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IPS Central Zone Meet and DSPP National Conference
on

Recent Advances in Plant Pathology and Innovative Approaches in Plant Disease Management (RAPPID)

ABSTRACTS

12-13th December, 2024

Organized by

Indian Phytopathological Society-Central Zone
Deccan Society of Plant Pathologists (DSPP), Hyderabad - 500 030.

Venue

Professor Jayashankar Telangana Agricultural University,
Hyderabad - 500 030, Telangana, India.

IPS Central Zone Meet and DSPP National Conference
on
Recent Advances in Plant Pathology and Innovative Approaches in Plant Disease Management (RAPPID)
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MESSAGE

With great pleasure I heartily congratulate the Deccan Society of Plant Pathologists, Hyderabad for organizing the Indian Phytopathological Society Central Zone Meet and the National Conference 2024 on an important theme, "Recent Advances in Plant Pathology and Innovative Approaches in Plant Disease Management" at Professor Jayashankar Telangana Agricultural University (PJTAU), Hyderabad, Telangana during 12-13th, December 2024 and extend my greetings to all the delegates.

This programme represents a significant milestone in our collective journey towards enhancing agricultural productivity and food security in India through the modern advancements in Plant Pathology and innovative disease management strategies. Under the climate change scenario, the challenges posed by plant pathogens are ever-evolving, necessitating a proactive approach that combines traditional knowledge with cutting edge research. This Conference serves as an important platform for subject experts, researchers and practitioners to exchange their knowledge, share insights, foster collaboration and explore innovative solutions to combat emerging plant diseases effectively.

I am confident that the deliberations of this conference will focus on creating a roadmap for identification of core research areas in the field of Plant Pathology, finding solutions to major disease problems, shaping future policies and practices that prioritize plant health.

I wish this National Conference a grand success.

T Nageswara Rao

(TUMMALA NAGESWARA RAO)

भा.कृ.अनु.प.- केन्द्रीय नीबूवर्गीय फल अनुसंधान संस्थान
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Dr. Dilip Ghosh
DIRECTOR

MESSAGE

With great pleasure and pride, I extend my heartfelt congratulations to the Indian Phytopathological Society-Central Zone and the Deccan Society of Plant Pathologists (DSPP), Hyderabad, for organizing the IPS Central Zone Meet and DSPP National Conference on *"Recent Advances in Plant Pathologyand Innovative Approaches in Plant Disease Management" (RAPPID),* scheduled to be held at the University Auditorium, Professor Jayashankar Telangana Agricultural University on 12-13 December, 2024.

This conference comes at a crucial time when agriculture, both in India and globally, is facing unprecedented challenges due to climate change, resource limitations, and the need for sustainable practices. The conference aims to bring together experts, researchers, and practitioners to share knowledge and explore cutting-edge solutions to ensure climate-resilient agriculture. The focus on innovative technologies and plant health management strategies is particularly relevant in today's context that will have immense agricultural potential. The exchange of ideas and research findings during this conference will contribute to strengthening our efforts toward achieving sustainable agricultural practices, which will benefit not only the farming community but also the nation's food security.

I commend the organizing committee for their dedication and effort in bringing together such a distinguished group of experts and participants. I am confident that this conference will serve as a platform for fruitful discussions, collaborative research, and the development of strategies that will address current and future challenges in agriculture.

I wish all the participants a successful and enriching conference.

(Dilip Ghosh)
President, Indian Phytopathological Society, New Delhi
&
Director, ICAR-Central Citrus Research Institute, Nagpur

Date: 04th November, 2024

PROFESSOR JAYASHANKAR TELANGANA AGRICULTURAL UNIVERSITY
(Formerly Acharya N.G. Ranga Agricultural University)
Administrative Office, Rajendranagar, Hyderabad-500 030, Telangana, India

Prof.Aldas Janaiah
Ph.D. PDF (IRRI, The Philippines)
Vice-Chancellor

Message - Hon'ble Vice Chancellor

It is a great pleasure to welcome all delegates to the IPS Central Zone meet and the national conference on "Recent Advances in Plant Pathology and Innovative Approaches in Plant Disease Management." At Professor Jayashankar Telangana Agricultural University, our goal is to strengthen the visibility of our institution as a leader in agricultural research, education, and extension. This conference serves as a vital platform to showcase our dedication to these objectives and to foster meaningful interactions within the scientific community.

Plant pathology plays a critical role in protecting crop health and ensuring food security. With challenges from climate change and evolving pathogens, advancing our understanding and developing innovative disease management strategies is essential. This gathering of experts, researchers, students, and industry professionals embodies our commitment to knowledge-sharing and collaborative solutions

As we move forward, let us continue to place PJTAU at the forefront of agricultural science, enhancing our contributions to sustainable farming and resilient food systems. I am confident that the discussions and insights generated here will further our collective mission and bring lasting benefits to the growth and development of agriculture sector.

I extend my best wishes for a successful organization of the conference and look forward to witness the impactful outcome to address the problems in the context of climate change.

With warm regards

(Pros. Aldas Janaiah)

Dr. R. Sarada Jayalakshmi Devi
Vice-Chancellor

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Message

Agricultural sector has transformed from subsistence activity to sophisticated agri-science and agribusiness connecting all the stakeholders in the agri-value chain nationally and globally. Science of Plant Pathology, an important core area of Agriculture, deals with the crop health starting prior to sowing concerning seed health till harvest and post-harvest care. Commercialization of agriculture, change in food consumption patterns, growth of rural economy, technology revolution led to huge growth opportunities in agribusiness associated with 'Make in India' programme aimed at export-oriented agriculture.

Commercialization of Agriculture and challenges associated with the open world trade pose challenges to the Science of Plant Pathology in terms of possibility of occurrence of hither to unknown diseases in India, role of quarantine, swift action needed for safeguarding plants from pest and disease attack, climate change, smart and precision agriculture, stringent food quality parameters of international trade *etc.*

At this juncture, it is necessary to focus our efforts on rapid detection of plant pathogens especially viral and phytoplasmal plant diseases, mapping occurrence of diseases and their prevalence and distribution using remote sensing techniques, development of resistant varieties / hybrids using molecular tools duly addressing biosafety and biosecurity concerns. It has also become necessary to work on microbiome *per se,* as is known that the total earth is switched on and off by microbes. Use of drones in agriculture, especially for plant protection, is one of the emerging areas that attracts entrepreneurship in agriculture, besides plant protection chemicals. It is also necessary to extend the use of drones in identifying the primary foci of infection, and occurrence and distribution of disease at district and village level for effective plant protection operations.

I congratulate the organizers of the National Conference on **Recent Advances in Plant Pathology and Innovative Approaches in Plant Disease Management (RAPID),** jointly organized by the Indian Phytopathological Society - Central Zone and Deccan Society of Plant Pathologists (DSPP), Hyderabad from 12th to 13th December 2024. I am sure the conference aptly abbreviated as **RAPPID** with themes appropriate for todays' changing world and Science of Plant Pathology will deliberate on the core topics and come out with fruitful outcome that support the enthusiastic Indian farmers, policy makers and other stake holders.

Saradalni

Date: 22.11.2024

(R. SARADA JAYALAKSHMI DEVI)

Dr. DANDA RAJI REDDY
M.Sc. (Ag), Ph.D.
Vice Chancellor

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MESSAGE

Agriculture is the backbone of Indian economy, providing employment for about 52% of the population and contributing 14% GDP. Though India has achieved self sufficiency in food production, it is still facing many challenges through biotic and abiotic stresses including pest and disease attack, natural disasters and climate change.

Plant diseases has become a major problem leading to significant economic losses and threatening the global food security. The average crop losses due to diseases in India ranges from 10-35% annually. Climate change and the response of pathogens to ever-changing conditions influence sustainable crop production and detecting plant pathogens and diagnosing diseases are critical components of efficient crop management.

Traditional methods to manage plant diseases have been extensively used, but they face significant drawbacks, such as environmental pollution, health risk, pathogen resistance, chemical residues above threshold levels and emergence of new races/biotypes in addition to significant increase in the cost of cultivation. Therefore, advanced techniques and recent innovations in disease management such as IPM, bio security, epidemology, host plant resistance, microbiome, biological control and pest and disease fore warning systems are to be promoted to attain eco friendly and profitable agriculture.

The National Conference on "Recent advances in plant pathology and innovative approaches in plant disease management (RAPPID)" provide platform for the researchers, policy makers and farmers for the productive interactions and elicit valid recommendations for future crop resilience against changing disease patterns. I congratulate Indian Phytopathological Society (IPS) –Central Zone and Deccan Society of Plant pathology, Hyderabad for selecting the relevant topics for the conference in view of increased concern for quality and pesticide residue free farm produce at reasonable price.

I wish RAPPID -2024 a grand success.

D. Raji Reddy

Dr.K.Gopal
VICE-CHANCELLOR

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MESSAGE

I am delighted to know that the Professor Jayashankar Telengana Agricultural University (PJTSAU) in collaboration with the Indian Phytopathological Society (Central Zone, Hyderabad) is organizing a National Conference on "Recent Advances in Plant Pathology and Innovative Approaches in Plant Disease Management (RAPPID)" to share and discuss the cutting-edge research and advancements in Plant Pathology.

Plant diseases are a major constraint to global food production, causing substantial losses in crop yield and quality. Emerging plant pathogens persist as a serious threat to the food security and stability of ecosystems, casting a looming shadow over the global economy. The early and accurate diagnosis of plant diseases, coupled with effective management strategies, is essential for minimizing these losses and ensuring food security. Recent advancements in plant pathology have provided new tools and approaches for disease diagnosis and management, enhancing our ability to protect crops from pathogens.

Innovative approaches in plant disease management are crucial for sustainable food security, enhancing crop productivity, and minimizing environmental impacts. Traditional methods such as chemical control and resistant varieties, are still widely used, but emerging technologies and research are shifting the focus towards more sustainable, efficient, and integrated approaches. Modern technical methods are becoming increasingly important, especially the use of remote sensing instruments that enable accurate and systematic pathogen surveillance, artificial intelligence and machine learning for early detection, smart sprayers, and the creation of novel, high-yielding disease-resistant cultivars. Genetic approaches and techniques including marker technology, plant-incorporated protectants and stacked traits are urgently needed and are a great challenge. The future of plant disease management will likely involve a combination of cutting-edge technologies and traditional practices, emphasizing sustainability, precision, and integration. The focus is shifting towards reducing chemical reliance, improving early detection, and fostering plant resilience, while considering environmental impact and climate variability. Collaboration between researchers, farmers, and policy-makers will play a key role to the successful implementation of these innovative approaches.

I convey my best wishes for the fruitful deliberations and the success of the National Conference on “RAPPID” and appreciate the efforts of organizers.

(Dr.K.Gopal)

PROFESSOR JAYASHANKAR TELANGANA AGRICULTURAL UNIVERSITY
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Foreword

It is with great pleasure and pride that I write the foreword for the Abstract Book of the National Conference on *Recent Advances in Plant Pathology and Innovative Approaches in Plant Disease Management (RAPPID)*, organized by Deccan Society for Plant Pathology (DSPP), and Indian Phytopathological Society (IPS), Central Zone. This conference marks a significant milestone, as it is the first IPS national-level event hosted in Telangana following its bifurcation, and it brings together the collective expertise of researchers, academicians, and industry professionals to discuss the advancements and challenges in plant pathology.

The conference is thoughtfully structured around five pivotal themes: advanced detection and diagnostic techniques for plant pathogens; biosecurity, epidemiology, and the role of climate change in plant disease epidemics; host plant resistance and molecular approaches to disease management; the exploration of microbiomes, biological control, and integrated disease management strategies; and entrepreneurship development in plant disease management. These themes encapsulate the present and future arenas of plant pathological research, emphasizing both scientific innovation and practical application.

This book serves as a comprehensive compilation of abstracts, offering a wealth of information that reflects the vibrant research culture of the Central Zone of India. It highlights not only ongoing research but also emerging challenges and opportunities in plant disease management. The insights shared during this conference will undoubtedly contribute to developing sustainable strategies for combating plant diseases, fostering agricultural resilience, and addressing global food security challenges.

I extend my heartfelt gratitude to the organizers, participants, and contributors for their dedication to advancing plant pathology. Let this conference and its proceedings inspire collaborative efforts and innovative solutions for a healthier, more sustainable agricultural future.

Yours Sincerely

(Dr. B. Vidya Sagar)

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MJ NARASIMHAN MERIT ACADEMIC AWARD-IPS CENTRAL ZONE

Keynote Addresses

KN-01

Biological Control: A Potential Approach for Plant Disease Management

R Sarada Jayalakshmi Devi

Vice-Chancellor, Acharya NG Ranga Agricultural University, Lam, Guntur - 522 034,
Andhra Pradesh, India.

Keynote

Plant pathogens, including fungi, bacteria and viruses, significantly impact crop yields, causing economic losses, threatening global food security. This study evaluates the effectiveness of biocontrol agents, particularly *Trichoderma* spp. and *Pseudomonas fluorescens*, against major pathogens in rice (*Pyricularia oryzae* and *Xanthomonas oryzae* p.v. *oryzae*), chickpea (*Fusarium oxysporum* f. sp. *ciceri*), groundnut (*Aspergillus niger, Sclerotium rolfsii* and *Rhizoctonia bataticola*), sugarcane (*Colletotrichum falcatum*) and maize (*Macrophomina phaseolina*). Laboratory experiments demonstrated that *Trichoderma* spp. effectively inhibited the growth of above soil-borne pathogens while *Pseudomonas* spp. showed strong antagonism against the rice blast and bacterial leaf blight pathogens. The *Trichoderma* and *Pseudomonas* isolates were molecularly characterized and identified as *Trichoderma viride, T. asperellum*, *T. longibrachiatum*, *T. harzianum,* and *P. fluorescens,* respectively. The antagonistic activity was mediated through mechanisms like mycoparasitism, production of antimicrobial compounds, and induction of systemic resistance. Comparative analysis with chemical fungicides revealed that while fungicides act rapidly, they have long-term drawbacks, including environmental pollution and resistance development. Biocontrol agents, on the other hand, enhance soil health, reduce dependency on chemical inputs, and align with consumer demand for sustainable and organic produce. Challenges such as inconsistent field efficacy and production costs persist but can be mitigated through integrated disease management strategies and further research. This study underscores the potential of biocontrol agents in achieving sustainable agriculture.

Keywords: Biocontrol agents, *Trichoderma* spp., *Pseudomonas fluorescens*, soil-borne pathogens, chickpea, groundnut, rice blast, sugarcane red rot, maize charcoal rot.

KN-02

Current Advances in Plant Pathogen Detection in Horticultural Crops

R Selvarajan

Director, ICAR-National Research Centre for Banana, Tiruchirappalli - 620 102, Tamil Nadu, India.

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Keynote

Horticultural crops are part of our daily life and mainly include fruits, vegetables, materials for beverages and fragrances, herbal medicine, and ornamentals. Horticulture contributes around 30.4% to the Gross Domestic Product (GDP) of agriculture GDP while using only 13.1% of the gross cropped area, making it a significant player in India's agricultural growth. Plant pathogens currently pose a major threat to horticultural industry. These pathogens cause up to 40% yield loss of economically important crops each year. In order to reduce yield losses, it is important to ensure disease free plants for which effective detection techniques and kits are needed. Effective diagnostic tools for timely determination of plant diseases become essential to the assurance of horticultural sustainability and global food security. Ideally, a plant pathogen detection technique should be affordable, sensitive, specific, user-friendly, rapid and robust, equipment-free or simple, and deliverable to end-users, and able to detect pathogens in complex matrices, such as soil samples or plant extract etc., Nucleic acid- and antibody-based molecular assays are gold-standard methodologies for the diagnosis of plant diseases, but the analyzing procedures are complex and laborious. However, there is a growing interest in developing techniques that can be based in real-time and thus facilitate in-field or onsite diagnosis. Several recent advances have demonstrated that CRISPR-associated (Cas) endoribonuclease systems may offer useful features for nucleic acid detection. Next-generation sequencing (NGS)-based innovative methods have been shown to possess great potential to detect multiple pathogens simultaneously. In this keynote lecture, main advantages and disadvantages of currently available and recent emerging detection techniques are discussed in detail, which should allow researchers and stakeholders to easily compare the different options that are available nowadays and select a method that is most suited for their specific use. Special emphasis is given to detection techniques adopted for banana diseases are discussed in detail.

Keywords: CRISPR-Cas, Next generation sequencing, detection, pathogen.

KN-03

Microbial Diversity and its Role in Sustainable Plant Health and Livelihood

Prof C Manoharachary

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Biodiversity has been discussed a lot in terms of large organisms but no organisms are more ubiquitous, abundant or diverse than microorganisms. Microorganisms are the first live forms that came in to existence prior to macroorganisms. The metabolic activities that the microbes carried out during this time were critical for creating the conditions for the evaluation of the other organisms. The microbial world includes bacteria, viruses, actinomycetes, archaea and

some fungi. Characterization of microbial diversity is an important aspect and challenging and thus operationally, DNA technology has played an important role in this regard. For microbial community studies, 70% of genomic similarity definition is impractical to apply instead many have used genetic markers to characterize microbial communities like OTU, 16s rDNA and other techniques. Microbes are so abundant that even minute fraction of their diversity is difficult to estimate. Currently, it is not feasible to completely quantify the diversity of a gram of soil or a liter of sea water. The abundance of bacteria and archaea in any habitat makes difficult to estimate. The earlier scientists calculated that there are more bacteria on earth than the other stars of universe. Because of taxonomic and evolutionary diversity bacteria are functionally diverse. Archaea requires particular effort to culture, and diversity of this group is less understood. This group has been found living at physical or chemical extremes. Molecular methods have revolutionized the understanding of bacteria and archaea diversity. Like prokaryotes fungal species have been traditionally defined morphologically and molecularly. Hawksworth and Lucking (2017) suggested that there are at least 1.5 to 6.8 million fungal species globally. Around 1,55,000 fungi have been described up to species level from the world and 35000 fungal species have been described from India. There is a necessity of studying the microbial diversity at length in soils, aquatic systems, extreme habitats and others. Microbial diversity exploration needs to be encouraged due to the fact that the microbes are vital for life since they perform numerous functions essential for the biosphere. Maintaining ecosystem functions and services, nutrient cycling, litter decomposition, primary production and climate regulations are some of the key roles performed by the microbial communities. Thus, the microbial diversity is important in the maintenance and conservation of global genetic resources. Aspects and prospects of microbial diversity in relation to plant health, livelihood, human health and other related aspects will be discussed in the presentation.

Keywords: Microorganisms, characterization, bacteria, archaea.

Lead Presentations

THEME 1:

Advanced Detection and Diagnostic Techniques of Plant Pathogens

LP-01

Facilitation of Global Export of Plant Genetic Resources of Consultative Group on International Agricultural Research Institutes for Research Purposes by ICAR-National Bureau of Plant Genetic Resources

K Anitha[1], B Bhaskar[1], B Parameswari[1], Prasanna Holajjer[1], L Saravanan[1], P Humayun[2], Rajan Sharma[2], V Celia Chalam[3] and G P Singh[3]

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Abstract

International germplasm exchange plays a pivotal role in addressing the flow of genetic diversity across the countries for crop diversification and improvement programmes for food security in most of the developing countries. Since this global exchange of crop germplasm enhances phytosanitary risks, the Government of India has empowered the Indian Council of Agricultural Research - National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi as the nodal organization to undertake quarantine processing of crop germplasm meant for research purpose both for public and private sectors. ICAR-NBPGR established its Regional Station at Rajendranagar, Hyderabad in 1986 as the plant quarantine authority to facilitate the exchange and quarantine of germplasm and breeding material of mandate crops of International Crops Research Institute for the Semi Arid Tropics (ICRISAT). ICRISAT has a Memorandum of Agreement with the Govt. of India for unrestricted movement of seeds and genetic material into and out of India as required by the institute for its cooperative research programs across the world, after ensuring appropriate quarantine inspection to avoid introduction or export of pests. NBPGR RS Hyderabad facilitates the pre-export crop inspection, issuance of phytosanitary certificate, as well as first and second level safety duplication of ICRISAT genebank accessions in various countries as a ‘Black box arrangement’.

ICAR-NBPGR facilitates the export of plant genetic resources for research purposes by considering the requests under three categories. (i) Indian Researcher/Government institution to carry/send biological resources for ***Non-commercial research*** or ***Research for emergency purposes*** other than collaborative research; (ii) Requests under ***Collaborative research*** projects; (iii) Request for ***Annex I crops*** designated by India under the Multilateral system (MLS) of the

ITPGRFA & ***FAO designated accessions*** of ICRISAT mandate crops. The material of Indian origin (Category I) is allowed for export with the prior approval from the National Biodiversity Authority. Export of genetic resources pertaining to category II is facilitated by ICAR-NBPGR with the prior consent from ICAR/DARE. The Annex I crops/FAO designated germplasm under Category III are exported with the approval of the Director, ICAR-NBPGR. Since inception, ICAR-NBPGR Regional Station, Hyderabad facilitated the export of more than 1.35 million samples of germplasm belonging to ICRISAT mandate crops and maize germplasm belonging to CIMMYT. An export inspection is conducted to ensure that the consignment meets the phytosanitary import requirements of the importing country, followed by the issuance of a phytosanitary certificate for the consignment. The diagnostic protocols are undertaken to meet the phytosanitary requirements for the export of seed as per the guidelines of ISPM 27 for the detection and identification of pests. In addition, ICAR-NBPGR facilitates the export of safety duplicates of crop germplasm for posterity in both the primary and secondary centres of conservation in global gene banks (USDA; IITA, Nigeria; ICARDA, Syria; WVC, Taiwan etc) and Global Seed Vault, Norway, respectively. The export procedures in line with India's quarantine regulations are discussed in this presentation.

