustilago scitaminea* Sydow is considered as one of the major disease next to red rot. Both plant and ratoon crops are affected by this devastating disease, however, ratoon crops are more prone to it. It has been reported to cause yield losses of 39-50 % in plant cane crop and 53-73 % in the ratoon crop. Many sugarcane commercial varieties like CoS 510, Co 453, Co 740, Co 975, Co 1158, Co 62175 and NCO 310 had been completely eliminated from cultivation due to high incidence of this disease. Due to lack of effective control measures, resistance breeding has remained the most suitable and viable option solution. Thirty-nine elite sugarcane clones of early and midlate-maturity groups were artificially evaluated against smut under Punjab conditions. Three budded setts of each clone were inoculated by steeping them for 30 minutes in freshly prepared teliospore suspension with a spore load of one million spores per milliliter before planting. The disease incidence was recorded at weekly intervals throughout the crop season as per the standard protocol. Based on the cumulative smut incidence, the clones were categorized into different disease reaction categories. Out of 39 clones, clones *viz.*, Co 15027, CoLk 15207 and CoH 14261 were found resistant (R) to smut disease whereas twenty-four clones namely Co 15023, Co 15024, CoLk 15201, CoLk 15205, CoPb 15211, CoPb 15212, CoLk 14201, CoPb 14211, CoPb 13181, CoS 13231, CoLk 15206, CoPb 15213, CoPb 15214, CoS 15231, CoS 153232, CoS 15233, CoS 15234, Co 14035, CoLk 14204, CoPb 14184, CoPb 14185, CoS 14233, CoH 13263 and CoPant 13224 were rated as moderately resistance (MR) having disease incidence >0-10 %. Nine clones were identified as moderately susceptible (>10-20%) and three clones were found susceptible (>20-30%). None of the clones showed highly susceptible (>30.0%) reaction. The resistant or moderately resistant genotypes can be further evaluated on large scale under varietal improvement programme for their commercial cultivation in the state.

OP-10: Evaluation of sugarcane (*Saccharum officinarum* L.) clones for high sugar yield and multiple disease resistance under subtropical conditions

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Sugarcane (*Saccharum* sp. hybrid complex) is one of the most important agro-industrial crops. In India, sugarcane is cultivated all over the country under wide range of climate, ranging from sub-tropical to tropical conditions. In the sub-tropics, Uttar Pradesh, Uttarakhand, parts of Bihar, Punjab and Haryana are the important cane growing States of the country. In Punjab state, sugarcane is being grown in an area of about 95 thousand hectares with sugar recovery of 9.94 %. Being a long duration crop, it gets attracted by number of fungal, bacterial, viral and phytoplasmal diseases and pose serious threat to sugarcane cultivation throughout India. The productivity of the crop is measured in terms of cane and sugar yield. The exploration of existing germplasm for genetic base broadening is of utmost importance in sugarcane as poor seed replacement rate limits the availability of quality seed of new sugarcane varieties. So beforehand screening of potential clones and multiplication will assist in extracting maximum potential cane and sugar yield of varieties. Improvement in yield has been achieved to some extent but there is an urgent need for identification of the improved sugarcane varieties producing higher sugar per unit area per unit time. Therefore present study is conducted to test the promising clones for their adaptability under Punjab conditions based on their performance for sugar yield and their reaction to major diseases for their further introduction as a new source in conventional breeding programme. Field experiments were conducted to evaluate the performance of 53 early and mid-late maturing sugarcane clones including standards at Punjab Agricultural University, Regional Research Station, Kapurthala which represents the subtropical conditions of the country. All the clones were evaluated for different quality traits and disease resistance against major diseases of sugarcane i.e. red rot, smut and wilt, using standard protocols. Analysis of variance revealed that clones used in the testing differed significantly with respect to all the characters studied. Among all the tested53 clones (43 tested clones + 10 standards) when assessed for quality parameter i.e. sucrose %

juice , 8 % of clones are among high sugared early maturing clones at par with best quality check CoJ 64, followed by 11 % clones which are in mid range and quality is at par with best quality yield check Co 238 and 23 % clones falls in the third group which has the best potential to serve as mid maturity group and quality matches with the national standards (CoS 767 and CoPant 97222). Out of 53 clones screened for major diseases of sugarcane, 31 were found moderately resistant/ resistant to both the red rot pathotypes by plug and nodal cotton swab methods of inoculation. One clone (K 2/1) was rated as resistant (R) to smut whereas 30 as moderately resistant (MR). For wilt, 33 genotypes were rated as resistant (R; grade 0), and 11 as moderately resistant (MR; grade 2). It can be concluded from the present study, that eleven elite clones namely K 2/1, K 2/2, K 2/9, K 3/1, K 31/1, K 6/3, K 57/1, K 58/2, K 66/1, K 71/3 and K 72/3 were high sugared clones possessing resistance to major diseases of sugarcane. Realization of higher sugar yield of these sugarcane clones in combination with disease resistance needs to be adjudged on large scale to enhance sugar recovery of the state in sugarcane command area by industry and growers.

OP-11: Antifungal metabolites from plant growth promoting bacteria

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The bacterial isolates were tested for antagonistic activity against a wide range of phyto-pathogens on potato dextrose agar medium by dual-culture technique. The antifungal activity of the culture filtrate was evaluated by measuring the diameter of inhibition zones. The antifungal activity of selected bacterial isolates was tested against various fungi namely *Fusarium oxysporum, Rhizoctonia solani, Alternaria alternata, Cladosporium* sp. and *Curvularia* sp. Antifungal activity was confirmed through clear zone formation around bacterial colonies. The antifungal metabolites were extracted and identified using various biochemical techniques. Different kinds of plant growth promoting bacteria, their isolation, PGP attributes, antifungal metabolites and their characterization will be discussed during the presentation.

OP-12: Identification of advance breeding materials through agro-physiological traits with high yield and stripe rust resistance

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Wheat is an important cereal crop giving directly ~21% of energy intake for the world's population and more than 50% of the energy intake in the Indian population. In India, wheat production increased from 11 Mt to 101.20 Mt from 1961 to 2019 due to selective breeding for high yielding semid-warf varieties. Since the cultivated area is limited, hence the productivity of wheat has to increase particularly in high fertility areas. A set of 38 advanced wheat genotypes were evaluated for the identification of superior genotypes targeting with high grain yield, physiological traits and stripe rust incidence during 2018-19 at ICAR-IIWBR, Karnal. The experiment was carried out in randomized block design with three replications. The plot size was kept six row of six meter length with spacing of 23 cm between rows and 10 cm between plants within rows. The observations were recorded on grain yield per plot, normalized difference vegetation index (NDVI) and stripe rust incidence. The genotypes namely LBP 18-1, LBP 18-13, LBP 18-16, LBP 18-15, LBP 18-17, LBP 18-18, LBP 18-20, LBP 18-19, LBP 18-25, BCW 2, BCW 5, BCW 6 and BCW 9 were observed as resistance for stripe rust incidence. The genotypes *viz*., LBP 18-1, LBP 18-16, LBP 18-15, LBP 18-17, LBP 18-19, LBP 18-25, BCW 2 and BCW 9 were found superior over the best check for better normalized difference vegetation index. However, the genotypes LBP 18-16, LBP 18-18, LBP 18-19 and BCW 6 were found better over the check for grain yield, NDVI and stripe rust incidence. In conclusion, the best genotype for grain yield was observed as LBP 18-20 with resistance for stripe rust. Thus, the genotypes could be used as donors in wheat breeding programs to develop high yielding, stripe rust resistance with suitable NDVI.

POSTER PRESENTATIONS

PP-1: Insight into *Ustilaginoidea virens* causing false smut of rice in India

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Claviceps oryzae-sativa Hashioka [*Ustilaginoidea virens* (CKe) Tak., Ascomycetes]causes rice false smut which is one of the emerging diseases in India. Disease incidence ranged from 10-30% in the affected rice plots. Yield loss to the tune of 0.2-49% has been reported in India. New cropping technology, including planting high N-responsive varieties, enhancing the moisture supply, and including late sown wheat in the crop rotation, aggravated the disease in farmers fields. False smut of rice is a major disease not only in India, but all over the world. Morphological characterization of *U. virens* isolates from PB showed creamy dull white, grey black, fluffy mycelium, undulated, compact, ring pattern growth of colonies. Spores were, circular to ovate, echinulated, double walled. The isolates from Delhi and UP showed creamy dull white-grey, cottony, undulated colonies. Spores were circular to ovate, highly echinulated, double walled, mass of spores covered with silvery membrane. The conidia (3-5 μm) of *U. virens* were globose to irregularly rounded and ornamented with prominent spines (200-500 nm). Out of the 20 tested culture media for the growth of *U. virens*, 4 media (Corn meal dextrose agar, Yeast malt agar, Potato dextrose agar, and Potato carrot agar) showed cultural growth (1cm in 10 days) which was at par with the standard PSA (Potato sucrose agar). A greenhouse trial was conducted to standardize the inoculation technique in false smut of rice (CV. Swarna) during the 2018 Kharif season by using syringe and spray inoculation methods at boot, early flowering and grain filling stages of the crop. Syringe inoculation of spore suspension (4x10^{6}) of *U. virens* at early flowering stage of the rice crop was most successful method in producing the disease as compared to the spray method. Syringe inoculation produced 10.0% disease incidence and 0.4% disease severity at early flowering stage of the crop respectively.

PP-2: Screening germplasm accessions for identification of diverse stripe rust and spot blotch resistance sources.

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For sustaining and realizing future wheat production goals in terms of increasing human population, wheat crop will have to be protected against biotic stresses. Wheat rusts have adversely affected yields in the past and still have been the major biotic production constraints. Breeding wheat for rust resistance relies on characterization and deployment of genetically diverse sources of rust resistance. A total of 166 exotic wheat germplasm accessions were used for identification of potential rust and spot blotch resistance sources. Most of these lines had some sort of resistance to either any of the three wheat rusts and spot blotch. The data for Adult Plant Resistance (APR) on leaf and stem rust was recorded at Wellington which is a hotspot location, as infection occurs under natural conditions. The stripe rust was artificially created at Karnal for identification of resistant lines. Based on APR data 85, 96 and 16 accessions were found completely resistant to leaf, stem and stripe rusts, respectively. Based on the seedling resistance data against different pathotypes (10 each for leaf & stripe and 5 for stem rust) of each rust, nine, fifteen and five accessions were found highly resistant, respectively. The APR and and SRT data identified 28 accessions which were highly resistant to either to one or two rusts. Evaluation for spot blotch was carried out at Wadura and Coochbehar, the scores obtained were recorded and arranged into three classes; resistant (upto 25 infection score), moderately susceptible (26-57 infection score) and highly susceptible (>57 infection score). Based on infection score, 26 accessions were found to be highly resistant. The resistant lines so identified in this study may be exploited for hybridization programs to diversify the sources of resistance or can be directly used in the plant breeding programs.

PP-3: Evaluation of barley germplasm / cultivars against spot blotch (*Bipolaris sorokiniana* Sacc. Ex. Sorok.) Shoe. of barley

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One hundred forty three Barley germplasm/cultivars obtained from various sources were evaluated against spot blotch (*Bipolaris sorokiniana*) under field condition by creating artificial epiphytotic conditions, during Rabi 2017-18 at Nawabganj Research Farm, C.S.A. University of Agriculture & Technology, Kanpur. The experiment was laid out in Randomized Block Design with three replicates. Each cultivar was sown in 2 m row spaced 22.5 cm apart in last week of December. The spore suspension of *Bipolaris sorokiniana* was prepared from 21days old cultivar. The inoculation with the pathogen was made by spore suspension (4.3 x 10^4 spore/ml of water) on barley genotypes. The progress of the disease in all barley genotypes was monitored from 2nd fortnight of March and disease severity at 10 days interval was recorded. Maximum disease severity was observed in RD2935, RD2937, RD 2938 (78.00%). However the minimum disease severity was recorded in barley genotypes *viz;* BH 1001, BH 1003, BH 1015, BHS 450, DWRB 123, DWRB 136, DWRB 141, and DWRB158 (35-36%).

PP-4: Evaluation of Harvest Plus Yield Trial (HPYT) genotypes for disease, agro-physiological and quality parameters

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Presently, breeding for quality is one of the prime research areas among scientific community. Development of high yielding genotypes coupled with superior quality and rust resistance is tedious and time consuming. Therefore, a study was conducted to characterize the advanced 9thHPYT genotypes for rust, agro-physiological and quality parameters. Fifty genotypes including check variety (HD 3086) were evaluated in a six-row plot of six meter length under timely sown irrigated conditions during crop season 2018-19 in Randomized Complete Block Design with two replications. The study was conducted at ICAR-IIWBR, Karnal research farm. The row spacing was 20 cm and between plants spacing was 10 cm. Data was recorded on days to heading, days to maturity, plant height (cm), 1000-grain weight (g), stripe rust, brown rust, normalized difference vegetation index at three stage (pre-heading, heading and post-heading), grain number per spike, grain iron content (ppm), grain zinc content (ppm), biomass (g) and grain yield (g). The 1000-grain weight ranges between 36-51g, grain number per spike ranged from 44-74, iron range from 27-39 ppm, zinc ranges from 28-39 ppm, biomass range was14kg-19kg and GY range from 4270-6965gm/plot. The range for stripe rust was 0-40S and 0-20S for brown rust, whereas the score for stripe rust was 5S and for brown rust 10S in check variety HD 3086, indicating that some tested genotypes were superior for both stripe as well as brown rust resistance. Six genotypes exhibited resistance for both stripe as well as brown rust resistance. 13 genotypes showed 1000-grain weight more than >46g which is higher than check (40g); 16 genotypes showed grain number per spike mean >64 which is higher then check (62); 08 genotypes for iron mean >37ppm which is higher then check (36 ppm); 12 genotypes for zinc mean >34 ppm which is higher then check (28 ppm); 08 genotypes for mean biomass and 06 genotypes for mean grain yield which is higher then check. The best genotype for 1000-grain weight was G 411 (51g), for iron and zinc G404 (39ppm) and for grain yield was G432. Further, G6 was found superior than check for 1000-grain weight, grain yield as well as brown and stripe rust resistance. In the present set of materials, appreciable amount of variability is present for all the yield traits along with stripe as well as brown rust resistance. Therefore, the genotypes which showed superior performance in comparison to check for rust incidence and other yield components could be used in active wheat breeding programme for improvement in respective traits.

PP-5: Identification of rust resistant donors under terminal heat stress environment

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Sizeable area of wheat production across the globe is exposed to heat stress at different stages of crop growth, which pulls down the genetic potential of the modern day cultivars which bred for normal crop growing environment. Current estimates indicated that wheat crop grown on around 13.5 mha in India is affected by heat stress. The climate change-induced temperature increases are estimated to reduce wheat production by 29% and rigorous threat particularly during reproductive and grain-filling phases that result into yield loss. The development of genotypes with potentially high yield under heat stress conditions has led to modest genetic gains. In order to meet the challenges of high temperature ahead of global warming, concerted efforts are being made to evaluate germplasm for heat tolerance and develop genotypes suitable for such stressed environments. The crop is exposed to high temperature stress due to late planting. Therefore, a study was conducted to evaluate a set of 18 high yielding genotypes for yield components and rust resistance under late sown irrigated conditions. The crop was sown during second fortnight (22nd) of December 2018 at ICAR-IIWBR, Karnal research farm. Each genotype was planted in a six-row plot of six meter length in an alpha-lattice design with two replications. Spacing between rows and between plants was 20 cm and 10 cm, respectively. Standard agronomic practices were followed to raise the crop. The data was recorded for days to heading, days to maturity, plant height, stripe rust, brown rust, grain filling duration, grain filling rate, 1000-grain weight and grain yield. Maximum temperature ranged between 23.7-39.20 C and minimum temperature ranged between 9.9-21.20 C during the grain filling period. The weakly temperature data revealed that the heat stress (>30°C) initiated after 16 days of heading during 2018-19 crop season. The maximum mean temperature during grain filling period was 31.84^0C. The required optimum temperature regime is 15-18°C during grain filling stage but daily temperature is 25-35°C or even higher is common across many regions of the world where wheat is grown, this affects the crop yield. Thus, the test genotypes faced heat stress environments. Negative correlation was found for days to heading (-0.384), days to maturity (-.269), lodging% (-0.133), stripe rust (-0.272) and brown rust (-0.418) with gain yield, while positive and significant correlation was found for 1000 grain weight (0.82**) and gain filling rate (0.95**) with gain yield. Positive and significant correlation (0.72**) among grain filling rate and 1000-grain weight was also observed, thus the selection could be effective based on these traits. In the present study, six genotypes were found free of stripe rust and four genotypes for brown rust. Four genotypes for 1000-grain weight and one genotype for grain yield. One genotypes QYT-RI-1823 was found superior than check (DBW173) for 1000 grain weight and stripe rust resistance, whereas, QYT-RI-1816 for 1000 grain weight, stripe as well as brown rust incidence, and QYT-RI-1825 for grain yield, 1000 grainweight and grain filling rate. These genotypes could be developed as new source for stripe and brown rust resistance in high yielding genetic backgrounds under terminal heat stress conditions after further testing of selected genotypes under multi years and/or locations.

PP-6: Host-bacterium interaction during disease development in plants

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Phytopathogenic bacteria constitute a large domain of prokaryotic microorganisms and are capable of inciting various diseases into host plants. A number of factors are responsible for successful disease development in plants such as virulence and abundance of bacteria, susceptibility of plant host in addition to totality of all congenial environmental conditions. The events that follow in successful disease development include host finding through chemotaxis, adhesion and entry, interaction between host plant cell and pathogen, growth and reproduction followed by dissemination of the pathogen. The chemotaxis signaling pathway in response to host secretions is mediated through a transmembrane receptor protein MCP (Methyl accepting chemotaxis protein) which, prior to ligand binding, is present in form of monomers. The attractant or repellent act as a ligand for MCP receptor and shows ligand binding activity to dimerise it in order to bring about conformational changes and activation of MCP causing MCP to recruit one transducer protein and another sensor kinase. The sensor kinase autophosphorylates itself on histidyl residues to activate another protein which further activates a protein complex that acts as a flagellar motor switch. This gives signals to basal body to rotate flagellum for direction change based on signal perceived from the host. After locating the host, bacteria adhere the plant surface and enter them through non-cuticularised areas and natural openings or wounds because they are incapable of direct penetration into the plant. Different bacteria have different modes of entry into plant viz., *Xanthomonas axonopodis* pv. *malvacearum* through stomata, *Pantoea stewartii* through wounds created by flea beetle, etc. Type III secretion system also plays important role in adhesion to plant surface and virulence through PAMPs or effector molecules leading to effector triggered immunity or susceptibility. A number of genes are found to be involved in host-pathogen interaction *viz*., hrp, avr, disease specific genes, harpins, etc. The interaction between host and pathogen falls into two general categories, i.e., compatible interaction, leading to symptom development, and incompatible interaction leading to absence of observable disease symptoms on plants. The incompatible interaction with non-host plants is often correlated with elicitation of hypersensitive response when bacteria are introduced at > 10^6 cfu/ml.

PP-7: Identification of rust resistant donors in high yielding genetic backgrounds under limited irrigated conditions

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In India, about 80% of wheat is cultivated under irrigated conditions, 66% of it receives only partial (1-2) irrigations, and the remaining 20% is grown under rainfed environments. The wheat demand is expected to increase about 60% by 2050, and production might go down by 29% as a result of climate change imposed environmental stresses. In the current era of global climate drift, plant growth and productivity are often limited by various environmental stresses, especially drought and heat. Thus, exploitation and utilization of drought resistant germplasm is of great importance to meet the challenges of wheat production under changing climatic conditions. The breeding for drought tolerance using novel genetic resources is the most viable strategy to cope with the changing climatic conditions. Therefore, the present experiment was conducted to identify the rust resistance donors in high yielding genetic backgrounds under restricted irrigated conditions. A set of 18 high yielding genotypes including checks (PBW644, DBW93, HD3171, HI8498 (d) and DBW110) were evaluated during crop season 2018-19 at ICAR-IIWBR, research farm. Each genotype was planted in a six-row plot of six meter length with two replications under Randomized Complete Block Design. The spacing between rows was 20 cm within the plot, and 10 cm between plants within the rows. All the recommended agronomic practices were followed to raise the crop under only one life saving irrigation at 40-45 days after sowing. The observations were recorded were on days to heading (days), days to maturity (days), plant height (cm), grain filling duration (days), grain filling rate (g/day), 1000-grain weight (g), grain yield (g), stripe rust and brown rust incidence. The positive but non-significant correlation of days to heading (0.447), days to maturity (0.304), plant height (0.210) and 1000-grain weight (0.331), while positive and significant correlation of grain filling rate (0.743**) with grain yield was recorded. The negative correlation was recorded among grain filling duration (-0.330), stripe rust (-.602*), while negative and significant correlation among stripe rust and 1000-grain weight under timely sown restricted irrigated conditions. Thus, the selection could be effective based on these traits. In the present study, 03 genotypes *viz.,* BST-18-1, QYT-RI-1828 and QYT-RI-1831 were found better than the three checks for grain filling rate, grain yield and stripe as well as brown rust resistance. Furthermore, 04 genotypes *viz.,* BST-18-3, BST-18-4, QYT-RI-1829 and QYT-RI-1831 were found better than checks for 1000- grain weight and stripe as well as brown rust resistance. Two genotypes *viz.,* QYT-RI-1829 and QYT-RI-1831 were found better than the checks for grain filling rate, grain yield and stripe as well as brown rust resistance. The selected genotypes could be used as potential donors to develop the lines exhibited resistance for stripe as well as brown rust disease under restricted irrigated conditions.

PP-8: The role of the shikimate and the phenylpropanoid pathways in plant parasitic nematodes infection and their management

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Plant-parasitic nematodes (PPNs), such as root-knot nematodes (RKNs) and cyst nematodes (CNs), are among the most devastating pests in agriculture. There is an increasing attention in studies on alternative methods for nematode management because of limitations on the use of chemical pesticides. Among the strategies of non-chemical nematode management, identification and implementation of host resistance is one of the option. Plants recognize pathogen-associated or damage-associated molecular patterns derived from PPNs. Plant immune responses against PPNs include the secretion of anti-nematode enzymes, the production of anti-nematode compounds, cell wall reinforcement, production of reactive oxygen species and nitric oxide, and hypersensitive response-mediated cell death. Resistant plant responses to PPN infection by recognizing PPN invasion through different but complementary systems, such as synthesis of important and diverse compounds from shikimate and phenylpropanoid pathways. These compounds can be developed for use as nematicides themselves or they can serve as model compounds for the development of chemical synthesized derivatives with enhanced activity. In addition, transcript profiling of key genes of the phenylpropanoid pathway during nematode infection could identify potential gene targets for nematode control strategies. Genes whose expression augments in response to nematode infection can be used as targets for knockout purposes. Overexpression of genes whose expression is downregulated during nematode can also be used as alternative method in nematode control strategies. Thus, significant challenges for future research in the field of plant and nematode interactions would be to understand the interactions of shikimate and phenylpropanoid pathways in PPN immunity and to identify their molecular components that define host specificity.

PP-9: Role of plant-pathogen interaction in crop improvement

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Plant pathogens represent a constant and major threat to global food production, with 20%–30% global crop losses estimated, principally in food-deficit areas. Pesticide use, breeding for resistance genes, and genetic manipulation of plant immune components have helped to mitigate this threat. Deciphering plant–microbe interactions is a promising aspect to understand the benefits and the pathogenic effect of microbes and crop improvement. The recent and ongoing developments provide a unique approach to describe these intricate interactions and test hypotheses. The plant innate immunity has always been an important aspect of research and leads to some interesting information like the adaptation of uniqueimmune mechanisms of plants against pathogens. The development of new techniques in the post - genomic era has greatly enhanced our understanding of the regulation of plant defense mechanisms against pathogens. In beneficial plant– microbe interactions, plants and microbes developed cooperative and beneficial relationship which helps in improving the host plant resistance to a wide variety of stresses, including diseases, drought, salinity, heavy metals, toxins, nutrient stresses, and extreme temperature. Plant and microbes both play important roles in the contribution of the beneficial plant–microbe interactions. The well-studied examples are symbiosis, where both plant and microbes are benefited, for e.g., nitrogen-fixing bacteria which survive in root nodules of leguminous plants and form a mutually beneficial relationship. Beneficial endophytes, the microbes which live within the plants without eliciting any disease response, in some way involved in triggering the plant induced systemic resistance (ISR) against some pathogenic bacteria. The different classes of plant–microbe interactions elicit different response mechanism. The *Agrobacterium tumefaciens*-plant interactions where plant derived signal molecules and plant immune responses are important in pathogenicity and transformation efficiency. The recent developments in *Agrobacterium tumefaciens* responses to various plant-derived signaling molecules which help in its pathogenicity and the activation of virulence genes induces the transfer and integration of T-DNA from its Ti-plasmid into the plant nucleus. Various defense components like MAPKs, defense gene expression, production of reactive oxygen species (ROS) and hormonal adjustments and its manipulation by the *Agrobacterium,* the transformation will occur.

PP-10: Evaluation of multiple diseases resistant in advanced wheat lines developed through pre-breeding

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Wheat (*Triticum durum* L.) is one of the most important cereal crops in the world and in the Indian sub-continent it is a major staple food crop giving highest calories to poors. The production of wheat was recorded all time high i.e. more than 102 mt and still we need to improve the productivity to the ever increasing population. The production and productivity of wheat crop is hampered by the biotic and abiotic stresses putting the world food security at risk. Among the biotic stresses, rusts are the major threat throughout the wheat growing areas in the world. A set of 65 advanced lines including amphidiploids were evaluated for multiple disease resistance including rusts and leaf blight during 2017-18 and 2018-19 crop seasons at ICAR-Indian Institute of Wheat and Barley Research, Karnal. These pre-breeding materials involved wild relatives of wheat like *Triticum Urartu, Triticum timopheevii,Aegilops mutica, Aegilops speltoides, Aegilops caudate, Secale cereal, Secale anatolicum, Aegilops umbellulata, Thinopyrum bessarabicum* in their pedigree.Experiments were conduct in 4 row of 2.5 mt length plot size for each genotype in Randomized block design (RBD). Mixture of the most virulent pathotypes for stripe rust (45s119, 110s119, 47s103 & 110s84), stem rust (11, 40A, 42, 122 & 117-6) and leaf rust (12-5, 77-9, 77-5 & 104-2) was used for disease creation. Most virulent leaf blight inoculums collected from UBKV, Coochbehar were used for disease creation. Out of 65 lines, 56 lines highly resistant to stripe rust, 49 for Leaf rust and all 65 for stem rust were identified. Most of the lines were found immune to all the three rusts. 63 genotypes showed immune reaction to powdery mildew and 02 recorded moderate resistant. Data obtained from spot blotch experiment revealed 57 lines immune to spot blotch infection while five lines recorded moderately resistant with 23-34ip HLB score infection. Powdery mildew (PM) resistance (5-10%) was observed in 02 lines. These genotypes may be used as donor parents for hybridization program in plant breeding of multiple disease resistant varieties in wheat.

PP-11: Multi-environment evaluation of wheat varieties and advance breeding lines for stripe rust resistance

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Stripe rust (yellow rust), caused by *Puccinia striiformis* f. sp. *Tritici* (pst), is a serious disease of wheat worldwide, including India. Growing resistant cultivars is the most cost-effective and eco-friendly approach to manage the disease. Stripe rust can cause upto 100% yield loss if infection occurs very early and the disease continues developing during the growing season. Therefore, there is urgent need to identify and exploit the existing variability in wheat for stripe rust resistance under changing climatic scenario. In this study, a set of 91 released varieties and advance breeding lines were evaluated for their reaction against stripe rust pathotypes during rabi 2018-19 under three environments *viz.*, timely sown-irrigated (TS-IR), late sown-irrigated, (LS-IR) and late sown-rainfed condition (LS-RF). The experiments for TS-IR and LS-IR was carried out under natural conditions in field while for LS-RF under rainout shelter. The stripe rust data was recorded at physiological maturity when disease pressure is maximum. The range of stripe rust incidence was observed as 0 to 80S in TS-IR and LS-IR conditions, while it was from 0-60S in LS-RF condition. Out of 91, 30 genotypes were resistant under TS-IR, 16 genotypes under LS-IR and 16 genotypes under LS-RF environments under natural field conditions. Furthermore, 10 genotypes namely AC-domain, CBW 38, DBW 246, HI 1612, PBW 698, PBW 701, PBW 703, PBW 712, PBW 725 and PBW 765 were found resistant for stripe rust incidence under all three environments. The correlation among stripe rust incidence and grain yield was highly significant under TS-IR (-.386**), LS-IR (-.594**) and LS-RF (-.343**). Thus, the selected genotypes could be used in hybridization to enhance stripe rust resistance in high yielding wheat/breeding lines.

PP-12: Assessment of advance bread wheat genotypes for grain characteristics, grain yield and rust incidence

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The primary objective of most of the breeding programme is the development of high yielding, disease resistance/ tolerance genotypes along with good grains appearance for end product uses. In this study, advanced wheat genotypes were evaluated for agronomic and grain characteristics along with rust resistance (brown and stripe rust), during rabi 2018-19. The experiment was laid out in a randomized complete block design with two replications with a plot size of six rows (5 m) with spacing of 23 cm between rows and 10 cm between plants within rows. The data recorded exhibited a wide range of variation in the present breeding materials for days to heading, days to maturity, plant height, stripe rust, brown rust, lodging percent, grain yield and some grain characteristics (grain color, grain texture, and 1000-grain weight). Sixteen genotypes were selected which exhibited higher grain yield than overall population mean. Similarly, 11 genotypes were selected which showed higher 1000-grain weight than overall population mean. Seven genotypes were found common for higher 1000-grain weight and grain yield than population mean. Disease incidence reported from 0 to 80S in the advanced genotypes. Genotype ST 122 showed no incidence of brown rust whereas, genotypes ST 115, ST 121 and ST 123 showed no incidence of yellow rust. The genotypes which exhibited medium thresh-ability, while grain color and soft grain texture is good for biscuit purpose. Similarly, easy thresh-ability, amber grain color and hard grain texture is good for chapatti making. Two genotypes (ST 101 and ST 114) could be used for the improvement in grain yield along with good biscuit making quality. Further, the selected genotypes could be used as donors in hybridization programme for improving 1000-grain weight, grain yield and minimizing the disease incidence in bread wheat for targeted areas.

PP-13: Effect of cereal cyst nematode (*Heterodera avenae*) infestation on total sugar and phenolic contents in barley

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To understand the biochemical changes taking place during the early response to nematode attack in barley, a pot experiments were conducted on four resistant cultivars (BH 939, BH 959, RD 2035 and DWRB 91) and one susceptible cultivar (BH 902) under screen house conditions. After germination one plant per pot was retained and nematodes were isolated and inoculated (1500 J2/pot) into the rhizosphere of seedlings. After 40 days of inoculation plants were uprooted and washed properly. Roots and shoots of all varieties were dried in an oven for two weeks. After drying plant parts were ground in pestle and mortal to make powder for biochemical analysis. The study indicates that *Heterodera avenae* infestation led to significant increase in phenolic content in roots as well as shoots of all the varieties. But the levels of rise were different in all the varieties. This showed that total phenolics were more in resistant plants which were responsible for imparting resistance against *Heterodera avenae.* Different levels of phenol in different varieties explains the varying levels of resistance in different varieties. Maximum increase in total sugar content in shoots as well as roots after infection were recorded in cultivar BH 902 (susceptible variety) and minimum increase in total sugar in shoot and root was recorded in RD 2035. Total sugar seems to play positive role in nematode penetration and development. As the nematode enters in the plant, it initiates establishing host-parasite relation i.e. development of feeding site. As a result of this, sugar content of plants was increased more so in susceptible one. Resistant varieties showed increase in total sugar content after infection in both shoots and roots.

PP-14: Evaluations of different types of potato seed tuber for their seed degeneration attribute

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Seed degeneration of potato seed tuber is an important phenomenon that affects it's both quality as well as production potency. Seed plot technique in potato crop production is very useful in maintaining its quality. To find out the extent of seed degeneration in different kinds of seeds of Kufri Bahar variety, a field experiment under AICRP-Potato was carried out at research farm, department of vegetable science in Randomized Block Design with three treatments in five replications. The treatments were: T1- fresh breeder seed, T2 – seed produced through seed plot technique and T3 – seed produced without seed plot technique. The size of each plot was 3 m x 3 m and spacing was 60 cm x 20 cm. Observations on seed emergence (after 30 and 40 days of planting) and incidence of potato apical leaf curl disease (PALCD) after 45, 60 and 75 days after planting were recorded. Experimental findings revealed that, use of the breeder seed results in highest emergence (90.7%) followed by seed plot technique and without seed plot technique. As far as disease incidence is concern, it was least in breeder seed (4.6%), followed by seed plot technique and without seed plot technique to the tune of 4.9 and 13.9%, respectively. Therefore, it is concluded that, use of seeds produced through seed plot technique could be a next better option of breeder seed to achieve comparatively better seed emergence, management of viral disease and ultimately desired crop production.

PP-15: Selection of host differentials for the identification of *Albugo candida* pathotypes and resistant sources against white rust disease of rapeseed-mustard

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White rust/ blister of rapeseed-mustard caused by *Albugo candida* is considered to be a serious disease of rapeseed-mustard causing a significant yield loss in India. Among various management practices, breeding for resistant genotypes/varieties is considered as most eco-friendly, economic and effective method for the management of this diseases. But resistant cultivars are also prone to show break down of resistance due to the attack of new pathotypes and virulent race of the pathogen. Present investigation was undertaken by cross inoculating different Brassica genotypes/ varieties (31 no.) with different *A. candida* isolates (32 no.) collected from different geographical locations of India for the identification of host differentials. On the basis of more or less similar phenotypic disease reaction different Brassica genotypes can be grouped as under and could be used as host differentials: Group 1: Varuna, Pusa Bold, RH-30, Kranti, RL1359; Group 2: EC 399313, EC399301; Group 3: Bioysr; Group 4: Heera; Group 5: Donskaja; Group 6: NRCDR 515; Group 7: Cutlass; Group 8: Tobin; Group 9: Wester, GSL1; Group 10: Torch; Group11: Candle; Group 12: YSPB 24; Group 13: *B. nigra* 2782; Group 14: Sangam; Group 15: E. sativa; Group 16: BSH-1; Group 17: *S.alba*; Group18: Ragini; Group 19: Pusa Kalyani; Group 20: TL 15; Group 21: Bhawani; Group 22: PT 303; Group 23: Kiran; Group 24: DLSC 1; Group 25: *B.olerecea.* These host differentials of Brassica genotypes/varieties could be used for further study for the identification of new possible pathogenic race of *A. candida* pathogen as well as resistant sources against the white rust disease.

PP-16: Identification of rust resistant lines for early sown conditions in wheat

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Forty Nine lines including 4 check varieties (DBW 168, HD 3086, HD 2967, HI 1544) were sown under early sowing (mid to end of October) and timely sowing in two replications in simple lattice design (4x4) following conventional tillage at eight environments *viz.,* IIWBR Karnal, IARI New Delhi, BISA Ludhiana, BISA Jabalpur, Dharwad, Indore, PAU Ludhiana and HAU Hisar. Each plot comprised of six rows of 6 meters length separated by 20 cm during the crop season 2018-19. The data were recorded for yield and anciallary traits. The average yield gain by early sowing was 0.31q/ha/day while the highest gain was at Karnal centre (0.73q/ha). At ICAR-IIWBR, Karnal high disease incidence was observed for yellow rust (upto 40S) and leaf rust (40S). From the multilocation yield analysis, rust reactions under natural and artificial conditions reported that nine entries viz., DBW327, DBW328, DBW329, DBW330, DBW331, DBW332, DBW333, WH1252 and HD3378 were found to be significantly superior than the best check (HD3086-62.7q/ha) under early sown conditions. These entries have been contributed in the special high yield potential trial to be conducted during 2019-20.

PP-17: Improving rust resistance in wheat through marker assisted backcross breeding

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The major limitation for wheat productivity is biotic and abiotic stress factors. Among them rusts are the most damaging pathogens since the domestication of the grain and have hindered global wheat production, and continue to threaten the world's wheat supply. The present research was aimed to introgress rust resistance genes (*viz.* Lr32, Sr26 and Yr15) in three wheat cultivars released from ICAR-IIWBR *viz.,* DBW88, DBW107 and DBW110 to enhance rust resistance through marker-assisted backcross breeding. Markers like wmc43 and barc135 were used for Lr32 gene, while marker gwm413 for Yr15 gene and markers Sr26#43 and BE518379 for Sr26 gene for foreground selection. Out of 655 SSR markers identified as polymorphic in the parents of the six cross combinations, 286 were used in the lines for identifying the recurrent parent in cross combinations. During 2018-19, the BC2F4 populations were screened for background selection. Individuals with significant background recovery were identified in each combination, i.e. DBW88/PBW703 (up to 72.7 per cent), DBW107/ PBW703 (up to 76.2 per cent), DBW107/FLW15 (up to 68.2 per cent), DBW88/FLW15 (up to 63.3 per cent), DBW110/ FLW15 (up to 63.6 per cent) and DBW110/Sunlin (up to 81.8 per cent). Out of total lines screened in each cross [DBW88/ PBW703 (19), DBW107/PBW703 (14), DBW107/FLW15 (18), DBW88/FLW15 (15), DBW110/FLW15 (21) and DBW110/ Sunlin (17)] agronomically superior lines were identified on the basis of yield in single row, TKW, grains per spike and other ancillary traits.

PP-18: Induced mutation in wheat varieties to develop yellow rust resistance

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The ever increasing population of India demands higher food grains production. Globally, it is predicted that 88% of world wheat production is susceptible to rusts. These are of three kinds: the black or stem rust (*Puccinia graministritici*), the brown of leaf rust (*P. recondita*), and the yellow or stripe rust (*P. striiformis*). Stripe rust has recently emerged as the most important biotic concern of global wheat production. Developing wheat lines with resistance to new virulent pathotypes is of utmost importance for national food security. Induced mutation breeding has been used as a tool to develop resistant lines in the high yielding and popular wheat varieties HD 2967 and WH 1105. The varieties were mutagenized and M2 were screened at IIWBR, Karnal (2017-18). M2 populations having 270 lines were screened for resistance to yellow rust and yield performance. Nearly, 96 variants showing maximum resistance and higher yield have been identified (2018-19) and these mutants showing resistance to virulent races will be confirmed in upcoming season. This may lead to development of useful mutants, which are excellent resources for improvement rust resistance in wheat. The current success in identifying resistance to virulent races of yellow rust without altering favorable combination of genes responsible for yield related traits using gamma rays induced mutation breeding can be seen a successful method in wheat improvement.

PP-19: Deploying disease resistant Wheat variety in northern India

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The wheat cultivation suffers from major biotic stresses in Northern India, where stripe and leaf rust are major hindrance in harvesting the full potential of the varieties. Development and deployment of resistant wheat varieties of wheat is an ecological and economical approach in mitigating the adverse effects of rust diseases. In modern agriculture, seed is a vehicle that delivers all agriculture-based technological innovations to farmers for exploiting the genetic potential of new varieties. The availability, access and use of seed of adaptable modern varieties is, therefore, determinant to the efficiency and productivity of other packages (irrigation, fertilizers, pesticides) in increasing crop production to achieve food security and alleviating rural poverty in developing countries. During the year 2018-19, around 4000 quintals of seed of popular varieties *viz*., HD 2967, HD 3086, DBW187, DBW173, WB02, etc. was produced by the ICAR-IIWBR. For the year 2019-20, the recent varieties were given to the seed producers from public and private sector, farmers, NGOs. DBW 187 and HD 2967 the recently released variety for NEPZ and NWPZ was strategically deployed in north and eastern part of the country to proofing against the emerging threat of wheat blast. High demand for recently released variety DBW187 was observed and during the seed fair around 10,000 farmers participated and procured the seed from the institute.

PP-20: Biochemical effects of Alternaria blight infection on oilseed *Brassica* species

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Oilseed crops play an important role in global agriculture and horticulture. *Brassica* species group of crops is the major oilseed crop of India; this contributes about 23% acreage and over 25 % production for the last five years. This crop has low average productivity due to the prevalence of various biotic and abiotic stresses. Among the various factors limiting their productivity, Alternaria blight caused by *Alternaria brassicae* (Berk.) Sacc., is an important and a widespread destructive disease of rapeseed-mustard worldwide. This disease infects host species at all growth stages from seed germination to ripening of siliquae and deteriorate both quality and quantity of oil. Biochemical traits for identifying tolerant genotypes in rapeseed- mustard would be used as indicators for biotic stress-tolerance to accelerate breeding associated with Alternaria blight resistance. A set of representative eight oilseed *Brassica* species (*B. brassica juncea* -domo yellow, *B. rapa, B. napus*-PB9501, *B. carinata-turnip* red, *B. nigra*-local, *Eurca sativa, B. alba*) evaluated in the field experiments using an Randomized Block Design (RBD) with two replications under control and infected with *Alternaria brassicae*. Total chlorophyll content, total phenol content, total protein content and antioxidant enzymes (Catalase, phenylalanine ammonia lyase, peroxidase and superoxide dismutase) participating in the scavenging of ROS were investigated. Accumulation of antioxidant compounds in foliage viz., Catalase (CAT), phenylalanine ammonialyase (PAL), peroxidase (POD) and superoxide dismutase (SOD) were observed significantly higher in all the *Brassica* species in response to blight infection in comparison to healthy leaves.In *Alternaria* infected leaves of *Eurca sativa,* activities of all the enzymes increased in terms of percent increase. Increasing all cell protecting enzymes, *viz.,* PAL (30.01 %), POD (23.58 %), CAT (37.49 %) and SOD (30.19 %) were in favour of highest resistant of *Eurca sativa* against Alternaria blight infectionin comparison to other Brassica species. Reduction in total chlorophyll content (-9.87%) and total sugar content (-17.26%), alongwith higher accumulation of total phenol (26.98%) and total protein content (29.68%) were also in favor of resistance to Alternaria blight infection in Eurca sativa. In nutshell it is revealed that higher activities of biochemical traits like superoxide dismutase (SOD) and peroxidase (POD), phenyl ammonia lyase (PAL) and catalase (CAT) in different genotypes of rapeseed-mustard can be utilized as indicator for identifying resistant genotypes in different species of brassica. *Eurca sativa* species has higher tolerance against Alternaria blight infection and this resistant capacity would be utilized in mustard breeding programme.