Keywords: Export, Phytosanitary certificate, ICRISAT, CIMMYT

LP-02

Multi-functional Microbial Surfactants for Plant Health and Disease Management

Bee Hameeda

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Abstract

Microbial surfactants produced by microorganisms (bacteria, yeast, fungi) have emerged as alternatives to surface active agents due to their low toxicity, biodegradability, multi-functionalities under extreme temperature, pH conditions. Microbial surfactants are classified as glycolipids, lipopeptides, lipoproteins, polymeric surfactants. In addition, they can be produced from renewable sources with aspect of sustainable economics and can be the focus to meet the sustainable development goals (SDGs). Biosurfactants are eco-compatible molecules of 21st century and there is increase in demand with Compound annual growth rate of 6 .1% from 2021 to 2030. In recent past, work on biosurfactants as emerging biomolecules has geared up due to their bio and interfacial activity, which is also dependent on the structure and composition of each with unique applications in field of agriculture, food, environment and pharmaceuticals. At the Plant Probiotic and Biosurfactant Lab (P2BL), we work on production of microbial surfactants from plant growth promoting bacteria (*Pseudomonas aeruginosa* DR1, *Bacillus velezensis* MS20, *Bacillus mojavensis* RHPR20, *Stenotrophomonas maltophila* GHG9, *Serratia marsecens* EB 67) and yeast (*Pichia occidentalis* MHY5, *Hanseniaspora guilliermondii* MHY3, *Hanseniaspora pseudoguilliermondii* MHY7, *Hanseniaspora opuntiae* MHY8), which have been identified by molecular methods. Antagonistic studies against different phytopathogens were tested by dual culture using microbes as mentioned above and also with the biosurfactants extracted. *P. aeruginosa* DR1 produced rhamnolipid which has potential application as biocontrol agent. *B. mojavensis* RHPR20 showed fengycin and surfactin production and was used to control charcoal rot disease of sorghum and biofortification of iron. *Bacillus velezensis* MS20 showed surfactin production and induced systemic resistance against *Rhizoctonia solani*. All the yeast showed significant antagonistic activity and also showed growth of green gram and black gram in greenhouse conditions when compared to control. Results of multifunctional microbial surfactants work we do at P2BL will be presented.

Keywords: Microbial surfactants, Pseudomonas, Bacillus, yeast, plant growth, biological control

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LP-03

Transboundary Movement of Pathogens: A Global Plant Biosecurity Threat

V Celia Chalam[1*], J Akhtar[1], P Kumari[1], P Kumar[1], K Anitha[2], B Parameswari[2], B Bhaskar[2], K Kalaiponmani[1], A Tripathi[1], Priya Yadav[1], A K Maurya[1] and S Lenka[1]

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Abstract

Trade and exchange of germplasm at international level play a key role in the long-distance dissemination of a destructive pathogen or its virulent strain. The worldwide distribution of many economically important pathogens is attributed to the unrestricted exchange of seed lots. Of the material being imported, bulk imports for sowing/ planting carry maximum risk as thorough examination becomes difficult and planting area required is also too large. Quarantine processing is often restricted to smaller samples derived from them and based on results of these samples the whole consignment is rejected/ detained or released. Certain small samples meant for research purposes especially germplasm or wild relatives of a crop are more likely to carry diverse biotypes/ races/ strains of the pathogen and are of immense quarantine importance. In India, the Directorate of Plant Protection, Quarantine and Storage under the Ministry of Agriculture and Farmers' Welfare is responsible for enforcing quarantine regulations and for

quarantine inspection and disinfestation of commodities meant for commercial purpose. The imported germplasm material including transgenics are subjected to quarantine processing at the ICAR-National Bureau of Plant Genetic Resources, New Delhi. The Plant Quarantine (Regulation of Import into India) Order, 2003 requires *Additional Declarations* to be included in Phytosanitary Certificate for seeds and other planting material as free from pests. As per the PQ Order, 1261 pests are regulated pests which are of quarantine significance for India. Early, sensitive and accurate diagnosis is necessary for detection of pathogens in quarantine. Just as communication networks, diagnostic networks are available in different countries to ensure biosecurity of crops. The United States of America has established the National Plant Diagnostic Network (NPDN) and it works with state and federal agencies to ensure quick, accurate and secure conveyance of information about new detections. Through NPDN's communications system, diagnosticians have access to expertise wherever it exists. NPDN labs follow standardized protocols for data acquisition and storage and practice secure communications to ensure that information of potential regulatory concern is not released inappropriately. Australia has established the National Plant Biosecurity Diagnostic Network (NPBDN). The NPBDN is the nationally integrated network for plant diagnosticians in Australia and plant diagnosticians involved with this network are located in every state and territory. Diagnostic services are provided from cities and regional centres in most of Australia's major agricultural production areas. India need to establish a National Plant Pests Diagnostic Network of interconnected diagnostic laboratories and strong surveillance programme to identify new pathogens. By closely monitoring which pathogens are most frequently reported from which countries, and what commodities tend to be infected, it may be possible to predict high-risk pathogens and commodities. Adopting a strategy of post-entry quarantine growing/inspection followed by use of combination of conventional, serological and molecular detection techniques 30 pathogens including 7 exotic fungi and 23 exotic viruses of great economic and quarantine importance were intercepted in imported germplasm including transgenics in the last 25 years at ICAR-NBPGR, New Delhi. The quarantine regulations and plant biosecurity diagnostic networks and capacity development are essential for global plant biosecurity.

Keywords: Quarantine, import germplasm, transgenics, regulations, exchange, detection, pests

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LP-04

An Overview of Biological Control in Rice Disease Management

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Abstract

Rice, *Oryza sativa* L., is a staple food for over 3.5 billion people, contributing 60-70% of their caloric intake. India is a leading producer and exporter, accounting for 50% of global rice production and consumption, with Basmati and non-Basmati exports generating $5.2 billion and $3.6 billion, respectively, in 2023-2024. However, diseases such as rice blast, bacterial leaf blight, sheath blight, false smut and bacterial panicle blight can cause annual global rice yield losses of 15-35%, equivalent to millions of tonnes of rice, posing a significant threat to food security. Integrated disease management (IDM) is an ecological approach that relies on an understanding of population biology at the local farm level. It is important to avoid relying on a single technology and instead integrate the control components that are available to farmers with limited resources. Biological control is a method of managing rice diseases using natural organisms, such as predators, parasitoids and pathogens. It can be an effective and safe way to control rice diseases. It can reduce chemical pesticide use, improved natural control of specific diseases, increased profits for rice farmers, and lower incidence of sickness for IDM farmers. The plant microbiome is a community of microorganisms that live in and around a plant and can impact plant health and disease resistance. It is an integral part of the host and increasingly recognized as playing fundamental roles in plant growth and health. Increasing evidence indicates that plant rhizosphere recruits beneficial microbes to the plant to suppress soil-borne pathogens.

Keywords: Biological control, microbiome, disease management, pathogens

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LP- 05

Host-Pathogen Interaction Studies using Whole Genome Sequencing and Transcriptomics

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Abstract

Host-pathogen interaction studies provide critical insights into molecular mechanisms underlying disease processes, paving the way for improved management strategies and therapeutic interventions. Whole-genome sequencing (WGS) and transcriptomics are transformative technologies that allow comprehensive analysis of these interactions both at genomic and transcriptomic levels. WGS provides detailed information on genetic composition of hosts and pathogens, enabling the identification of key genes involved in pathogenicity, resistance and susceptibility. Transcriptomics complements this by analysing gene expression patterns during host-pathogen interactions, elucidating dynamic changes in response to infection. Integrating these approaches reveals intricate signalling pathways, virulence factors and immune responses, facilitating the discovery of molecular targets for disease control. Additionally, comparative studies across species and conditions enhance our understanding of evolutionary adaptations in pathogens and host defenses.

Keywords: Whole genome sequence, transcriptomics, host-pathogen interaction, gene expression

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LP-06

Seed Mycoflora - A Possible Cause for Low Seed Viability in Soybean

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Abstract

Soybean is an important oilseed cum pulse crop majorly grown in temperate countries and is being expanded to several other tropical and subtropical countries like India. Soybean seeds are considered the rich source of protein (40-45%) followed by carbohydrates (20-26%) and oil (20-22%), hence holds a greater share in meeting the requirement of human diet. The most common complaint encountered in soybean production is loss of seed viability and vigour during storage under ambient conditions which adversely affects the plant stand especially in warm and humid parts of the world. Besides its inherent poor storability and mechanical damage, soybean seeds undergo rapid deterioration during storage owing to several seed associated mycoflora. Among these, *Phomopsis sojae, Cercospora kikuchi, Colletotrichum truncatum, Fusarium oxysporum, Macrophomina phyaseolina, Aspergilles flavus* and *A. niger* are found predominant in occurrence causing several detrimental effects on soybean seeds.

According to the reports published, precipitation at maturity and delayed harvesting associated with exposure of mature seeds to high relative humidity are the main reasons for soybean to become prone to seedborne infections. On the other hand, the seeds with cracks and bruises absorb moisture from the atmosphere and remain as best substrate for several microbial populations. In order to increase the production of soybean and make its cultivation profitable, a source of high quality and disease free seeds must be made available to soybean growers. A series of experiments conducted at Seed Research and Technology Centre, PJTAU have indicated that the seedborne infections appear both under field and storage conditions can effectively be managed by adopting pre-storage seed treatment with carboxin + thiram (Vitavax power) @ 3g/kg coupled with pre-harvest sprays with pyraclostrobin + metiram (Cabriotop) @ 2g /l at R3, R5 and R7 stages of soybean. It was also found that the storability of soybean seeds with 7 - 9% initial moisture content was doubled when seeds were subjected to fungicidal treatment. The seeds with higher moisture content were also get protection against seed associated mycoflora and could sustain the viability up to 6 months after storage (MAS). Further, it was observed that polyline gunny bag was found to be the best storage container for soybean seeds with 10% initial moisture content which recorded the germination at above IMSCS (>70%) up to 8 MAS.

Keywords: Soybean, seedborne fungi, storage, seed viability

LP-07

Recent advances in sustainable management of diseases of oilseed crops

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Abstract

Oilseed crops play a vital role in global edible oil production and industrial applications. India, a leading oilseed producer of oilseeds, cultivates nine major oilseed crops *viz.,* soybean, mustard, groundnut, sesame, niger, sunflower, safflower, castor and linseed. These crops significantly contribute to the national economy and nutritional security, supplying edible oils and industrial raw materials. However, their productivity is often reduced by biotic stresses, particularly plant diseases, causing yield losses of 10–80% depending on the crop, region and environmental conditions. Soybean, the leading oilseed crop globally is often affected by diseases like rust, root rot and stem canker. Mustard is affected by white rust and alternaria blight. Groundnut, suffers from collar rot and leaf spot. Sesame, impacted by diseases such as alternaria leaf spot and phyllody. Niger, faces losses due to powdery mildew and alternaria blight. Sunflower, is prone to downy mildew, rust and alternaria blight. Safflower, is affected by wilt and rust. Castor, threatened by wilt, root rot and grey mold. Linseed, suffers from rust and powdery mildew.

To combat these diseases, Integrated Disease Management (IDM) is a sustainable solution. This strategy combines multiple approaches, including cultural practices such as crop rotation, timely sowing, use of resistant varieties and sanitation to reduce the initial inoculum load. While chemical control remains effective, its application must be judiciously managed to prevent pathogen resistance and reduce environmental pollution. Biological control, utilizing beneficial microbes such as *Trichoderma* spp., *Pseudomonas fluorescens* and *Bacillus subtilis*, has emerged as a promising alternative. Furthermore, advancements in molecular biology and biotechnology have enabled the development of resistant cultivars by leveraging insights into host-pathogen interactions, providing durable disease resistance. Recent advancements have further enhanced IDM strategies including the use of nanotechnology for precise fungicide delivery, biopolymers for targeted and controlled release of biocontrol agents, genome editing tools such as CRISPR/Cas9 for developing disease-resistant cultivars and artificial intelligence tools for disease prediction and management. These technologies, combined with traditional IDM practices, ensure a sustainable and environmentally friendly approach to managing diseases in oilseed crops, enhancing productivity and profitability for farmers while reducing the ecological footprint.

Keywords: Oilseed crops, Integrated Disease Management (IDM), CRISPR/Cas9 and sustainable disease resistance.

LP-08

Biofilmed Biofertilizers for Improving the Nutrient Minerlization and Plant Health for Sustainable Production of Cotton

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Abstract

Biofilmed biofertilizers are emerged as promising strategies for improving soil health and mineralizing nutrients for plant growth. The present study was focused to develop fungal based bacterial biofilms, performed their functional characterization and evaluated potential and novel biofilmed biofertilizers as plant growth promoting and biocontrol agents in cotton crop. The biofilms were developed using *Trichoderma viride* as a matrix and agriculturally important bacteria - *Bacillus subtilis, Pseudomonas fluorescens* and *Azotobacter chroococcum,* as partners. Microscopc observations revealed significant differences in the progress of growth of biofilms as dual cultures. In the biofilms, the bacteria were observed growing intermingled within the fungal mycelial mat. Biofilms exhibited higher values for various biochemical attributes as compared to the individual organisms and dual cultures. Biofilmed formulations significantly improved the germination (%), growth and nutrient uptake parameters, microbiological activity and yield attributes, including 15-20% increase in boll weight in cotton. In *Rhizoctonia solani* infested sick plots at Sirsa, seedling mortality reduced with microbial seed treatments *viz., T. viride + B. subtilis* and *T. viride + P. fluorescens* biofilms. This was significantly correlated

with increased activity of hydrolytic enzymes like β-1, 3 and β-1, 4 endoglucanases and chitosanase in plant roots. Scanning electron microscopy further confirmed their colonisation on roots, especially the *T. viride* + *B. subtilis* biofilms. Significant correlation of plant parameters with polyphenol oxidase activity, mortality of cotton plants with MBC, defense enzyme activity with mortality were also observed. Synergistic effects of the partners in these biofilmed formulations illustrated their potential *vis a vis* use of mixtures/individual cultures as inoculants. Such formulations may represent a more viable inoculation option for integrated nutrient and pest management strategies in agriculture. Our field level experiments illustrated that the novel microbial inoculants developed in our study, offer a promising alternative, which can help reduce the use of chemicals and lead to improved crop productivity and soil health.

Keywords: Fungal bacterial biofilms, PGPR, cotton, yield.

LP-09

Parthenium hysterophorus L. - A Biosecurity Threat to Agricultural Crops and Management Options

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Abstract

Parthenium hysterophorus L. is a species of herbaceous, erect and annual flowering weed in the *Asteraceae* family and the origin is considered to be from Mexico, America, Trinidad and Argentina. Locally known as carrot weed, congress grass, star weed, white top and it is an invasive weed and about 35 M.H. land was estimated to be invaded with Parthenium today in India. It spreads through seeds and in south India, it is spreading viral and bacterial diseases and causing considerable yield loss (14-27%) in both agricultural and horticultural crops and also causes allergy for both animals and human beings. It requires 100-120 days to complete its life cycle under normal conditions. It is a symptomless carrier of Tobacco streak virus (TSV) by supplying TSV infected pollen in south India. The pollen is carried by thrips to main crop hosts (sunflower, groundnut, sunflower, black gram and green gram) and cause the disease. Stem necrosis disease epidemic occurred on groundnut during the year 2000 in Anantapur district due to TSV spread by parthenium and loss was estimated around Rs.300 crores. Subsequently, TSV incidence on groundnut was recorded up to 2-16.5% during 2004, 5-25% in 2006 and 2-25% in 2007. Parthenium was also identified as natural host for Groundnut bud necrosis virus (GBNV) and acts as reservoir for GBNV in nature. Both TSV and GBNV are causing

losses in yield in many crops. Recently in 2021, phytoplasma infection was also reported on parthenium and identified as *Ca*. Phytoplasma Australasia 16SrII-D. Parthenium also harbours sucking pests *viz*., thrips and jassids, which in turn act as vectors for many viral and bacterial diseases. Spread of virus infected pollen of parthenium can be curtailed by growing 4-6 rows of tall barrier crops like bajra or jowar around the groundnut field. Parthenium should be removed before flowering to avoid spread of diseases. Parthenium spread and growth can be restricted by promoting other competitive weeds like *Cassia sericea* or *Cassia tora, Tephrosia* in waste lands. Beetle, *viz*., *Zygogramma bicolorata* was identified as best biocontrol agent against parthenium as it feeds on both foliage and flower. Non-selective herbicide, paraquat @ 1 litre per acre, pre-emergence herbicides *viz*., alachlor @ 1 litre per acre and pendimethallin 50 % EC @ 1.2-1.5 l/acre were proved to be effective against parthenium. Integrated weed management practices are to be followed to combat the parthenium menace. Strict enforcement of parthenium eradication programme, establishment of taskforce committee for monitoring and control of parthenium, linking up of parthenium eradication programme with ongoing National Rural Employment Guarantee Act (NREGA) should be taken up on war foot basis.

Keywords: *Parthenium hysterophorus*, TSV, GBNV, phytoplasma and thrips

Oral Presentations

THEME 1:
Advanced Detection and Diagnostic Techniques of Plant Pathogens

OP-01

Phenotypic and Genotypic Identification of Rice Genotypes against Bacterial Leaf Blight Caused by *Xanthomonas oryzae* pv. *oryzae*

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Abstract

Rice, *Oryza sativa* L., is an important crop in Telangana that covers a major area of nearly 60 lakh acres. Bacterial leaf blight (BLB), caused by the Gram-negative bacterium, *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is the second most devastating disease of rice after blast, causing substantial yield loss in major rice growing areas of Telangana. The seed borne infection of Xoo is the primary source of inoculum and leads to extremely high field incidence. Weather conditions play a predominant role in determining the course and severity of epidemics of a disease. It is critical to explore and identify the new resistant resources to control the races of the bacterium. In the present study, screening of 135 rice genotypes that were developed at different rice research stations of PJTAU in Telangana, *viz*., Rajendranagar, Rudrur, Kampasagar, Jagitial, Warangal and Kunaram were screened against BLB during *Kharif* 2023 at Regional Agricultural Research Station, Warangal, Telangana. Phenotypic identification of resistant genotypes was done by artificial inoculation of *X. oryzae* pv. *oryzae* using leaf clipping technique at 45 days after transplanting. The genotypes, which were found resistant against BLB at field level were screened genotypically to confirm the presence of two resistant genes *i.e., Xa21* and *xa13*. Out of 135 rice genotypes screened, one entry *viz.,* RNR 37986 including resistant check, "Improved Samba Mashuri" were found "Highly Resistant" to BLB with disease score 1; five genotypes *viz.,* KNM 12472, KNM 12510, KPS 12531, WGL 1868 and RNR 44476 were found "Resistant" with score '3'; four genotypes *viz.,* WGL 1837, WGL 1869, RNR 44583 and RNRH 316 were found "Moderately Resistant" with score '5'; two genotypes *viz.,* KNM 12469 and WGL 1843 were found "Susceptible" with score '7', 123 genotypes including susceptible check 'Taichung Native 1' were found "Highly Susceptible" with score '9' to BLB of rice phenotypically under field conditions. The genotypes that were found highly resistant, resistant, moderately resistant in field screening were again screened genotypically for the presence of two BLB resistant genes *i.e., Xa21* and *xa13.* Genotypic results showed that two entries *viz.,* RNR 44476 and RNR 44583 were observed to be positive only for *xa13* gene, while phenotypic resistance for BLB in other genotypes may be due to the

presence of other resistant genes. The identified promising rice entries can be used as donors in breeding programmes for the development of disease resistant/tolerant varieties against bacterial leaf blight.

Keywords: Rice, bacterial leaf blight, phenotypic screening, genotypic screening, resistance

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OP-02

Detection of Variation in Tobacco streak virus Isolates from Sunflower by Serological and Reverse Transcription Polymerase Chain Reaction Method

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Abstract

Among different diseases infecting sunflower, *Helianthus annuus* worldwide, sunflower necrosis disease (SND) caused by Tobacco streak virus (TSV) poses a potential threat to the cultivation of sunflower in India. Various methods have been developed to detect TSV, including Enzyme linked immunosorbent assay (ELISA), Reverse Transcription-polymerase chain reaction (RT-PCR), and probe-based techniques. The presence of TSV in necrosis disease-affected leaf samples collected from major sunflower-growing areas of Andhra Pradesh, Karnataka, Maharashtra, and Tamil Nadu was confirmed by direct antigen-coated enzyme-linked immunosorbent assay (DAC-ELISA) using TSV-specific polyclonal antiserum. All the isolates showed a positive reaction in the ELISA test using TSV-specific polyclonal antiserum, confirming the presence of TSV. The absorbance values varied from 0.57 to 1.18 as compared to the positive control, *i.e.,* TSV-infected cowpea (1.59) and healthy control (0.07). Disease reaction and symptomatology of three test plants, *viz*., cowpea cv. C-152, sunflower cv. Morden, and *Nicotiana tabacum* cv. Samsun, to these virus isolates were studied under artificially inoculated conditions. Infectivity assays of the eight virus isolates of SND collected from various locations on cowpea cv. C-152 and *N. tabacum* cv. Samsun showed no variation in symptom expression. On sunflower cv. Morden, the isolates produced mosaic (AP-2, MH-2, KA-2, TN-1, and TN-2), while necrotic lesions were produced by AP-1, MH-1, and KA-1 within 6-7 days. Using primers specific to the coat protein region of TSV, RT-PCR was successful in amplifying the TSV-CP gene from sunflower tissue. A DNA band of expected size (approximately 700 bp) was observed in all the necrosis disease-affected sunflower samples collected from Maharashtra, Karnataka, Tamil Nadu, and Andhra Pradesh. The CP gene of TSV isolates collected from different locations of four states, when compared, showed uniform banding patterns and expressions suggesting that the TSV population is homogenous and perhaps has a common origin. There is a necessity to characterize the isolates of the virus through cloning and sequencing to ascertain the occurrence of serotypes from different sunflower-growing locations of the country.

Keywords: Sunflower necrosis disease, variation, ELISA, RT-PCR, TSV-CP gene

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OP-03

Isolation, Purification and Pathogenicity of *Fusarium oxysporum* Schl. f.sp. *ciceris* Inciting Wilt Disease in Chickpea

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Abstract

Wilt disease caused by *Fusarium oxysporum* f.sp. *ciceris* in chickpea remains a persistent threat, leading to substantial losses in both quantity and quality. The present study was conducted during November-March, 2022-23 in the Department of Plant Pathology and Central Instrumentation Cell, College of Agriculture, Professor Jayashankar Telangana Agricultural University, Rajendranagar, Hyderabad with an aim to isolate, purify and pathogenicity assessment of wilt inciting pathogen in chickpea. The pathogen was isolated from infected chickpea fields and purified, with its cultural and morphological characteristics utilized for identification. The analysis revealed that pathogen grown on potato dextrose agar medium exhibited morphological and cultural characteristics such as mycelium-superficial colour-pinkish white, texture-cottony, pigmentation-light orange, type of growth-radial and speed of growth-fast, consistent with *Fusarium oxysporum* f.sp. *ciceris*, possessing macroconidia-sickle shape, microconidia-oval shape and chlamydospores-thickwalled. Furthermore, a pathogenicity test was conducted on the chickpea cultivar JG-62 by inoculating the pathogen culture into pots using the sick pot soil method under controlled conditions in a net house. Within 30 days of inoculation, seeds treated with the fungus developed wilting symptoms, and the per cent disease incidence was recorded, effectively satisfying Koch's postulates. This investigation provided valuable insights into understanding the pathogen, thereby contributing to the development of cost-effective solutions for managing wilt disease in chickpea by the farmers of Telangana.