PP-21: Management of wheat diseases through deployment of resistant varieties in North-Western Himalaya

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Wheat is an important winter cereal of North-Western Himalaya, occupying 1.39 million hectare area in its hill states *viz.,* Jammu & Kashmir, Himachal Pradesh, Uttarakhand and hilly regions of West Bengal and North Eastern states. Among rust diseases, yellow and brown rusts are the foremost pathogens, capable of causing huge losses to wheat crop grown in this region. Incidence of yellow rust is growing as a major concern not only to the wheat crop grown in the Himalayan region but also to the crop grown in North-Western Plains, because it receives primary inoculum of yellow rust from off-season crop and volunteer plants grown in different altitudes of Himalaya. Powdery mildew and hill bunt are also important diseases of this region causing substantial loss to the wheat crop. The rust diseases can be controlled through the use of fungicides but it increases production cost as well as health hazards by polluting the environment. Deployment and saturation of Northern hills with high yielding rust resistant wheat varieties, is an environment by safe and viable solution to tackle the rust menace. Keeping in view, wheat varieties *viz*., HS 507, HS 542 and HS 562 were released and notified by CVRC for commercial cultivation in the hill states. HS 507 is suitable for timely sown production conditions of Northern Hills Zone (NHZ). It is giving mean grain yield of 2.66 tons/ha under rainfed and 4.68t/ha under irrigated production conditions with 5.9% and 9.3% grain yield advantage, respectively over best check VL 907. It also possess brown and yellow rust resistance with Average Coefficient of Infection=0.9 and 1.1), respectively to contain the rusts in the Himalayas. Besides, HS 507 has very good chapatti and bread making qualities. HS 542 is suitable for early sown rainfed production conditions of NHZ. It is giving mean grain yield of 3.3 t/ha under rainfed conditions with 6.1% grain yield advantage over the best check VL 829. It possess brown and yellow rust resistance with ACI=2.0 and 7.1, respectively with diverse combination of Yr2+, Lr13+10+, Sr5+8a+9b+11+ genes. HS 562 is suitable for timely sown production conditions of NHZ. It is giving mean grain yield of 3.6 t/ha under rainfed and 5.27t/ha under irrigated production conditions. HS 562 possess field resistance to stripe rust (ACI=6.0). Breeder seed of these wheat varieties is made available to the seed producing agencies. About 50.5 tons of breeder seed of wheat varieties HS 507, HS 542 and HS 562 has been supplied to the seed producing agencies for producing foundation and then certified seed for its distribution among the farmers of this region.

PP-22: Assessment of tomato leaf curl virus in different locations of Jammu division

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Tomato leaf curl disease caused by tomato leaf curl virus (ToLCV) of genus *Begomovirus* of the family Geminiviridae is one of the most devastating disease in many tropical and subtopical regions in the world. Extension survey was conducted in different locations of Jammu and Udhampur districts to assess the incidence of the tomato leaf curl virus and the result showed that the per cent disease incidence varied from different locations surveyed. However, the disease was prevalent in almost all the locations surveyed. In Jammu district the incidence of disease ranged from 19.75 to 24.00 per cent and maximum disease incidence of 24.00 per cent was recorded from Akhnoor and minimum from R. S. Pura (19.75%). While in Udhampur district the per cent disease incidence ranged from 18.75 to 23.7 per cent with maximum incidence of 23.75 per cent from Udhampur while minimum 18.75 per cent from Ramnagar.

PP-23: Screening of different germplasm of tomato against tomato mosaic disease under field conditions

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Tomato (*Solanum lycopersicum* L.) is an important annual and short lived perennial vegetable cultivated throughout the world for it's edible fruits. Among the viral diseases, tomato mosaic is one of the most destructive disease in India and is the major limiting factor responsible for low productivity of the crop. Different germplasm of tomato were evaluated against the tomato mosaic disease under field conditions in research field Skuast-J, Chatha and it was observed that out of twenty germplasm EC-771607 and Hisar Anmol were found resistant while Kashi Vishes, HisarArun and ArkaAnanya were found moderately resistant. However, EC-677049, Avinash 2, Money Maker, EC-620417 and EC-617048 showed susceptible reaction and Pusa Ruby was found highly susceptible against the disease. The germplasm *viz.* EC-620406, ArkaVikas, EC-676791, EC- 514109, EC- 514109, EC-677191, EC-677123, Local, Kajal and Arka Sourabh were found moderately susceptible.

PP-24: Varietal Screening of different chilli germplasm against mosaic

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Chilli (*Capsicum annum* L.) is among the most frequently consumed spices and condiments throughout the world. Screening of different germplasm of chilli against chilli mosaic disease were carried out at research farm Skuast-Jammu during the year 2016-17 and the result showed that out of the fifteen germplasm Pusa Sadabhar, Punjab Gucchedar and Punjab Lal were found resistant while CH-1, Arka Meghna and Anmol BSS-273 were found moderately resistant. However Pusa Jwala, NP-46-A and Local showed susceptible reaction and Surajmukhi, G-4, Nishant, Crystal 906, K-Long 1 and Chandani showed moderately susceptible reaction against the disease.

PP-25: Impact of inoculation of promising pearl millet root bacterial endophytes on seed quality parameters

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Endophytes can be defined as a group of microorganisms that infect internal tissues of plant without causing any immediate symptom of infection and / or visible manifestation of disease and live in mutualistic association with plants for at least a part of their life cycle. Endophytic microbes play significant role in growth and development of host plants by producing a range of nutrient products and facilitating primary and secondary nutrient uptake through atmospheric nitrogen fixation, formation of iron siderophores and solubilization of minerals such as phosphate, potassium and zinc. They also supply roots with growth promoting phytohormones such as auxin, cytokinin and gibberellin. A total of 30 pearl millet root bacterial endophytes (PMRBE1 - PMRBE 30) were obtained from crushed roots of pearl millet streaked on Nutrient agar plates and on the basis of various biocontrol traits exhibited under *in vitro* conditions, twenty pearl millet root endophytic bacterial isolates *viz.* PMRBE1, PMRBE2, PMRBE4, PMRBE5, PMRBE6, PMRBE7, PMRBE9, PMRBE10, PMRBE11, PMRBE14, PMRBE16, PMRBE17 ,PMRBE18,PMRBE20,PMRBE23, PMRBE24, PMRBE25, PMRBE26, PMRBE27 and PMRBE28 were selected to study their effect on germination, seedling vigour index and germination speed of different pearl millet cultivars *viz.* HHB226, HHB67 Imp and 7042 S. Seed germination was improved on seed treatment of HHB226 and HHB67 Imp with isolate PMRBE4 and PMRBE6 and 7042 S on inoculation with isolate PMRBE23. Germination speed of HHB226, HHB67 Imp and 7042 S was higher on treatment of seeds of HHB226 and HHB67 Imp with isolate PMRBE17 and 7042 S cultivar seeds with PMRBE20 as compared to check. Seedling vigour index of HHB226, HHB67 Imp and 7042 S was higher on inoculation of seeds with PMRBE1, PMRBE6 and PMRBE23 while seedling vigour index II was maximum on inoculation of HHB226 and HHB67 Imp seeds with isolate PMRBE4 and 7042 S seeds with PMRBE1. However, Pearl millet root bacterial endophytes exhibiting plant growth promoting abilities could be explored on different crops for development of effective biocontrol agent and to minimize the uses of fungicides.

PP-26: Perception and signal transduction in plants

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Molecular communication between plant and pathogen commences almost immediately after the pathogen makes contact with the plant surface. Plant disease resistance and susceptibility are governed by the combined genotypes of host and pathogen, and depend on a complex exchange of signals and responses occurring under given environmental conditions. Susceptibility or resistance is determined by the winner; if the pathogen is able to overcome the toxic environment in the plant tissue, the disease develops and if the plant is able to ward off the pathogen's toxic weapons, disease resistance develops. Moreover, this principle appears true for different levels of resistance, since similar compounds of signal transduction are active in species-specific resistance, in race-specific resistance and in quantitative resistance of susceptible plants. Plants are able to recognize conserved microbe-associated molecular patterns (MAMPs) or pathogen associated molecular patterns (PAMPs) that trigger a number of induced defenses in plants. However, many PAMPs have been shown to be general elicitors of defense that can obscure host pattern recognition receptors as to avoid recognition but without compromising their function. The recognition of a potential pathogen results in activation of several intracellular signaling events including rapid ion fluxes, activation of kinase cascades and the generation of reactive oxygen species (ROS). Many of the plant defense responses are mediated by an interacting set of endogenous signal molecules including jasmonic acid (JA), ethylene (ET) and salicylic acid (SA). However, these are not the only endogenous signals for defense gene activation but other molecules such as ROS and nitric oxide (NO) also appear to be involved in plant defense signaling. These signaling events lead to defense responses including induction of hypersensitive response (HR), a localized form of programmed cell death (PCD) limiting pathogen spread, further reinforcement of the cell walls, and production of antimicrobial compounds such as defense proteins and phytoalexins. Its repeatation of the abstract under M.J. Narasimhan Academic Award Contest.

PP-27: Utilization of SSR markers for screening of maize inbred lines for MLB disease

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Though, maize is one of the most important and well known cereal crops in terms of its adaptability and importance worldwide but the incidence of a range of foliar diseases has become a severe yield limiting factor in most maize producing regions throughout the country. A major fungal foliar disease of maize called maydis leaf blight (MLB) or southern corn leaf blight (SCLB) caused substantial yield losses worldwide during the past few decades. The most effective way to control MLB is to use resistant cultivars. Most maize breeders prefer the use of quantitative MLB resistance in their cultivar development programs. Thus, improvement of genetic resistance to the foliar diseases remains an important objective in maize breeding programs. In the past decades, growing resistant cultivars in most maize producing regions has effectively controlled some foliar diseases. The aid of molecular markers may help in selection and adoption of breeding approaches suitable for improving yield, quality and disease resistance. Therefore, the genetic nature of resistance was studied. The experimental material comprised of eight inbred lines out of which four inbred lines (HKI 209, HKI 1332, HKI 325-17AN and HKI 488-1RG) were susceptible and four inbred lines (HKI 1128, HKI 163, HKI 164D-4-(O) and HKI 193-2-2) were resistant to maydis leaf blight on the basis of disease reaction in the field. These inbred lines were used to generate sixteen crosses by Line x Tester design at CCS Haryana Agricultural University, Regional Research Station, Karnal during Kharif 2013 and Rabi 2013-14. The sixteen crosses *viz.,* HKI 209 x HKI 1128, HKI 209 x HKI 163, HKI 209 x HKI 164D-4-(O) , HKI 209 x HKI 193-2-2, HKI 1332 x HKI 1128, HKI 1332 x HKI 163, HKI 1332 x HKI 164D-4-(O) , HKI 1332 x HKI 193-2-2 , HKI 325-17AN x HKI 1128 , HKI 325-17AN x HKI 163 , HKI 325-17AN x HKI 164D-4-(O), HKI 325-17AN x HKI 193-2-2, HKI 488-1RG x HKI 1128, HKI 488-1RG x HKI 163, HKI 488-1RG x HKI 164D-4-(O), HKI 488-1RG x HKI 193-2 along with eight parental inbred lines were screened for maydis leaf blight disease using artificial inoculation condition using standard procedure of disease rating scale of 1-5. A total of 43 SSR primers were used to screen five parental genotypes for polymorphism with the polymorphic primers to detect segregation pattern and association of DNA markers for maydis leaf blight resistance. Variation in allelic profile for SSR markers were depicted on agrose gel electrophoresis. Out of 43, 37 primers showed amplification in all parents under study, of which 5 were monomorphic *viz.,* p-umc2253, p-umc1525, p-bnlg1732, p-bnlg2241and p-umc1159 and 32 were polymorphic. The six primers viz., p-umc1500, p-umc1250, p-umc1622, p-umc1641, p-umc1184, p-bnlg2248 did not show amplification. All of these 37 markers that showed amplification were run on agrose gel electrophoresis to get the clear differences among the base pairs and thus were used for further analysis. As an indication of polymorphism, the number of alleles along with their frequency at each locus were analyzed and the number of alleles each locus ranged from 2 to 4. Based on the morphological data of disease reaction and molecular screening, the results showed that the inbred lines of high resistance to maydis leaf blight create high resistance hybrids.

PP-28: Wheat blast proofing in India: An anticipatory measure

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In order to restrict the entry of wheat blast in the country ICAR-IIWBR has adopted several quarantine as well as anticipatory breeding approaches. As a part of quarantine measures, several awareness as well as continuous survey and surveillance programmes were organized in the bordering Bangladesh. Secondly blast resistant wheat varieties are being developed involving resistant sources and screening in Bolivia and Bangladesh so as to deploy resistant material in the eastern parts of the country. ICAR-IIWBR as a part of preparatory breeding program sent a set of 100 wheat genotypes comprising popular released varieties, AVT and NIVT entries toJassore (Bangladesh) and Quirseore (Bolivia) during 2017-18 for screening against wheat blast disease. Again during 2018-19 same set of 100 genotypes was sent to Jassore (Bangladesh) for confirmatory screening during 2018-19 another set of 353 lines (including 100 previous year lines) involving popular released varieties, AVT, NIVT and registered genetic stocks were screened against wheat blast disease at one of the hot spot location (Jassore, Bangladesh). Based on the disease reaction of the 353 lines, two wheat blast resistant genotypes *viz*., DBW 187 (IR-TS) and DBW 252 (RI-TS) of ICAR-IIWBR and one variety HD 3249 (IR-TS) of IARI have been recommended for release by CVRV. More than 600q breeder and TL seed of the two IIWBR varieties has been distributed among the farmers and seed growers. Breeder seed of DBW 252 was also supplied to >25 public (KVKs, SAU) and private seed growers for seed multiplication and further distribution to the farmers of NEPZ. In addition anticipatory breeding for blast resistance has been initiated at IIWBR, Karnal in collaboration with research organizations in West Bengal, Bihar, Jharkhand and Assam. Forty eight crosses made during 2018 and 2019 involving resistant donors were sent for generation advancement at Dalang Maidan. More than 15q seeds of latest blast resistant variety DBW 187 was distributed to the farmers of Gorakhpur, Motihari and BCKV, Kalyani during crop season 2018-19. Beside this created three foster breeding centres *viz*., BAU, Sabour, BISA Pusa and BAU, Ranchi for the supply of seed of DBW was distributed 187 (Blast resistant) to the farmers and public sector organizations during 2019-20 crop season. In addition, some preventive measures (no wheat zone, wheat holiday in two districts of West Bengal) were taken to restrict entry of the disease into the country and also issued advisory to use only certified treated seed of the latest recommended varieties of wheat.

PP-29: Development of chilli leaf curl virus disease resistant line and its commercialization

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Chilli (*Capsicum annuum* L.) is an important spice-cum-vegetable crop of the family Solanaceae. Out of the major diseases infecting chilli like powdery mildew, fruit rot, fusarium wilt and bacterial wilt, the leaf curl disease caused by various species of begomoviruses is the most disparaging disease. The begomoviruses which cause huge production losses to this crop belongs to family Geminiviridae and their transmission is carried out by whitefly (*Bemisia tabaci*). Control measures, such as natural and synthetic pesticidal sprays for vector management, eradication of diseased plants and various cultural control methods have been tried for different virus disease management without much success. Therefore, the phenomena of host plant resistance is a better option to control diseases, especially which are caused by viruses to a larger extent of a certain period of time. In view of this, a line resistant to leaf curl virus disease namely S-343 was developed by Punjab Agricultural University, Ludhiana. This line was further used to develop leaf curl virus disease resistant hybrid namely, CH-27 by using S-343 as male parent and nuclear male sterile line, MS-12 as female parent. The hybrid covers more than 75% area of the Punjab state in a short span of time from 2015-2019. During 2019, the hybrid was also released at national level in the AICRP (VC) testing. Due to the popularity of hybrid among chilli growers, 18 different multinational/national private seed companies/farmers signed an agreement with the university to produce and market hybrid seed of CH-27 within the country. The work on identification of linked marker to leaf curl disease resistant gene is in progress so that the gene may be transferred to other lines possessing good horticultural traits which in turn further strengthen the chilli breeding programme in India.

PP-30: Screening of advance lines against tomato leaf curl virus in tomato

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Tomato cultivation, especially in autumn season in north India and in summer season in south India is adversely affected due to the high incidence of tomato leaf curl virus disease (ToLCVD) and economic losses often exceeds 90 per cent. The disease is reported to be caused by different species of genus *Begomovirus* (Family Geminiviridae), which are transmitted by whitefly (*Bemisia tabaci Genn.*). Among the different begomoviruses, Tomato leaf curl New Delhi virus and Tomato leaf curl Palampur virus have wide distribution and infect many other crops. The typical symptoms of the infected susceptible plants are severe leaf curling, shrinking of leaves and stunted plant growth. Managing the disease with pesticides has been a difficult task therefore, use of host resistance against virus or vector is astute approach. Only field screening could not be reliable because there is chance to escape of disease due to irregular visit of white fly and unavailability of inoculums therefore, further confirmation of resistance against ToLCVD, artificial screening is more trustworthy. Advance tomato lines (50 nos) were subjected to artificial screening under net house with high inoculum pressure by viruliferous whiteflies. The observation of disease incidence and symptom severity was recorded at 45 days after inoculation. The mild to severe infection was noticed in different genotypes. On the basis of coefficient of infection, out of 50 advance lines screened, 4 lines were highly resistant, 9 resistant, 7 moderately resistant, 6 moderately susceptible, 14 susceptible and 10 highly susceptible while resistant check (Punjab VarkhaBahar-4) showed no incidence of ToLCVD but susceptible check (Punjab Chhuhara) showed 100% disease incidence. Under artificial screening, level of resistance decreased due to high and uniform pressure of viruliferous whiteflies inoculations. It was found that several lines showing resistant reaction in field screening were found to be either moderate resistant or susceptible during artificial screening. All those lines which showed resistant reaction in artificial screening also showed resistant reaction in field screening against ToLCVD. The line namely RSTW-8-1E-1-13 was found to be completely free from ToLCVD during both artificial and field screening possessing good horticultural traits.

PP-31: Identification of sources with resistance to powdery mildew and yellow rust among differentials lines and promising wheat genotypes

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Powdery mildew (PM) and yellow rust (YR) caused by *Blumeria graminis* f.sp. *tritici,* (Bgt) and *Puccinia striiformis,* respectively are the major constraints for wheat production in NHZ and NWPZ of India including Himachal Pradesh. These can be effectively managed by cultivation of resistant varieties. However, majority of the varieties released for disease prone areas are susceptible to PM and YR. Moreover, fast emergence of new virulences make the resistant varieties susceptible after short period. Hence, identification of new, stable and diverse sources of resistance and their utilization in the breeding program is a pre-requisite to evolve new varieties. Keeping this in view, 81 genotypes comprising some powdery mildew, leaf rust and loose smut differentials and promising genotypes were evaluated against PM and YR at hot spot locations i.e. RWRC, Malan (2016-17), CSKHPKV, Palampur (2016-17 and 2017-18) and HAREC, Kukumseri (summer, 2016) and Keylong (2017). The data for PM at seedling stage (ST) were recorded on '0-4' scale whereas, at Adult Plant Stage (APS) on terminal disease reaction (TDR) using '0-9' scale. At APS, data were also recorded periodically on % disease severity (DS), which was used to determine Area Under Disease Progress Curve (AUDPC), infection rate (r) and relative AUDPC. The data for YR was recorded on modified Cobb's Scale. It was observed that Rye (*Secale Cereale* L.) was free from PM and YR at ST and at APS. Genotypes Amigo, Maris Dove, near isogenic line (Pm1), and NIL Pm3a were free from PM at seedling stage. Genotypes AJAIA/Ae Squarrosa, 330 (1), CROC_1/Ae. Squarrosa, 662 (1), 68.111/ RGB-U//WARD /3/FGO/4 /RABI/5/Ae. squarrosa, 905(1), Amigo (4), Kavkaz (4), Maris dove (2), NILPm1(2), Pm2 (1), Pm3a (3), Pm3c (3), Pm4 (3), Citr 14125 (2), NC96BGTA5 (3), Citr 15888 (3), ALDAN (4), CMM 77308 (4), SAW 71(4) and SAW 74 (5) showed mean disease reaction of 0-5, terminal disease severity (TDS) ≤15% and AUDPC, rAUDPC and 'r' ranging between 20.63-494.44, 2.75-40.05 and 0.01 0.04, respectively in comparison with susceptible cultivar Lehmi showing TDR, TDS, AUDPC, rAUDPC and 'r' of 7, 41%, 1510.88, 99.18 and 0.04, respectively. Hence, these were categorized as slow mildewing genotypes. Genotypes Maris Dove, Chul Bidai, Ra 3765, K 88046, HD 2189, Thew, HP 1633LR 9, TD 1, TD 2, SHANGAI, TL 1210, RYE, ALDAN, CMM 77308, H 56771, HD 29 and SAW 74 showing YR severity <5 and genotypes Lr 23, UP 2338, WEBSLER Lr 29, and TD 4 showing YR severity <10S. Only seven genotypes AJAIA/Ae. squarrosa (330), Maris dove, RYE, ALDAN, CMM 77308, SAW 71 and SAW 74 showed multiple resistance to both the diseases which may be harnessed in breeding programme to develop genotype with multiple disease resistance.

PP-32: Evaluation of wheat genotypes for powdery mildew resistance under northern hill zone conditions

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Powdery mildew caused by *Blumeria graminis* f.sp. *tritici* (Bgt) has appeared as one of the most important fungal diseases of wheat (*T. aestivum* L.) worldwide. In India, it has become a potential threat to wheat cultivation in the north-western and hilly wheat-growing areas of the country comprising Punjab, Haryana, Uttar Pradesh, Himachal Pradesh, Uttrakhand and Jammu & Kashmir. The disease causes severe losses in the hilly areas as the temperature remains conducive for its development and spread throughout the crop season. It is the need of hour to find new sources of resistance to broaden and diversify the genetic base of the cultivars for this disease. A set of thirty-six diverse germplasm sources including lines from national and international germplasm nurseries, high yielding varieties and some local landraces was screened for powdery mildew resistance. These lines were evaluated at Malan under field and controlled conditions during Rabi 2016-17 to 2018-19 and at Dalang Maidan, a hotspot location for Bgt infestation, during off season 2016-17 to 2018-19. Scoring for severity of infection was done using 0-9 scale. Based on this scale, out of thirty- six lines, four lines (ONS 29, ONS 27, YRC-1 and PMC-1) showed immune response (0), while three lines (EIGN 33, MDSN-15, MDSN-17) were found to be resistant (1-3) against powdery mildew at both the locations over last three years. These resistant lines can be used as new sources of resistance to develop new cultivars to diversify the resistance base of wheat varieties.