Keywords: *Cicer arietinum*, wilt, isolation, pathogenicity, Telangana

OP-04

Identification of Resistant Rice Genotypes for Neck Blast and Identification of Pi^{54} Gene Using ssr Marker

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Abstract

Rice is the main staple food crop for more than 50% of the world population. The rice crop is affected by several diseases, of which blast caused by *Magnaporthe oryzae* is one of the most devastating disease, can infect rice plant right from seedling to late vegetative/reproductive stages affecting leaves, nodes, collar, panicles and neck region. Use of resistant rice varieties is the most effective way to control this disease. In the present study, 542 entries were screened for neck blast resistance during *Rabi* 2023-24. The neck blast scoring was done based on SES Scale (2014). The results indicated that in neck blast screening, two entries i.e., TTBDR 106-2-4 and RP 5084-58-33-2-2-3-B recorded score 0, 1 in two successive years (2022 and 2023) and five entries i.e., KAU-PTB-0627-2-24-1, AE-1261 AE-1262, AE-1283, RTCNP-120 recorded score 1, 1 in two consecutive years and seven entries i.e., BM-574, AE-1264, RTCNP-77, RTCNP-78, RTCNP-93, NLR-2 OLF-43, NLR LBR 8 (UB1058) recorded score 0,3 in two consecutive years. During *Rabi* 2023-24 season, Machilipatnam entries i.e., MTM-13, 43, 47, 50, 51, 59, 67, 73, 74, 85, 86, 88, 89, 89, 91, 92, 97, 98 recorded immune reaction to neck blast with 0 score. Under early duration entries i.e., AE-1340, 1341, 1343, 1344, 1346, 1347, 1348, CE-695: medium duration entries i.e., AM-946, 950, 951, 954, 962, 963, 964, 966, 967, 970, BM-588, 589, 590, 592, 594, 595; CM-463, 466, 467, 469, 470; YS-12, YS-21; late duration entries i.e., AL-1085; BL-1078, 1081; CL -509 recorded score 0 with immune reaction. Under multi-location, one entry i.e., MST-108; submergence trial entries i.e., ADW-308, 319, CDW-183, 187, 194 recorded score 0 with immune reaction. Out of 542 entries, 231 and 112 entries showed the highly resistant and resistant reaction with score 1 and 3 for neck blast. The present study represents valuable neck blast resistance genetic resources that could be used for rice breeding programmes as donors for blast resistance and genomic studies. Presence of PiK^{h} (Pi54) blast resistance gene was detected in MTU 1001, MTU 1064, MTU 2077, MTU 1172, MTU 1262, MTU 1223, MTU 1224, BPT 1768, BPT 2595, NLR 3041, NLR 33358, NLR 40054, RGL 11414, RGL 1880, NDLR-7, NDLR-8, PLA 1100 through SSR marker with primer RM206 (147 bp).

Keywords: Neck blast, resistance, Pi^{54}, SSR marker

OP-05

Deciphering *Fusarium* Diversity in Pokkah Boeng Disease of Sugarcane in Andhra Pradesh

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Abstract

Pokkah boeng is a fungal disease that affects sugarcane and the etiology of the disease is still controversial. Hence, the present study was aimed to identify the pathogens associated with the disease. Forty diseased sugarcane samples were collected from the Regional Agricultural Research Station, Anakapalle, and its surrounding areas in Andhra Pradesh, India, encompassing various popular sugarcane varieties. Pathogen isolation was carried out from the collected samples and the isolates were characterized using both morphological and molecular approaches, focusing on ITS, β-tubulin, and tef-1 regions. Morphological examination revealed that four isolates were identified as *Fusarium proliferatum*, eight isolates as *F. subglutinans*, seven as *F. sacchari*, and 12 as *F. moniliforme/F. verticillioides*. However, molecular identification based on ITS sequence data from the NCBI database indicated that each isolate exhibited over 95% similarity with multiple *Fusarium* species. To achieve more precise species identification, additional molecular analyses were performed using tef-1 and β-tubulin regions. Based on these analyses, the isolates were further confirmed as either *F. sacchari* or *F. andiyazi*. Overall, the combined morphological and molecular data suggest that the pathogens involved belong to various species within the *Fusarium fujikuroi* species complex.

Keywords: Sugarcane, pokkahboeng, *Fusarium* species, ITS, β-tubulin, tef-1

OP-06

Advanced Diagnostic Techniques for Sustainable Disease Management in Indian Agriculture: Integrating Precision Tools within IPM Frameworks

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Abstract

Accurate and timely detection of plant pathogens is essential for sustainable agriculture, especially in India, where plant diseases significantly impact food security and the livelihoods of farmers. Advanced diagnostic techniques, when integrated within Integrated Pest Management (IPM) frameworks, present transformative potential for effectively managing plant diseases with precision. Traditional molecular methods, such as polymerase chain reaction (PCR) and loop-mediated isothermal amplification (LAMP), are now enhanced by cutting-edge technologies like CRISPR-based diagnostics and RNA interference (RNAi). CRISPR allows for rapid, specific pathogen detection by utilizing gene-editing tools, while RNAi enables targeted gene silencing of pathogenic genes, supporting both diagnostic and protective roles. In addition, metagenomics and next-generation sequencing (NGS) expand pathogen identification capabilities to detect known, emerging, and previously uncharacterized threats. Field-deployable biosensors, such as electrochemical and fluorescence-based devices, offer immediate and on-site pathogen detection, making them valuable for real-time disease monitoring. Remote sensing tools, including hyperspectral imaging and satellite-based sensors, provide large-scale monitoring of crop health, detecting early signs of disease over vast areas. Artificial intelligence (AI)-powered diagnostics further enhance IPM by analyzing complex data patterns related to plant health, improving the precision of field-adapted disease management strategies.Adapting these advanced diagnostic tools for India's diverse agricultural landscape enables the application of cost-effective, scalable solutions accessible to smallholder farmers. Incorporating these methods within IPM frameworks promotes sustainable agriculture by reducing dependency on chemical inputs and enabling timely, targeted interventions. Advanced diagnostics thus support resilience and productivity in Indian agriculture, empowering farmers with efficient disease management tools to safeguard crops and improve yield stability.

Keywords: Integrated pest management, CRISPR, RNA interference, next-generation sequencing, artificial intelligence.

OP-07

Identification of 16Sr-IID Subgroup of Phytoplasma in Bamboo in Tirupati District of Andhra Pradesh

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Abstract

Bamboos are perennial grasses (Family: Poaceae) that thrive in various climates, from tropical to temperate. They are commonly found in the Indian subcontinent, China, and Southeast Asia. As an economically valuable plant worldwide, bamboo significantly contributes to the livelihoods and socioeconomic well-being of those involved in its cultivation. There are over 1,400 species of bamboo, with a diverse range of sizes and growth habits. Typical witches' broom symptoms were identified from the bamboo plantations at Seshachalam forest, Tirupati. An investigation was carried out to determine the association of phytoplasma with these symptoms. DNA was extracted from symptomatic as well as healthy bamboo leaves. The nested PCR amplification of the 16S rRNA gene was performed using primer sets P1/P7 and R16F2n/R16R2, yielding ~1.8 kb and ~1.25 kb amplicons, respectively. The results of phytoplasma identification in the symptomatic samples were further substantiated by using the *rp*multilocus gene, resulting in ~1390 bp amplicon using the primer pair rp (II) F/ rp (I) R1A. The nested PCR amplified ~1.2kb of 16S rRNA products and direct amplified ~1390 bp of *rp* gene products were purified, cloned, sequenced, and further analyzed for phytoplasma strain identification. BLAST and phylogenetic analysis revealed thatphytoplasma associated with bamboo belonged to the 16SrII group. To further confirm the classification at the subgrouplevel, virtual RFLP analysis was performed, which classified the phytoplasma associated with bamboo as *Candidatus* Phytoplasma citri (16SrII-D subgroup).

Keywords: Bamboo, witches' broom, phytoplasma, nested PCR, P1/P7, rp gene, *Candidatus* Phytoplasma citri

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OP-08

Mating-Type Analysis in (Rice False smut) *Villosiclava virens* Populations Based on PCR-Based Approach

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Abstract

Rice false smut disease caused by *Ustilaginoidea virens* (Cooke) Takahashi (teleomorph *Villosiclava virens* (Nakata) E. Tanaka & C. Tanaka is a destructive fungal disease of rice crop. The disease has gained national importance because of its effect on grain yield and quality. The individual rice grain infected by the fungus, transforms it to a powder form and the grain looks like an enlarged size ball known as smut ball. Fifty-two *U. virens* isolates collected from different zones *viz*., Western Zone, Eastern Zone, Central Zone and Southern Zone of different parts of rice growing regions were selected for the study. DNA of the respective isolates was isolated using modified CTAB method and all the *U. virens* isolates were confirmed with the specific ITS primer US1-5/US3-3 with the amplified product size of 380 bp. The PCR assay was standardized for *V. virens* idiomorph-specific primers to identify the mating type genes *viz*., MAT-1-1 and MAT-1-2. The genomic DNA of all 52 strains was subjected to PCR. The primer pair MAT-1-1F/MAT-1-1R amplifies 185bp of the MAT-1-1 idiomorphs and MAT-1-2F/MAT-1-2 primer pair amplifies 285bp of the MAT-1-2 idiomorphs. Among the 52 *V. virens* isolates collected, 34 (65.38%) isolates contained MAT1-1-1 idiomorphs and classified as MAT1-1-1 heterothallic mating type, 47 isolates (90.38%) had the MAT1-2-1 idiomorph and were classified as MAT1-2-1 heterothallic mating type, and 29 isolates (55.77%) contained both MAT1-1-1 and MAT1-2-1 idiomorphs and were classified as the homothallic mating type. Among the collected isolates, all the isolates from southern zone showed the presence of MAT1-2-1 idiomorph.

Keywords: False smut, idiomorph, mating type.

OP-09

Development of Reverse Transcription Recombinase Polymerase Amplification Assay for Rapid Diagnostics of Peanut mottle virus

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Abstract

Peanut mottle virus (PeMoV) is a single-stranded RNA virus transmitted through seeds and aphids that affects peanut crop worldwide. Enzyme-Linked Immune-Sorbent Assay (ELISA) and Reverse Transcription Polymerase Chain Reaction (RT-PCR) techniques are widely

employed to detect PeMoV in infected plants. ELISA is labour-intensive and time-consuming, involving preparation of buffers and production of polyclonal antibodies. Eventhough RT-PCR bypasses the need for buffer preparation and antibody production, it demands skilled manpower, requires expensive equipment like thermal cyclers, and involves complex procedures such as RNA isolation and cDNA conversion. The present study optimized the Reverse Transcriptase Recombinase Polymerase Amplification (RT-RPA) method by eliminating the steps of ribonucleic acid extraction, cDNA conversion, and the use of a thermal cycler. The optimized RT-RPA assay successfully detected PeMoV at concentrations as low as 10^{-6} and 10^{-7} dilutions (1µg/µl and 0.1µg/µl) of both RNA and crude sap templates, demonstrating high sensitivity comparable to the routine RT-PCR assay. The new RT-RPA technique was tested against other viruses that infect peanuts like the Peanut stunt virus, Tomato spotted wilt virus, and Peanut bud necrosis virus, this technique demonstrated great specificity and no cross-reactivity. The developed RT-RPA using a crude leaf sap template is time-saving, less laborious, not very complicated, high specificity, sensitivity, economical, and efficient. Therefore, laboratories with limited resources can use the RT-RPA assay for preliminary screening of PeMoV in nurseries, field and glasshouse conditions, and quarantine stations. The current study reports the development, optimization, and validation of Reverse Transcriptase Recombinase Polymerase Amplification (RT-RPA) using crude sap as a template for the onsite detection of PeMoV infection in peanut crops under field conditions for the first time.

PeMoV infection was confirmed by amplifying the expected size of 920 bp from the CP gene using the PeMoV1/2 primer pair. The RT-RPA was standardized by using the designed primer pairs PeMoV 2F/2R. Different lysis buffers were used for the preparation of crude leaf sap such as nuclease-free water, CTAB 5%, CTAB 10 %, phosphate buffer, TRIzol-TM reagent, RLT-buffer, RLC-buffer, EDTA, 1N-NaOH, and NaOH: EDTA (1:1). The assay was optimized with different temperatures and times of 5 °C - 50 °C (5 °C increment) and 5 to 50 minutes respectively. Among these, 1N NaOH followed by NaOH: EDTA (1:1) yielded the best results with an amplicon size of 300 bp at 45 °C for 40 minutes consistently. The detection limit of the RT-RPA assay was compared with that of RT-PCR using different dilutions of crude leaf sap, purified RNA, and plasmid. RT-RPA can detect upto 10^{-7}, 10^{-6}, and 10^{-12} dilutions, respectively. PeMoV was detected in 45 samples of 51 field-collected samples through RT-RPA whereas 42 samples were detected through RT-PCR indicating its comparable efficacy to RT-PCR. The results indicated that the developed assay was an efficient and sensitive method for detecting PeMoV and could be effectively utilized on samples collected from field. A rapid, reliable, robust RT-RPA assay was developed for the detection of PeMoV from infected peanut leaves by using crude leaf sap lysed from the 1N NaOH buffer. The assay required minimal resource setting dispensing off the need for sophisticated equipment like thermal cycler and template preparation, thereby reducing the associated cost and time and valuable for onsite detection and management of PeMoV in India.

Keywords: Peanut mottle virus, Recombinase polymerase amplification assay, on-site detection, Point-of-care testing.

OP-10

Characterization and Identification of *Dickeya zeae* Causing Bacterial Stalk Rot of Maize by Polyphasic Approaches

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Abstract

Bacterial stalk rot (BSR), caused by *Dickeya zeae* (syn. *Erwinia chrysanthemi* pv. *zeae*), has emerged as a significant disease affecting maize crop worldwide. In this study, infected symptomatic maize plants were collected from diverse agroclimatic zones in India during *Kharif* season over a period of three years from 2019 till 2021. Various approaches, including pathogenicity tests, cultural characteristics, biochemical profiling, and molecular analysis, were employed to accurately identify the collected bacterial isolates as *D. zeae*. The pathogen was isolated on semi-selective (crystal violet pectate) medium. Pathogenicity test was performed on 40-day-old maize plants by following Koch's postulates, as well as potato maceration assays. Their cross-infectivity study was conducted on rice, potato, tomato, and banana plants. Phenotypic and biochemical characterization confirmed that all the pathogen isolates belonged to the *Dickeya* genus. Based on specific amplification of a 420 bp fragment in the PCR assay, all 17 pathogenic isolates were further confirmed as *Dickeya*. Molecular characterization studies were performed on four isolates (UKMDZ-3, PBMDZ-7, TSMDZ-11, and HPMDZ-16), selected to represent distinct maize agroclimatic zones and four states of India (mention the names of states), and which caused severe infections on susceptible maize cv. Early Composite. Amplification of six characteristic genome regions (16S rRNA, recN, gyrB, dnaX, recA, and dnaJ) from these isolates facilitated individual and concatenated gene phylogenetic analyses, confirming their resemblance to *D. zeae*. This study represents the first comprehensive molecular analysis of *D. zeae* isolates from India, providing valuable insights for future crop improvement strategies. The findings contribute to our understanding of the genetic basis of BSR in maize and offer potential avenues for genetic enhancement to mitigate the disease's impact on maize cultivation.

Keywords: Bacterial stalk rot, maize, *Dickeya zeae*, cultural, biochemical and molecular analysis.

OP-11

Defining Genetic Diversity in *Fusarium udum*: A Study of Vegetative Compatibility Grouping among Pigeonpea Fusarium Wilt Isolates

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Abstract

Vegetative compatibility grouping (VCG) has emerged as a powerful tool to identify and differentiate closely related fungal isolates, providing insights into their genetic structure. Although widely applied to various fungi, VCG characterization has seen limited application for *Fusarium udum*, the pathogen responsible for wilt in pigeonpea. The present study was aimed to establish VCGs for *F. udum* isolates collected from major pigeonpea growing areas of Telangana during the year 2019-20. Fifty isolates were assessed through the generation of nitrate non-utilizing (nit) mutants using Puhalla's modification of Cove's method. Mutants were induced by culturing isolates on minimal agar medium with chlorate (MMC), which produced 286 chlorate-resistant sectors. The sectors were identified as nit mutants and classified phenotypically into nit1, nit3, and NitM based on growth patterns on specific nitrogen sources.

A total of 154 nit mutants were isolated, with 88.3% being nit1, 7.8% nit3, and 3.9% NitM. These mutants were subjected to complementation tests to identify vegetative compatibility among the isolates. Six NitM mutants served as testers to determine compatibility with nit1 and nit3 mutants. Compatibility was assessed based on the formation of robust aerial mycelia, which signified wild-type growth when complementary nit mutants interacted, indicating a positive vegetative compatibility reaction. Among the 342 tests, 82.4% exhibited wild-type or positive compatibility (++ or + reactions), indicating significant heterokaryon formation within these isolates. The study identified two major VCGs. Group VCG I included 48 isolates that showed strong reaction with at least one NitM tester, while VCG II comprised of two isolates (Fu-13 and Fu-42), which displayed moderate to weak or ambiguous reactions with NitMs, suggesting genetic differentiation. Pathogenicity analysis showed that the isolates within VCG I exhibited pathogenic variations, with six distinct pathogenic variants identified. Interestingly, isolates in VCG II were non-pathogenic, highlighting a potential link between VCG classification and pathogenicity. These findings provide valuable insights into the genetic diversity of *F. udum* in Telangana. The identification of distinct pathogenic and non-pathogenic groups within VCGs can improve disease management by helping to target pathogenicity-linked genetic groups. These results contribute to understanding the pathogen's genetic structure and highlight VCG analysis as a powerful tool for pathogen characterization. Implications extend to breeding efforts, where identifying and leveraging resistant pigeonpea varieties can aid in managing Fusarium wilt through targeted, genetics-based strategies.

Keywords: *Fusarium udum*, vegetative compatibility groups (VCG), genetic diversity, pigeonpea, Fusarium wilt, pathogenicity.

PP-12

Characterization of *Colletotrichum truncatum* Isolates from Soybean Growing Regions of India

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Abstract

Soybean is a globally grown oilseed and pulse crop where India occupies fifth position in soybean production. Anthracnose disease, caused by *Colletotrichum truncatum*, has a broad host range and may become a major threat to soybean yield in the coming years owing to climate change. Assessment of deviation among the *Colletotrichum* isolates is important with respect to host and climatic conditions of different soybean-growing regions of India. Cultural, morphological, and molecular approaches were applied to establish variation among the species. The majority of *Colletotrichum* isolates had identical morphology that was making it impossible to determine the species-level variation. Therefore, PCR-based sequencing was carried out to establish the difference among the isolates at the micro-level. The morphological characterization of 20 *C. truncatum* isolates revealed significant variations in growth, colony morphology, microsclerotia production, and spore dimensions. Molecular profiling using ITS primers identified distinct phylogenetic groups, with isolates clustering into two clades (C1 and C2). Sequence analysis showed 100% similarity within each clade, indicating genetic homogeneity. Clade C1 exhibited 95% resemblance to *Colletotrichum capsici*, while Clade C2 showed 93% similarity to *Colletotrichum dematium*. Notably, all isolates shared a common origin with *C. capsici*, *C. dematium*, and *Macrophomina phaseolina*. This study provides comprehensive insights into the morphological and molecular characteristics of *C. truncatum*

isolates. The current study on soybean anthracnose caused by *C. truncatum* investigation was crucial for reducing risk exposure and the possibility of a disease incidence in Indian soybean-growing regions under climate change scenario.

Keywords: Anthracnose, *Glycine max*, *Colletotrichum truncatum,* morphological and molecular characterization.

OP-13

Uncovering the Genetic and Morphological Landscape of *Ustilaginoidea virens*: A Deep Dive into False Smut Diversity in Rice

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Abstract

A detailed study of 22 isolates of *Ustilaginoidea virens*, the fungus that causes false smut in rice, uncovered considerable diversity in both their physical and genetic characteristics. The isolates varied in colony size and growth rates, with Uv3 growing to a maximum of 77 mm at a rate of 2.85 mm per day, while Uv11 was the smallest at 40 mm, growing at 1.48 mm per day. They showed differences in features such as colony color, height, patterns, sectoring, and formation of chlamydospores. Using cluster analysis based on these physical traits, the isolates were grouped into five main clusters, each with unique characteristics. Molecular analysis with PCR, using both universal and species-specific primers, produced products of 700 bp and 380 bp. Phylogenetic analysis placed Uv3 and Uv15 in clades X and VII, respectively, which included only Indian isolates, while Uv4 fell under clade II, grouping both Chinese and Indian isolates. A separate clustering based on 14 SSR markers created four groups, which differed from the morphological clusters. Genetic clustering aligned with geographical regions for 60% of the isolates, compared to only 30% alignment with morphological grouping, suggesting that genetic markers more accurately reflect relationships among *U. virens* isolates than physical traits do.

Keywords: False smut, paddy, *U. virens*, diversity, molecular and morphological characters, phylogenetic tree.

OP-14

Molecular Identification of *Bemisia tabaci* Biotypes and their Association with Secondary Endosymbionts

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Abstract

This study aimed to characterize *B. tabaci* biotypes and their associated secondary endosymbiotic bacteria in four districts of Andhra Pradesh. The existence of two genetic groups was revealed based on partial mitochondrial cytochrome c oxidase I gene sequence analysis. Isolates from YSR-Kadapa and Nellore belong to Asia-II-1 genetic group andAsia-II-8 genetic group was first time identified in Anantapur and Tirupati district of Andhra Pradesh. The association of secondary bacterial endosymbionts with *Bemesia tabaci* populations was also studied using16S rRNA/23S rRNA gene sequences. *Wolbachia,* as secondary endosymbiont was identified in all four isolates which belongs to super group B. Whereas, the association of *Cardinium* and *Arsenophonus* was observed from YSR -Kadapa *B. tabaci* population. The phylogenetic analysis identified *Cardinium* connected to C2 subgroup and *Arsenophonus* to A2 subgroup. *Rickettesia* was absent in all *B. tabaci* populations. Thus, Asia -II-1 genetic group from YSR-Kadapa was found in association with *Wolbachia, Cardinium* and *Arsenophonus*, while Asia-II-8 genetic group associated with only *Wolbachia.* This study highlights significant genetic diversity within *B. tabaci* populations on particularly on horse gram in Andhra Pradesh and emphasizes the importance of monitoring invasive biotypes like Asia II-8. Additionally, the detection of specific endosymbionts provides insights into potential biotype-specific interactions that could influence whitefly management strategies. Future research should explore the role of these endosymbionts in whitefly biology and vector competence.