PP-33: Isolation and morphological analysis of rhizosphere soil microflora for the assessment of conducive and suppressive soils

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Soil microorganisms comprise of an important component of soil biological properties. More microorganisms occur in soil than all other ecosystem combined. There are several microorganisms which are found in rhizosphere such as bacteria, fungi, actinomyctes and their availability depends upon soil physico chemical properties which renders the soil conducive soil or suppressive soil in nature. The suppressive soil is the best examples of natural microbes based plant defense against pathogenic microflora which fails to establish due to occurrence of antagonists. The experiments were conducted to assess the biodiversity of microorganisms from the rhizosphere soil of rice and wheat in the Malwa region which included Talwandi Sabo, Faridkot, Sardulgarh locations in Punjab during year 2018-19 at three different times. The fungal colonies obtained from soil of wheat-rice rhizosphere by serial dilution and plating method were largely *Acremonium* sp., *Aspergillus* spp., *Alternaria* spp., *Curvularia lunata., Cladophialphora* sp. *Helminthosporium* sp., *Fusarium* spp., *Mucor* sp., *Penicillium* spp. Mainly the Bacillus spp. and Pseudomonas spp. belonging to were also isolated from the soil sample. The accessions from rhizosphere soil of rice were more favourable for growth during the Kharif season as compared to rhizosphere soil of wheat. The genera of fungi, bacteria and actinomyctes in the soil ranged from 5 - 8 (per gm), 6-9 (per gm) and 1 - 3 (per gm), respectively in all three regions. The two bacterial isolates 2B10 and 2C5 of Sardulgarh and Faridkot regions showed appreciable inhibitory effect against *Fusarium* sp. Based on morphology, gram staining and biochemical tests both these strains were identified as *Bacillus subtilis*. During secondary screening *Bacillus subtilis* 2B10 showed a maximum zone of inhibition against *Penicillium* spp. and *Aspergillus* spp., while *Bacillus subtilis* 2C5 showed best inhibition against *Penicillium* spp., *Helminthosporium* sp., and *Curvularia lunata*. The findings of present study reveal that the soil sample of Talwandi sabo contains more diversity of pathogens and hence, conducive for soil borne diseases whereas, soil sample of Sardulgarh and Faridkot is rich in antagonistic bacterial diversity rendering it suppressive against the pathogens.

PP-34: Supplementary protein and carbohydrate source feeding suppress European foul brood incidence in *Apis mellifera colonies*

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European foul brood (EFB) caused by the gram-positive Streptococcus bacterium *Melissococcus pluton* is statuary notifiable, threatening and infectious disease prevalent among the uncapped *A. mellifera* larval brood at the age of 3-4 days. Under favorable conditions, disease may turn into epidemic with malignant manifestation, seriously damaging even very strong bee colonies. EFB disease appears in a pronounced seasonal cycle beginning from mid-February and continue up to August with maximum severity from March to June in weakened and malnourished colonies. Hence, supplementary feeding of *A. mellifera* colonies with freeze dried bee collected pollen and carbohydrate sources (sugar, jaggery, liquid glucose and high fructose rice syrup) was investigated during 2017 and 2018 dearth periods to strengthen colonies and render them safe against the incidence of EFB. In present studies, the EFB was consistently present during entire dearth period in 2017 as well as 2018. During 2017, incidence of EFB diminished significantly with the onset of minor honey flow season with similar level of infestation both in without and with pollen fed colonies (0.8 EFB infected cells/colony). During 2018, incidence of EFB among different treatments in the apiary was insignificant that too confined to the early dearth period in June (0.0-1.3 EFB infected cells/colony). Among the different carbohydrate treatments the incidence of EFB was quite low and ranged from 0.1-1.7 EFB infected cells/colony during 2017 and from 0.2-1.0 EFB infected cells/ colony during 2018. Present studies confirm the importance of supplementary feeding of carbohydrate sources in suppressing the incidence of EFB. The incidence further got lowered with superimposition of protein feeding through bee collected stored pollen.

PP-35: Diversity in Trichoderma under chickpea rhizosphere of Uttar Pradesh

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Chickpea (*Cicer arietinum)* wilt is a major and frequently occurring diseases, causes considerable yield loss. The disease is usually caused by coplex of pathogens and is referred to as a multipathogenic disease in which *Fusarium oxysporumf.* sp. *ciceriing* (Padwick) Synd. &Hans. is considered to be the primary cause of wilt disease in chickpea under Indian conditions. Morphological characters *viz.,* conidiation (effuse/ flat putulation) colour, conidiatium shape, length and width, conidiophore (divergently branched at 90° and clustered terminating with penicullus) phialide characters namely fertile or sterile apex; shape; length; width and chlamydospore production of 16 different isolates of *Trichoderma* were studied with the help of stereomicroscopy, bright field microscopy and phase contrast microscopy. Results revealed great variation among the strains of individual species and also between the species of *Trichoderma*. Out of five isolates of *T. longibrachiatum,* MTAT 4 recorded both effuse and flat pustule condition, whereas others possessed flat pustule conidiation. Out of eight isolates of *T. harzianum,* three isolates MTAT 5, MTAT 11 and MTAT 15 recorded both effuse and flat conidiation and others recorded only effuse conidiation. Isolates of T. atrobrunnea (MTAT 8 and MTAT 10) recorded uniformly both effuse and flat conidiation. Maximum average length of conidium was recorded with MTAT 10, measuring

4.10 µmwith effuse and flat both conidiation dull white colour, elleptical conidium with divergent conidiophore at 90°, sterile stipe, cylindrical phialide measuring 05.95 µm average length and 03.30 µm average width. Extreme variability in phialide were recorded in different chickpea rhizospheric isolates of *Trichoderma*. Maximum 08.95 µm of average phialide length was measured with MTAT 9 along with 03.10µm width, sterile stipe, cylindrical shape without chlamydospore and statistically at par with MTAT 13 isolate measuring 08.85 µmlength and 02.65 µm width, cylindrical shape, fertile apex and chlamydospore. *Trichoderma* isolate MTAT 8 measured maximum average width of 03.40 µm phialide with cylindrical shape, sterile stipe and chlamydospore followed by MTAT 10 (03.03 µm) having same characters and at par to MTAT 8. MTAT 1 was observed dull white, flat conidiation, oblong conidium measuring 03.75 µm and 02.80 µm average length and width of conidium, clustered terminating with peniculluse conidiophore, ellongated fertile phialide measuring 08.80 µm average lengths without chlamydospore.

PP-36: Endophytes of sugarcane with special reference to variety COLK 8102 to explore induced systemic resistance

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Exploring the potential endophytes and their importance in plants as Induced Systemic Resistance is the recent attention towards disease management and plant growth promotion. A plant exhibits an increased level of resistance power without any changes of its basic genotypic combination by shifting of its physiological phenomenon. Salicyclic acid, acibenzolar-S-methyl, iso-nicotinic acid, jasmonic acid and several others are the known chemicals to induce resistance in certain plants, but only few of them fulfils the criteria being real plant activating compounds. Initiative work has been done to investigate in antagonistic microorganism *viz.,Trichoderma* spp. and *Pseudomonas* spp. in inducing systemic resistance insugarcane against challenge with the red rot pathogen. In *Pseudomonas* spp., involvement of different PR-proteins such as -1.3-glucanases, chitinases and thaumatin-like proteins (TLPs) were also found to be associated with *Pseudomonas*-mediated induced systemic resistance. In sugarcane, red rot disease caused by the fungus *Colletotrichum falcatum* is one of the major limiting factors to the growers and the sugar industry. Breakdown of red rot resistance of a resistant variety is common in case of sugarcane due to wide adoptability of a promising variety by the farmers. Therefore, in addition to breeding for durableredrot resistance, other viable options need to be explored for successful management of the disease. In the line a red rot resistant variety, Bo 91 was used to isolate and characterize beneficial fungal endophytes that are intimately associated with plant and have the potential for diseases management and growth promotion. Standard Blotter Paper Method (ISTA 2013) and Standard Agar Plate Method (ISTA 2013) were used to isolate the endophytic mycoflora associated with root, leaf and cane. After fungal growth, the colonies were counted and grouped by morphological characteristics. The single spore isolation techniques were followed to purify the culture for further studies. Identification keys developed by Baijal and Mehrotra, 1980; Bissett, 1991; Domsch *et. al.,* 1993; Pitt, 1998; Hammil, 1970; Raper and Fennell, 1975; Refai, 1969; Samuels *et al.,* 1998; and Sutton, 1980 were used to identify the endophytic mycoflora.The fungal endophytes found associated with the root, leaf and cane of variety CoLk 8102 were from the fourteen genera *viz., Rhizoctonia, Curvularia, Epicoccum, Fusarium, Alternaria, Colletotrichum, Cladosporium, Chaetomium, Trichoderma, Acremonium, Rhinocladiella, Gliocladium, Penicillium,* and *Aspergillus.*The antagonistic characterization of different isolates revealed that two isolated of non-pathogenic *Colletotrichum* and two isolates of *Trichoderma* were potentially antagonistic to red rot pathogen.

PP-37: Distribution of sugarcane smut (Sporisorium Scitamineum) in Uttar Pradesh

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Sugarcane is one of major cash crops of the country. India is the second largest sugarcane producing country after Brazil. In India, Uttar Pradesh holds the first position in the sugarcane production. Biotic stresses major constraint to sugarcane production and among these are the diseases cause significant loss all over the world. Smut disease of sugarcane is one of the most serious diseases. Susceptible varieties of sugarcane are severely stunted and cause considerable yield losses and reduction in quality of cane and about 30-100% production losses. Smut is a fungal disease and is caused by a fungus, *Sporisorium scitamineum.* The spread of spores is by wind dispersal or infected planting material. Smut of sugarcane was first time reported in 1877 in Natal, South Africa thereafter it was reported in India by several scientists. 25-30°C temperature is optimum for the disease development. Several reports indicate 52-73% yield loss in moderately susceptible varieties. Use of susceptible varieties and favourable environmental conditions for disease development causes up to 100% crop loss. Smut infection leads to loss of 3-7% sucrose content alongwith loss of guide quality. Disease incidence was found to be linked with increasing age of the crop and varietal susceptibility. A disease survey conducted during 1917-18, 1918-19 and 2019-20 crop seasons revealed that there is considerable increase in the incidence of red rot in the Uttar Pradesh. In crop seasons 17-18 it was noticed to the tune of 2 to 10 % and crop seasons 2018-19 it was 2 to 18 %, whereas during crop season 2019-20, smut incidence was recorded 5 to 30 % Uttar Pradesh in all commercially cultivated varieties.

PP-38: Screening and characterization of potential suppressive soils against soil borne pathogens in maize-rice agro ecologies

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Identification and characterization of soils for suppressiveness are key steps for the development of eco-friendly and sustainable management of soil borne diseases. The suppressive soils have a rich diversity of native soil microorganism and hence provide a biologically healthy environment in which plants comparatively suffer less soil-borne diseases than expected. Suppressiveness is reduced due to repeated monoculture and lost upon soil sterilization, however, it can recover even by adding 1% of the natural soil, thus, suppressiveness is closely associated to the soil microbiome community composition. Long-term extensive maize/rice cropping, can generate acclimatization in the soil born pathogens. Application of synthetic fertilizers and agrochemicals further worsens soil health by posing a threat to the beneficial microbes which may be antagonists to the pathogenic organisms. This makes the soil sick or conducive for the pathogens. Suppressive soils can be used as effective microorganism sources for bio intensive management of soil borne diseases. The main concerns in modern agriculture are the crops vulnerable to emerging races/strains of pathogens under climate change. The biotic and abiotic parameters in arable soils and their impact on crop yields and food supply at global level serve as key components of suppressive soils. The trend of soil borne diseases in maize-rice cropping zones is drastically changing and the pathogens infecting rice are also spreading to maize ecologies. Climate change may contribute to certain soil-borne pathogen migration toward niches or regions previously uncolonized by these pathogens. Soil-borne pathogen incidence in cereal cropping is difficult to control due to their natural persistence in soils and the inefficiency of chemical controls; thus, biological control becomes a very promising alternative to prevent soil diseases. The “suppressive” soils occur as naturally and prevent soil-borne pathogen in establishing and hence, reducing disease incidence even if the host is susceptible and climate is conducive. Thus, a long-term land-use plan and crop rotational models could represent a natural and effective source of suppressive soils against soil-borne pathogen diseases. The vast potential of native soil microorganisms as soil inoculants can improve plant growth and prevent soil-borne pathogen disease incidence in cereal cropping. The present paper recommends extensive screening of soil for its biological properties. Soil chemical properties and microbial community composition may be characterized based on their potential for pathogen inhibition *in vitro,* and their efficacy in controlling the diseases. Suppressive soils are being lost by an increase of intensive agriculture practices worldwide. The understanding of microbial communities in suppressive soils as well as the mechanisms acting in disease suppression in the rhizosphere may be used as a valuable tool for the development of sustainable control of soil-borne pathogen *(Rhizoctonia Solani, Fusarium sp., Macrophomina phaseolina)* in soil.

PP-39: Genetic inheritance of stripe rust and leaf rust in hulless barley cultivar PL891

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The present study was undertaken to study genetic inheritance of stripe rust pathotypes G, M, 24 and leaf rust pathotypes H1, H4 and H5 in hulless barley cultivar PL891. Genetic segregation of F2 population of PL891(resistant) x Jyoti(susceptible) revealed single dominant gene (3 resistant: 1 susceptible) for stripe rust pathotype M (2(1df) =0.08ns at 5% level of significance) and 24 (2(1df) =0.38ns at 5% level of significance) while for pathotype G, F2 showed inhibitory gene action (13 resistant: 3 susceptible, 2(1df) =0.57ns at 5% level of significance). For leaf rust, F2 population of PL891 x Jyoti segregated for two independent dominant resistant genes showing duplicate gene action (15 resistant: 1 susceptible) for pathotypes H1(2(1df) =0.21ns at 5% level of significance) and H4 (2(1df) =1.621ns at 5% level of significance) while for pathotype H5, F 2 population segregated for inhibitory gene action (13 resistant: 3 susceptible, 2(1df) =6.24ns at 5% level of significance). These inheritance studies for rust diseases will be helpful in further gene mapping and transfer of resistance genes into other elite barley cultivars which have become susceptible to rust diseases.

PP-40: Improving spot blotch resistance in wheat by marker-aided backcross breeding

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Spot blotch has been a serious constraint in wheat production in the Eastern Gangetic Plains (EGP) of North Eastern India. Therefore, to enhance spot blotch resistant in high yielding cultivar i.e. HD 2967, marker assisted backcrossing programme is initiated at ICAR-IIWBR. BH 1146' (Fronteira/Mentana//Ponta Grossa1) a Brazilian cultivar carrying resistance to spot blotch was used as a donor parent. Transfer of targeted QTLs 'QSb.iiwbr-7B'and 'QSb.iiwbr-7D' responsible for conferring resistance to spot blotch was monitored by diagnostic markers (Xwmc758-7B and Xwmc653-7D) for foreground selection. Background selection was achieved based on a set of well distributed SSRs. Based on foreground selection, 89 BC3F1 individuals were found positive. Selection of desirable plants were done on the basis of desirable QTLs, contribution of recurrent parent genome, 1000 grain weight (TGW), grain yield (GY) and low disease severity in BC1F1, BC2F1, BC3F1 in HD 2967 and BH 1146 cross. Further selections will be made in BC3F2 and BC3F2 plants which would show improved spot blotch resistance in the field, and also yield better than the recipient parent in presence of the disease.

PP-41: Mapping of QTLs conferring resistance to Karnal bunt in bread wheat

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Karnal bunt (KB) of wheat, caused by *Tilletia indica,* is one of the biggest challenges to the grain market, as it affects the grain quality and also causes yield loss. Genetic resistance is one of the best ways to cope up with this disease. Although there are several different sources of resistance, which have been identified to date, very few of them have been subjected to genetic analyses. Understanding the genetics of resistance and characterization and mapping of new resistance loci can help in development of improved germplasm. A study was carried out to identify and characterize resistance loci (QTL) in a set of 217 wheat recombinant inbred lines (RILs) developed from a cross between susceptible (KBRL22) and resistant (PBW343) parent. This population was screened for Karnal bunt for two consecutive cropping seasons (2015-16 and 2016-17) with the pathogen populations prevalent in Northern India. More than 550 SSR markers were used for the parental screening which covers almost all the chromosomes. We identified two consistent QTLs for Karnal Bunt (KB) resistance mapped on chromosome 2B (Qkb.iiwbr-2B) and 5B (Qkb.iiwbr-5B) accounting 15-20% phenotypic variation. The resistance at these loci was contributed by the parent ‘KBRL22’. The best lines from the population (in agronomy, end-use quality and KB resistance) carrying resistance alleles at all identified loci, may be used for selection of improved germplasm in future.

PP-42: Preliminary assessment of Yellow Leaf Disease (YLD) at initial clonal stage of sugarcane (*Saccharum* spp. hybrid complex)

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Sugarcane is an important industrial crop of Punjab after cotton, cultivated on 96.0 thousand ha in command area of 16 sugar mills. Its varietal improvement programmes aim to develop new varieties with higher cane yield and sugar content along with resistance to major diseases. During hybridization at ICAR-SBI, Coimbatore attempts are being made to use maximum parental diversity of clones planted in National Hybridization Garden from different zones. Since this disease is not an important one under subtropical conditions but important in tropical zone of the country, affecting sugarcane production globally including India. Its infection lowers the photosynthesis in sugarcane and, in turn mobilisation of photosynthates decreases from leaves to stalk, hence sugar content reduced. Severe YLD infection significantly reduces the cane yield and sugar content. Present study reports the natural occurrence of YLD in clones advanced to clonal stage II.

A panel of 169 clones was evaluated under field conditions at Regional Research Station, Kapurthala during crop season spring 2019-20. YLD was scored on the scale of 0-5 (zero to in the highest susceptibility level). It was observed that YLD was very severe in progenies of a diverse cross combination *viz*, CoV 89101 x Co1148 having rated 4-5. Incidence was little higher in some clones used from east coastal zone, however, it was lower in clones used North x North and North x Southern cross combinations and the clones showed YLD score ranged from 0 to 2. Therefore, it is advised that an utmost care should be taken while selecting parental diversity in hybridization garden to develop high yield and sugared clones resistant to YLD in future varietal development programme.

THEME-III

PLANT DISEASE MANAGEMENT UNDER CLIMATE CHANGE

LEAD LECTURES

LL-1: Damping-off disease of tomato and its management

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Tomato (*Solanum lycopersicon*) is an important off-season vegetable cash crop of Himachal Pradesh. In mid hills the crop is transplanted in the month of March and fruits are available from June onwards, which are transported to the Northern plains where they fetch remunerative prices. At various stages of plant growth, the crop is infected with various diseases of fungal, bacterial and viral nature, which not only reduce the quantity but also the quality of the produce. During the surveys of nurseries of tomato crop in Solan district of the State, the seedlings were found severely infected with damping-off disease and both pre- and post emergence symptoms were observed. Keeping this in view, the present investigations were carried out with the objectives to study the prevalence of the disease in tomato nurseries, identification of associated pathogen (s) and to devise suitable management strategies.

The incidence of damping-off in tomato ranged from 41 to 85 per cent at different locations in Solan district. Diseased samples were collected and the associated pathogen was isolated in pure culture. On the basis of coenocytic mycelium, production of sporangia (23.08-34.87 × 22.3-33.56 µm), germination of sporangium by zoospores and production of oospores (18.58-26.95 × 18.36-26.78 µm), the associated pathogen was identified as *Pythium* spp. On the basis of ITS amplification of genomic DNA, the pathogen was identified as *Pythium ultimum* Trow (NCBI Accession No. MF185175). *P. ultimum* caused both pre and post-emergence damping-off of tomato under artificial inoculation conditions and took 168 and 192 hr incubation period for pre and post-emergence damping-off, respectively.

In epidemiological studies, 25-30° C temperature along with high soil moisture (60-75%) were found favourable for the development of damping-off of tomato. Among different biocontrol agents evaluated, *Trichoderma harzianum* was found to be most effective both under *in vitro* and pot conditions, while *Bacillus subtilis* was least effective. Among various fungicides tested under *in vitro* and pot conditions, Metal, Apron XL, Curzate M8, Ridomil Gold and Sectin were found highly effective in the management of damping-off of tomato. Integration of soil solarization with seed treatment and soil application of *T.harzianum* was found best in reducing the incidence of both pre and post-emergence damping-off, while drenching with Ridomil Gold was also found effective in reducing post-emergence damping-off.