Keywords: *Bemisia tabaci*, Mitochondrial cytochrome oxidase 1, endosymbiont, *Wolbachia, Cardinium Arsenophonus, Rickettesia.*

OP-15

Pathogenic Diversity of *Xanthomonas oryzae* pv. *oryzae* Causing Bacterial Leaf Blight of Rice in Andhra Pradesh

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Abstract

The study examines the pathogenic diversity and virulence of *Xanthomonas oryzae* pv. *oryzae* (Xoo) isolates from rice-growing areas of Andhra Pradesh, India, focusing on their interactions with bacterial blight (BB) resistance genes in rice. Twelve Xoo isolates were collected from varied locations and assessed for virulence using near-isogenic rice lines (NILs), each carrying single or combined BB resistance genes (Xa genes). Significant pathogenic diversity was observed across the isolates, which were subsequently grouped into seven pathotypes (APXoPt-1 to APXoPt-7). Each pathotype exhibited unique interaction with the resistance genes, reflecting varied levels of virulence. Pathotype-2 was found to be the most prevalent and is widely distributed across multiple districts. Pathotype distribution analysis also indicated geographic influence on pathogenic diversity, with isolates from different regions showing distinct virulence patterns. Virulence frequency analysis revealed that resistance genes such as Xa8, Xa4+Xa21, and Xa13+Xa21 demonstrated higher effectiveness across the isolates tested, while single genes like Xa1 and Xa3 exhibited only moderate effectiveness. These findings suggest that pathogenic diversity exists within the *Xoo* population and the presence of region-specific pathotypes pose challenges to BB management. Regular monitoring of virulence patterns and continuous profiling of new pathotypes are essential for enhanced BB resistance in rice. This research underscores the need for developing rice cultivars with durable resistance through careful selection and combination of effective resistance genes tailored to regional pathogenic profiles, thereby supporting sustainable rice production in bacterial leaf blight endemic areas of Andhra Pradesh.

Keywords: Pathogenic diversity, pathotype, resistance genes, virulence pattern.

THEME 2:

Biosecurity, Epidemiology and Climate Change of Plant Disease Epidemics

OP-16

Bacterial Canker: An Upcoming Threat to Mango Cultivation and Export in South India

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Abstract

Mango, *Mangifera indica* L., is considered as 'King of fruits". India is the major exporting country in world. Mango, mainly suffer from disease such as anthracnose, powdery mildew and malformation, and infestation of various pests resulting in reduced fruit yield. Under the changed climatic scenario, the minor disease, mango canker caused by *Xanthomonas campestris* pv. *mangiferae indicae*, is becoming one of the important diseases causing considerable losses ranging from 18 -26 % of yields. It is an upcoming threat in major mango growing states in South India such as Andhra Pradesh, Karnataka and Telangana states. An investigation was conducted at Mango Research Station, Nuzvid to record the detailed symptomatology. In addition, evaluation of mango cultivars against bacterial canker under natural condition was also carried out from 2019-2020 to 2023-2024. The symptoms were recorded on almost all aerial parts of the plant including leaves, petioles, fruits, flower stalks, tender stems and branches. The pathogen induced raised, angular, black leaf lesions with a chlorotic halo. It was recorded that severe leaf infection resulted in abscission and immature green leaf fall of 30 to 42 %, which directly depends on the orchard management by the farmers. Severe leaf fall was recorded in many mango orchards in January to March months. The fruit symptoms appear as small, water-soaked spots on the lenticels that later become star shaped, erumpent, and exude an infectious gum. Often, a "tear stain" infection pattern is observed on the fruit. Severe fruit infections caused premature drop. It was observed that dried twigs on trees are potential sources of inoculum. Yield loss up to 45% has been reported at grove scale for susceptible cultivars such as Banaganapalli in Andhra Pradesh and Telangana. Among 18 cultivars evaluated against mango bacterial fruit spots, Banaganapalli (Baneshan) and Cherukurasam were recorded as susceptible. However, Kothapalli Kobbari, Totapuri, Mallika, and Dasheri were resistant. The cultivars Pandhurivarimamaidi, Alfonso, Suvarnarekha, Panukulu and Nuzvid Chinnarasalu, and Tella Gulabhi recorded as moderately resistant, while Neelum, Kesari, Himampasand and Jalal were moderately susceptible. This information will be useful for future breeding programmes and for selecting mango cultivars during establishment of a new orchard.

Keywords: Bacterial disease, mango black spots, *Xanthomonas* sp., germplasm, screening.

OP-17

The Impact of Climate Change on Occurrence Pattern of Major Maize Diseases in Telangana, India

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Abstract

Maize (*Zea mays* L.) is one of the important cereal crops and nearly 61 diseases infect maize in India. Climate change is affecting the occurrence, prevalence and severity of plant diseases. Changes in rainfall distribution, temperature, excessive soil moisture or water logging or drought in maize producing areas lead to alteration in disease occurrence. The survey results in parts of Telangana on incidence of maize diseases during 2014-2015 to 2023-2024 indicated that there are consistent changes in disease occurrence based on local weather conditions. The decreasing trend of monsoon and scanty rainfall in some parts of Telangana led to the increased occurrence of post flowering stalk rot disease, caused by a fungal complex of *Macrophomina phaseolina* and *Fusarium verticilloides,* in majority of maize growing districts during *Kharif* and *Rabi* seasons as per the disease trap nursery and maize disease survey reports since 2015. Post flowering stalk rot occurrence was changed from 31% in 2015 to 73% in 2023 based on the local weather conditions. The foliar disease *viz*., Turcium leaf blight, which was 20-25% in 2015 was changed to less than 5% in 2023. Sporadic incidence of bacterial stalk rot, *Erwinia caratovora* (*Dikeya zea*), which was less than 2% in 2015, reached to 32% in 2016, 15% in 2017, 10% in 2018 and 8% in 2023 was noticed on few susceptible genotypes. In recent times, erratic excessive rains/soil moisture or water logging has become a regular feature at least once in the *Kharif* season, which is a predisposing condition to bacterial stalk rot of maize. Previously, bacterial stalk rot disease was never noticed or in very negligible proportions. There is a shift in disease pattern for the past few years as major maize diseases such as Pythium stalk rot, Turcicum leaf blight and Maydis leaf blight, downy mildew diseases, which are gradually becoming less important due to climate change effect, and development of hybrids with new sources of resistance. Hence there is an urgent need to develop suitable disease forecasting modules, breeding for climate resilient genotypes, rescheduling of crop planting, sensitization of farmers, extension workers, plant pathologists about the diversification of major diseases of maize in Telangana and development of disease management strategies to cope with the situations arisen due to climate change.

Keywords: Maize, climate change, post flowering stalk rot.

OP-18

Climate Change Impact on Fungi and Its Consequences on Life

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Abstract

The Earth's climate has been changing rapidly since the mid-twentieth century and this has consequences for all living organisms. These changes will affect the evolution of species and their ability to adapt, to migrate and reside within ecosystems. The climate change has direct effects on fungal growth and indirect effects on their habitats. Fungi play a dominant role in terrestrial decomposition and nutrient cycling, as well as plant nutrient uptake, plant health and the diet of many animals. Changes in fungal growth resulting from climate change will have considerable effects on ecosystem functions. Environmental disruptions due to climate change such as floods, storms, and hurricanes can disperse and aerosolize fungi, leads to increase in the geographic range of very rare unknown fungal pathogenic species or their vectors, causing the emergence of diseases in areas where they have not previously been reported. *Candida auris* is considered as the first novel pathogen to have evolved in response to climate change. *Fusarium* head blight (FHB) by *Fusarium graminearum* infection leads to reduced cereal yield and quality. Stripe rust is one of the most devastating global diseases of wheat recently seen to invade warmer regions. *Cryptococcus deuterogattii*, traditionally associated with tropical and subtropical climates, acquired greater capacity for thermal adaptation. *Batrachochytrium dendrobatidis* (*Bd*) is an emerging pathogen of amphibians causing most spectacular loss of amphibian diversity. It is surprising that black fungal yeast is found to survive in harsh habitat caused serious problems in covid time. *Talaromyces marneffei* occurring in immune compromised host has become an emerging pathogen. Unless action is taken to drastically reduce carbon emissions, the global temperature will continue to rise and the fungi are likely to continue to affect crops, native plants, and human beings with expanding ecological range and long-distance dispersal events producing new risks. Therefore the mycologists have to find out ways and means to stop these consequences, and need to explore the fungi that can provide the solutions to the global challenges.

Keywords: Biodiversity, climate change, fungi, pathogen, soil, temperature.

OP-19

Development of CRISPR Based Diagnostic Tools for Detection of Seed Transmitted Viruses in Quarantine

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Abstract

The exchange of germplasm exposed the world to greater risk of introducing exotic pests. ICAR-NBPGR Regional Station, Hyderabad was established to cater to the needs of plant quarantine activities of research institutes located in the southern part of the country, including international organizations. Several diagnostic methods are available for detection of different seed-transmitted viruses in quarantine and post-entry quarantine detection, *viz*., Enzyme linked immunosorbent assay (ELISA), Reverse transcription polymerase chain reaction (RT-PCR), and real-time quantitative RT-PCR. However, ELISA-based assays have insufficient sensitivity and require high-quality antibodies, and RT-PCR-based assays consume time and require expensive thermal cyclers. Recently, the collateral activities of clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated nuclease Cas systems like Cas12 have been exploited to develop highly specific, rapid, and sensitive diagnostic platforms. Currently, there is a need for the development of simple and user-friendly on-site diagnostic kits for the detection of seed-transmitted viruses in post-entry quarantine inspection. This diagnostic method can be performed at a single temperature in less than 30 minutes and integrated with a fluorescence visualiser to facilitate rapid, in-field diagnosis of seed-transmitted viruses. Peanut mottle virus (PeMoV) is a single-stranded RNA virus transmitted through seeds and aphids that affects peanut crops worldwide. For the diagnostics PeMoV, we developed a CRISPR/Cas12a-based visual nucleic acid detection system targeting the PeMoV coat protein gene. The whole process can be completed within 45 minutes with high sensitivity. This system could detect cDNAs diluted up to 10^{-5} when 2000 ng of total RNA was used for reverse transcription. The Cas12a/crRNA complex designed for PeMoV detection could recognise and cleave the targeted double-stranded DNA and ultimately cleave the single-stranded DNA probes and produce fluorescent signals. The green fluorescence produced under blue light (440-460 nm) in this procedure could be observed by the naked eye. The current study reports the development, optimisation, and validation of CRISPR-based diagnostic tools using crude sap as a template for detection of PeMoV infection in peanuts under quarantine for the first time. The development of CRISPR-based tools for detection of Cucumber mosaic virus infecting tomatoes and chilli is under way.

Keywords: Diagnostic tools, quarantine, clustered regularly interspaced short palindromic repeats, Peanut mottle virus

OP-20

Predicting Potential Climatic Suitability for *Ditylenchus dipsaci* in India Using MaxEnt Modeling

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Abstract

The stem and bulb nematode, *Ditylenchus dipsaci* is a major nematode parasite of plants that causes economic damage to a wide range of plants, particularly in areas with a temperate climate. This nematode is not reported to occur in India and has been listed as a quarantine pest as per the Plant Quarantine Order (Regulation of import into India) 2003. Understanding the suitable habitat and potential geographic distribution areas of *D. dipsaci* in India would greatly increase the understanding of its establishment and extent of its spread. The maximum entropy (MaxEnt) model was used in this study to identify the potential geographic distribution in India under current climatic conditions. Spatial analysis software, DIVA-GIS was used for visualization of the maps. The model-predicted suitable areas for *D. dipsaci* are distributed in the parts of Himachal Pradesh and Uttarakhand states, and the Jammu and Kashmir Union Territory in northern India besides Sikkim, Arunachal Pradesh and a few parts of Manipur in the northeastern region. The climatic envelopes (annual mean temperature and annual precipitation) for *D. dipsaci* based on the occurrence data revealed that maximum occurrence points are present in the temperature range of 5 to 25 °C and precipitation range of 200 to 1500 mm. Among the bioclimatic variables, annual mean temperature (Bio1) and precipitation seasonality (Bio15) have more influence on the geographic suitability for *D. dipsaci*. The study revealed that congenial climatic conditions are available for *D. dipsaci* in India for their establishment. Therefore, strict quarantine vigilance is required for this regulated nematode due to its extensive dissemination abilities through planting material, its serious damage and survival potential, and subsequent management challenges.

Keywords: Distribution, *Ditylenchus dipsaci*, MaxEnt modeling, prediction

OP- 21

Mapping of Risk Areas Associated with Brown Spot Disease of Rice in Jharkhand and Chhattisgarh States Using Inverse Distance Weighed (IDW) Spatial Interpolation Method

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Abstract

Brown spot disease in rice caused by *Bipolaris oryzae* (*Syn: Helminthosporium oryzae*; telemorph=*Cochliobolus miyabeanus*) is known to cause both qualitative and quantitative loss. An extensive roving survey was conducted during *Kharif* 2023 across major districts in both the states to assess the incidence and severity of brown spot disease in rice. Inverse distance weighed (IDW) spatial interpolation technique was used to estimate the value of unknown point by using weighed average of nearby known points.In the investigation, IDW method was used to identify the risk associated with brown spot disease in Jharkhand and Chhattisgarh states. In Jharkhand and Chhattisgarh, the overall disease incidence ranged from moderate to severe in most areas surveyed. However, high to very high disease severity (50-70%) was reported in certain districts of Jharkhand, *viz*., Chaibasa, Khunti, Hazaribagh, Koderma, and Giridih, while moderate to severe (30-50%) brown spot disease was observed in different villages of Deoghar, Jamtara, Dumka and Bokaro districts. On the contrary, villages in Gumla, Lohardaga, Latehar, Daltonganj, Chatra, Dhanbad, Saraikela and Palamu exhibited moderate severity (25-30%), while regions like Ramgarh, Rampur and parts of Jamshedpur recorded very low disease severity (<5-10%). In Chhattisgarh, brown spot severity was notably higher in villages of Jagdalpur, Bilaspur, Bemetara, Mungeli, Korba, and Ambikapur districts. However, areas in Kabirdham, Kanker, and Kondagaon showed low to moderate severity, with the lowest levels recorded in Raipur district. Overall, disease severity was more pronounced in fields planted with local rice varieties and those managed poorly, while rice hybrids showed lower incidence and severity in both states. Based on IDW spatial interpolation method, areas such as Chaibasa, Kunti, Gumla, Hazaribagh, Dumka and Jamtera in Jharkhand; Jagdalpur, Bilaspur, Bemetera, Mungeli, Korba and Ambikapur districts of Chhattisgarh were identified as risk associated areas for brown spot disease.

Keywords: Inverse distance weighed spatial interpolation, IDW

OP- 22

Influence of Initial Inoculum Load and Distribution on Sheath Blight Epidemic Progression in Rice Cultivars under Coastal Ecosystem of Andhra Pradesh

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Abstract

Sheath blight disease caused by *Rhizoctonia solani* is a major threat to rice cultivation. Field investigations in Andhra Pradesh revealed that higher inoculum levels significantly increased disease incidence, with susceptible cultivars like MTU 7029 showing the highest diseased area (97.2%), lesion length, and disease severity compared to tolerant cultivars such as MTU 1001 and TETEP. Inoculum distribution also influenced disease progression, with random distribution intensifying the impact compared to aggregated distribution. Field trials at Regional Agricultural Research Station, Maruteru, confirmed that both inoculum density and distribution patterns affected disease spread in susceptible and tolerant cultivars. Principal component analysis identified per cent diseased tillers and diseased area as major contributors to sheath blight incidence. Simulated epidemics using the *r* algorithm aligned well with observed data, highlighting primary infection rate as a key factor in disease progression, while secondary infection had minimal impact, particularly at high inoculum densities and random distribution. However, discrepancies like the misclassification of tolerant cultivars based solely on diseased area indicated the need for integrating additional parameters, including host and pathogen dynamics, to refine the model. This study underscores the importance of inoculum management and improved simulation tools for effective sheath blight management in the coastal rice ecosystem of Andhra Pradesh.

Keywords: *Rhizoctonia solani*, infection rate simulation, rice, inoculum levels, epidemics.

OP-23

Influence of Weather Parameters on Powdery Mildew Disease of Sunflower

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Abstract

An experiment was conducted at Regional Agricultural Research Station, Nandyal, during *Rabi* 2021-22 to study the influence of weather parameters on powdery mildew disease of sunflower using the susceptible hybrid KBSH-44. The crop was sown on four different dates: November I fortnight (FN), November II FN, December I FN, and December II FN. Results showed that the lowest disease severity (PDI: 10.5%) was observed in the fourth sowing date (December II FN), while the highest severity (PDI: 36.6%) was recorded in the first sowing date (November I FN). Disease initiation occurred earlier in the first sowing (January, flowering stage) compared to the fourth sowing (February, star bud stage). Correlation studies revealed that PDI was positively correlated with maximum temperature (0.36) and temperature range at a 1% significance level, as well as with mean temperature and wind velocity (0.34) at a 5% significance level. Conversely, PDI showed a negative correlation with evening relative humidity (-0.3) and relative humidity range. These findings highlight the role of weather factors in influencing disease severity, aligning partially with earlier studies by Karuna et al. (2016). The study concludes that to minimize powdery mildew severity and associated yield losses, sowing sunflower in the second fortnight of December is recommended during the *Rabi* season.

Keywords: Sunflower, powdery mildew, *Golovinomyces cichoracearum*, weather parameters, date of sowing, disease severity, PDI

OP-24

Epidemiological Studies of the Anthracnose Disease in major soybean growing areas of Telangana state

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Abstract

Soybean (*Glycine max* L.), known as the "Golden Bean," is a major oilseed crop in India with high nutritional value, containing 20% oil and 40% protein. Globally, soybean production is 385.5 million tonnes, with a productivity of 2.51 t/ha over 132.5 million hectares. In India, Madhya Pradesh leads in soybean production, while Telangana ranks fourth. Among soybean diseases, anthracnose is a significant concern in Telangana, often appearing in epidemic proportions in major growing areas and causing extensive crop damage. Favourable conditions for the disease include temperatures of 22-29°C, relative humidity >80%, and optimal rainfall. A two-year survey conducted during *Kharif* 2023 and 2024 in Telangana revealed anthracnose incidences of 40% and 45%, respectively. In 2023, the disease first appeared in August (34th meteorological week) under conditions of 30.9°C maximum and 23.9°C minimum temperatures, 3.4 cm cumulative rainfall, and 87.4% relative humidity. It peaked (PDI: 40) in October (40th week) with 33.9°C maximum and 22.7°C minimum temperatures, 4.2 cm rainfall, and 79.3% relative humidity. Similarly, in 2024, disease onset was in August (35th week), peaking (PDI: 45) in October (41st week). This survey highlights the disease progression and emphasizes the need for timely management strategies to prevent yield losses.

Keywords: Soybean**,** anthracnose, epidemiology, weather factors, disease incidence

THEME 3:
Host Plant Resistance and Molecular Approaches of Disease Management

OP-25

Secreted in Xylem (*SIX*) Genes Profiling of *Fusarium oxysporum* f. sp. *ricini* Isolates from Castor Growing Regions in India

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Abstract

The cultivation of castor crop (*Ricinus communis* L.) is economically significant due to its diverse industrial applications. However, wilt disease caused by *Fusarium oxysporum* f. sp. *ricini* leads to substantial yield losses in castor. This pathogen produces *Secreted in Xylem* (*SIX*) effectors, which are critical in host-pathogen interactions and determine pathogen virulence. A study was conducted on 20 isolates of *F. oxysporum* f. sp. *ricini* (*For*) collected from various castor growing regions in India to analyze the presence of 14 *SIX* genes (*SIX*-1 to *SIX*-14). Ten complements of genes (*SIX*-1, *SIX*-3, *SIX*-5, *SIX*-7, *SIX*-8, *SIX*-9, *SIX*-10, *SIX*-11, *SIX*-12 and *SIX*-13) were identified, ad *SIX*-1 and *SIX*-8 genes were consistently present across all the isolates. Highly virulent *Fusarium* isolate *For*-1 from Palem, Telangana exhibited highest number of gene complements comprising eight *SIX* genes (*SIX*-1, *SIX*-3, *SIX*-5, *SIX*-7, *SIX*-8, *SIX*-9, *SIX*-10 and *SIX*-11) indicating a strong potential for pathogenicity. Expression profiling of the *SIX* genes in the highly virulent isolate *For*-1 was conducted in resistant (cv. AP-33) and susceptible (cv. JI-35) castor genotypes at 0, 24 and 48 hours after inoculation (hai). The results indicated that the susceptible genotype exhibited increased expression of *SIX* genes with increase in time, reflecting a breakdown in defense mechanisms, whereas the resistant genotype maintained a balanced expression profile. Notably, in susceptible cv. JI-35, strong expression of genes was noticed at 48 hpi with *SIX*-8 and *SIX*-10 showing the highest expression, followed by *SIX*-11 and *SIX*-7, while the expression levels of *SIX*-1 showed a slight alteration. This differential gene expression emphasized the distinct roles of *SIX* genes in the infection process, underscoring their potential as diagnostic markers for assessing virulence in *F. oxysporum* f. sp. *ricini* isolates.

Keywords: *Secreted in Xylem genes,* wilt disease, *F. oxysporum* f. sp. *ricini*, resistant, susceptible, castor, genotype

OP-26

Identification of Resistant Sources for Brown Spot of Rice from Wild Rice Introgressed Lines

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Abstract

Brown spot disease in rice caused by *Bipolaris oryzae* (*syn-Helminthosporium oryzae*; telemorph=*Cochliobolus miyabeanus*) is known to cause both qualitative and quantitative loss. Host plant resistance to brown spot disease in rice has remained a relatively unexplored area, largely due to the lack of a precise and reliable artificial screening methodology. The development of an effective artificial screening method depends heavily on obtaining consistent and abundant sporulation of the causal fungus, *B. oryzae*. In our investigation, we studied the inter-relation of different light and nutritional sources on the sporulation of the fungus and found that, among the different nutrient sources, Rabbit food agar (RFA) followed by corn meal agar could induce good vegetative growth and excellent sporulation in fungus after exposure of fungus to near ultra violet light. A field based high throughput artificial mass screening method was standardized at ICAR- Indian Institute of Rice Research, Hyderabad to identify the donors. Sandwich method of layout with spray of conidial suspension was adapted in this method. Around 185 wild rice introgression lines derived from *O. rufipogon x Samba Mahsuri* were artificially screened for three consecutive seasons (2021-23). Out of 185 wild rice introgression lines screened, four lines showed good level of resistance (CGIL-1, 2, 8, and 33 recorded score of 3). The AUDPC and rate infections were computed based on periodical increase in disease severity, which varied among different lines. Among the popular varieties, BPT 5204, Swarnadhan, Gangavathi Sona and Purple rice were identified as highly susceptible while CH-45, Tetep, Tadukan and IR-64 were moderately resistant (score of 4-5) varieties. The lines identified for brown spot resistance in the present study are employed in breeding for brown spot resistance.

Keywords: Brown spot, rice, wild rice

OP-27

Hypersensitive and Absolute Resistance to Bean common mosaic virus (BCMV) and Bean common mosaic necrosis virus (BCMNV) Conferred by the Dominant *"I"* and Recessive *"bc-3"* Genes in Common Bean

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Abstract

Bean common mosaic virus (BCMV) and Bean common mosaic necrosis virus (BCMNV) are among the most challenging threats for common bean production in India due to their easy transmission through aphid vectors and also through infected seeds. Highly valuable Indian common bean varieties and landraces are more susceptible to BCMV and BCMNV. However, some varieties that exhibit high resistance to these viral strains are often went un-noticed. The genetic control towards these both viruses are governed by a single dominant (*I*) gene and few recessive (*bc-1, bc-1*^{2}*, bc-2, bc-2*^{2}*, bc-3* and *bc-u*) genes. Our aim was to identify common bean genotypes, bearing the dominant *I* gene, which confers resistance through a hypersensitive response resulting in a localized vein necrosis on the primary inoculated leaves and recessive *bc-3* gene that together can provide durable resistance towards BCMV and BCMNV. In the current study, 150 genotypes of common bean were mechanically inoculated with a mixture of BCMV and BCMNV strains maintained on *Nicotiana benthamiana* plants. Both SCAR and SNP markers were utilized to screen common bean germplasm for the presence of these two resistant genes. The genotypes showing resistance towards the virus were re-confirmed by repeated inoculations using the same set of strains used earlier. The expression of BCMV in the resistant genotypes was also understood properly through a time course experiment in a qPCR assay. Those genotypes bearing single dominant, recessive resistant genes and valuable gene combination of *I, bc-3* was established in the screened germplasm. This extensive identification of resistant common bean genotypes against BCMV and BCMNV can be readily included for the common bean breeding program of India for virus resistance.

Keywords: *Phaseolus vulgaris*, poty virus, resistance, genotype

OP-28

Screening of Rice Genotypes for Resistance against Bacterial Leaf Blight of Rice Caused by *Xanthomonas oryzae* pv. *oryzae*

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Abstract

Rice yield is affected by a number of diseases among which bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv *oryzae* (Xoo) is one of the oldest and most severe diseases. It is a significant vascular disease of irrigated and rainfed rice and severe infection may lead to substantial yield losses. As chemical control is found to be ineffective against BLB, the only feasible and economical way of controlling disease is the use of resistant rice cultivars. Hence, the present study was undertaken with the aim of evaluating 158 entries received from the PJTAU Rice Research Stations of Kunarum, Warangal, Kampasagar, Jagtial and Rajendranagar under MRST trials, 31 entries of Warangal released varieties and promising cultivars and 35 entries under conformation and identification of differentials. These genotypes were screened against BLB during *Kharif* 2018 at Regional Agricultural Research Station, Warangal, Telangana. Identification of resistant genotypes was done by artificial inoculation of *X. oryzae* pv *oryzae* using leaf clipping technique at 45 days after transplanting. Among 236 entries screened against BLB disease, only 16 entries (Jagital-JGL 24423, JGL-28547 and JGL-33510 entries, Rajendranagar- RNR-28360, RNR-28362, RNR-26116, RNR-25980 and RNR-25979 entries, Warangal promising varieties- WGL-915, differentials- IRBB-63 and IRBB-64; biotechnology- IBTR 2, ML-S8-3, ML-S3-1, ML-S1-1 and TPL-56-3 entries) showed the lowest disease incidence of about 1-5% (scale 1). The key recommendations from this study is the following entries Jagital- JGL 24423, JGL-28547 and JGL-33510 entries, Rajendranagar- RNR-28360, RNR-28362, RNR-26116, RNR-25980 and RNR-25979 can be used in crossing programmes for development of high yielding and disease resistant/tolerant to BLB disease in rice.

Keywords: Rice, bacterial leaf blight, genotypes screening, resistance

OP-29

Lupeol: A Predisposing Factor for the Pathogenesis of Gray Mold, *Amphobotrys ricini* Pathogen in Castor

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Abstract

Gray mold caused by *Amphobotrys ricini* is one of the most destructive diseases of castor and is a serious constrain in castor production. The wax layer, which serves as a protective barrier during plant-pathogen interaction, is vital in determining the plant's resistance or susceptibility towards the pathogen. This study was aimed to understand the castor wax layer's multifaceted contribution to *A. ricini* pathogenesis. The hydrophobic components of cuticular wax from waxy and non- waxy castor genotypes were analyzed by Gas Chromatography-Mass Spectrometry (GC-MS) technology, which enabled the stable detection of various fatty acids and terpenoids. The investigation revealed a significant presence of triterpenoid compound, 'lupeol', accounting for approximately 53.6% of the wax composition in the waxy genotype (DCH-519), which was absent in non-waxy genotype (ICS-324). On exposure to lupeol, about 93.3% of conidia germinated leading to rapid mycelial growth and sporulation of *A. ricini.* Scanning electron microscopy (SEM) analysis of waxy and non-waxy genotypes infected with *A. ricini* confirmed faster germination and production of longer germ tubes on waxy genotype compared with non-waxy genotype. The pathogen's growth was highly stimulated in the presence of lupeol, which may likely due to early recognition of the suitable host, ultimately aiding in speedy germination and growth of the pathogen setting pace for pathogenesis. Thus, it was inferred that castor capsule epicuticular wax containing lupeol as predominant triterpenoid, aiding in pathogen infection.

Keywords: Castor, gray mold, pathogenesis, wax layer

OP-30

Screening of Sesame Genotypes for Resistance against Powdery Mildew Disease

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Abstract

Sesame, *Sesamum indicum* L., a vital oilseed crop of the family *Pedaliaceae*, is among the oldest oilseed crops cultivated for its high oil (38-54%) and protein (18-25%) content. India leads globally in sesame production, cultivating in 15.23 lakh hectares with an output of 8.02 lakh tonnes and a productivity of 527 kg/ha. In Andhra Pradesh, it is grown over 39,000 hectares, producing 14,000 tonnes with a productivity of 343 kg/ha during 2021-22. Sesame thrives in well-drained soils and diverse agro-climatic regions, demonstrating resilience to biotic and abiotic stresses. However, powdery mildew, a significant foliar disease prevalent in humid conditions with low night temperatures, can cause yield losses of 25-50%. Cultivar resistance is an eco-friendly and effective strategy for managing this disease. During the *Rabi* seasons of 2020-21 and 2021-22 at Agricultural Research Station, Yellamanchili, 20 sesame genotypes were screened for powdery mildew resistance using artificial inoculation and a 0-5 severity scale after 50-60 DAS. Results revealed that IC260713 and IC208567 as the most resistant (5% severity), followed by LT-10 (6%), VZM-9 (7.5%), IC179934 and YLM-142 (8%), YLM-146 (9%), and YLM-66 (10%). In contrast, the Local Check "Madhavi" showed 55% disease severity. These resistant genotypes offer potential for breeding high-yielding, disease-resistant varieties. Their adoption can enhance productivity and reduce dependence on chemical control measures, contributing to sustainable sesame cultivation.

Keywords: Sesame, powdery mildew, resistance

OP-31

Screening of Blackgram Genotypes for Yellow Mosaic Disease Resistance and Validation of Molecular Markers Linked to YMD Resistance

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Abstract

Blackgram genotypes (126 numbers) were screened for yellow mosaic disease (YMD) resistance under natural conditions during summer 2024 in a randomized block design with two replications. To provide uniform disease pressure, the YMD susceptible check, LBG 648, was seeded on both sides of the test genotypes. The disease reaction in the genotypes was recorded using 0-9 disease rating scale at harvesting stage and were categorized into Immune (I), Resistant (R), Moderately Resistant (MR), Moderately Susceptible (MS), Susceptible (S) and Highly Susceptible (HS). Out of 126 genotypes screened, 22 genotypes were found to be disease free, 65 as R, 24 as MR, 9 as MS, 3 as S and 3 as HS. A set of 24 SSR markers were validated for yellow mosaic disease resistance in 36 selected blackgram genotypes. Thirteen markers out of 24 (54.2%) showed polymorphism among the genotypes tested. Twelve markers were producing two distinct alleles among the genotypes. These markers amplified a total of 38 alleles with Polymorphic Information Content (PIC) values ranging from 0.11 (VMGSSR83) to 0.65 (CEDG97) with an average of 0.42. DARWIN cluster analysis revealed that most phenotypically resistant genotypes grouped together, while susceptible genotypes formed separate clusters. These genotypes can serve as useful sources of YMD resistance in blackgram breeding programme.

Keywords: MYMV, SSR markers, urdbean, resistant sources

OP-32

Comparing the Efficiency of Field Artificial Screening Methodology with the Natural Disease Screening at Hot Spot Areas for Rice False Smut Disease

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Abstract

False smut of rice, caused by *Ustilaginoidea virens* (Cooke) Takah., has emerged as a most important grain disease in India. It has increased considerably both in terms of its intensity and geographical spread resulting in considerable yield loss. The major constraint in development of resistant varieties against false smut was lack of resistant/tolerant donors due to difficulty in the establishment of artificial screening technique. Injection of conidial suspension at booting stage of the crop is the promising methodology and we have modified and improved the mass multiplication methodology for harvesting high number of *U. virens* conidia for large scale screening of rice genotypes. In this study, through All India Coordinated Research Project on Rice Program, we evaluated one hundred and twelve (112) National Screening Nursery 1 (NSN-1) entries with the duration of early and mid-early under natural hot spot areas and also by standardized artificial screening methodology at Plant Pathology Co-ordinated centers. Natural screening was carried at three locations *viz*., Gangavathi, Gudalur Masodha and entries were artificially screened at the established screening facility at ICAR-IIRR, Hyderabad. Under natural disease infections, observations were recorded as number of hills infected and maximum number of smut balls per Hills. Number smut balls per panicle were recorded in case of artificial screening. At Gudalur, Tamil Nadu, under natural infestation, the percentage of disease infection was 100% and all the entries were infected and the infection level was varied between the entries. At Gangavathi, Karnataka, level of false smut infection was around 72% and 84 % at Masodha, Uttar Pradesh. At ICAR- IIRR, Hyderabad under the established facility, the entries were screened and artificial the percentage of infection was around 93% and maximum of 64 smut balls recorded in the susceptible variety CO-51.

Keywords: Rice, false smut, artificial inoculation, screening methodology

OP-33

Screening for Multiple-Resistance of Pigeonpea Genotypes against Fusarium Wilt and Sterility Mosaic Disease

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Abstract

Pigeonpea, *Cajanus cajan,* is one of the important grain legume crops cultivated in the semi-arid tropics, playing a crucial role in the economic well-being of subsistence farmers. India is the major producer of pigeonpea, accounting for over 75% of the world's production. Fusarium wilt and Sterility mosaic disease (SMD) are the major constraints to pigeonpea cultivation in the Indian subcontinent, leading to potential yield losses up to 70-100%. To overcome these issues, host plant resistance is considered to be one of the economically cost-effective methods. Thirty-eight genotypes including checks *i.e.,* ICPL-2376 (Fusarium wilt); ICP-8863 (SMD) were screened for Fusarium wilt and SMD resistance by adopting Sick plot and leaf stapling techniques, respectively under field conditions during *Kharif* 2022-23 at Regional Agricultural Research Station, Warangal. Based on the percent disease incidence, the genotypes could be classified as Resistant (0-10%), Moderately resistant (11-35%) and Susceptible (35-100%). Variable reaction of resistance was observed among the tested genotypes against both the diseases. Out of 38 genotypes screened, three genotypes *i.e.,* WRGE-167, WRG-443 and WRG-476 showed resistant reaction (0-10%) against both the diseases *i.e.,* Fusarium wilt and SMD. Twelve genotypes (WRGE-150, WRGE-155, WRGE-147, WRGE-165, WRGE-160, WRGE-169, WRGE-177, WRG-447, WRG-486, WRG-500, WRG-504 and WRG-512) were moderately resistant to both diseases and nine genotypes (WRGE-173, WRGE-174,, WRGE-178, WRG-468, WRG-476, WRG-488, WRG-503, WRG-505 and WRG-507) showed resistance only to sterility mosaic disease, while five entries (WRGE-171, WRGE-176, WRGE-181, WRG-446, WRG-464) showed resistance to Fusarium wilt disease alone. Therefore, the genotypes with multiple disease resistance can be utilized in varietal developmental programme for better sustainability of the crop.

Keywords: Genotypes, pigeonpea, resistance, Fusarium wilt, Sterility mosaic disease

OP-34

Evaluation of Resistance to Stem Rot in Groundnut Lines through Field, Glasshouse, and Laboratory Screening

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Abstract

Stem rot, caused by *Sclerotium rolfsii* Sacc., is a significant constraint in groundnut cultivation across Asia, sub-Saharan Africa, and the Americas. This study was aimed to identify resistant groundnut lines through rigorous screening under laboratory, glasshouse, and field conditions. Two experiments conducted during the rainy seasons of 2022 and 2023 at ICRISAT, India, evaluated disease incidence at intervals of 15-, 30-, 45-, and 60-days post-inoculation. Five lines, namely ICGV 171025, ICGV 181035, ICGV 181458, ICGV 211107, and ICGV 171002, demonstrated moderate resistance with disease incidence below 30%, while other lines exceeded 30%, marking them as susceptible. In laboratory assays, oxalic acid solutions at concentrations of 20mM and 50mM were used to assess the wilt response in detached main and lateral stems. The stems were immersed in these solutions, and wilting symptoms were recorded at 12, 18, and 24-hour intervals. Significant wilting was observed at 20mM after 24 hours in lateral stems, while at the higher concentration of 50mM, wilting symptoms appeared earlier, at 18 hours for lateral stems and between 18 and 24 hours for main stems when compared with control (0 mM concemtration). This differential response highlighted oxalic acid's role in distinguishing resistant from susceptible lines, with the four lines (ICGV 171025, ICGV 181035, ICGV 171002, and ICGV 211107) consistently showing moderate resistance across field, glasshouse, and laboratory assays. To further validate these findings, gene expression studies focused on defense-related genes, specifically Polyamine biosynthesis genes (Ornithine decarboxylase, Spermine synthase), Ethylene biosynthesis genes (ACCS, ACCO2), and lipoxygenase genes, with actin as a reference gene. RNA from the second leaf from the base was extracted at 24-, 48-, and 72-hours post-infection to evaluate cDNA expression levels. These studies provide a deeper understanding of genetic resistance mechanisms, potentially contributing to breeding programs aimed at combating stem rot disease in groundnuts.

Keywords: Groundnut, stem rot incidence, screening, host plant resistance, *Sclerotium rolfsii*

OP-35

Modified *in vitro* Infection Models for Charcoal Rot Pathogen and Identification of Potential Fluorescent Pseudomonads against *Rhizoctonia bataticola*

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Abstract

Rhizoctonia bataticola, the causal agent of charcoal rot disease in soybean, affects numerous economically important crops, including cereals, legumes, vegetables, and fruits. *In-vitro* semi artificial experiment set-ups offered several advantages but lack the root-soil interface. Interlinked multi-component complexity of the rhizosphere required experimental designs and at present, there is no described methodology for *in-vitro* interaction involving root-soil interface in semi-artificial experimental set-ups. In the present study, we report a method to raise plantlets of different crops, and soybean in particular, in modified Petri plates/rings for *in-vitro* interaction, involving root-soil interface in semi-artificial experimental setups. We also monitored the colonization of fluorescent *Pseudomonas* isolate 9704 in soybean cultivar CG-SOYA1 roots following the root imprinting methods. The model demonstrated bi- and tri-partite interaction studies, validated by the inhibition of *R. bataticola* (61%) by *Pseudomonas* isolate 9704, which inhibited *R. bataticola* by 61% in confrontation assays. In tripartite setups, microsclerotia of *R. bataticola* showed reduced germination on soybean CG-SOYA1 roots colonized by *Pseudomonas* compared to *Pseudomonas*-uncolonized roots, highlighting the protective role of the bioagent. This innovative infection model provides a controlled platform for evaluating pathogen-host interactions and the efficacy of biocontrol agents, fungicides, and botanical formulations against charcoal rot disease.

Keywords: *Pseudomonas*, *Rhizoctonia bataticola*, Bi and Tri partite interaction, modified Petri plate technique

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OP-36

Identification of Parents and Superior Crosses for Yield Components, Quality Traits and Powdery Mildew Tolerance in Sesame

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Abstract

This study was conducted at Regional Agricultural Research Station (RARS), Polasa, Jagitial with an objective to identify superior sesame parents and crosses for yield components, quality traits and powdery mildew tolerance. Eighteen crosses were generated using six lines and three testers in line × tester model during late *Kharif* 2023. These crosses along with parents were evaluated during summer 2023 in RBD with three replications. Data on fifteen yield components and oil quality traits were recorded. The infector row technique was followed to screen the genotypes for powdery mildew tolerance, where two rows of susceptible check Swetha, was sown all around the bed. The data were recorded at 50-60 days after sowing when the disease incidence was maximum on the susceptible check adopting the 0-9 grade (TNAU 1980) and PDI was recorded as per the formula given by Mc Kinney (1923). Combining ability analysis revealed predominance of non additive gene action in inheritance all the traits except number of capsules per plant. Among parents, Swetha and Rajeswari were found to be good combiners for major yield and oil quality parameters. Among the crosses, Swetha × BRT-04, JCS DT 26 × BRT-04, JCS 3202 × ES-139-2-84 and Swetha × JCS 4019 exhibited best specific combining ability for seed yield and quality traits. Three parents *viz.*, Swetha, Rajeshwari and JCS DT 26 shown susceptible (54, 50.24 and 50.61%) reaction against powdery mildew disease respectively, whereas BRT -04 was found resistant. Six crosses *viz.,* JCS 2454 × BRT-04, JCS 1020 × BRT-04, Rajeshwari × JCS 4019, JCS 1020 × ES-139-2-84, Swetha × ES-139-2-84 and Rajeshwari × ES-139-2-84 were found resistant to powdery mildew. These crosses also had good yield characters such as 1000 seed weight and seed yield per plant with range of 3.15 to 3.38 g and 7.28 to 9.01 g, respectively. These crosses may be advanced to further generations for isolation of transgressive segregants for yield and disease resistance.

Keywords: Sesame, combining ability, yield components, oil quality parameters, powdery mildew

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OP-37

Genetic Resistance to Fusarium Wilt in Safflower Core Germplasm

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Abstract

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *carthami*, poses a significant challenge to safflower, *Carthamus tinctorius* L. production, with a potential yield loss up to 80% globally. Despite its impact, research on genetic resistance within diverse safflower germplasm has been limited, creating a critical gap in disease management strategies. Moreover, current breeding programs often fail to incorporate a wide range of resistant sources, hindering the development of cultivars with strong resistance to Fusarium wilt. To address these challenges, we evaluated a core set of 283 safflower genotypes obtained from ICAR-National Bureau of Plant Genetic Resources, New Delhi. These genotypes were screened for disease resistance in wilt-sick pots under greenhouse conditions using a virulent isolate of *F. oxysporum* f. sp. *carthami* sourced from the culture collection unit of ICAR - Indian Institute of Oilseeds Research. Plants were assessed for disease incidence using a standardized disease severity scale. Our results demonstrated significant variation in disease response, with disease incidence varying from very low to high resistance levels. In particular, 182 genotypes were classified as highly resistant, 23 as resistant, 13 as moderately resistant, 4 as moderately susceptible, 5 as susceptible, and 56 as highly susceptible. These findings provide valuable insights into the genetic diversity of Fusarium wilt resistance in safflower. A genome-wide association study (GWAS) is currently in progress to identify genome regions associated with wilt resistance in this core set. Furthermore, the identified resistant genotypes have the potential to be utilized in breeding programs to develop Fusarium wilt-resistant safflower cultivars, thus contributing to management and improving safflower productivity.

Keywords: Safflower, Fusarium wilt, *Fusarium oxysporum* f. sp. *carthami*, resistance, breeding, core germplasm

OP-38

Unravelling the Interaction of Rice Tungro Disease with Rice Phytoplasmas and its Transgenic Resistance

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Abstract

Rice occupies 25% of India's cultivated land and is a primary food source for half of the population. Rice Tungro Disease (RTD) leads to annual economic losses of around $340 million in Southeast Asia, causing 5-10% yield reductions in Asia and with a 2% drop in India's national production posing a significant threat. RTD results from a co-infection of two viruses: Rice tungro bacilliform virus (RTBV) and Rice tungro spherical virus (RTSV) with symptoms, including stunted growth and yellow-orange leaf discoloration. The tungro virus complex is semi-persistently transmitted by the green leafhopper (GLH), *Nephotettix virescens*. The most practical current approaches for tungro control are growing resistant varieties (host plant resistance) and implementing appropriate cultural practices. RNA-mediated resistance has been the underlying principle in some of the examples of successful transgenic virus resistance. The study discusses the introgression of PB 1 transgene into the widely grown rice variety ASD 16 in southern India. Several backcrossed progenies were evaluated for their resistance to RTD, focusing on traits such as reduced plant height, chlorophyll content, agronomic performance, and viral DNA accumulation. Lines like ASD 16-59-4, ASD 16-88-3, and ASD 16-115-3 exhibit a favourable combination of key agronomic traits from the parent variety and resistance to RTD. Other lines BPT 5204-45-10, BPT 5204-90-4, CR 1009-8-4 and CR 1009-10-4 also demonstrated resistance against RTBV. These lines provide significant value and can be utilized as donors for marker-assisted backcross breeding to introduce RTBV resistance into susceptible varieties in the future. Rice plants that exhibited typical symptoms of orange yellow discoloured leaves were suspected to be phytoplasma as testing for RTD with PCR gave negative results and the bacterial blight pathogen could not be isolated. Attempts to conduct a transmission assay with the Zigzag leafhopper failed to produce the typical symptoms of tungro. This indicated that there was no interaction between the phytoplasmal agent and tungro-associated viruses. Although the symptoms of both diseases are similar, the Zigzag leafhopper transmitted the phytoplasma agent alone.