LL-2: Potential of botanicals in plant disease management

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Overuse and misuse of synthetic pesticides can result in harmful effects on humans, non-target organisms and the environment. Constituent compounds of synthetic pesticides have been attributed to chronic human ailments either due to consumption or exposure. Plants with bioactive compounds have been used to manage different crop pests with notable success. The active compounds in plants include phenols, quinones, alkaloids, steroids, terpenes, alcohols and saponins. plants like Bougainvillea (*Bougainvillea glabra)*, Artemisia (*Artemisia roxburghiana*), tulsi (*Ocimum sanctum)*, karvya (*Roylea elegans*), dudhali (*Cryptolepsis buchanani*), darek (*Melia azedirach*) have been reported to possess excellent potential against different diseases. Home made botanical formulations have been found effective against number of foliar diseases including fruit rots of strawberry, apple and citrus. Apple trays impregnated with cow urine based botanical formulation reduced post-harvest losses caused due to fungal pathogens and also increased the shelf life of the fruits. Botanical formulations were found effective with 84.2 per cent reduction in the disease index of buck-eye rot of tomato caused by *Phytophthora nicotianae* var. *parasitica* and 4.74 times increase in yield. Cow urinebased botanical formulation was also found effective against Phytophthora leaf blight and fruit rot of capsicum with 70.5 per cent reduction in disease index of leaf blight, 81.9 per cent reduction in the incidence of fruit rot along with 3.58 times increase in marketable fruit yield. Botanical formulations based on the local plants were also found effective against black rot of cauliflower with 74.8 per cent reduction in the disease index. The recent years have witnessed the introduction of nanotechnology mediated bio-pesticides. Nano-formulations of botanicals have been found more effective. Efficacy of pure silver nano-particles was found approximately 10,000 times higher than the water-based botanical formulations. Foliar spray of pure formulation of neem SNPs (150 ppm) was found most effective and incidence of buckeye rot was reduced by 82 per cent with 31.7 per cent increase in the fruit yield compared to control. Tomato plants sprayed with neem-based SNPs indicated highest content of ascorbic acid, lycopene content and total phenolics in the fruits.

INVITED LECTUERS

IL -1: Repercussions of climate change on plant disease

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Climate change is the result of acceleration in the increase in temperature and CO_2 concentration over the last 100 years. The repercussions are being felt more in developing countries, where damage to agricultural production from extreme weather linked climate change is contributing to deaths from malnutrition, poverty and associated diseases. Throughout the 21st century, India is projected to experience warming above the global mean. Climate change is the reality now and biggest threat of the present century. The repercussions of climate change have been observed in many dimensions such as effects on biodiversity, food grain production, insects and plant diseases. Out of this, repercussions on plant diseases is also one of the important dimension that has to be seen in broader prospective. Since environment and diseases are closely linked, climate change probably alter the geographical and temporal distribution of phyto-sanitary problems. Change in temperature directly influence infection, reproduction, dispersal, and survival between seasons and other critical stages in the life cycle of a pathogen. Moisture is particularly important for fungal and bacterial pathogens on plants. Rising CO_2 level, atmospheric pollutant and ultraviolet B components play important impact on host pathogen system in cultivation practices. The climate change has various repercussions on biotic, abiotic and mesobiotic stress on plants. Therefore, 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. 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 again may influence the 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; a lack of understanding of epidemic processes at relevant environmental and spatial scales has hampered progress. In such scenarios, weather-based disease monitoring, inoculums monitoring, especially for soil-borne diseases and rapid diagnostics would play a significant role. There is need to develop integrated disease management strategies to decrease dependence on fungicides. In addition, monitoring and early warning systems for forecasting disease epidemics need to be developed for important host-pathogens which have a direct bearing on the earnings of the farmers and food security at large. The use of information technology can also help in proper compilation of the data for forecasting as per the climate change and management of plant diseases.

IL-2: Combining rust resistance with non-structural carbohydrates (NSC) in wheat to achieve food security

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Wheat crop is a major contributor to the agricultural economy in India, occupying 30.7 mha area with 98.38 mt production. Yellow rust is a major constraint to wheat production on about 12.0 m ha in the irrigated area of Punjab and Haryana, Northern Hills and North Western region of India. Varieties resistant at the time of release become susceptible usually within a few years due to evolution of new pathogen races. In addition, wheat production is also affected by abiotic stresses. Adaptability to stress can be facilitated by resilient wheat cultivars with inbuilt mechanisms. Non structural carbohydrates (NSC) serve as reserve to support grain filling under stress conditions. These reserves improve yield stability in grain crops by providing an alternative source when photosynthetic capacity is reduced during the later phases of grain filling, or during periods of abiotic and biotic stresses. Since resistance to rust diseases in new wheat cultivars is among the important criteria for release, evaluation of NSC among rust resistant germplasm would produce germplasm ready for use in breeding programs. Although pathologists and physiologists have been serving wheat breeding programs independently, scientists from these disciplines have not yet worked together on a common goal to save wheat production from abiotic and biotic threats. In this study we aim to use knowledge of pathology, genetics, physiology and molecular biology to develop wheat germplasm combining rust resistance with high amount/activity of NSC through evaluation of genetically diverse rust resistant germplasm under managed/natural stress conditions.

IL-3: Multipronged strategy to manage pathogens associated with varroa mite in Apis mellifera honey bees

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Worldwide economic value of honey bee mediated pollination amount to 153 billion. In India, at $ 22.5 billion, it benefits more than 600 commercial crops spread over 48.5% area. About 2.42 lakh beekeeper families directly earn their livelihood by rearing 1.6 million domesticated honey bee colonies, producing 1.05 lakh MT honey exporting 61,333.88 MT worth $105.48 million. Inherent vulnerability of social bees to pests, diseases and stresses demand major effort in beekeeping operations. Colony losses have steadily increased to 33% in America and EU. Ectoparasitic mite, *Varroa destructor* is the dominant threat to *Apis mellifera* bees globally and in India killed more than 50% colonies during its epidemic in 2004. These losses occurred in parallel with global spread of Varroa whose infestation is considered the key explanatory factor. Varroa induced collapsing colonies has close association with a range of pathogens including 22 viruses (single-stranded positive sense RNA viruses; Iflaviruses; taxonomically unclassified viruses) predominated by Deformed wing virus, Israeli acute paralysis virus, Acute bee paralysis virus, Kashmir bee virus, Acute bee paralysis virus, Black queen cell virus, Chronic bee paralysis virus that are transmitted both horizontally and vertically enhanced by crowding and trophallaxis. Two firmicute bacteria, *Paenibacillus larvae* and *Melissococcus plutonius* are infective agents behind American and European foulbrood disease, of bee larvae, protozoan *Nosema* sp., etc. and finally the complex of "parasitic mite syndrome". Disease management entails expensive treatment, quarantine regimes. Antibiotics and chemical pesticides used indiscriminately lead to collateral losses of beneficial microbes, residues in honey and development of resistance that were the prime reasons of Indian honey being banned for export to EU in 2009. India specific strategies to counter these threats have been developed by author that include preventive, biotechnological, organic or biochemical, chemical and finally breeding of honey bee colonies resistant to multiple pathogens and form part of this paper. For the first time in India, a novel approach of breeding honey bees resistant to Varroa and multiple pathogens employing hygienity test was developed that may provide lasting solution. Three apiaries (194 colonies) screened for hygienic behaviour through "pin-prick method" reported wide range of sensitivity. It was encouraging to find 4.6% colonies with highly sensitive (HS) trait and 22.2% to moderately sensitive (MS) group. Majority of colonies exhibited (75 colonies, 38.7%) sensitive (S) and least sensitive (LS) reaction (67 colonies, 34.5%). Hygienic behaviour was independent of colony strength and the time of dead brood removal, confirming its heritable nature. Further, HS and MS colonies recorded lower *V. destructor* population (3.47 and 7.85 mites/colony) compared to LS colonies and S colonies (16.69 and 11.37 mites). Based on a combination of hygienic behavior and colony growth parameters, 52 colonies were selected for future breeding programme.

ORAL PRESENTATIONS

OP-1: Application of nanotechnology in crop protection as nanofungicides

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Application of nanotechnology in crop protection as nanofungicides holds a significant promise in management of pathogens. Government organizations, scientists, inventors as well as industries are coming up with new techniques, protocols and products that have a direct application of nanotechnology in agriculture for crop protection. Recent manufacturing advancements have led to the fabrication of nanomaterials of different sizes and shapes with unique properties targeted toward specific applications in crop protection. Among nanomaterials, polymers are biocompatible and biodegradable and can be successfully employed as nanovehicles for delivery of pesticides for plants protection. However, use of nanotechnology in agriculture, especially for plant protection and production, is an under-explored area in the research community. Preliminary studies show the potential of nanomaterials in improving seed germination and growth, plant protection and pathogen detection. This talk summarizes agricultural applications of nanomaterials as fungicides and the role these can play in future crop protection.

OP-2: Recent status of the biotic and abiotic stresses in cotton crop in the South Western Region of Punjab, India

Rupesh Kumar Arora and Paramjit Singh

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Cotton is a major fibre crop of Punjab, grown over 2.84 lakh hectares with production of 11.50 lakh bales of cotton with an average productivity of 688 kg/ha. The production of cotton crop has been unable to touch the production potential due to number of biotic and abiotic stresses. The stresses with a particularly disease are mainly associated with the leaves of plant, which drastically affect the photosynthesis and ultimately reduces the yield. Among the biotic stresses, diseases caused by the viral, fungal and bacterial pathogen i.e Cotton leaf curl virus diseases, Root rot, Fungal foliar Leaf spots and Bacterial blight and Vein blight are the predominant one. Cotton leaf curl virus disease (CLCuD) caused by Gemini virus and transmitted through whitefly (*Bemisia tabaci*) is one of the major biotic stress affecting the yield and productivity of the cotton in the South Western Region of Punjab but at present severity of the CLCuD are on decreasing trend. An incidence of Root rot (soil borne) usually appeared in the month of June or July during the time of first irrigation or at the time of rainfall in few isolated scattered plots. Diseases like Fungal foliar leaf spots and Vein blight are the diseases of less economic importance, usually appear late in the cropping season in last week of August or September (around 120-130 DAS) and can occurs in severe form if coincides with the high humidity at that time. An incidence of Sooty mould in the cotton crop came into notice in 2015 at the time of epidemic of whitefly in Punjab. During 2015, congenial environmental conditions for the multiplication of whitefly, delayed sowing and tank mixing of insecticides lead to outbreak of sucking pests i.e. whitefly and lead to cause the Sooty mould in cotton crop. Abiotic stresses i.e Para wilt, Leaf reddening, Droppings, Tirak, Damage or injury of cotton crop due to hailstorm, drying of the cotton crop due to water stagnation, etc. are the predominant ones. Among all the abiotic stresses i.e. Para wilt (physiological disorder) widely noticed and widespread followed by Leaf reddening and droppings. Tirak in cotton crop is of least economic concern since last 3-4 years. The problem of Tirak in cotton crop noticed in the few scattered plots adjoining border areas of the Rajasthan. Incidence and severity of the biotic and abiotic stresses during the cropping season of the cotton are related to erratic weather conditions in Punjab. The optimum sowing time of the Cotton in Punjab, India is April 1 to May 15 and more than 90 per cent area of the cotton crop is covered with the Bt cotton hybrids. Delayed sowing, uniform cultivation of the particular hybrid, application of excess dosages of fertilizers particularly Urea, tank mixing of insecticides, lack of awareness among farmers, etc. are the important factors leading to the enhancement of stresses in the cotton crop in Punjab.

OP-3: Cultivation of Cordyceps militaris in Haryana

Rakesh Kumar Chugh, Satish Kumar, Ajay Singh and Surjeet Singh

Department of Plant Pathology, CCSHAU HIsar, *HAIC, Murthal, Sonepat

Mushrooms have been used for both edible and medicinal purposes from thousands of years in almost all parts of the world. Especially, medicinal mushrooms have history of their usage in traditional medical practices. They are utilized worldwide as potent source of nutritionally and pharmacologically bioactive compounds. Biological formulations derived from medicinal mushrooms are part of modern clinical practices in Japan, Korea, China, Russia and several other countries. For modern clinical practices, medicinal mushrooms attain special position as they possess unlimited source of polysaccharides, proteins, polysaccharides-protein complexes, vitamins, nucleosides and other secondary metabolites with several biological effects including immune-enhancing, anticancer, antiaging, antimicrobial activity, etc. Literature shows that about 65% of cancer related deaths could be prevented by adding mushrooms to daily diet as mushrooms are rich source of antioxidants. Cordyceps sinensis (also known as *Ophiocordyceps sinensis*) is one of the most important medicinal mushroom, which is a storehouse of enormous number of bioactive compounds with remarkable pharmacological properties. Genus *Cordyceps* have a history for its usage in almost all parts of Asian continent from last thousands of years. Cordyceps name is a combination of two latin words i.e., cord and ceps which means club and head, respectively. It is popularly known as “yartsa-gumba” or “Dong Chong Xia Cao” (winter worm summer grass) and naturally distributed in China, Bhutan, Nepal and India. This wild macrofungi in different forms such as fruiting bodies, cultured mycelia and extracts possess immense medicinal properties. Considering medicinal properties of *C. sinensis,* it has been utilized to treat various disorders such as hyperglycemia, hyperlipidaemia, hyposexuality, cancer, lung disorders, cardiovascular disorders, renal dysfunction, arrhythimias and liver related disorders, etc. Apart from medicinal properties, it is popularly marketed as dietary health supplement approved by the FDA and it has huge market potential in many countries. In addition to medicinal and nutraceutical properties, this medicinal mushroom is considered as “soft gold” in China, and Indian origin of *C. sinensis* is found in Himalayan range at about 5000 meters altitude in Arunachal Pradesh, Uttarakhand and Sikkim states . In Uttarakhand state of India, it is known by common names, Kira Ghas, Kira Jhar and Ghas ka kira, etc. This macrofungi is a rich source of secondary metabolites such as cordycepin, cordycepic acid, adenosine, ergosterol, mannitol, polysaccharides, fatty acids, steroids, flavonoids, polyphenols, vitamins and mineral elements. An attempt has been made to cultivate. *Cordyceps militaris,* which is an entomopathogenic fungus belonging to Ascomycota, Sordariomycetidae, Hypocreales and Cordycipitaceae and is one of the most important traditional Chinese medicinal mushrooms. *Cordyceps militaris* is the type species of *Cordyceps,* which internally parasitizes larva or pupa of lepidopteran insects and forms fruiting bodies on their insect hosts. Different workers have studied the effects of working volume, carbon sources, nitrogen sources, inorganic salts, growth factor, nucleoside analogue and amino acid additions in order to improve the cordycepin production by static liquid culture of *C. militaris* and suggest the optimization medium conditions that were helpful for improved large scale cordycepin production. As artificial cultivation for production of fruiting bodies of this precious medicinal mushroom is very costly and time consuming, mycelial biomass production through liquid fermentation can be an alternative to utilize its biological potential. Various research studies have claimed that mycelial biomass is rich in bioactive metabolites (essential amino acids, antioxidants, vitamins and minerals) as compared to biomass derived from fruiting bodies. The reason behind this is that the nutrients access to the mycelia is easy from the culture media due to penetration into the substrates by using physical pressure and through enzymatic secretion.

OP-4: Sugarcane diseases management in Punjab

Rajinder Kumar, Anuradha, Lenika Kashyap and Paramjit Singh

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Sugarcane is not only the cash crop for the growers, but it is the main source of white crystal sugar and also a very good substitute of sugar in the form of 'gur' and 'khandsari' (brown sugar). Agricultural production continues to be constrained by a number of biotic factors. Sugarcane crop requires hot and humid climate for its development, which is also conducive for the development of diseases. Number of diseases caused by fungi, bacteria, viruses and phytoplasmas cause considerable losses approximately 10-15 per cent in terms of yield and quality. The foremost disease of sugarcane is red rot. Red rot: caused by the fungus *Colletotrichum falcatum* is widely prevalent in tropical and sub-tropical India. The disease appears from July to till the crop is harvested. Initially yellowing of the third or fourth leaf from top occurs which later appears on other leaves as well, leading ultimately drying of the cane top. Later, on splitting open the diseased cane longitudinally, the tissue exhibits red discoloration interspersed with white patches running inside the cane. Varieties like CoPb 92, Co 118, CoJ 85, CoPb 93, CoPb 94, CoPb 91, Co 238 and CoJ 88 have been resistant to red rot. Use disease free seed of sugarcane, do not plant sugarcane in the disease affected fields for one year, rogue out and burn the diseased canes. The other important diseases are wilt and smut. Wilt: caused by *Fusarium sacchari,* is a serious constraint to sugarcane production. Stress due to water logging and drought along with root injury greatly enhanced the expression of wilt syndrome. Management of this disease could be achieved by growing fairly resistant variety, rogueing and removal of the infected canes. Smut:- caused by the fungus *Ustilago scitaminea* is prevalent throughout the year, but is severe from May to July and again October to November. It is easily recognized by the appearance of long whip like shoots covered with dusty black mass of spores. Cultivate fairly resistant varieties, use disease free seed material for planting and discard even non-whipped healthy looking canes from diseased stools are some of the remedies for its management. Red stripe/Top rot: caused by *Pseudomonas rubrilineans* was first reported by Desai in 1933. There has been a lot of controversy among the researchers about the taxonomic position of the pathogen of red stripe. Keeping in view, isolation and identification of the associated pathogen was carried out by using rDNA ITS (Internal Transcribed Spacer) region molecular marker. Thirteen markers were used for the identification of the isolated pathogen. The amplification of the targeted ITS (Internal Transcribed Spacer) region of the rDNA revealed the pathogen as *Acidovorax avenae* sub sp. avenae. This confirmed that a new pathogen *Acidovorax avenae* sub sp. *avenae* is associated to the red stripe/top rot of sugarcane in Punjab State. Affected plant should be removed and burnt and growing of resistant variety is the best method to control this disease. The occurrence of the pokkah boeng disease has been recorded in Punjab on most of the commercial varieties. Symptoms of pokkah boeng initially seen on the young leaves which become chlorotic towards the base, accompanied by malformation or distortion in the form of wrinkling, twisting and shortening of leaves with often narrowed base. Later on, the whole base of the spindle gets rotten and dries up very fast and finally, it formed a 'Top-Rot' of the tender tissues of the apical part of the cane. Growing resistant variety, roguing and removal of the infected canes reduce the pokkah boeng disease. Integrated disease management using resistance varieties and physical methods are the way for the management of sugarcane diseases.

OP-5: From farm to fork individual solutions to meet the essential requirements for food safety

Amod Arora

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Analytik Jena technologies are creating innovations in the field of food safety and provide better solutions for food and agriculture analysis. Food safety covers many aspects of the food chain – from point-of-origin to the nutritional value, the presence of pathogens, toxic metals, and other biological contaminants, to the elemental composition of animal feed and soil that affect animal and plant health. National and international directives help to regulate the industry and define limits along the food chain from primary agricultural production to food processing and consumption.

OP-6: Impact of seed treatment with bio-fertilizers on wheat production

Satyavir Singh, Anuj Kumar, Sendhil R, Anil Khippal, Mangal Singh, RameshChand and GP Singh

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At global level, India is the second largest producer of wheat in the world. Higher yield of wheat can be obtained through judicious use of plant nutrients. The minerals will continue to play the key role in the argumentations of the food production in the entire world. In recent past due to escalation in cost of chemical fertilizers and with objective to minimize environmental pollution, awareness is being created on the use of organics including bio-fertilizers, which are the sources of macro, micro and secondary nutrients to sustain the soil fertility and productivity also. During last five years, bio-fertilizers like Azotobactor and Phosphorus Solubilising Bacteria (PSB) which are eco-friendly and low cost agriculture inputs, have shown tremendous potential to increase yield of wheat under frontline demonstrations conducted in different wheat producing zones of India. The seed treatment with bio-fertilizers along with recommended inorganic fertilizers were compared with untreated seed with recommended inorganic fertilizers. A total of 254 demonstrations on seed treatment with bio-fertilizers were conducted from 2014-15 to 2018-19 to show its potential impact on wheat yield. Bio-fertilizers such as Azotobactor and PSB were demonstrated at farmers' field across the country at 254 locations. Seeds of newly released varieties were treated with Azotobactor and PSB cultures. The whole method of seed treatment was demonstrated to all the Frontline Demonstration farmers for its better adoption. The results of demonstrations on bio-fertilizers were encouraging across the country. The yield gain ranged from 0.68 q/ha to 6.02 q/ha while the overall yield gain was 2.58 q/ha. The percent yield gain ranged from 3.37 to 14.11 per cent averaging 8.66 across zones. The highest yield of 54.75 q/ha was recorded with HD 2967 variety in NWPZ whereas the lowest yield i.e.11.61q/ha was recorded in NEPZ. The possible reason of increase in yield level was due to increased availability of N and P to the plants due to increased microbial activities in the root zone triggered by Azotobactor and PSB. Hence it could be inferred from the above findings that seed treatment with bio-fertilizers is a low cost technology but its impact is high so there is a need to popularize this technology across the country on wider scale for the benefit of the farmers.

OP-7: Agilent genomics solutions in applied Plant & Crop research

Gaurav

LCGC India Pvt Ltd, -----------

Plant viruses, viroid's, and phytoplasmas are known to cause considerable losses in crop yield, quality of plants, and plant products. It's a high demand for more precise and reliable techniques to detect foreign (transgenic or pathogenic) DNA in edible plants. Now a days various methods are apply in research laboratories to improve the crop production. Quantitative real-time PCR (qPCR) is a very powerful technique incorporates traditional polymerase chain reaction (PCR) which efficiently produces a specific fluorescent signal, measuring the kinetics of the reaction in the early PCR phases. The most influential characteristic of real-time PCR is its suitability for quantitative analyses. In recent years, real-time PCR as a valuable and versatile tool to use with accuracy for quantification of specific target in most agricultural fields such as plant protection and plant biotechnology. qPCR is widely use for viral and bacterial detection, pathogen identification in human, animals and plant samples. It's one of the widely accepted technique to assess the candidate gene expression. In multiplex real-time PCR assays several targets can be simultaneously detected from different microorganisms by differences in emission of wavelength and also analyze the expression of multiple genes in between different experimental groups. However, qPCR provides a higher sensitivity and specificity for the detection of DNA and RNA but still consider as candidate gene approach, which allow to analyze DNA and RNA at genome level.

Microarrays have become an important technology for the genome wide analysis of gene expression in humans, animals, plants, and microbes. Implemented in the context of a well-designed experiment, cDNA and oligonucleotide arrays can provide high throughput, simultaneous analysis of transcript abundance for thousands of genes. However, despite widespread acceptance, the use of microarrays as a tool to better understand processes of interest to the plant physiologist is still being explored. To help illustrate current uses of microarrays in the plant sciences, several case studies demonstrate the emerging application of gene expression arrays in plant physiology. Agilent Microarray provides full range of DNA and RNA applications in a variety of fields, starting from gene expression analysis to detection of complex chromosomal defects. Agilent microarray covers vast applications in basic research studies. Agilent microarray enable researcher to study under a large area of applications like a detection and identification of plant pathogens.

POSTER PRESENTATIONS

PP-1: Management of collar rot disease of groundnut through fungicides as seed treatments and soil drenching

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Groundnut (*Arachis hypogaea* L.) is a leguminous oilseed crop and India occupies the first position, both with regard to area and production of groundnut in the world. Groundnut is a crop which is mainly cultivated under rain-fed conditions, thus, pathogens have more of a chance to attack the crop. The crop suffered from many divastating disease such as early and late leaf spot, rust and collar rot which are economically important in India. Among the soil borne diseases of groundnut, collar rot caused by *Aspergillus niger* is an important disease. The collar rot of groundnut is an important seed and soil borne disease. Collar rot disease of groundnut is one of the major constraints for taking optimum production of groundnut by the farmers. By keeping in view the importance of this disease the experiment was laid out at Regional Research Station, Bawal during Kharif, 2018 in order to find out effective control measure. The treatments included different fungicides with variable doses applied as seed treatments before sowing and soil drenching after first irrigation. The results revealed that seed treatments with Captan @ 3gm /kg seed + soil drenching with carbendazim @ 0.1 % was found superior for minimizing the collar rot disease as compared to all other treatments along with control under field conditions. Minimum collar rot incidence was observed in treatment (T3) where, seed treatments with Captan @ 3 gm /kg seed + soil drenching with carbendazim were applied @ 0.1 % (2.40%) followed by T2 i.e seed treatments with Captan @ 3 gm /kg seed (3.19%) and T4 (3.83%) with seed treatments with carbendazim @ 2gm/kg seed. The maximum pod yield was also recorded in treatment T3 (33.90 q/ha) as compared to all other treatments.

PP-2: Comparative efficacy of fungicides and biocides against *Bipolaris sorokiniana* incitant of wheat spot blotch

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Bipolaris sorokiniana is a most destructive fungus causing foliar disease of wheat and spreading in all the wheat growing areas of country. The present investigation was under taken to evaluate the potentiality of different seven fungicides (Raxil 060 FS, Trifloxystrobin 500 SC, Trifloxystrobin + Tebuconazole 080 FS, Vitavax, Flint (Trifloxystrobin) 50 WG, Nativo (Trifloxystrobin 25%+Tebuconazole 50%) 75 WG, Tebuconazole 2% DS) and two biocides (*Trichoderma viride,* Neemexcel-Neem based product) for standardization of effective dose of fungicides and bioagent against *B. sorokiniana*. The effect of the treatments was studied on germination percentage and seedling growth parameters of wheat, foliar diseases and yield component, and phytotoxicity effect due to foliar spray. Four doses *viz.* 0.03%, 0.06%, 0.12% and 0.25% of fungicides and bioagent (Neemexcel) were used in food poison technique against *B. sorokinana*. Nativo 75WG was found most effective in reducing the spore germination (94.40%) with concentration @ 2.50 ml/lit. of the spot blotch followed by Raxil 060 FS (94.00%). *In vitro* condition, Nativo 75 WG was found most effective rather than any fungicides and biocides. Seed treatment with *T. viride* was found most effective against seed borne infection and also stimulate the germination of seed (100%) followed by Vitavax (98.64%). Effect of biocides (T. viride, 85.00%) on growth parameter of wheat (shoot and length) was found better than fungicides (Raxil, 76.90%). In foliar spray with fungicides, Nativo 75 WG was found highly effective against spot blotch, Powdery mildew and Alternaria blight than biocides in glass house condition. Under natural condition, Nativo 75 WG and Trifloxystrobin + Tebuconazole 080 FS were found much effective against spot blotch, Powdery mildew, Alternaria blight, rust, lose smut and reduced the disease severity (60.53%,+%, +%,+%,+%) and (60.33%,+%, +%,+%,+%) in control (68.68%), respectively.

PP-3: Antagonistic activities of biocontrol agents for guava wilt fungus caused by *Fusarium oxysporum*

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Guava is an important crop cultivated worldwide in tropical and subtropical climate. Soil borne pathogenic fungus *Fusarium oxysporum,* is a major catastrophe of guava wilt disease. It limits productivity of guava. Since use of chemicals is field are harmful to humans and it is not easy to control soil borne fungus. Therefore, biocontrol agents have been studied for wilt management under *in vitro* conditions. In present study an experiment was conducted to evaluate maximum inhibition efficiency of four species of *Trichoderma* obtained from ITCC (*T. viride, T.asperellum* (7447), *T. hamatum* (7272), *T. harzianum* (7229) and one culture of *Aspergillus niger* (6738) against guava wilt fungus. Three *F. oxysporum* culture were isolated from soil samples, collected from wilt affected areas of IARI, New Delhi, and Tamil Nadu. Morphological characterization of isolates was done by studying its conidial characters. After confirming, culture was submitted to ITCC and accession number of cultures was obtained as Fop-6 (8287), Fop-7 (8288) and Fop-39 (8291). Dual culture assay technique was done for *in-vitro* screening of four species of *Trichoderma* (*T. hamatum, T. asperellum, T. viride, T. harzianum)* and *Aspergillus niger.* Study shows that A. niger was found to give maximum inhibition percent which was in 71.9%-77.9% range. Among *Trichoderma* species, *T. viride* was found to give maximum inhibition ranging from (60.3%- 73.6%), followed by *T. harzianum* (50%-61.8%) and *T. asperellum* (52.3%- 60%). *T. hamatum* was least significant in its antagonistic activity which was in range of 47-49%. *In- vitro* assay suggested the use of *A. niger, T. harzianium, T. viride* for evaluation on a larger scale under field conditions.

PP-4: Strategies for disease free seed cane production to manage varietal yield decline in sugarcane (*Sacchraum* spp.)

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Sugarcane cultivation and the development of sugar production industry run in parallel to the growth of human civilisation and are as old as agriculture. Sugar industry is a focal point for socio-economic development in rural areas, mobilizing rural resources, generating employment and higher incomes, and supporting the development of transport and communication facilities. Sugarcane, thus, plays a major role in the economy of sugarcane growing areas and, hence, improving sugarcane production will greatly help in economic prosperity of the farmers and other stakeholders associated with sugarcane cultivation. Sugarcane yields are deteriorating day by day because of lack of good quality seed and latent infection of pathogens (like red rot, wilt, smut, ratoon stunting and grassy shoot diseases) that adversely affect the realization of potential cane yield of varieties. Sugarcane is vegetatively propagated and it favours accumulation of pathogens of most of the diseases over a period of time, which makes minor disease into major one. Several epidemics due to red rot, smut, wilt, grassy shoot, ratoon stunting, yellow leaf and leaf scald occurred in the past indicated that disease infected seed can play significant role in their creation and further spread. Affected planting material poses a major problem in propagation and exchange of germplasm, and eventually in breeding and distribution of superior genotypes. The bulky cane cuttings used for planting as seed harbor many pests and diseases thereby decreasing cane yield and quality drastically. In fact, poor quality seed is a major constraint in sugarcane production. For increasing sugarcane production availability of good quality seed material of high yielding varieties is very essential. To increase output and profitability in the sector, there is need to increase on farm production and productivity of cane, and to increase the recovery rate of sugar in mills. Also, there is need to improve the efficiency and to reduce the cost of cultivation by adopting the latest technologies like system of sugarcane initiative (SSI) involving single bud and bud chip techniques, spaced transplanting technique (STP) and community-based seed cane production (CBSS) approach; to have rapid multiplication through tissue culture/ micro-propagation of disease-free seed of new improved varieties of sugarcane using hot water, moist hot air therapy (MHAT); elimination of viruses in sugarcane crop using meristem tip culture technology, disease indexing of micro-propagation raised plants for freedom from viruses and virus-like diseases through enzyme linked immune sorbent assay (ELISA) and molecular methods, certification of micro-propagated plantlets through accreditation laboratories and finally application of general seed cane certification standards to safeguard the interests of cane growers and the sugar industry by saving cane that could be used for seed purposes. There is a need to spresd awareness among farmers for use of right methods and procedures for seed production. Healthy and good quality seed cane provide assured germination of disease free canes that helps the farmers to rejuvenate and retain high yielding sugarcane varieties for longer duration.

PP-5: Integrated disease management of banded leaf and sheath blight in maize using different biorational products

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Maize (*Zea mays* L.) is one of the most versatile emerging crops having wider adaptability under varied agro-climatic conditions. Among various fungal, bacterial and viral diseases of maize, banded leaf and sheath blight (BLSB) caused by *Rhizoctonia solani* f. sp. *sasakii* has become one of the most devastating disease and resulted in severe yield losses (100%). Therefore, a study was conducted for integrated disease management of BLSB through organic supplements/ amendments under field conditions during Kharif, 2018. The experiment consisted of following treatments i.e. T1= Beejamrit @ 10% + Jiwamrit @ 5%, T2= Beejamrit @ 10% + *Pseudomonas fluorescens* @ 0.2%, T3= Beejamrit @ 10% + *Trichoderma harzianum* @ 0.2%, T4= *Azotobacter chroococcum* @ 50 ml/acre + Jiwamrit @ 5% and T5= *Trichoderma harzianum* @ 0.2% + *Pseudomonas fluorescens* @ 0.2% were used as seed treatment and soil drenching to control the BLSB disease. The results revealed that all the five treatments combination significantly reduced BLSB disease. A minimum disease incidence (33.18%) and disease severity (22.1%) was recorded with the treatment T5 i.e. seed treatment with *T. harzianum* @ 0.2% and soil application with *P. fluorescens* @ 0.2%. It was also observed that above treatment found to be most effective in controlling the disease upto 66.89 per cent, while T4 i.e. seed treatment with *Azotobacter chroococcum* @ 50 ml/ acre and soil application with Jiwamrit @ 5% was found second best treatment in controlling disease upto 60.67 per cent. However, a maximum disease incidence (59.6%) and disease severity(39.02%) was recorded with the treatment T1 i.e. seed treatment with Beejamrit @ 10% and soil application with Jiwamrit @ 5%.

PP-6: Effect of fungicide and different containers on germination and mycoflora incidence of sorghum (*Sorghum bicolor*) seeds

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Sorghum [*Sorghum bicolor* (L.) Moench] an important food and fodder crop of India belongs to family poaceae. It is the fifth major cereal crop in the world after wheat, rice, maize and barley, and serving as a staple food for millions of people particularly in semi-arid tropics of the world. One of the reasons reported to stumble the green fodder production is non-availability of quality seed in sufficient quantities. Therefore, this study was designated to evaluate the effects of different fungicide treatments, and storage containers on seed germination and mycoflora incidence of sorghum seeds. Seeds were treated with seventeen different fungicides and stored for fifteen months in different containers. Maximum germination was observed in the seeds treated with carboxin + thiram followed by carbendazim + mancozeb. Among containers, polythene bag found better than cloth bag and metal box. Treated sorghum seed developed less mycoflora particularly *Alternaria,Helminthosporium, Curvularia* and *Penicillium* while more association of *Asperigillus, Fusarium* and *Mucor* were observed with the seeds during storage period in different containers. Fungicide carboxin + thiram, carbendazim + mancozeb and carbendazim were found most effective against the four genera *viz. Alternaria, Helminthosporium,Curvularia* and *Fusarium* of sorghum seed in all the three containers. Among the fungicides treatments carboxin + thiram was found most effective against the fungi followed by carbendazim + mancozeb in all the three containers. Polythene bag was found superior to protect the seed from the seed mycoflora of sorghum during storage.

PP-7: Assessment of disease appearance, percent disease index and management of white rust of mustard

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Mustard (*Brassica juncea* L.) belongs to family *Brassicaceae* (Cruciferae) and genus *Brassica. Albugo candida,* the causal organism of the white rust/ blister of the rapeseed mustard occurs in particularly in northern and north eastern states of India. It is one of the important diseases of rapeseed-mustard in India causing a yield loss of 17-34 per cent. The effect of weather parameters and sowing dates play an important role in the severity of white rust of rapeseed-mustard and its impact on yield. In the Rabi season (2017-18) a periodical increase in the disease severity was found with the delay in sowing and the Percent Diseases Intensity (PDI) progression was higher during 3rd sowing at 100 Days, 110 Days, 120 Days and 130 Days after sowing of Giriraj variety followed by RLC-3. The disease severity differed significantly among the sowing dates and varieties; such as the Giriraj exhibited highest PDI (37.60%) whereas; PC-6 and GSC-7 exhibited lowest PDI (0%) at lowest temperature (11.4-14°C) and lowest relative humidity (62-89%). Highest seed yield (20.37 q/ha) was recorded on 1st sowing (D1) followed by 2nd sowing (D2) (12.59 q/ha) and the seed yield was lowest in case of 3rd sowing (D3) for all the four varieties. Disease management evaluation of fungicides, bio-agent and botanical extract revealed that Carbendazim 50% WP 3g was the most effective against the white rust and it reduced the disease by 73.52-78.69 %, followed by the *Trichoderma viride*@500 ppm reduced the disease by 68-65.32 % and Neem extract10% reduced the disease 60.18-61.28 %, respectively.

PP-8: Management of early blight of potato through different approaches

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Potato (*Solanum tuberosum* L.) is one of the most important vegetable crop growing in the century. It originated in Peru-Bolivian in the Andes (South America). It is a popular source of carbohydrate, and can be used both for table consumption as well as in processed world. In India, it was introduced from Europe in early 19th century. Fresh potato tubers contain around 80% water and 20% dry matter. More than 75% of the dry matter is starch but it also contains protein, fibers and small amount of fatty acids. It is also rich in minerals such as potassium, phosphorus, magnesium and vitamins like B1, B3 and B6. Potato is affected by various diseases caused by fungi, bacteria, plant parasitic nematodes, viruses and phytoplasma, etc. Major diseases of potato are late blight, early blight, black scurf, dry rot, etc. in the fungal group and bacterial wilt, soft rot/blackleg of potato and common scab in the bacterial group. Sometime, these diseases may cause losses up to 75%. Early blight of potato caused by *Alternaria solani* (Ell. and Mart.) Jones and Grout, is very common and is found in almost all the potato growing states including in Uttar Pradesh, Madhya Pradesh, Andhra Pradesh and Maharashtra. Early blight has been found very destructive and gaining importance day by day because of the destructive potential of *Alternaria solani* raising temperature due to global warming and gradual deterioration of soil health, which pose a new threat to potato cultivators. For the investigation susceptible cultivar of potato 'Pusa Bahar' was grown in a randomized blot design during rabi 2017-2018 with seven treatments. Among all the treatments, the highest Percent Disease Control (50.95%) was recorded with Fenamidone (@ 0.1%), followed by Copper oxychloride 45.25 (50 % WP @ 0.2%) over control, while among the botanicals, the Neem seed kernel extract the PDC was followed by Garlic. The fungicide Fenamidone @ 0.1% was found more efficacious in inhibiting the growth of *Alternaria solani* in potato, while on the other hand, the maximum growth inhibition among the botanicals tested was found in Neem seed kernel extract @ 5%.

PP-9: Role of chitosan in plant disease management and increasing shelf life of agricultural produce

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In recent years environmental-friendly measures have been developed for managing crop diseases as alternative to chemical pesticides, including the use of natural compounds such as Chitosan. Chitosan is a deacetylated derivative of chitin that is naturally present in the fungal cell wall and in crustacean shells from which it can be easily extracted. Chitosan has been reported to possess antifungal and antibacterial activity, and has been found effective against seed borne pathogens when applied as seed treatment. It can form physical barriers (film) around the seed surface, and it can act as vehicular for other antimicrobial compounds that could be added to the seed treatments. Its nano formulations can also be used to increase shelf life of various agricultural produce. Conversion of macro materials in to nano size particles (1-100nm) gives birth to new characteristics and the material behaves differently. Nanomaterials can be potentially used in the crop protection, especially in the plant disease management. Nanoparticles may act upon pathogens in a way similar to chemical pesticides or the Nanomaterials can be used as carrier of active ingredients of pesticides, host defense inducing chemicals, etc to the target pathogens. Because of ultra small size, nanoparticles may hit/target virus particles and may open a new field of virus control in plants. The disease diagnosis, pathogen detection and residual analysis may become much more precise and quick with the use of nanosensórs.

PP-10: Integrated management of root-knot nematode in cucumber under protected cultivation

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Cucumber (*Cucumis sativus*) is an economically important crop grown in open as well as in protected cultivation. More and more farmers in Haryana are opting for cucumber cultivation in protected structures. Due to controlled environmental condition and continuous growing of crops, the root-knot nematode (*Meloidogyne* spp.) has emerged as a major problem, causing enormous yield loss. About 88% yield loss due to root-knot nematode has been observed under protected cultivation. The damage progressively increases if proper sanitation control measures are not followed during the polyhouse cultivation of crops. Such huge losses necessitate the use of management practices against nematode pests in this crop. Looking into the hazards of chemical nematicides to the environment and human health, an urgent need to adopt alternative control and long term integrative approaches for their replacement is felt. The present study was conducted to know integrated management of root-knot nematode (*Meloidogyne incognita*) in cucumber cultivation. The results indicated that removal of previous crop residues with soil solarisation and application of *Purpureocillium lilacinum* @ 2 kg in 1 ton FYM in beds reduced final nematode population as well as number of galls/plant (69.6 %). Subsequently, it increases the cucumber yield to the extent of 20.6% over untreated check under protected cultivation.

PP-11: Management of lentil collar rot with biocontrol agents

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Lentil (*Lens culinaris* L.) is an important Rabi crop of Madhya Pradesh, which is highly susceptible to wilt and root rot diseases resulting huge yield loss. Use of fungicides, cultural and biological control are in some common management practices for this disease. Due to the harmful effect of chemical pesticides on the environment, biological control is emerging as an alternative management option. In an effort to develop eco-friendly management strategy for lentil collar rot the present study was initiated, in which vermi compost (VC) and neem cake (NC) were used as soil amendments with or without *Trichoderma harzianum* in different treatments to evaluate their efficacy in suppressing *Sclerotium rolfsii*. Application of a combination of *T. harzianum* strains as seed treatment @ 4 g kg-1plus soil treatment of neem cake @ 80g/pot at the time of sowing and 30 days after sowing showed minimum collar rot incidence with maximum colonies of *T. harzianum* and reduced population of the pathogen. Maximum yield was found in the treatment having vermi compost and seed treatment, followed by soil treatment. Increasing frequency of application of the *T. harzianum* along with organic amendments increased the growth and yield of lentil crop.

PP-12: *In vitro* evaluation of fungicides on the pathogenic fungi *Fusarium oxysporum* f. sp. *ciceris,* the incitant of Fusarium wilt of chickpea

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Chickpea (*Cicer arietinum* L.) is the world's third most important legume crop, predominantly consumed as a pulse. Fusarium wilt incited by *Fusarium oxysporum* f. sp. *ciceris* is one of the major soil / seed borne disease of chickpea.Four fungicides namely mancozeb 75%WP, azoxystrobin 23%SC, tebuconazole 25.9% EC and captan 50%WP were evaluated for their efficacy against *Fusarium oxysporum* f. sp. *ciceris in vitro* by employing "Poisoned food technique". The results obtained on the fungitoxicity of fungicides *in vitro* differed considerably in their toxicity to mycelial growth of test fungi. The EC50 values of fungicides ranged between 1.57 to 4.79 ppm a.i. among various fungicides, azoxystrobin 23%SC proved to be the most toxic fungicide in inhibiting mycelial growth of the *Fusarium oxysporum* f. sp. *ciceris* with least EC50 value i.e. 1.57 ppm a.i., followed by *tebuconazole* 25.9 % EC in which EC50 value was 4.6 ppm a.i., respectively.

PP-13: Potential impacts of climate change on plant pathogens and plant diseases management

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Human activities have had a major impact on climate and ecosystems, resulting in increased temperature, changes in the quantity and pattern of precipitation, increased CO_2 and ozone levels, drought, etc. Any change in ecosystems can affect plant diseases, because plant disease is the result of interaction between a susceptible plant, a virulent pathogen and the environment. Climate change influences the occurrence, prevalence, and severity of plant diseases. Predicted climatic changes are expected to affect pathogen development and survival rates, and modify host susceptibility, resulting in changes in the impact of diseases on crops. These effects have been predicted to result in shifts in the geographical distribution of pathogens and their hosts, altered crop losses due to disease, and a change in the selection and efficacy of management strategies with regard to timing, preference and efficacy of chemical, physical and biological control measures and their utilization within integrated pest management (IPM) strategies. IPM is an analytical method used to analyze the agro-ecosystem and its different elements in order to optimally manage these elements to control and minimize pests while protecting the environment and the economic health. The prediction and the management of climate change effects on plant health are influenced by interactions with global change drivers. The models of plant disease development can vary under different forms of climate change, requiring different management strategies based on more participatory approaches and multidisciplinary science. All these efforts and integrations will produce effective crop protection strategies using novel technologies as appropriate tools to adapt to altered climatic conditions.