Keywords: Rice tungro disease- RTBV-transgenic resistance-rice phytoplasma

OP-39

Evaluation of Maize Genotypes for Charcoal Rot, *Macrophomina phaseolina* Disease in Northern Telangana Zone

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Abstract

Maize (*Zea mays* L.) is the third most important staple food crop in Telangana in terms of area and production, after rice and cotton. Charcoal rot, also known as dry weather wilt, caused by *Macrophomina phaseolina* (Tassi) Goid., has been reported in all maize growing areas of Telangana during both *Kharif* and *Rabi* seasons. The disease attacks maize from post- flowering to maturity stages, causing severe losses (30 to 90 per cent) in grain yield depending upon the severity of the disease. The present studies were aimed to evaluate 471 maize entries for resistance against charcoal rot disease in randomized block design using a check at Agricultural Research Station, Karimnagar, Telangana State, India during *Rabi* 2022-2023 and *Kharif* 2023. Out of two hundred seventy seven entries against charcoal rot disease during *Rabi*-2022-2023, One line KMH-42283 was identified as resistant, 23 promising entries namely KML-1, KML-6, KML-10, KML-29, KML-34, KML-52, KML-54, KML-72, KML-75, KML-79, KML-80, KMH-422752, KMH-422838, KMH-422730, KMH-422758, KMH-422753, KMH-42229, KMH-421353, KMH-422788, KMH-422777, KMH-42247, KMH-422972 and KMH-42284 were identified as moderately resistant, one hundred and ninety three lines were recorded as moderately susceptible and remaining 59 lines were recorded as susceptible and Kaveri-50 (check) entry was recorded as highly susceptible. Out of 194 entries screened during *Kharif*-2023, one line KML-39 was identified as resistant, 31 entries viz., KML-5, KML-25, KML-65, KML-95, KML-102, KML-107, KML-114, KMH-422518, DKC-9178,P-3401, KMH-422307, KMH-422475, KMH-422325, KMH-422381, KMH-422382, NK-7702, P-3302, PAC-751elite, GK-3237, KMH-422383, KMH-422384, KMH-422391, KMH-422397, KMH-131, KMH-422302, KMH-422333, KMH-422599, DKC-9233, DHM-121, KMH-422480 and KMH-422520 were identified as moderately resistant to charcoal rot disease, one hundred and ten lines were moderately susceptible, 51 lines were recorded as susceptible and one line Kaveri-50 was noticed with high 8.20 disease scale and severely affected by charcoal rot and rated as susceptible during *Kharif,*2023. The 56 entries (24 in *Rabi* and 32 in *Kharif*) were identified as promising sources of resistance against charcoal rot disease and can be used to develop disease resistant and high yielding hybrids to enhance maize productivity in Telangana State.

Keywords: Charcoal rot, *Zea mays*, resistance, susceptibility.

OP-40

Histological Insights into Early Infection Strategies of *Puccinia arachidis* in Groundnut Genotypes

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Abstract

Groundnut, *Arachis hypogaea* L., is an important oilseed crop globally and in India. Rust caused by *Puccinia arachidis* is one of the most destructive foliar diseases causing substantial yield losses. While resistance to rust is well-characterized, histological differences leading to visual variations in symptoms among the genotypes with varying resistance levels remain unclear. This study was aimed to understand early infection mechanisms of *P. arachidis* in six genotypes of groundnut using detached leaf assay with urediniospore inoculation (5×10^4 ml^{-1}). Spore germination occurred by 12 hours after inoculation (hai) and continued until 24 hai, without any genotypic differences in pre-penetration and penetration events. However, at 3-5 days after inoculation (dai), differences in hyphal growth and colonization were observed in the mesophyll tissue. In genotypes TMV 2 and K 6, profuse hyphal colonization spanning 30 to 40 mesophyll cells was observed by 7 dai. In contrast, genotypes ICG 11426 and GPBD 4 exhibited mesophyll cell death by 3 dai, ceasing the hyphal growth by 4 to 5 dai. These early infection-stage differences likely influence resistance components among genotypes with varying resistance levels. Molecular quantification of fungal DNA can complement histological analyses, enabling early insights into resistance mechanisms before the onset of visual symptoms.

Keywords: Groundnut, detached leaf assay, histology, *Puccinia arachidis*, rust

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THEME 4:

Microbiome, Biological Control and Integrated Disease Management

OP-41

Laboratory Evaluation of Homeopathic Drugs against Stem Rot of Groundnut Caused by *Sclerotium rolfsii*

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Abstract

Stem rot caused by *Sclerotium rolfsii* is a common major disease of groundnut (*Arachis hypogaea* L.) in India. The efficacy of 33 commercially available homeopathic drugs at different potencies was evaluated in the laboratory for their anti-fungal activity against *S. rolfsii* isolated from groundnut fields, Seed Research and Technology Centre, Rajendranagar, Professor Jayashankar Telangana Agricultural University, Hyderabad. The homeopathic drugs were screened for their effect on mycelial inhibition, sclerotial reduction and other growth parameters using poisoned food technique. All the tested drugs inhibited the mycelial growth, delayed the initiation of sclerotial development, sclerotial germination, and decreased the production of number of sclerotia and also delayed the sclerotial maturity when compared to the positive control. Among the tested homeopathic drugs, *Chelidonium* @ 30C (88.88%, 60.80) and *Colchicum* @ 1000C (82.21%, 75.20%), *Thuja occidentalis* @ 200C (73.33%, 34.00%) predominantly inhibited the mycelial growth and sclerotial number, respectively. It is widely recognized that homeopathic drugs are used against plant pathogens and act as the most important alternatives to fungicides and thus need to be exploited for the future requirements within the frame work of integrated plant disease management.

Keywords: *Sclerotium rolfsii,* homeopathic drugs, mycelial inhibition

OP-42

Studies on Seed Biopriming using *Trichoderma* G2 Mutant for Improved Plant Growth Promoting Activity

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Abstract

Beneficial microorganisms are introduced directly to the soil and plant tissues or by seed inoculation, however soil application is recommended when there is a possibility of antagonistic or inhibitory microbes on the plant tissues. Insufficient microbe survival, difficulties in applying fungicides to the seeds, and exposure to heat and sunshine during subsequent seed storage in traditional inoculation procedures need the investigation of suitable and effective administration techniques. In some crops, seed priming (Hydrating seeds to stimulate metabolism without germination and then drying them) increases germination, stand establishment, and stress tolerance. Biopriming, which includes applying rhizobacteria or other beneficial microbes that promote plant growth, is the process of priming seeds with a living micro-organism inoculum. Biopriming guarantees quick, consistent, and high crop establishment and speeds up and evens out germination, which enhances harvest quality and production. On biopriming of rice seeds using *Trichoderma* G2 mutant improvement was seen in germination percentage, no. of tillers, and root volume. It is speculated that through seed biopriming, G2 mutant has entered and sticked to seeds and become acclimated to the common circumstances. Biopriming is suggested as a potential way for applying helpful microorganisms to the seeds.

Keywords: Beneficial microorganisms, biopriming , Seed, *Trichoderma* G2 mutant

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OP-43

Integrated Management of Gummy Stem Blight in Bottle Gourd

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Abstract

During field survey in 2021-22, disease incidence of gummy stem blight (15%) was noticed in few vines of bottle gourd in Shamshabad (Rangareddy dist.) and Shamirpet (Medchal dist.) areas in Telangana. The pathogen was isolated from collected diseased samples and identified as *Didymella bryoniae.* A field experiment was taken up during the years 2021-22, 2022-23 and 2023-24 for integrated management of gummy stem blight in bottle gourd at Vegetable Research Station, Sri Konda Laxman Telangana Horticultural University, Rajendranagar, Hyderabad. Seven treatments, including seed treatment, soil drenching and foliar application of different combinations of fungicides *i.e.* zineb, carbendazim, azoxystrobin, chlorothalonil; different bioagents *i.e.* talc-based consortia of *Trichoderma* (TCV-2) + *Bacillus subtillis* (CRB-7), *Trichoderma asperellum* and micronutrients were chosen in the experiment. Among all the treatments, seed treatment by carbendazim 50% @ 2.5 g/kg seed + application of micronutrients @ 5 kg/ha in root zone near collar region at the time earthing + foliar spray of azoxystrobin 4.8% + chlorothalonil 40% SC @ 0.25% at 10 days interval twice starting from first sign of disease showed minimum per cent disease severity (10.91%) due to gummy stem blight disease and highest marketable yield *i.e.* 30.35 t/ha with highest B:C ratio (2.78).

Keywords: Gummy stem blight, *Didymella* sp., *Trichoderma asperellum*, *Bacillus subtillis.*

OP-44

Biorational Management of Banded Leaf and Sheath Blight of Maize Caused by *Rhizoctonia solani* with Bio-fumigation and Plant Growth Promoting Rhizobacteria

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Abstract

Banded leaf and sheath blight (BLSB) of maize caused by *Rhizoctonia solani* f. sp. *sasakii* is an economically significant disease world-wide. Sustainable management of BLSB is possible by integration of environmentally safe practices such as Plant growth promoting rhizobacteria (PGPR) and bio-fumigation. In our study, we have evaluated certain fungal bioagents (*Trichoderma* spp.) and PGPR (*Pseudomonas* spp and *Bacillus* spp.) against *R. solani* under *in vitro*, greenhouse and field conditions. Further, the compatibility of these PGPR with bio-fumigation extracts of mustard leaves, shoots, roots and whole plant was evaluated under laboratory conditions. Greenhouse and field studies were carried out in a randomized complete block design with 10 treatments, replicated three times including untreated control against BLSB by integrating PGPR and bio-fumigant substrate. Elite strains of *T. harzianum* and *P. fluorescens* were selected and evaluated as seed treatment, soil drenching and foliar spray alone and as consortia. The standard chemical check, azoxystrobin was included as a chemical check. Commercially available *P. fluorescens* and *T. harzianum* were also evaluated. The population levels of these PGPR were monitored. Our results showed that *T. harzianum* (Th1) and *P. fluorescens* (Pf1) have shown higher antagonistic ability against BLSB under *in vitro* conditions. Further, the PGPR strains were less sensitive to volatiles released by the bio-fumigant substrate under laboratory conditions. Our greenhouse and field studies showed that the integration of bio-fumigation and consortia of *P. fluorescens* and *T. harzianum* as seed treatment, soil drench and foliar spray and in combination with azoxystrobin as foliar spray, the BLSB incidence was significantly suppressed. Further, this treatment showed highest seed germination, root, shoot, cob length, number of kernels per cob and seed yield (5266.7 kg/ha) compared to untreated and chemical control. Soil enumeration of fungal and bacterial strains showed highest population levels irrespective of bio-fumigation substrates used. Our findings suggest that BLSB disease could be effectively managed to enhance maize yield by integrating bio-fumigation and consortia of *T. harzianum* and *P. fluorescens* as seed treatment, soil drench and foliar spray under the conditions evaluated.

Keywords: Banded leaf and sheath blight, maize, *Rhizoctonia solani, bio-fumigation* and PGPR.

OP-45

Development of Microbial Consortia for the Management of *Fusarium* Wilt of Banana Caused by *Fusarium oxysporum* f. sp. *cubens* Tropical Race 4

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Abstract

The present study was investigated under *in-vitro* conditions in Fruit Pathology Laboratory, Department of Plant Pathology and Nematology, PGCA, RPCAU, Pusa, Samastipur, Bihar. The pathogen and nine biocontrol agents (5 fungal and 4 bacterial) were procured from Fruit Pathology Laboratory and Biocontrol Laboratory, Department of Plant Pathology and Nematology, RPCAU, Pusa. All the BCAs possessed promising antagonistic potential against FoC TR4 (>65% PI), and have been identified and characterized molecularly. The fungal and bacterial BCAs were combined together and total 24 test consortial combinations were prepared. Upon *in vitro* evaluation of compatibility among the constituent BCAs in each consortial combinations, 09 (E1+F4, B1+F2, B2+F2, E1+F2, E2+F2, E1+F5, E2+F5, F5+F3 and F5+F1) consortial combinations were screened based on ≤1% inhibition of fungal constituent BCA in each combination. Meanwhile for conducting glass house experiment, 09 screened consortial combinations, 09 individual BCAs, 01 negative check (only pathogen, no BCA treatment) and 01 check (no pathogen, no BCA treatment) were selected for *in planta* evaluation of the consortial combinations. The results reveals that the highest value of PDI was recorded for negative check (100%) followed by consortium *Bacillus velezensis* strain 2 (E2) + *Trichoderma harzianum* (F5), *Bacillus subtilis* (B1) + *T. asperellum* (F2) and *T. asperellum* (F2), *T. asperellum* (F3), whereas remaining treatments check had shown no disease incidence (0 PDI). The plant vigour index (PVI) was highest for check (5514) followed by combination of E1+F2 (5070) and F5+F3 (4691). Also, PVI was considerably higher in treatments F1(4397) followed by B2+F2 (4111), E2+F2 (3927). PVI was least in case of negative check (588) followed by E2+F5 (1676) and B1+F2 (1833), F2 (1882).

Keywords: Banana, *F. oxysporum* f. sp. *cubens,* tropical race 4, *Bacillus* and *Trichoderma*, per cent vigour index, percent disease index.

OP-46

Novel and Broad Spectrum Combination Fungicide for Managing Multiple Diseases of Rice

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Abstract

In rice, diseases account for yield losses ranging from 9.6 to 85.0% wherein, blast and sheath blight are major concerns for the farmers of Telangana state. Prolonged and repeated use of fungicides with similar mode of action often results in pathogen developing fungicide resistance, as is evident with most extensively used blast fungicide, tricyclazole. Amid increasing concerns of its hazardous effects on human health and residue issues while exporting rice, tricyclazole has now been notified under judicious use / banned category fungicide. Further, use of individual fungicide molecules to combat different diseases adds to the cost of protection. Therefore, identification of combination molecules effective against multiple diseases of rice having broad spectrum activity saves the protection costs by reducing number of sprays apart from delaying the resistance development. Studies conducted against blast and sheath blight over three years with seven fungicides, alone and in combination, revealed that application of azoxystrobin 18.2% w/w + difenoconazole 11.4 %SC @ 500 ml/ha, at initiation of disease followed by another spray at 15-20 days interval recorded the highest control efficacy of neck blast (78.5%) and sheath blight (41.6%) and accrued 38.0% increased grain yield over untreated control. The cost of fungicide is Rs. 4,414/- (for two sprays @ 500 ml/ha in each spray). This novel combination fungicide was effective against multiple diseases of rice and Rs. 854/ha would be saved on crop protection with ICBR of 1:7.9. The unique combination of triazole and strobilurins group together have achieved broad spectrum fungicidal activity against blast and sheath blight and demonstrated highest per cent reduction of neck blast (62.7%) and sheath blight (18.3%) over existing widely used fungicide molecules such as isoprothiolane and propiconazole, respectively. The novel combination fungicide is also capable of managing blast pathogen that has already developed resistance to triazole and dithiolane fungicide groups.

Keywords: Combination fungicides, blast, sheath blight, paddy, triazole, strobilurin.

OP-47

LC-MS Profiling of *Bacillus* and *Trichoderma* Metabolites: Combating *Stagonosporopsis cucurbitacearum*-Induced Gummy Stem Blight

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Abstract

Gummy stem blight, caused by *Stagonosporopsis cucurbitacearum* (anamorph) or *Didymella bryoniae* (teleomorph), is a devastating disease that significantly impacts cucurbit crops, resulting in severe economic losses. Given the environmental and health concerns associated with chemical fungicides, the current study was focused on harnessing its own microbiome for managing the disease. The isolates (8APSO, 1TS, TRI-3), which exhibited potentiality at *in vitro* and pot experiment against gummy stem blight were subjected to metabolic profiling using liquid chromatography–mass spectrometry (LC-MS). This study examined the antifungal potential of culture filtrates from *Bacillus subtilis* (8APSO), *Bacillus amyloliquefaciens* (1TS) and *Trichoderma asperellum* (TRI-3) against *S. cucurbitacearum*. The findings indicated that the antifungal activity observed is largely attributed to bioactive compounds present in the culture filtrates of these organisms. Metabolic profiles were assessed and used to identify major metabolites based on the scores of variable importance in the projection and the plot scores of principal component analysis (PCA). A total of 357 differential metabolites were screened, including positive and negative ion modes. Among these, several key compounds were identified including surfactin C, stearic acid, indole-3-acetonitrile, norharmane, ethyl gallate etc. These metabolites were shown to disrupt the internal mycelial structure of *S. cucurbitacearum*, resulting in suppression of fungal growth. This research provides valuable insights into the potential of biological control agents and their associated metabolites as effective alternatives to conventional chemical treatments. It also opens new avenues for the exploration of unexplored antifungal compounds produced by biological agents, positioning them as promising solutions for managing gummy stem blight in cucurbit crops.

Keywords: Gummy stem blight, *Stagonosporopsis cucurbitacearum*, *Bacillus*, *Trichoderma*, LCMS.

OP-48

Potential of *Bacillus* sp and *Pseudomonas* sp in Reducing Groundnut Seedling Diseases: A Biocontrol Approach

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Abstract

Collar rot and stem rot diseases caused by *Aspergillus niger* and *Sclerotium rolfsii* are the important seed and seedling diseases of groundnut, which are more extensive in the *Kharif* than the *Rabi* and Summer seasons and cause more damage in sandy loam and medium black soil during early stages of crop growth. Harnessing the bioagents for the management is an alternative solution to prevent the ill effects of chemicals on environment and soil health. Nine fungal and 88 bacterial colonies were isolated from groundnut rhizosphere (39 no.), healthy plant parts [internal collar (IC) and root (IR)-42 no.], cow urine (3 no.) and cow dung (4 no.) from farmers' fields of Wanaparthy, Warangal and Mahaboobnagar districts. The isolated microflora was tested for their antagonism against *S. rolfsii* and *A. niger.* Of the 97 microbial populations evaluated using dual culture technique, only seven isolates were found effective in inhibiting mycelial growth of *S. rolsfii* (65.25 to 90.50%) and *A. niger* (60.75 to 80.50%). Among these bioagents, *Bacillus* sp. (IR 10) and *Pseudomonas* sp. (IC 8) were selected and evaluated two methods of applications *viz*., seed treatment and seed treatment cum soil application of the selected bioagents were evaluated under artificial inoculation conditions in green house with both the pathogens. Seed treatment with *Bacillus* sp. recorded maximum per cent seedling emergence (68.50%) against *S. rolfsii* as compared to seed treatment cum soil application (65.83%) and minimum seedling mortality of 22.67% and 26.50%, respectively was recorded. However, seed treatment with *Pseudomonas* sp showed 60.17 % seedling emergence. With respect to *A. niger*, maximum per cent seedling emergence (66.50 %) and minimum seedling mortality of (21.83%) was recorded by seed treatment cum soil application of *Bacillus* spp. with no significant difference with seed treatment by *Bacillus* sp (65.50%) for seedling emergence. However, the per cent improvement of seedling emergence by seed treatment with *Bacillus* sp. was 54.49% and 57.36% reduction of seedling mortality over pathogen control against *S. rolfsii*. While, the per cent improvement of seedling emergence by seed treatment cum soil application of *Bacillus* sp was 55.38% and 61.13 per cent reduction of seedling mortality against *A. niger*. The study proved that seed and soil method of application of bioagents is an effective management strategy against the seedling diseases during initial stages of groundnut crop.

Keywords: Groundnut, bioagents, *Bacillus* sp., *Pseudomonas* sp., seed treatment, soil application, *Sclerotium rolfsii* and *Aspergillus niger.*

OP-49

Field Evaluation of Fungicides Against False Smut of Rice Caused by *Ustilaginoidea virens*

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Abstract

Rice, *Oryzae sativa* L. is one of the leading food crops in the world and the most important staple food in Asia. False smut disease caused by *Ustilaginoidea virens* (Cooke) (Takahashi) is regarded as a minor disease earlier but the disease has been observed in severe form since 2001 in India. In the present investigation, seven different fungicides were evaluated against false smut in randomized block design under field conditions at Agricultural Research Station, Nellore during *Rabi* 2023-24. Results revealed that all the fungicides significantly reduced the severity of the false smut. Among the seven fungicides, picoxystrobin 7.05% + propiconazole 11.7% SC@ 2ml/l recorded highest per cent reduction of false smut severity (98.71%) with highest grain yield (6301kg/ha), which was at par with propiconazole 25EC@ 1ml/l. Rest of the fungicides *viz*., azoxystrobin 18.2% + difenoconazole 11.4SC @1ml/l, fluopyram 17.7% w/w + tebuconazole 17.7% w/w @1.1/l, trifloxystrobin 25% + tebuconazole 50% WG @0.4g/l, tebuconazole 25.9% EC @ 1.5 ml/l and krysoxymethyl 44.3% EC@1 ml/l recorded 93.56%, 93.13%, 92.70% 91.41% 61.80% reduction of the disease severity respectively.

Keywords: Rice, false smut, fungicides.

OP-50

A New Biological Way to Suppress the Storage and Rhizome Rot in Ginger by Priming of Seed Rhizomes with Trichoprime

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Abstract

The gingerm *Zingiber officinalis* crop is badly affected by a number of diseases *viz*., soft rot, Phyllosticta leaf spot, bacterial wilt, rhizome rot and storage rot. To manage the storage rot and rhizome rot, a field experiment was conducted for three years (2020-21 to 2022-23) at Turmeric Research station, Kammarpally with technical support of Indian Institute of Spices Research, Kozhikode. These trials were carried out to assess the potential of trichoprime to suppress the storage rot and rhizome rot by priming to ginger seed rhizomes before 2 to 4 weeks of sowing. It designed in Randomized block design, four treatments (T1-Rhizome treatment with trichoprime, T2 - Rhizome treatment with metalaxyl-mancozeb @ 1.25g/L+ imidacloprid 0.5 ml/L for 30 minutes, T3 - Rhizome treatment with tebuconazole @ 1ml /L+ imidacloprid 0.5 ml/L for 30 minutes and T4- Recommended state package of practices) with six replications. Significant differences were observed with all the growth parameters and the mean maximum sprouting percentage (87.33), mean maximum plant population (55.23), maximum mean plant height (51.84 cm), mean maximum fresh weight of clump (313.77gm), maximum mean fresh rhizome yield per plot (7.33 kg/plot) and maximum mean fresh rhizome yield (18.54 t/ha) was recorded in T1-Rhizome treatment with trichoprime. The percent disease incidence (PDI) of rhizome rot was scored using the 1 to 5 grading scale. It was observed that, minimum PDI of 0.0, 4.94 and 5.95 at 30, 60 and 90 DAP, respectively in treatment (T1) with application of trichoprime followed by minimum PDI of 5.95, 11.16 and 14.25, at 30, 60 and 90 DAP respectively with T2 - Rhizome treatment with metalaxyl - mancozeb @ 1.25 g/l+ imidacloprid @ 0.5 ml/l for 30 minutes

Keywords: Trichoprime, priming, rhizome and storage rot, fresh rhizome yield

OP- 51

Integrated Management of Root Rot and Powdery Mildew Diseases in Sesame

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Abstract

The present investigation was conducted during two consecutive summer seasons (February to April) of 2022 and 2023 at Regional Agricultural Research Station, Polasa, Jagtial, Telangana to determine ecofriendly, cost effective and potential disease management strategy for the management of root rot and powdery mildew diseases in sesame. Three modules were tested in randomized block design each with five replications. Among the tested modules, Module M3, [Seed treatment with *Trichoderma asperellum* @ 10 g kg^{-1}; soil application of enriched *Trichoderma* (2.5 kg *T. asperellum* + 100 kg vermicompost) @ 250 kg ha^{-1}; spray of tebuconazole 50% + trifloxysrobin 25% @ 0.5 g l^{-1} at 30-35 DAS and second spray at 50-60 DAS] showed minimum root rot incidence (8.17%) with 78.57% reduction and powdery mildew per cent disease index - 11.24 with 76.30% reduction over untreated control with highest seed yield of 776.8 kg ha^{-1} and B:C ratio of 3.22. The next best treatment was Module M2 [Seed treatment with carbendazim @ 2 g l^{-1} + spray of tebuconazole 50% + trifloxystrobin 25% @ 0.5 g l^{-1} at 30-35 DAS and second spray @ 0.5 g l^{-1} at 50-60 DAS]. This integrated disease module can be used for the effective management of root rot and powdery mildew diseases in sesame for ensuring sustained yields, particularly in the Northern Telangana Zone of Telangana, India.

Keywords: Sesame, root rot, powdery mildew, incidence, PDI, ID.

OP-52

Management of Stem Rot in Groundnut Using Bioagents and Organic Formulations

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Abstract

Groundnut is the second most important oilseed crop after soybean. India accounts for 27% of global area and contributes to 19% of world groundnut production. The crop is known to suffer from several fungal, bacterial and viral diseases. Among many soil borne fungal diseases, stem rot caused by *Sclerotium rolfsii* in many groundnut growing areas reduces yields to an extent up to 80%. Keeping this in view the present study was undertaken to evaluate the efficacy of bioagents and organic formulations against *S. rolfsii* of groundnut at Seed Research and Technology Centre, Rajendranagar, Hyderabad during 2022-23. The efficacy of bioagents and organic formulations *viz*., *Trichoderma asperellum*, *Preudomonas fluorescens* were tested by dual culture technique and organic formulations *viz.*, Beejamrit @ 2% and 5%, Jeevamrit @ 2% and 5%, Kunabjal @ 2% and 5% and fungicide check, carboxin + thiram @ 0.3% were tested by poisoned food technique against *S. rolfsii.* The results indicated that, *T. asperellum* was found effective in inhibiting the test pathogen (72.1%) followed by *P. fluorescens* (60.4%). In case of organic formulations tested, Beejamrit @ 5% inhibited pathogen growth to an extent of 51.4% followed by Kunabjal (42.1%) and Jeevamrit (38.5%). Organic formulations *viz*., Jeevamrit @ 2 % inhibited pathogen growth (11.1%) followed by Beejamrit (2.9%) and Kunabjal (2.1%). Whereas, carboxin + thiram inhibited 100 % inhibition in pathogen growth over control. Bioagents, *T. asperellum*, *P. fluorescens* inhibited pathogen growth by 72.1% and 60.4% and organic formulations *viz.,* Beejamrit @5% inhibited pathogen growth of 51.4%, which was followed by Kunabjal (42.1%). Organic formulations with 2% concentration were not found effective against test pathogen. The research findings of the study would suggest suitable low cost input technology in the form of seed treatments.

Keywords: Groundnut, stem rot, bioagents, organic formulations and in vitro studies.

OP-53

Characterization of Rice Stem Rot Pathogen and Integrated Disease Management

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Abstract

A roving survey on incidence of stem rot of rice in major growing regions of Andhra Pradesh, Telangana and Tamil Nadu states of southern India. A total of 36 *Sclerotium oryzae* isolates were isolated from 60 diseased samples. Koch postulates were proved on susceptible rice cultivar Prabhat (MTU3626). Among the isolates, So15 has produced the highest mean per cent disease index (PDI) (39.51) with maximum AUDPC (489.52 units) and an infection rate of 0.065 units day^{-1}. *In vitro* evaluation of efficacy of six organic amendments (OAMs) against the virulent isolate of *S. oryzae* (So15) was carried out. Karanja cake has shown cent per cent mycelial growth inhibition followed by vermicompost (76.67%) and poultry manure (74.44%) at 5 per cent concentration. The bioefficacy of 12 fungicides was evaluated against the virulent isolate So15 in *in vitro*. All fungicides at all five concentrations inhibited the mycelial growth when compared to control except validamycin 3% L at 250ppm. Among the fungicides tested, tebuconazole 250 EC (25.9% w/w) had completely (100%) inhibited the mycelial growth of the pathogen. A biointensive management study for control of stem rot was conducted in farmer's field at Kaikaram village, Unguturumandal of West Godavari district of Andhra Pradesh on susceptible cultivar MTU1121. Among the treatments, root dipping of seedlings with *Bacillus subtilis* strain BsIIRR (ON024393) at 10% + soil application of karanja cake @ 125 kg ha-1 + spraying of tebuconazole 250 EC (25.9% w/w) @ 1ml/L at 45 and 60 days of crop age (T7) recorded the lowest PDI (15.74) and the highest yield (6.26 t/ha) over all other treatments including control with B:C ratio of 1.76. Hence for the cost-effective management of stem rot, root dipping of seedlings with *B. subtilis* strain BsIIRR (ON024393) at 10% + soil application of karanja cake @ 125 kg ha-1 + spraying of tebuconazole 250 EC (25.9% w/w) @ 1ml/L at 45 and 60 days of crop age proved to be the best.

Keywords: Stem rot, organic amendment, biointensive management, paddy

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OP-54

Identification of Effective Volatile Compounds Emitted from *Bacillus aryabhattai* against Root-knot Nematode, *Meloidogyne incognita* Infestation in Tomato

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Abstract

Tomato, *Solanum lycopersicum*, is an important vegetable grown worldwide. It is a rich source of antioxidants, phytochemicals, and many essential nutrients. *Meloidogyne incognita* infestation causes an estimated yield loss of 11-35% in tomato in India. *Bacillus aryabhattai* is an important rhizobacterial species that significantly reduces the host's biotic stress due to nematode infestation. Bacterial metabolites induce physiological changes in the host plant, thus promoting a defense response against nematode infestation. A study was conducted to assess the efficacy of volatile compounds emitted from *B. aryabhattai*-treated tomato roots infested with *M. incognita*. Among the several compounds emitted by the bacteria-treated tomato roots, the antimicrobial properties of propanoic acid, octadecanoic acid, 1,2-benzene dicarboxylic acid, bis (2-ethylbutyl) ester, and hexadecanoic acid were confirmed through a literature search. All four compounds were reported from the nematode-bacteria-treated plant roots, while hexadecanoic acid was reported in the nematode-alone-infested plants besides the above-mentioned treatments, but the compound's concentration was lower in the nematode-infested roots than the bacteria-treated roots. An *in silico* docking analysis with the above four compounds against the endoglucanase of *M. incognita* resulted in the compound 1,2-benzene dicarboxylic acid, bis (2-ethylbutyl) ester, having the most virulent effect on the nematode endoglucanase with a binding energy of -8.6 kcal/mol. The present study proves the nematicidal properties of biomolecules emitted by *B. aryabhattai,* which can be developed as an alternative to chemical nematicides.

Keywords: *Bacillus aryabhattai*, metabolites, nematicidal activity, tomato.

OP-55

Assessment of Fungal Bioagents against *Tilletia indica* Inciting Karnal Bunt of Wheat

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Abstract

Karnal bunt of wheat incited by *Tilletia indica* is a quarantine-important disease and it has a zero-tolerance limit in the international market. The present investigation was conducted at ICAR-Indian Agriculture Research Institute, New Delhi to find promising biocontrol agents, that can be used as eco-friendly alternatives to pesticides against *T. indica*. In this study, 18 isolates of *Trichoderma asperellum* and 15 isolates of *Trichoderma harzianum* were tested against *T. indica* under *in vitro* and *in planta* conditions. Under *In vitro* analysis, the highest per cent inhibition was shown by *T. asperellum* 6413 (T17) with 42.07% and 63.97% inhibition of Ti12 and Ti18 isolates of *T. indica,* respectively, followed by *T. asperellum* 8619 (T2) with 37.93% inhibition of Ti12 and 61.07% inhibition of Ti18 isolates of *T. indica. T. harzanium* isolates were not found effective. GC-MS analysis revealed the presence of several volatile organic compounds (VOCs) common in *T. asperellum* 6413 (T17) and *T. asperellum* 8619 (T2). However, volatile organic compounds having antifungal properties like heptanes, 2,3-Butanediol, and 1-Hexanol were common in both the *T. asperellum* 6413 and *T. asperellum* 8619 and 2H-Pyran-2-one, acetic acid and toluene were exclusively present in *T. asperellum* 8619. In case of *In planta* assay pre-inoculation treatment with biocontrol agents revealed that T2 treatment (*T. asperellum* 6413) showed percent disease control (PDC) of 26.85% against Ti12 and 28.08% against Ti18. Post-inoculation application of biocontrol agents revealed that T2 treatment gave 20.57% PDC with Ti12 and 23.68% with Ti18. Pre- and post-inoculation application of biocontrol agents, T2 treatment showed 29.49% and 30.75% PDC against Ti12 and Ti18 respectively. T1 and T2 were found significant in all methods of biocontrol application. Propiconazole 0.1% gave 100% disease control. *In planta* studies, *T. asperellum* 6413 showed significantly constant and good results in all three assays.

Keywords: Biocontrol, Karnal bunt, *Tilletia indica*, *Trichoderma* sp., volatile organic compounds.

OP-56

Molecular Characterization and Evaluation of Novel Management Options for *Burkholderia glumae* BG1, the Causative Agent of Panicle Blight of Rice

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Abstract

Bacterial panicle blight, incited by *Burkholderia glumae,* has impacted rice production globally. Despite its significance, knowledge about the disease and the virulence pattern of the causal agent is very limited. Bacterial panicle blight is a major challenge in the rice-growing belts of North-western India, resulting in yield reduction. Twenty-one BG strains using the 16S rRNA and the *gyrB* gene-based sequence approach have been characterized in the present study. The *gyrB* gene-based phylogenetic analysis resulted in geographic region-specific clustering of the BG isolates. The virulence screening of 21 BG strains revealed the variation in the disease severity and the grain yield of rice plants. The most virulent BG1strain resulted in the highest disease incidence (82.11%) and lowest grain yield (11.12 g/plant), and BG10 came out as the least virulent strain. The BG10 strain resulted in lowest disease incidence of 18.94% and highest grain yield of 24.62g per plant. However, the management of *B. glumae* has become a challenge due to the lack of proper management strategies. *In vitro* evaluation of various biocontrol agents and nano copper at different concentrations by agar well diffusion method revealed that nanocopper at 1000mg/L inhibited the colony growth of *B. glumae.* The application of nano copper at 1000mg/L reduced the disease severity to 21.23% and increased the grain yield by 20.91% (31.76g per plant) compared to the positive control (COC 0.25% + streptomycin 200 ppm). Remarkably, pre-inoculation with nano copper at 1000mg/L followed by challenge inoculation with *B. glumae* enhanced the activity of enzymatic antioxidants *viz.,* Phenyl ammonia-lyase (PAL), Polyphenol oxidase (PPO), Peroxidase (POX) and non- enzymatic antioxidant phenol. Additionally, we observed a substantial transcript level upregulation of six defense-related genes to several folds *viz., OsPR2, OsPR5, OsWRKY71, OsPAL1, OsAPX1,* and *OsPPO1* in comparison to the pathogen control and healthy control. Overall, our study provides valuable insights into the potential and practical application of nano copper for the mitigation of bacterial panicle blight, offering promising prospects for commercial utilization in disease management.

Keywords: *Pseudomonas glumae*, paddy, management, nano copper, panicle blight.

OP-57

Integrated Management of Bitter Gourd Yellow mosaic virus Disease in Telangana

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Abstract

Bitter gourd, *Momordica charantia,* is one of the world's major vegetable crops and has great economic importance, grown extensively in India and throughout south-east Asian countries. It is an excellent source of minerals, vitamins, dietary fibers and antioxidant properties. Presently, bitter gourd production is declining due to various pests and diseases. Among them, viral diseases, especially Yellow mosaic virus are becoming a serious threat, which is significantly reducing the yield year by year. A field experiment was conducted for three consecutive years from 2020 to 2023 to evaluate the seven different integrated disease management (IDM) modules against viral diseases in bitter gourd at Vegetable Research Station, Sri Konda Laxman Telangana Horticultural University, Rajendranagar, Hyderabad, Telangana. The IDM module comprising of growing two rows of maize as border crop, use of black silver polythene mulching along with spraying of acephate @ 1.5g/l + neem oil @ 2ml/l (10,000 PPM) followed by Pyriproxifen @ 1ml/l at 10 days interval was effective for bitter gourd viral disease management. Lowest Percent Disease Index (PDI) of 22.84% and also highest yield (8.75 t/ha) with highest benefit-cost ratio (3.47) was recorded.

Keywords: Bitter gourd, yellow mosaic, virus disease, percent disease index, IDM.

OP-58

Potency of *Bacillus thuringiensis* and *Bacillus subtilis* against *Sclerotium rolfsii,* Incitant of Stem Rot Disease of Groundnut

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Abstract

Among the soil borne diseases of groundnut, Stem rot disease caused by *Sclerotium rolfsii* is regarded as potent threat owing to its significant yield loss of up to an 80-90% and its occurrence on all stages of crop growth under favourable conditions. Similarly, yield loss of 47% due to one of the important pests, *Spodoptera litura* can also be expected. Management of both these pest and disease is challenging due to their soil borne and polyphagous nature. The present study aims at use of combination of biocontrol agents or microbial consortium i.e *Bacillus thuringiensis* and *Bacillus subtilis* having different antagonistic mechanisms for management of *Sclerotium rolfsii*. Among the 20 isolates of *Bacillus thuringiensis* and 10 isolates of *Bacillus subtilis* tested, all the twenty *B.t* isolates significantly inhibited *S. rolfsii* with per cent inhibition ranging from 26.67% to 71.11%, and all the ten *B. subtilis* isolates recorded 55.56% to 86.30% per cent inhibition. The potential *B. thuringiensis* and *B. subtilis* isolates against *S. rolfsii* obtained were tested for their compatibility and consortium of the most compatible isolates (TTLK1+ SPVP1) were developed in different proportions. Consortium of *Bt*:*Bs* in the ratio 1:2 recorded maximum inhibition (87.41%) of *S. rolfsii,* which was on par with the *Bt*:*Bs* in the ratio 2:1 (81.48%), while least per cent inhibition was recorded in case of *Bt*:*Bs* in the ratio 1:1 with 73.70% inhibition. Under pot culture conditions too, combined treatments of seed + soil application with consortium was found to be more effective with maximum disease control, when compared to individual bioagents and pathogen check and by use of individual chemical treatments like hexaconazole and tebuconazole. Thus, the present study reveals that combined use of the biocontrol agents with different mechanisms of actions can improve the insect pest and disease control with minimal interference with the biological equilibrium in nature.

Keywords: *Bacillus thuringiensis*, *Bacillus subtilis,* Groundnut stem rot , Microbial consortium, *Sclerotium rolfsii.*

OP-59

Integrated Approach for the Management of Phytophthora Blight in Redgram: An Extension Study

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Abstract

Redgram, *Cajanus cajan,* is an important legume crop grown under rainfed conditions in an area of more than one lakh acres in Vikarabad district of Telangana. Phytophthora blight caused by *Phytophthora cajani* emerged as an economically significant disease in the district for the past 4-5 years. The pathogen causes severe seedling mortality when heavy rains coincide with high relative humidity and hot conditions particularly under low lying areas. Keeping this in view, DAATTC, Tandur conducted Front Line Demonstration on integrated disease management of Phytophthora blight in the years 2022 and 2023. The disease was managed through agronomic interventions like deep summer ploughing of soil to desiccate the pathogen and modification of field with raised bed planting of redgram in place of flat-bed sowing. Seeds were treated with *Trichoderma viride* @10 g/Kg seed, followed by soil drenching with metalaxyl @ 25% W.P - 2.5 g/l under severe conditions. Demo fields showed 11.2% disease incidence compared to farmers' practice (32.8%), which showed significant reduction in disease throughout the crop growth stage. Yield increase upto 42% was observed in demo fields with the grain yield of 1893 kg/ha in comparison with 1448 kg/ha in farmers' practice. High net returns of Rs. 1,19,910 /- were gained with 1:3.6 cost benefit ratio compared to farmers' practice (Rs. 71756.5 /-) with 1:2.5 cost benefit ratio. The results of this study indicate that through integrated disease management approach, especially seed treatment with *Trichoderma* as well as raised bed formation, protected the crop right from the seedling stage.

Keywords: Front line demonstration, disease, integrated, management, *Phytophthora*, pigeonpea, *Trichoderma.*

OP-60

Trichoderma -A multiweaponery soldier in managing major fungal diseases of groundnut

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Abstract

Groundnut is a major oil seed crop with high nutritional value as Poorman's peanut.It will be infected with major fungal diseases including soil borne, seed borne and soil borne pathogens. Soil-borne pathogens include *Sclerotium rolfsii, Rhizoctonia bataticola.* Foliar pathogens include *Mycosphaerella* or *Cercospora* causing tikka leaf spot(early or late leaf spot).Seed-borne pathogens include *Aspergillus flavus, A.parasiticus,A.niger, S.rolfsii. Sclerotium rolfsii* (*Athalium rolfsii*)is a facultative parasite with a wide host range of more than 500 host plants. In groundnut *Sclerotium* causes both seed borne and soil borne infection causing stem rot,root rot and even post-harvest diseases like blue seed disease.*Aspergillus niger* infection in groundnut leads to the production of aflatoxins in seeds and also leads to collar rot in groundnut. In the present investigation on stem rot of groundnut, *Trichoderma asperellum* (GT4)inhibited mycelial growth to 78.43 per cent and sclerotial population of *S.rolfsii* to cent per cent. In another *in vitro* investigation on dry root of groundnut, *T.asperellum* GT_6 was found to inhibit the dry root rot pathogen to 80.74 percent .Commercial formulation of *Trichoderma* reduced seed borne pathogens of groundnuts like *A.niger* associated with collar rot .Seed treatment and soil application of *T.asperellum* has reduced disease incidence of stem rot and collar rot of groundnut ,disease severity of late leaf spot of groundnut whereas *T.asperellum* GT6 has reduced the disease incidence of dry root pathogen to 20.38 per cent. *Trichoderma* is an ecofriendly biocontrol agent with different mechanisms (direct and indirect).In dual culture mycoparasitism and lysis was observed. Siderophores were also produced by *Trichoderma* spp. that help in killing the pathogens. Directly *Trichoderma* spp. infected sclerotia and also reduced oxalic acid produced by *S.rolfsii* .By enzymatic weapons also,*Trichoderma* spp. have contributed for phosphate solubility with the production of phosphatases.Plant growth was also found to be influenced by *Trichoderma* by the production of auxins like Indole-3-Acetic acid.

Keywords: *Trichoderma,*groundnut,*Sclerotium rolfsii, Rhizoctonia bataticola, Aspergillus niger.*

OP-61

Alternaria Fruit Rot of Chilli in Telangana: Survey, Pathogenicity and Effective Fungicidal Management

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Abstract

Chilli (*Capsicum annuum* L.) is a globally important vegetable. Among various biotic constraints, Alternaria fruit rot is one of the most significant diseases in Telangana. A roving survey was carried out in major chilli growing districts of Telangana *i.e.,* Warangal, Mahabubabad and Khammam in December 2023. During this survey eight *Alternaria* isolates were collected from 19 fields. Highest fruit rot incidence was recorded in Jagguthanda village (67.48%) of Khammam and lowest in Banjarathanda village (9.08%) of Mahabubabad. Pathogenicity test using pink prick method confirmed all the eight isolates of *Alternaria* spp. on chilli fruit. Each isolate initially produced small brown lesions on the fruit, which expanded into sunken dark patches and leads to rotting. Among them, isolate A7 showed highest virulence with 55.44% infection on 9th day. Consequently, isolate A7 molecularly identified as *A. alternata* was selected for further management studies. *In vitro* evaluation of 14 fungicides was done against the *Alternaria* isolates using poisoned food technique. Among the four systemic fungicides, difenoconazole (93.88%) showed maximum inhibition of radial growthwhile minimum was observed for carbendazim (32.33%). Among the five contact fungicides, mancozeb (67.38%) was found to inhibit the maximum radial growth and minimum was observed for propineb (58.10%). Among the combination fungicides, captan + hexaconazole (100.00%) showed maximum radial inhibition and minimum was observed in pyraclostrobin + metiram (84.65). Additionally, the fungicides were also screened for their effectiveness in managing *Alternaria* spp. under glasshouse conditions at their recommended dosage. Out of all the treatments, captan + hexaconazole (97.10%), difenoconazole (92.41%), tebuconazole + trifloxystrobin (91.18%), azoxystrobin + tebuconazole, azoxystrobin+ difenoconazole, propiconazole, pyraclostrobin+ metiram and copper hydroxide showed more than 80 per cent reduction of disease over the control. The fungicide carbendazim recorded minimum per cent (18.62%) of inhibition. It was found that Captan + Hexaconazole proved to be most effective fungicide in controlling the disease.

Keywords: Chilli, *Alternaria*, fruit rot, *in vitro*, glasshouse

OP-62

Bacillus spizizenii induces resistant to nematode-fungus disease complex through anti-microbial compounds synthesis and defense related enzymes activity in Castor (*Ricinus communis*)

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Abstract

Castor is a highly valuable non-edible oilseed crop that is grown all over the world. In castor growing regions, there are number of factors that limit the productivity of the crop, in which pests and diseases play a key role. The fungus, *Fusarium oxysporum* f. sp. *ricini* and reniform nematode, *Rotylenchulus reniformis* are the major causes of the highly harmful disease, castor wilt. Using 16S rRNA technology, the rhizobacterial isolate RB65, which was proven effective against the nematode-fungus disease complex *in vitro*, was molecularly characterized and confirmed as *Bacillus spizizenii* (1518 bp). *In vitro* studies conducted with the crude metabolite extract of *B. spizizenii* revealed that 100% concentration of the extract of the bacteria was found to not only decrease mycelial growth of the fungi (77.36%) but also result in juvenile mortality (92.00%) of the nematode. Two lipopeptide genes *viz*., Bacilysin and β-1,3-glucanase were identified from the bacteria. A pot culture experiment was carried out to assess the effect of bacteria on the nematode-fungus disease complex in castor. It was observed from the studies that *Fusarium* wilt incidence and nematode population were significantly reduced in plants treated with *B. spizizenii* (5 ml / kg soil) by up to 80.00%. Additionally, plant growth parameters, such as shoot and root length, fresh shoot and root weight, and dry shoot and root weight, were significantly increased upon the bacterial treatment, coupled with an increase in defense enzyme activities of peroxidase (PO), polyphenol oxidase (PPO), phenylalanine lyase (PAL), and total phenol contents (TP). Hence, to mitigate the negative effects of fungicides and nematicides, *Bacillus spizizenii* can be used as an eco-friendly alternative solution.