PP-14: Module analysis for fruit drop management of kinnow mandarin (*Citrus reticulata* Blanco) under changing climatic conditions of Western Region of Punjab State

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The agro-ecological conditions of Punjab, western Rajastahan and Haryana are best suited for the production of citrus fruits. Among citrus species, kinnow mandarin (*Citrus deliciosa* x *Citrus nobilis reticulata* Blanco) proved a boon for the farmers due to its higher yield, quality, taste and flavor superior. Due to change in climate conditions cultivation of kinnow mandarin is plagued with various problems, among them physiological and pathological (*Colletotrichum gloeosporioides, Diplodianatalensis*) fruit drop is a major problem and causes13-28 percent fruit yield reduction. Currently, more than 80% of farmers rely only on injudicious use of fungicides at the peak of fruit drop. Efforts were made to evaluate Integrated fruit drop IFDM module and Farmers' Practice (FP) based on the earlier field studies for the management of fruit drop in kinnow mandarin. Farmers participatory field experiments were conducted at farmers filled of Punjab (Fazilka), Rajasthan (Sri Ganganagar) and Haryana (Sirsa) during two consecutive years (2016-2018). Integrated fruit drop management module (IFDM) proved with 70 -80 per cent reduction in fruit drop and 10.5 to 18.4 percent increase in yield, in comparison to farmers practices. This study is designed to educate the kinnow orchardist to adopt the sustainable integrated fruit drop management module

(IFDM) to combat the adverse effect of climate change and increase the production of fruit yield.

PP-15: Nanotechnology in crop improvement

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Nanotechnology is defined by the US Environmental Protection Agency as the science of understanding and control of matter at dimensions of roughly 1–100 nm, where unique physical properties make novel applications possible. NPs can be used as biomarkers or as rapid diagnostic tool for detecting phytopathogens. Nano chips are a type of microarray that contains oligo capture probe through which hybridization can be detected. They are highly sensitive and specific. In Nano-encapsulation of active ingredient of pesticide leads to "controlled release of the active ingredient". Karate® ZEON and Gutbuster are nano pesticides available in market for insect pest control. NPs which are sensitive to temperature, humidity and nutrient variation are sprinkled over field and thus act as sensors for monitoring. There are numerous reports revealing the use of nano-particles in crop improvement. Mostly carbon and metal-oxides based engineered nano-particles have been subject of studies like Nano-particles of TiO2 improved spinach growth by enhancing nitrogen metabolism. Silver NPs display a strong inhibitory activity to microorganisms and has been significantly used for phytopathogens management. Ag NPs inhibited the colonization of *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *E coli*. Ag+ions bind to cysteine-containing proteins on plasma membranes, causing both physiological and biochemical damage. NPs act as carrier in transferring gene into other genome. It has been reported that PAMAM dendrimer acts as a nanocarrier for delivering GFP gene in turf grass. Nano pore sequencing is fastest, cheapest and accurate method of DNA sequencing. It is a label-free and amplification-free single-molecule approach, in which DNA molecules are driven through channels, producing signals that allow researchers to identify the corresponding sequences.

PP-16: Antagonistic activity of volatile compounds producing bacterial endophytes from wheat (*Triticum aestivum*) against *Bipolaris sorokiniana*

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Wheat is the second largest cultivated crop in the world mainly due to its presence in the diets of most nations. Wheat is a major staple food crop being consumed by 30 percent population of the world and is grown in all the continents. The present investigation was carried out at division of Crop Protection, Indian Institute of Wheat and Barley Research, Karnal to exploit diverse endophytic bacteria from 8 recommended wheat varieties. Total 101 endophytic bacteria were isolated (40 from leaf, 30 from stem and 31 from root tissues of wheat) on nutrient agar, Pseudomonas and Actinomycetes selective media. *In vitro* assays revealed that bacterial endophytes could produce volatile organic compounds (VOC) that inhibited mycelia growth of *Bipolaris sorokiniana*. Among all, 8 bacterial endophytes were effective of which HD3272-18 (72.70%), UP2950-7 (50.90%) and WB2-5 (69.10%) were found to be more effective. Based on molecular characterization 3 bacterial endophytes were identified as *Bacillus subtilis* subsp. *subtilis*. (HD3272-18), *Bacillus cereus* (UP2950-7) and *Bacillus subtilis* (WB 2-5).

PP-17: Integrated plant disease management and changing climate

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Threats of changing climate have been well documented across agriculture sector. Effect of changing climate on agriculture or more precisely on insect-pests and diseases of agricultural crops is multi-dimensional. The enormity of this effect could vary with the type of species and their growth patterns. The higher agricultural crop production could be off-set partly or completely by insect-pest and diseases. With the change in the temperature and rainfall pattern, the natural vegetation over a region is facing a new phase of competition for survival. Global rise in temperature and CO_2 due to climate change may modify aggressiveness and fecundity of plant pathogens, increase in host susceptibility and host-pathogen interaction. Climate change would influence the emergence of new disease, biology of plant pathogen, disease development and their management. It is therefore, important to consider all the biotic components under the changing pattern of climate. Crop diversification and use of diverse cultural practices, such as crop rotation, plant residue management, adjusting sowing dates, etc. are effective strategies for crop disease management under changing climate.

PP-18: Efficacy of *Pasteuria penetrans* for the management of root-knot nematode in brinjal

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The efficacy of the obligate bacterial parasite, *Pasteuria penetrans* against the root-knot nematode, *Meloidogyne incognita* infestation was assessed in brinjal. The experiment was laid out in a complete randomised block design with four treatments along with untreated check i.e. *Pasteuria penetrans* @ 1 x 10^3 spores/g soil, *Pasteuria penetrans* @ 1 x 10^4 spores/g soil, *Pseudomonas putida* @ 1 lt. of culture broth (2 day old on NB) and carbofuran @ 1 kg a.i./ha. The observations were recorded on the following parameters- plant height (g), seedling weight (g) per 10seedling, No. of galls/plant per 10 seedlings, No. of eggs perroot and No. of J2/200cc soil. Results indicated that *Pasteuria penetrans* @ 1 x10^4 spores/g and *Pseudomoans putida* were found promising in increasing plant height, fresh seedling weight of brinjal seedling and reduced root-knot nematode reproduction and multiplication. Maximum and significantly higher seedling height (20.4 cm) and fresh seedling weight (50.3 g) were observed in treatment where *P. putida* was applied @ 1 lt. of culture broth (2 day old on NB), which was statistically at par to that *P.penetrans* @ 1x10^4spores/g soil. Minimum numbers of galls (67.0) were observed treatment where carbofuran was applied @ 1kg a.i/ha followed by *P. putida* while number of eggs per root system (3,393.0) and final nematode population (93.3) were observed in *P. penetrans* applied @ 1 x10^4 spores/g soil as soil application.

PP-19: Utilization of diverse resistance genes to fight fast changing wheat rust pathogens

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Yield potential of wheat, a major cereal crop is limited due to various abiotic and biotic stresses. Rust disease of wheat, caused by *Puccinia* spp., is known to cause severe yield loses worldwide. The emergence of new pathotypes of wheat rusts and spread of the pathogens to new habitats due to climate change and human interventions have further intensified the threat. In the last two decades, the stripe rust pathogen has adapted to relatively higher temperature regimes and has spread to wheat-growing areas that were non-conducive for its development. The Noble Laureate NE Borlaug said 'rust never sleeps'and it emphasizes that breeding for disease resistance is a continuous expedition. Resistance to rust diseases is controlled by genes that are effective during all stages (all stage resistance; ASR) and those that express at the post seedling stages (adult plant resistance; APR). Ancestral hybridization events involving only a limited number of founders created a genetic bottleneck which led to a narrow genetic base of the modern wheat germplasm. This narrow genetic diversity of wheat, however, can be compensated by introgression of genetic variability from the landraces, related wild and cultivated species of wheat. More than 250 resistance genes against leaf, stripe and stem rusts have been identified from the primary and secondary gene pools and successfully transferred to cultivated wheat. However, only a handful of these genes have been used in the commercial cultivation due to linkage drag and not enough level of resistance. Wheat breeders have continuously been breeding for rust resistance under changing temperature regimes. The wheat breeding programme at ICAR-IIWBR, Karnal has successfully used Lr24/Sr24, Lr19/Sr25, Yr10, Yr18/Lr34Sr57,Yr5, Yr10, Yr15, Yr24, Yr18/Lr34/Sr57, Yr46/Lr67/Sr55, etc. through precise phenotyping in the field as well as glasshouse and applying marker-assisted selections. A coordinated effort to utilize the genetic diversity for rust resistance in the national wheat breeding programme has the potential to deliver a broad genetic base for developing climate-resilient wheat cultivars.

PP-20: Management of maydis leaf blight of maize caused by *Bipolaris maydis* through biocontrol agents

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Maize (*Zea mays* L.) is one of the most important cereal crops in the world and popularly known as queen of cereals. It is third major crop in India after wheat and rice. About 65 pathogens infect maize and out of these, maydis leaf blight (MLB) caused by *Bipolaris maydis* (Nisikado and Miyake) Shoemaker is considered as one of the most serious disease. The disease is widely distributed in India during Kharif season. MLB appears every year with incidence ranging from 20-85 per cent in Haryana. The disease has the potential to reduce the grain yield upto 41 per cent in susceptible cultivars. Keeping in view of environmental pollution and ecological imbalance caused by the use of chemical fungicides, an effort has been made in the present experiment to control the pathogen by using bio control agents. Five bio-control agents (*Trichoderma harzianum, T. viride, Pseudomonas fluorescens, P.maltophila and Bacillus subtilis*) were evaluated against maydis leaf blight of maize under field conditions during Kharif 2015. Among the various bio control agents tested, *Trichoderma harzianum* was found to be most effective as it showed minimum percent disease intensity and maximum per cent disease control followed by *T. viride*. The bio control agents *Bacillus subtilis* was found least effective with maximum per cent disease intensity and minimum per cent disease control. The disease control by different bio control agents ranged from 23.51 to 40.47 per cent. These finding will be helpful in developing integrated disease management strategies for the control of maydis leaf blight of maize.

PP-21: Management of stem gall of coriander caused by *Protomyces Macrosporus* Unger using different approaches and its effect on disease severity, incidence and yield

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Seed spices play an important role in our national economy because of large domestic consumption and continuously growing demand for export. Coriander production was 861thousand MT from an area of 664 thousand ha with 1.3 MT per ha productivity during 2017-18. Coriander suffers from various diseases, amongst those the stem gall disease caused by *Protomyces macrosporus* is one of the destructive disease. In spite of development of several technologies *viz.,* cultivation practices, high yielding varieties for different qualities and traits, management of pest and diseases, harvesting and post harvesting processing, for boosting coriander production, of yield level is still less in comparison to other countries, due to lack of stem gall resistance variety and climate change which enhanced biotic and abiotic stress. This requires high prioritized research on eco-friendly management aspects like using organic amendments, botanicals, bio control agents with reduced use of pesticides.The aim of this research was to find out cost effective, economical and ecofriendly method to manage stem gall of coriander and to examine the effect of biological control agents, some botanicals and fungicides on yield attributes, and the incidence and severity of stem gall disease of coriander caused by *P. macrosporus* under field conditions. Therefore, this experiment was carried out to examine the effect of some biocontrol agents (*Trichoderma viride, T.har-zianum, Pseudomonas fluorescens*), botanicals (neem, eucalyptus, datura, aloevera and parthenium) and fungicides on yield, disease severity and disease incidence of stem gall of coriander (*Coriandrum sativum* L.) caused by *P. macrosporus* Unger. Maximum stem gall incidence and disease severity was recorded in control i.e. 18.44% and 16.66%. The results revealed that, application of biocontrol agents, botanicals or fungicides caused significant reduction in stem gall incidence and severity as compared to control. Among the tested biocontrol agents, *Pseduomanas fluorescens* was found most effective to inhibit the growth of pathogen whereas amongst botanical leaf extract datura was found to be most effective and in case of fungicides Ridomil MZ and Blitox 50 WP were found most effective and significantly superior among the treatments with 100 per cent growth inhibition of the pathogen at 0.2 per cent concentration under in vitro conditions. Under field conditions, seed treatment and foliar spray of Ridomil MZ and Blitox 50 WP at 0.2 per cent was found most effective to manage the disease severity and incidence, resulting in comparative higher yield i.e. 1493.06Kg/ha and 1284.72kg/ha, respectively.

PP-22: Management of wheat diseases through deployment of resistant varieties in North-Western Himalaya

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Wheat is an important winter cereal of North-Western Himalaya, occupying 1.39 million hectare area in its hill states viz., Jammu & Kashmir, Himachal Pradesh, Uttarakhand and hilly regions of West Bengal and North Eastern states. Among rust diseases, yellow and brown rusts are the foremost pathogens, capable of causing huge losses to wheat crop grown in this region. Incidence of yellow rust has been growing a major concern not only to the wheat crop grown in the Himalayan region but also to the crop grown in North-Western Plains, because it receives primary inoculum of yellow rust from off-season crop and volunteer plants grown in different altitudes of Himalaya. Powdery mildew and hill bunt are also important diseases of this region causing substantial losses to the wheat crop. The rust disease can be controlled through the use of fungicides but it increases production costs as well as health hazards by polluting the environment. Deployment and saturation of Northern hills with high yielding rust resistant wheat varieties, is an environment safe and viable solution to tackle the rust menace. Keeping in view, wheat varieties viz., HS507, HS542 and HS562 were released and notified by CVRC for commercial cultivation in the hill states. HS507 is suitable for timely sown production conditions of Northern Hills Zone (NHZ). It is giving mean grain yield of 2.66 tons/ha under rainfed and 4.68t/ha under irrigated production conditions with 5.9% and 9.3% grain yield advantage, respectively over best check VL907. It also possesses brown and yellow rust resistance with Average Coefficient of Infection=0.9 and ACI=1.1, respectively to contain the rusts in the Himalayas. Besides, HS507 has very good chapatti and bread making qualities. HS542 is suitable for early sown rainfed production conditions of NHZ. It is giving mean grain yield of 3.3 t/ha under rainfed conditions with 6.1% grain yield advantage over the best check VL829. It possesses brown and yellow rust resistance with ACI=2.0 and ACI=7.1, respectively with diverse combination of Yr2+, Lr13+10+, Sr5+8a+9b+11+ genes. HS562 is suitable for timely sown production conditions of NHZ. It is giving mean grain yield of 3.6 t/ha under rainfed and 5.27t/ha under irrigated production conditions. HS562 possess field resistance to stripe rust (ACI=6.0). Breeder seed of these wheat varieties is made available to the seed producing agencies. About 50.5 tons of breeder seed of wheat varieties HS507, HS542 and HS562 has been supplied to the seed producing agencies for producing foundation and then certified seed for its distribution among the farmers of this region.

PP-23: Enhancing ground nut yields by managing soil borne diseases through seed treatment: A technology assessment at farmers' fields

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Soil borne diseases *viz.,* stem rot and collar rot are potential threat to groundnut cultivation. Although some plant diseases may be managed through resistant varieties and alteration of cultural practices, some diseases are only managed effectively with the application of suitable fungicides. The fungicides viz., hexaconazole, tebuconazole, propiconazole, difenconazole, vitavax, carbendazim along with captan and mancozeb and various combinations were applied as seed treatment at recommended doses. In this context, we evaluated seed dressing fungicides and their combinations for management of major soil borne diseases of groundnut during rabi 2017 and 2018 at Krishi Vigyan Kendra, Amadalavalasa. The experiment was laid out at Krishi Vigyan Kendra, Amadalavalasa adopted villages with three treatments and five replications. The treatments include: T1: Seed treatment with Tebuconazole@ 1 gm/kg + soil application of *Trichoderma viridae* 2 kg/acre + fungicidal spray with hexaconozole 2 ml/lit; T2: Seed treatment with mancozeb @ 3 gm/kg + soil application of *Trichoderma viridae* 2 kg/acre;T3: Farmers practice : No seed treatment. The yield data of groundnut revealed that maximum pod yield (25.5 q/ha) was obtained with application of Seed treatment with Tebuconazole@ 1 gm/kg + soil application of *Trichoderma viridae* 2 kg/acre + fungicidal spray with hexaconozole 2 ml/lit followed by Seed treatment with mancozeb @ 3 gm/kg + soil application of Trichoderma viridae 2 kg/acre (22.8q/ha). An increase of 24.5 % in yield was observed in the demo plot over farmers practice. In case of demo plots only 2% disease infected plants were observed compared to the 28 % disease infected plants in farmers practice. Further 3.51: 1 B:C ratio was recorded in demo plot against 3.17:1 in farmers practice.

PP-24: Efficacy of organic amendments against *Colletotrichum truncatum* causing anthracnose of soybean

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Eight sources of organic matter *viz.,* tea waste, poultry manure, wheat straw, cow dung, sugarcane bagasse, neem cake, mustard leaves and saw dust were evaluated under greenhouse conditions for their effectiveness to manage anthracnose of soybean caused by *C. truncatum.* All eight treatments were significantly effective in minimising the diseases severity out of which Neem cake was found most effective and gave highest seed germination (82.20%), vigour index (3504) and nodulation (26.66), and showed least disease severity (13.85%). Whereas minimum pre-emergence mortality was in tea waste with 12.99% ,while the post emergence mortality was found least in Neem cake with 4.60%. The current finding concentrates on the eco-friendly alternatives to manage anthracnose of soybean in the field over the conventional chemical pesticides.

PP-25: Chemical management of chilli mosaic disease under field conditions

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Chilli (*Capsicum annum* L.) is one of the world's most popular vegetable consumed as fresh or processed and used mainly as a spice and condiment. Viral diseases are one of the most severe constraints in the production of the crop. Among viral diseases, chilli mosaic disease is the most important one. Effect of various chemicals *viz.* imidacloprid, malathion, demeton-o-methyl, dimethoate, acetamiprid and botanical insecticides (neem oil) was studied against chilli mosaic disease under field conditions at Skuast Chatha research farm in the susceptible variety Pusa Jwala. The results revealed that foliar application of imidacloprid was found most effective with minimum mean disease intensity of 9.01 per cent followed by dimethoate, acetamiprid, seedling treatment of imidacloprid, demeton-o-methyl, and seed treatment with imidacloprid, malathion and neem oil.

PP-26: Antifungal activity of important botanicals

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The medicinal plants are rich source of natural chemicals as they possess a diverse range of secondary metabolities that are used for producing new antibiotics and different types of medicines which protect the human as well as plants against various diseases. The extracts of many higher plants have been reported to exhibit antibacterial, antifungal and insecticidal properties under laboratory trails. Plant diseases, caused by bacteria, fungi, virus and insect, reduce the productivity, yield and leading to huge loss. Among the different causal organisms, fungi caused the greatest impact to plants with regard to diseases and crop production losses. The phytopathogenic fungi are generally managed by fungicides that are hazardous to environment as well as human health therefore, there is a need of new antibiotics and chemotherapeutic agents that are highly effective, possess low toxicity, and have a minor environmental impact. The use of plant extracts to control various phytopathogens came into existence as the plant extracts are safe, cheap, ecofriendly and produce various secondary metabolites which perform defensive role in plants. In the present investigation, the methanol and aqueous extracts of leaves as well as rhizome of three different medicinal plants *viz. Azadirachta indica, Lantana camara* and *Curcuma longa* were used against five fungal phytopathogens *viz. Curvularia lunata, Bipolaris specifera, Rhizoctonia solani, Macrophomina phaseolina* and *Alternaria alternata* by agar well diffusion method. Methanolic extracts of plant parts showed higher antifungal activity against the phytopathogens than the aqueous extract. *C. longa* rhizome extract showed antifungal activity against all the plant pathogens and maximum zone of inhibition was showed at conc. 200µl/ml against *R. solani, B. specifera, C. lunata* and *M. phaseolina* (11mm, 7.66mm, 8mm and 7mm respectively), followed by leaf extract of *C. longa* and *A. indica.* The minimum activity was showed by *L. camara*.

PP-27: Influence of mycorrhizal fungi (*Glomus mosseae*) on damping off in chilli nursery

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An experiment was conducted in department of Plant Pathology, CCSHAU Hisar to evaluate the effect of different doses of mycorrhizal (*Glomus mosseae*) fungi i.e. 300, 400 and 500 sporocarp/kg soil on damping off of chilli. The culture of mycorrhizal fungi was maintained in the pots. The sporocaps were separated by Wet sieving technique. The counted spores were put in the nursery pots. The plot size of 1 x 1 mt. and three replications of each treatment were maintained. From the data it is clear that as the dose of mycorrhizal fungi increased the damping off decreased (22.50 to 11.50 percent) as compared to control. The mycorrhizal colonization and sporocarp number also increased as the dose of mycorrhiza increases.

PP-28: Integrated management of Fusarium wilt of clusterbean

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Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] commonly known as guar belongs to family Leguminosae or Fabaceae and use for cattle feed or otherwise fodder of the livestock. The present experiment was carried out during Kharif 2018-19 with four different treatments of integrated wilt management practices i.e. Check, Carbendazim (seed treatment) + *Trichoderma harzianum* (Soil application), *T. harzianum* (SA) + Neem extract (ST), Carbendazim + Neem extract (ST). The experiment was carried out in cage house condition with five replications in Randomized Block Design. All the Integrated disease management practices for wilt in guar resulted in significantly low incidence and maximized seed yield over the check. Result revealed that Carbendazim (ST) + *T. harzianum* (SA) showed lowest wilt incidence with 5.71 and 14.28 per cent at 40 and 60 DAS, respectively, followed by Carbendazim + Neem extract (ST) with 8.57 and 17.14 per cent; however the highest wilt incidence (11.42 and 20.00 per cent) with lowest per cent disease control (60.03 and 66.67 per cent) at 40 and 60 DAS was observed in seed treatment with *T. harzianum* + Neem extract; while the wilt incidence in Check was 28.57 and 60.00 per cent at 40 and 60 DAS, respectively.

PP-29: Evaluation of cow urine based formulations of plant extracts against wheat powdery mildew caused by *Blumeria graminis* f.sp. *tritici*

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Powdery mildew (PM) of wheat caused by *Blumeria graminis* f.sp. *tritici* (Bgt) is a serious disease causing considerable losses throughout the world. The disease has become a potential threat in North Western Plain Zone (NWPZ) and North Hill Zone (NHZ) of India including Himachal Pradesh. The disease can be successfully managed by cultivation of resistant varieties. However, all recommended varieties grown in NWPZ and NHZ are susceptible and PM can be managed by fungicides. However, the global awareness regarding the soil, water and environmental pollution due to excessive use of fungicides, and the political and administrative will of the government, to decide Himachal Pradesh will be converted into an organic and natural farming state. Under these situations, suitable alternatives are required for management of PM. In this context, cow urine based plant extracts were evaluated for the management of *B. graminis* under *in vitro,* polyhouse and field conditions. Under *in vitro* conditions, *Azadirachta indica* (20%) exhibited the least conidial germination (20.82%), followed by *Calotropis gigantia* (24.08%) and *Justicia adhatoda* (24.58%) with corresponding conidial inhibition of 82.57, 77.06 and 76.15 per cent, respectively. In potted experiment, *A. indica* sprayed @ 20 per cent was highly effective both in preventive and curative treatment resulting in the least disease severity i.e. 15.65 per cent with disease control of 88.72 per cent in preventive treatment, whereas, in curative treatment the disease severity was 15.92 per cent with disease control of 88.21 per cent. In the field experiment, the least plant disease index (PDI) of 19.05 per cent with corresponding disease control of 85.28 per cent, was recorded in plots sprayed with leaf extracts (15%) of *C. gigantia* followed by *J.adhatoda* (21.39%) and A. indica (25.74%) with corresponding disease control of 81.73 and 74.11 per cent, respectively. The highest grain yield of 34.63 q/ha was recorded in plots sprayed with *C. gigantia* followed by *J. adhatoda* (32.93 q/ha) and *A. indica* (32.20 q/ha). It is evident from the studies that cow urine based plantextracts were highly effective in the management of wheat powdery mildew.

PP-30: A new promising sugarcane clone CoH 13263 for cultivation in Haryana under mid late group

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A new promising clone CoH 13263 was developed from Co 89003 GC at CCS HAU, Regional Research Station, Uchani, Karnal. It was tested against the popular standards Co 05011, CoPant 97222, CoS 767 and CoS 8436 for its performance under AICRP yield trials from 2017-18 to 2018-19 in two plant and one ratoon crops. The clone CoH 13263 recorded an average yield of 89.06t/ha and commercial cane sugar yield of 12.08t/ha that was found superior to the standard varieties Co 05011(83.54/10.89 t/ha), CoPant 97222(77.57/9.28 t/ha), CoS 767(81.76/10.13 t/ha) and CoS 8436(71.39/9.32 t/ha). The clone CoH 13263 has recorded higher or at par with standards Co 05011, CoPant 97222, CoS 767 and CoS 8436 tested under two plant and one ratoon crops for no. of millable canes, cane diameter, cane girth and single cane weight. The clone CoH 13263 recorded mean sucrose of 19.37% at harvest stage which was numerically higher than standard varieties Co 05011(18.65%), CoPant 97222(17.08%), CoS 767(17.75%) and CoS 8436(18.84%). The mid late CoH 13263 had shown resistant (R) to moderately resistant (MR) reactions against red rot pathotypes cf 08 and cf 09 under artificial inoculation by both plug as well as nodal method during three consecutive years of testing in Haryana. The reaction to yellow leaf disease was also resistant (R) to moderately resistant (MR) for mid late clone CoH 13263. The clone CoH 13263 is a medium thick cane with erect growing habit and non lodging nature. This clone can be easily distinguished by yellow green cane with semi drooping leaves, deltoid auricle and bobbin shaped internode.

PP-31: Efficient callus induction and regeneration using immature inflorescence to develop somaclones in wheat

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This study was conducted using six different wheat genotypes (WH 542, WH 147, Raj 3765, UP 2338, DI 9 and PBW 343) by using immature inflorescence as explants. In this study, the effect of EMS (Ethyl Methane Sulphonate) treatment, genotypes and their interaction on callus induction and plant regeneration was observed. Immature inflorescences derived from non treated plants and from EMS treated (0.5%, 4hr) wheat seeds were cultured on MS medium supplemented with 2.5mg/l 2,4-D + 0.2mg/l NAA for callusing in six different genotypes. An average of 77.03% explants (non treated) and 79.59% (EMS treated) explants could induce callus and the most responsive genotype was WH 147(96.9%) followed by PBW 343(85.1%) in non treated while WH 542 (90.7%) followed by WH 147(88.3%) in EMS treated ones. Such inflorescence derived callus after sub culturing on same medium for 5-6 months were transferred to regeneration medium (MS medium +0.5mg/l 2, 4D+0.2mg/l NAA). Shoot regeneration occurred in about 10 days from non treated (79.59%) while it took 6 days from EMS treated calli (71.03%). PBW 343 showed highest regeneration for both non treated (93.2%) and EMS treated (86.1%) explants derived calli. Survival was 81.0% when regenerants were transferred to potted soil. The EMS treated regenerated plants exhibited physical variation also. This variation in tissue culture derived plants is somaclonal variation which also exhibit disease resistance under field condition when tested.

PP-32: Biological management of corm rot of saffron

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Saffron (*Crocus sativus* L.) is considered as one of the most expensive spices due to its therapeutic and aromatic value. In this study, corm rot was recorded as a major biotic stress, occurred in different saffron growing areas of Kishtwar district of Jammu province, with maximum disease incidence of 59.33 per cent and severity 35.00 per cent from Lower Poochal. Different myco-pathogens viz., *Fusarium oxysporum* f.sp. *gladioli, Fusarium oxysporum, Rhizoctonia* sp., *Aspergillus* sp., *Penicillium* sp. and *Macrophomina* sp., were isolated from the diseased corms of saffron having per cent occurrence of 34.67, 20.33, 15.67, 15.00, 11.67 and 2.67 per cent, respectively. Under *in vitro* conditions, *Trichoderma viride* and *T. Harzianum* significantly reduced the mycelial growth of the *Fusarium oxysporum* f.sp. *gladioli* with the inhibition of 77.60 and 76.60 per cent, respectively, using dual culture assay as compared to control on potato dextrose agar. Under field conditions, dipping of saffron corm in 0.2% carbendazim @ 50% WP exhibited maximum reduction in the disease incidence (70.33%), followed by corm treatment with *T.viride* and *T. harzianum* (1×10^7cfu/ml), which was statistically at par with soilsolarization having reduction in incidence of corm rot of saffron by 61.55, 57.15, 59.90 per cent respectively, over control. Population density of *F. oxysporum* f.sp. *gladioli* was significantly reduced (72.50%) by soil solarisation treatment after 90 days of sowing of saffron as compared to its population before planting of corms. In case of growth promotion traits viz., emergence of sprouting, flowering and number of flowers in saffron, corm treatment with *Bacillus subtilis* @ $1\text{x}10^9$cfu/ml significantly reduced the number of days of sprouting and flower emergence along with increase in number of flowers (23 & 74 DAS and 3, respectively) as compared to control (31 & 86 DAS and 1, respectively).

PP-33: Plant diseases: A threat to global food security

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Plant pathogens are estimated to cause around 12.5% of global crop loss, threatening many commercially and socially valuable crops like wheat, rice, and coffee. The pathogens reduce the yield, crop quality, kill their host, reduce food and marketing, affecting trade (import and export) and ultimately leading to scarcity of food. This problem is serious threat in the tropical and subtropical areas as the environment is favourable for the pathogens to grow. Global movements of people and goods also increase the risk of diseases spreading to new regions. There are different crop protection strategies that aim at limiting the impact of pathogen through a number of approaches like eradication, treatment, selective breeding and genetic engineering. Climate change adds an additional layer of risk to global crop production. However, the system as a whole remains vulnerable to these threats, and if we limit the impact of plant disease especially with the uncertainty of climate change we need to look towards making our farming system more resilient by diversifying our agriculture system, by introducing tolerant varieties of crop, crop rotation, improving crop microclimate. The diversification will not just benefit in limiting the plant diseases, but will likely make agriculture more robust to other abiotic and biotic threats and will lead to global food security.

PP-34: Effect of bio-agents, neem leaf extract and fungicides against Alternaria leaf blight of wheat (*Triticum aestivum* L.)

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The experiment was conducted under in vitro and field conditions to observe the effect of bio-agents, botanical and fungicides against *Alternaria triticina.* Eight treatments were taken up with three replications each and data collected was analyzed using CRD. Maximum inhibition per cent mycelial growth was observed in propiconazole (89.72%), of hexaconazole (88.44%), followed by *Trichoderma harzianum* (85.50), *Trichoderma viride* (83.30%), *Pseudomonas fluorescens* (80.73%) and neem leaf extract (73.57%) as compared to control (0). An experiment was conducted under field condition to observe the effect of bio-agent, neem leaf extract and fungicides against *Alternaria triticina.* Eight treatments were taken up to with three replications each and data collected was analysed using RBD. Maximum plant height (cm) was observed in *T. viride* (78.82cm) followed by *T. harzianum* (78.27%) as compared to control (70.04%). *T.viride* was significantly superior as compared to other treatments. Minimum disease intensity per cent and production of wheat was recorded in treatment propiconazole @0.1% (18.24% and 37.00q/ha, respectively) followed by *Pseudomonas fluorescens* @0.5% (20.51% and 30.44 q/ha), as compared to control (43.18% and 20.41q/ha). Propiconazole was significantly superior as compared to other treatments.

PP-35: Nanotechnology: Potential and use in plant disease management

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Nanotechnology is the engineering of functional systems at the molecular scale, deals with particles sizes between 1 and 100 nanometre at least one dimension. Particle size reduced to nanometre length scale exhibit high surface area to volume size ratio, thus showing unusual properties, making them enable for systematic applications in engineering, biomedical, agricultural and allied sectors. “Nanotechnology” is a brain child of late Richard Feynman, Nobel laureate in Physics in the year 1965. Nanotechnology for the control of plant diseases is a promising technique in plant pathology either by providing controlled delivery of functional molecules or as diagnostic tool for disease detection, an important step in plant disease treatment. Various nanoparticles like biopolymer nanoparticles, silver, chitosan, carbon nanotubes, alumina silicate, etc. are employed in plant disease management. Most importantly, biological synthesis of silver nanoparticles (AgNPs) has offered a consistent, nontoxic and ecofriendly approach for plant disease management due to their strong antimicrobial properties. There is big future waiting for the tiny technology. It has potential to change the course of time. As the size decreases computing speed and computing power increase, materials will be stronger, and small doses of medicines will cure diseases rapidly and more efficiently than ever.

PP-36: Eco-friendly management of Powdery mildew of green gram (*Vigan radiate* L.)

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Present study was conducted during consecutive Kharif season of 2014-2015.An experiment was conducted to evaluate the efficacy of selected fungicide, bio-agents, botanicals against powdery mildew (*Erysiphe polygoni*). To manage the disease an investigation was carried out in the Division of Plant Pathology, SHIATS-DU-Allahabad to evaluate the efficacy of bio-agents *viz., Pseudomonas fluorescens* @2%, *Trichoderma viride*@ 2.5%, *Trichoderma harzianum* @ 2.5%, plant extracts *viz.,* neem leaf extract @10%, garlic clove extract @10% and fungicide *viz.,* carbendazim @0.1 against powdery mildew (*Erysiphe polygoni*). *In-situ* (field) experiment was carried out in randomized block design with seven treatments and three replications. *T. viride* @2.5% was found to be most effective treatment and recorded minimum disease intensity (15.98%) followed by Pseudomonas fluorescens @ 2%(18.04%), *T. harzianum* @2.5% (20.26%), neem leaf extract @10% (21.55%), garlic clove extract @10% (22.87%) and fungicide *viz.,* Carbendazim @0.1% (14.27%). Use of *T. viride* @2.5% (65.99cm) recorded maximum plant height (42.62cm and 65.99cm at 45 and 75 DAS, respectively). Maximum number of pods recorded in *T. viride* (13.30 and 14.27, respectively) followed by P.fluorescens (13.00%,14.07%,respectively) as compared to control which recorded minimum number of pods per plant (8.50 and 9.60, respectively). The highest seed weight (g/plot) was recorded in *T. viride* (37.95g) followed by *P. fluorescens* (37.47g) as compared to control.

PP-37: Shiitake mushroom-A macrofungus with medicinal value

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Shiitake mushroom (*Lentinula edodes*) is the first medicinal macrofungus to enter the realm of modern biotechnology. It is the second most popular edible mushroom in the global market which is attributed not only to its nutritional value but also to possible potential for therapeutic applications. *Lentinus edodes* is used as medicine for diseases involving depressed immune function (including AIDS), cancer, environmental allergies, fungal infection, frequent flu and colds, bronchial inflammation, heart disease, hyperlipidemia (including high blood cholesterol), hypertension, infectious disease, diabetes, hepatitis and regulating urinary inconsistencies. It is the source of several well-studied preparations with proven pharmacological properties, especially the polysaccharide lentinan, eritadenine, shiitake mushroom mycelium, and culture media extracts (LEM, LAP and KS-2). *Antibiotic* Shiitake mushroom might be used directly in enhancement of antioxidant defenses through dietary supplementation to reduce the level of oxidative stress they have been related to significant antioxidant properties due to their bioactive compounds, such as polyphenols, polysaccharides, vitamins, carotenoids and minerals. Anti-carcinogenic and antiviral compounds have been isolated intracellularly (fruiting body and mycelia) and extracellularly (culture media). The potential of this macrofungus is unquestionable in the most important areas of applied biotechnology.

PP-38: Management of sheath rot disease of paddy incited by *Sarocladium oryzae*

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Rice (*Oryza sativa* L.) is the one of the major crops grown around world. Sheath rot caused by *Sarocladium oryzae*, is an important seed-borne fungal disease of paddy which is becoming a major concern to the rice growing farmers in our country. In bio-assay study, different fungicides *viz.,* Carbendazim 50% WP (Bengard), Tebuconazole 50% + Trifloxystrobin 25% (Nativo), Carbendazim 12% + Mancozeb 63% WP (Saaf), Hexaconazole 5% SC (Contaf plus), Tebuconazole 25.9% EC (Folicur), Mancozeb 75% (Tata M-45), Metalaxyl 8% + Mancozeb 64% WP (Matco), Propiconazole 25% EC (Zerox) and Propineb 70% WP (Antracol) were tested against *Sarocladium oryzae* at 25, 50, 75 and 100 ppm using poisoned food technique under laboratory conditions. After 8 days of incubation, Bengard, Nativo and Folicur (all at 100 ppm conc.) were most effective fungicides giving 100%, 91.34% and 90.95% control of this pathogen, respectively whereas Matco (at 25ppm) caused minimum inhibition (22.05 %) in radial growth. The field experiments were conducted at ICAR-IARI, RS, Karnal during Kharif 2016, 2017 and 2018 to find out suitable management strategy to control this potential threat to rice production. Different management options were evaluated against *Sarocladium oryzae.* Among the treatments assessed, seed treatment with Carbendazim 12%+Mancozeb 63% (Saaf) @ 2.5 g/kg seed + seedling dip in Streptocycline 200 ppm and one foliar spray with Tebuconazole 50% + Trifloxystrobin 25% (Nativo) @ 1.0g/l water, gave minimum incidence (4.34%) of sheath rot disease as against control (27.78%).

PP-39: Effect of fertilizers on larval emergence from cyst of *Heterodera avenae*

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Experiments were conducted in laboratory and pot conditions to determine the effects of Urea, Di-ammonium phosphate (DAP), Single super phosphate (SSP), Muriate of potash (MOP) and Zinc sulphate (ZS) on larval emergence of *Heterodera avenae* from cysts. Two concentrations of each fertilizer (urea=80, 160; DAP=65, 130; SSP=187, 375; MOP=50, 100; ZS=60, 120 ppm) with water as control were taken as treatments for lab study. Ten cysts and 5 ml of each solution were taken in 5 cm diameter Petri plates. Observations were recorded at weekly intervals upto six weeks. Urea, DAP, SSP and MOP inhibited larval emergence from cysts. Total larval emergence was found minimum (136) in higher dose of urea and maximum (866) in ZS. Total larval emergence after six weeks in control was 642. Maximum larval emergence in all the treatments was recorded in fourth week. In pot experiment, two dosages of urea (81, 163 mg/kg soil) and single dose of other fertilizers (SSP=187; MOP=50; ZS=60 mg/kg soil) were applied in *H. avenae*-infested soil sown with wheat variety WH-1105. Observations on juveniles in wheat roots, soil and left over cyst content were recorded 40 days after sowing. Among all the fertilizers, minimum number of nematodes in soil and roots (140) were found at higher dose of urea. Maximum nematode populations (289) in root and soil were recorded in ZS although it was less than water (346) but higher than other fertilizer treatments. ZS stimulated hatching in laboratory but not in pots.

PP-40: Endophytes mediated disease resistance in Zea mays: A potential strategy for bio intensive management of soil borne diseases

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The endosymbiotic microorganisms are of common occurrence in plants and colonize inter and intracellular spaces of plant compartments without causing disease or significant morphological changes in plants. Endophytic bacterial community is influenced by plant genotype, abiotic and biotic factors (environment conditions, microbe–microbe interactions and plant – microbe interactions) and agricultural practices, such as soil tillage, irrigation, use of pesticides and fertilizers. Therefore, for sustainable agriculture with promising yields choice of agricultural practices that maintain natural diversity of plant endophytic bacteria is very crucial. Endophytic bacteria induce growth promoting activity, modulation of plant metabolism and phytohormone signaling that helps in adaptation to environmental abiotic or biotic stress. Thus use of endophytic bacteria in agricultural applications can potentially ensure improved crop performance under cold, draught or biotic soil stress conditions and enhance disease resistance. The bacterial strain *Bacillus subtilis* DZSY21 isolated from the leaves of *Eucommia ulmoides* oliver. was labeled by antibiotic marker and found to effectively colonize the leaves of maize plant. Volatile organic compounds (VOCs) released by soil microorganisms influence plant growth and resistance against pathogens. The bacterial VOC, 2, 3-butanediol (2,3-BD) and promotes plant growth, exerts pathogen and herbivore resistance, and the attraction of natural enemies (parasitoids) in maize as observed by colonization of maize seedlings by *Enterobacter aerogenes,* an endophytic bacterium which renders maize plants more resistant against the Northern corn leaf blight fungus *Setosphaeria turcica*, however, *E. aerogenes* treated plants show susceptibility to caterpillar *Spodoptera littoralis*. Fungal endophytes also have potential in disease management due to commercially valued secondary metabolites. They inhibit plant pathogen mainly by inducing phytoalexins production and ecological occupation. There are four groups of phylogenetically distinct endophytes: (1) Rhizobiaceae bacteria; (2) plant-obligate arbuscular mycorrhizal fungi (AMF); (3) selected endophytic strains of fungi in the genus *Trichoderma;* and (4) fungi in the Sebicales order, specifically *Piriformospora indica* which induce gene expression that produces proteins which detoxify reactive oxygen species (ROS). Management strategies involving endophytic symbiosis can help achieve sustainability in agriculture in an eco-friendly manner by reducing excessive fungicide use. Development of endophytes-based bio-formulations can be effectively applied on seeds or aerial parts and once the microbe is inside the plant tissue, it can regulate the host metabolism directly transferring the benefits to the host in a closed-circuit system with no leakage of metabolites. However, for commercial application, an understanding of the (i) genetic and molecular basis of plant-endophytes interactions, (ii) strategies to establish symbiotic association between endophyte and host plant, and (iii) mode of transmission of endophytes could be of interest.

PP-41: Prospects of entomopathogenic nematodes in the management of insect-pests of crops

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In the past few years, there has been an intensive worldwide search for novel bio-control agents, and researchers have gained advances or breakthroughs in this field by the proper formulation and commercialization of some strains of bio-control agents. Among these, nematodes belonging to the families Steinernematidae and Heterorhabditidae drew the attention of research practitioners and growers, as these nematodes have a short life cycle and a wide insect host range, as well as the ability to persist under unfavourable conditions and environmental extremes. These beneficial nematodes are called entomopathogenic nematodes (EPNs), which are obligate parasites of insects and kill their hosts with the aid of symbiotic bacteria (*Xenorhabdus* or *Photorhabdus*) carried in their alimentary canal. Most of the bio-pesticides require days or weeks to kill the insect pest but EPNs kill the insect within 24-48 hrs. EPNs are biological control agents for the next generation due to their variety of habitats. EPNs are used successfully to control a variety of agricultural and horticultural insect pests in different countries. Moreover, no difficulties to apply EPNs as they are easily sprayed using standard equipment and can be combined with almost all chemical control compounds. Several workers have used EPNs against cutworms, stem borers, white grubs and other insect pests in laboratory and field conditions, and have found EPNs compatible with existing integrated pest management (IPM) programmes.