Keywords: Castor, *Bacillus spizizenii Fusarium oxysporum* f. sp. *ricini,* defense enzyme.

OP-63

Integrated Management of Root Rot Disease in Castor Using Soil Amendments, Biocontrol Agents, Botanicals and Fungicides

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Abstract

The cultivation of castor crop, *Ricinus communis* L. assumes paramount economic significance owing to its diverse applications across industries. However, its production is threatened by the root rot disease caused by *Macrophomina phaseolina*, which leads to considerable yield losses. This study evaluated the efficacy of various biocontrol agents, soil amendments, botanicals and combination fungicides against *M. phaseolina* under both *in-vitro* and pot conditions to develop an effective integrated management strategy. The results of *in-vitro* studies revealed that, of soil amendments tested, neem cake was the most effective with maximum mean mycelial inhibition of 54.7 %, while groundnut cake showed the lowest mean mycelial inhibition of 2.9 %. Among the various biocontrol agents tested, *Trichoderma harzianum* 4d and *T. asperellum* 2, achieved complete mycelial inhibition (100%), while *Bacillus subtilis* displayed the lowest inhibition of 37.4 %. Among the botanicals tested, *Allium sativum* extract showed the maximum mean mycelial inhibition of 59.9 %, whereas *Ocimum sanctum* recorded minimum mean mycelial inhibition of 9.8 %. Among the combination fungicides tested, tebuconazole + trifloxystrobin recorded 100 % mean mycelial inhibition, whereas zineb + hexaconazole recorded the lowest mean mycelial inhibition of 50.0 %. Results also demonstrated a substantial decrease in radial mycelial growth of the pathogen with increasing the concentrations of soil amendments, botanicals and fungicides tested under in vitro conditions. Based on these findings, the most effective treatments were combined and further evaluated in pot culture experiments under shade net conditions. Among the various treatments, seed treatment with tebuconazole + trifloxystrobin @ 0.4 g/kg and soil application of neem cake @ 150 g/kg, *T. harzianum* 4d @ 10 kg/ha and A. *sativum* @ 150 g/kg at 15 days after sowing recorded the lowest disease incidence of 8.7 %. These findings highlighted the potential of integrating selected combination fungicides, botanicals, bio-agents and soil amendments for the management of root rot disease effectively in castor cultivation.

Keywords: Castor, *M. phaseolina,* root rot, integrated disease management

THEME 5:

Entrepreneurship Development for Plant Disease Management

OP-64

Eco-Friendly Business Ventures: 2-Methylpyrazine and 6-Pentyl Pyrone as the Future of Bio-fungicides

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Abstract

This study explores the extraction, purification, and characterization of secondary metabolites 2-methylpyrazine (2MP) and 6-pentyl-2H-pyran-2-one (6PP) from the potent biocontrol agents, *viz*., *Pseudomonas putida* PIK1 and *Trichoderma asperellum* TAIK1, respectively, for the management of rice diseases caused by *Sclerotium hydrophilum* and *Ustilaginoidea virens*. Using ethyl acetate as a polar solvent, the metabolites were purified *via* thin-layer chromatography (TLC) and column chromatography, and their molecular structures were confirmed through advanced spectroscopic techniques, including Nuclear magnetic resonance (NMR) and high resolution mass spectrometry (HRMS). Bioassays revealed that 2MP and 6PP effectively inhibited pathogen growth at concentrations of 50 ppm and 100 ppm, respectively. To enhance their efficacy, the metabolites were encapsulated into nanoscale formulations using maltodextrin and gelatin as wall materials through spray drying. The resulting particles (400–500 nm) exhibited sustained release and prolonged antifungal activity. These eco-friendly bio-fungicides demonstrate significant potential as scalable, next-generation solutions for managing stem rot and false smut in rice. By integrating innovation and entrepreneurship, the development and commercialization of these bio-products offer transformative opportunities for sustainable agriculture. This study underscores their potential to replace chemical pesticides, providing eco-friendly, cost-effective, and profitable plant disease management strategies while improving crop productivity.

Keywords: 2-Methylpyrazine (2MP), 6-Pentyl-2H-Pyran-2-One (6PP), bio-fungicides, sustainable agriculture, agri-entrepreneurship

OP-65

Phytochemical Quantification in Oyster Mushroom Cultivated on Different Agri- wastes

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Abstract

Secondary metabolites of higher fungi like mushrooms are an unexplored resource compared to plant-derived secondary metabolites. In India, mushrooms are cultivated on varied agri-wastes, hence this study was taken up to study the effect of these substrates on the production of phytochemicals in mushrooms. One replicated trial was taken up with mushroom beds laid out with agricultural by-products like sesamum stalks, castor stalks, sunflower stalks, maize stalks, sorghum stalks, coconut coir pith, groundnut shells and paddy straw during *Kharif* and *Rabi* seasons for growing oyster mushrooms. The sporocarps of mushroom samples were chopped into small pieces, dried at 40°C in hot air oven for 48 h and powdered. The air dried powder was stored in an air tight container and used for the quantification of the phytochemicals like alkaloids, flavanoids, glycosides, saponins and triterpenoids. Results were analysed with paired t-test and interpretations revealed that high amount of alkaloids (20.90 mg/100 g of sample) and flavonoids (23.36 mg/100 g of sample) were recorded in the mushrooms grown on the paddy straw substrate. Maize substrate was found to be the next best with alkaloids (19.90 mg/100 g of sample) and flavonoids (21.50 mg/100 g of sample). Paddy straw stubbles were found ideal with high amount of saponins (17.10 mg/100 g of sample), glycosides (23.21 mg/100 g of sample) and triterpenoids (06.50 mg/100 g of sample) as compared to other substrates, followed by maize substrate (saponins: 16.21mg/100 g of sample; glycosides: 20.15 mg/100 g of sample) and sesamum substrate (triterpenoids: 05.36 mg/100 g of sample). Among all the eight substrates evaluated for the phytochemicals, the best source of substrate is paddy straw, recorded high amount of alkaloids, flavonoids, saponins, glycosides and triterpenoids and this is widely used source of substrate in Telangana.

Keywords: Oyster mushroom, substrate, alkaloids, paddy straw

OP-66

Adaptability and performance of shiitake mushrooms (Lentinula edodes) on different substrate combinations

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Abstract

Shiitake mushroom (*Lentinula edodes*) is one of the six popular edible mushrooms in the world. Itoriginated from East Asia is cultivated and eaten in many Asian countries as well as in Europe due to its flavour and medicinal properties. Shiitake is known as the most efficient lignin degrader in nature. They have lignocellulosic enzymes, enabling them to be cultivated in a wide range of lignocellulosic substrates. The most widely utilized base component in artificial substrate formulations for production is sawdust. The production and quality of the basal substrate were enhanced by the addition of certain additional supplements. *L. edodes* grows in cold climates with high relative humidity. A laboratory experiment was conducted to investigate the seven different substrate compositions on the mycelial growth of *L. edodes* for production of fruiting bodies. The results showed that all vegetative growth stages of shiitake mushrooms were recorded on seven substrates.S1 (Teak sawdust + sorghum grains) substrate which took 63 days for mycelial run, 15 days for mycelial coat formation, 43 days for bump formation and 26 days for browning period and shiitake mushrooms were harvested after 10 days of cold shock treatment with 550 g yield for1 kg of dry weight. Meanwhile, other substrates recorded vegetative growth with no yield. Normally, shiitake mushrooms were grown on oak and teak hardwood sawdust substrates, but the combination of sawdust supplemented with sorghum grains substrates, was able to produce shiitake mushrooms and the eucalyptus bark being available locally can be suggest for the best production of mushroom.A standard substrate composition has been developed to enhance shiitake mushroom production in Telangana.

Keywords: Shiitake mushroom (*Lentinula edodes*), substrate, sawdust, sorghum grains

Poster Presentations

THEME 1:

Advanced Detection and Diagnostic Techniques of Plant Pathogens

PP-01

Morphological and Genetic Variability among *Sclerotium rolfsii* Isolates Inciting Collar Rot of Chickpea

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Abstract

Morphological and genetic variability was studied among 14 *Sclerotium rolfsii* isolates infecting chickpea. Colony characters were recorded seven days after incubation, and the isolates have shown variation in the mycelial growth with three patterns, *viz*., fluffy, thin fibrous, and thin compact, with the presence and absence of concentric rings. The isolates also varied in colony color, such as extra white, white, and dull white. The data on sclerotial characters were recorded 20 days after incubation. The shape and color of sclerotia of different isolates varied from spherical to irregular, with light brown to dark brown color. Correspondingly, large variation was observed among the isolates in the number, size, and weight of sclerotia. Maximum number of sclerotia (221) was recorded with isolate CSR 13, and the minimum number of sclerotia (15) was recorded with isolate CSR 6. The size of sclerotia produced by different *S. rolfsii* isolates ranged from 1.20 mm to 3.20 mm, and the sclerotial weight ranged from 0.02 g to 0.50 g. The genetic variability among 14 *S. rolfsii* isolates was studied with seven Inter simple sequence repeat (ISSR) and four Sequence-related amplified polymorphism (SRAP) markers. Theresults of polymorphic data of *S.rolfsii* isolates with ISSR markers and SRAP markers showed 100 percent polymorphism with almost allmarkers except ISSR 827 (84.5 %). Cluster analysis based on ISSR markers groupedthe 14 *S. rolfsii* isolates into five clusters and most of the isolates were grouped under cluster IV. Correspondingly SRAP markers divided the 14 *S. rolfsii* isolates into seven clusters and hence large variation was observed among the isolates. From the variability studies using ISSR and SRAP techniques, it is revealed that even in the absence or mere presence of sexual stages, *S. rolfsii* had shown high variability and also elucidated that molecular methods can be well employed for analyzing variability.

Keywords: Chickpea, *Sclerotium rolfsii*, morphology, genetic variability

PP-02

Morphological and Molecular Variability of Macrophomina phaseolina Isolates Causing Dry Root Rot in Mungbean

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Abstract

Macrophomina phaseolina is a pathogenic fungus that causes dry root rot disease in various crops, including mungbean, *Vigna radiata*. It is a soil-borne fungus that survives in the form of sclerotia in soil and acts as a primary inoculum and germinates repeatedly throughout the harvest season. Hence, understanding the variability of *M. phaseolina* isolates is essential for developing resistant genotypes and implementing effective disease management strategies. The morphological, cultural, and molecular variation among different isolates of *M. phaseolina* was studied in the laboratory. Variation in morphological characteristics such as colony colour, texture, radial growth (mm/day), shape, size, and number of sclerotia was observed. Molecular characterization of 32 isolates was done using 12 SSR primers. Six primers, *viz*., MP-04, MP-11, MMP-16, MP-25, MP-32, and MP-35, have shown polymorphism among the isolates, and based on this data, isolates were grouped into clusters. At a 0.71% coefficient matrix, the isolates were grouped into 7 clusters. Further, allelic richness was studied, and it ranged from 1 to 14 unique alleles with all six SSR primers. The polymorphic information content values for SSR primers ranged from 0.61 to 0.91. The similarity coefficient matrix of *M. phaseolina* using SSR primers was recorded with a minimum of 0.25 to a maximum of 0.87. The average similarity across all the genotypes was found to be 0.37, showing that the isolates were highly diverse genetically. The results from the above study showed that there was a variation among the isolates with morphological as well as molecular characters. The results revealed that the isolates were highly diverse and further research is needed to fully understand the mechanisms underlying this variability and its implications for the biology and management of *M. phaseolina*.

Keywords: Variability, morphological, molecular, *Macrophomina phaseolina*, mungbean

PP-03

Diagnostics of Cucumber mosaic virus (CMV) in Chilli through Reverse Transcriptase Recombinase Polymerase Amplification Assay

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Abstract

Chilli is a major commercial vegetable and spice crop grown all over the world and about 35 viruses are known to infect chilli globally. Among the viruses, the Cucumber mosaic virus (CMV) is the most significant constraint to chilli production worldwide. CMV is a member of the *Cucumovirus* genus from the family *Bromoviridae*. Enzyme-Linked Immune-Sorbent assays and Reverse Transcription Polymerase Chain Reaction techniques are widely employed to detect CMV in infected plants. However, these techniques demand skilled manpower, expensive equipment and involve complex procedures. Thus, there is a need for a quick, reliable, efficient, and economical detection method for CMV. The present study optimized the Reverse Transcriptase Recombinase Polymerase Amplification (RT-RPA) method for the detection of CMV from infected chilli plants. Initially, primer optimisation was done using RT- PCR and then optimised primer was further used for the optimisation RT- RPA assay. The assay was optimized with different temperatures and times of 5°C-50°C (5°C increment) and 5 to 50 minutes, respectively. The optimized RT-RPA assay successfully detected CMV at 37 °C for 30 minutes consistently. Thus, developed RT-RPA assay for CMV can be utilised for further optimisation on field studies. CMV infection was confirmed by amplifying the expected size of 720bp from the CP gene using the CMV F/R primer pair. The RT-RPA was standardized by using the Coat Protein specific primer pairs using RT-PCR. The primer, which amplified the desired amplicons respectively with clear and bright band was used for the RT-RPA assay. The primer pair CMVFP2/RP2 gave a clear and bright band of amplicon size 239 bp was used for further RT-RPA assay. The temperature and time that gave bright and clear result was at 37 °C for 30 minutes consistently. Thus, a rapid, reliable, robust RT-RPA assay was developed for the detection of CMV from infected chilli leaves. The assay required minimal resource setting dispensing off the need for sophisticated equipment like thermal cycler and template preparation, thereby reducing the associated cost and time and valuable for on-site detection and management of CMV in India.

Keywords: Cucumber mosaic virus, chilli, recombinase polymerase amplification assay, on-site detection, point-of-care testing.

PP-04

First Report of *Cephalerous virescens* Causing Algal Leaf Spot of *Averrhoa carambola* in India

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Abstract

Averrhoa carambola (Star fruit) is a drought resistant edible fruit, belongs to the family Oxalidaceae. In early January 2023, we observed the symptoms of raised, more or less circular, orange to dark-brown, velvet textured, scattered algal leaf spots (1-4 mm) on the upper surface of *A. carambola* leaves at college farm, Agricultural College, Aswaraopet, Telangana, India. Transverse section cutting of algal spots revealed the algal thalli at subcuticular region and causing necrosis of epidermal cells. Sporangiophores raised from algal leaf spot were cylindrical, 4 to 5 celled, 200-450 µm long x 8-20 µm wide, and forming a head cell with suffultory cells and sporangia on the top. Sporangia were spherical to elliptical, rusty brown and 17.5-29 µm long × 18-23.6 µm wide. Setae were filamentous with three to six celled, 17.5-50 µm long × 2.5-7.5 µm wide. Fresh algal thalli were scraped from host tissue, surface sterilized (70% alcohol (30 s), 1% sodium hypochlorite (30 s) and sterile distilled water (3 × 60 s), inoculated to trebouxia liquid media and incubated at 25 ± 2°C with a 12 hours photoperiod for 72 hours. The resultant algal filaments were subjected to PCR amplification. The primer pair PNS1/NS41 was used in a PCR to amplify a fragment of 18S rRNA. The 18S rRNA gene sequences of the algae were compared using the Basic Local Alignment Search Tool showed that our partial sequence with 1625 bases long had 100% similarity to *C. virescens* (KM020142.1). Hence, it was classified as *Cephalerous virescens* and sequence was deposited in NCBI-GenBank. For proving pathogenicity, zoosporangial spore suspension was prepared by mixing algal thalli with sterile distilled water and sprayed on healthy, surface sterilized leaves of *A. carambola* and incubated in green house (T: 25^{0}C, H: 80%), three replicates of plants without inoculation served as control. The initial symptoms were produced 60 days after inoculation and complete algal thalli were observed on 90 days after inoculation, control plants were without any symptoms up to 150 days. Reisolated algal thalli from symptomatic plants were morphologically and molecularly similar to the identified *C. virescens*. The available literature suggests that, this is the first report of algal leaf spot on *A. carambola* caused by *C. virescens* in India.

Keywords: Carambola, algal leaf spot, pathogenicity, molecular characterization.

PP-05

Race Identification of *Fusarium oxysporum* f. sp. *ciceris,* Inciting Chickpea Wilt in Nandyal District of Andhra Pradesh

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Abstract

The chickpea wilt, caused by *Fusarium oxysporum* f.sp. *ciceris* (Foc), is a seed and soil borne disease that causes economic losses of 10-100% under favourable conditions. The emergence of new races poses a significant risk that reduces wilt resistance in the resistant cultivars of chickpea. Eight races (race 0, 1A, 1B/C, 2, 3, 4, 5 and 6) were reported all over the world; among them, four races (race 1, 2, 3 and 4) were reported in India. In the present study, 48 isolates (Foc 1 to Foc 48) from Nandyal district were characterized based on its cultural and morphological characters. For race identification of these 48 Foc isolates, six primers including four ITS based (FDP-2, FDP-3, FDP-9 and FDP-25) and two SCAR primers (FocR0-M15 and FocR5- L10) were used. Out of these forty-eight, 43 isolates were amplified at 700bp with FDP-3 and FDP-25 primers and identified as race-1. Four isolates (Foc-6, Foc-42, Foc-43 and Foc-46) were also identified as race-1 with FDP-3 primer alone, and one isolate (Foc-3) was not identified with any of the selected primers. Hence, we concluded the predominance of race-1 in the Nandyal district of Andhra Pradesh.

Keywords: *Fusarium oxysporum* f.sp. *ciceris* (Foc), ITS, SCAR, race and chickpea wilt.

PP-06

Genetic Fingerprinting of *Xanthomonas euvesicatoria* Isolates Inciting Bacterial Leaf Spot on Tomato in Telangana Region

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Abstract

Tomato, *Solanum lycopersicum* L. is the second most widely cultivated vegetable globally due to its sensory appeal and high nutritional value. However, bacterial diseases, particularly bacterial leaf spot (BLS), significantly constrain commercial cultivation, causing productivity losses of 23-44% in warm and humid climates. Identifying the pathogen is crucial for managing BLS, and molecular-based approaches, especially PCR, have emerged as effective tools for detecting pathogens at the species level. In a study employing Rep-PCR with the BOX element, DNA fingerprints consisting of multiple bands of varying sizes were generated, facilitating species-level differentiation. These fingerprints are widely used in phylogenetic and taxonomic studies. The similarity matrix from the study revealed a close genetic relationship among isolates, confirming their species identity. Additionally, DNA fingerprinting patterns indicated significant genetic diversity among isolates, with clustering patterns independent of their geographical origin. Similar correlations have been observed in other pathogens like *Xanthomonas campestris*. Understanding the genetic diversity of these isolates is crucial for developing effective breeding and management strategies to control BLS. The Rep-BOX PCR profile analysis demonstrated diversity among *Xanthomonas euvesicatoria* isolates, with some clustering within the same group regardless of their geographic origin.

Keywords: Bacterial leaf spot, *Xanthomonas*, tomato, PCR.

PP-07

Identification and Prevalence of Phytoplasmas Infecting Flower Crops in Andhra Pradesh, India

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Abstract

Andhra Pradesh (A.P) is one of the leading flowers producing states in India. In 2022-23, phytoplasmas were identified in all major flower crops of the state. The key symptoms identified were witches-broom, phyllody, little leaf, virescence, stunting and yellowing of leaves. We performed a nested polymerase chain reaction (PCR) assay using the universal P1/P7 and R16F2n/R16R2 primers and gene specific SecAfor2/Rev3 primers for detection and characterization of phytoplasma from the symptomatic tissues. PCR products of the expected size were obtained from the 16S rDNA and secA genes of the phytoplasma. Phylogenetic analysis revealed that marigold phytoplasma strains from Andhra Pradesh, India, belong to the 16SrI group, while those infecting crossandra, china aster, chrysanthemum, rose, and jasmine belong to the 16SrII group, which is associated with Aster yellows and peanut witches'-broom phytoplasma. The restriction fragment length polymorphism profiles were generated through an iphy classifier and indicated that all samples were infected by the same phytoplasma.

Keywords: Phytoplasma, Andhra Pradesh, marigold, crossandra, chrysanthemum, rose, jasmine, China aster, phyllody, witches broom, polymerase chain reaction.

PP-08

Exploring the Genetic Landscape in *Xanthomonas oryzae* pv. *oryzae* through Multi Locus Sequence Typing (MLST) and CRISPR-Cas Gene Profiles

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Abstract

In recent years, multilocus sequence typing (MLST) has become a widely used and highly discriminatory system for studying genetic diversity and evolutionary relationships among microbes. MLST analysis was performed using seven housekeeping genes to understand the genetic diversity and relationships among the isolates. Additionally, the presence or absence of Cas genes associated with the CRISPR-Cas immune system was examined in bacterial leaf blight, *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) isolates of paddy. The MLST analysis revealed genetic diversity among the 38 *Xoo* isolates, with different isolates exhibiting varying degrees of genetic relatedness. Some isolates shared identical sequence types (STs), indicating close genetic similarity, while others displayed unique STs, suggesting genetic divergence. Notably, the *dnaK* gene exhibited more sequence length variability than other housekeeping genes, indicating potential evolutionary pressures or genetic variation specific to this gene. Furthermore, the analysis of gene-specific diversity showed that most housekeeping genes had highly conserved sequences across the *Xoo* isolates, while the *dnaK* gene displayed greater variability in sequence lengths. This information provides insights into the genetic stability and diversity of these housekeeping genes within the *Xoo* population. These results highlight the complexity and diversity within the *Xoo* population in India and provide valuable insights into its evolutionary history. Regarding the CRISPR-Cas immune system, it was shown that certain *Xoo* isolates had a comprehensive complement of Cas genes, indicating the presence of an operational and effective defence mechanism against exogenous genetic elements. Nevertheless, it is noteworthy that two isolates exhibited the absence of the *Cas4* gene, a crucial component in spacer acquisition and adaptation. This genetic variation may affect their capacity to counteract novel challenges effectively.

Keywords: Bacterial leaf blight, paddy, multilocus sequence typing, CRISPR-Cas

PP-09

Identification of Groundnut bud necrosis virus Strain Infecting Tomato in Andhra Pradesh by Coat Protein Gene Analysis

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Abstract

Tomato, *Solanum lycopersicum* is an important vegetable crop grown worldwide, with Andhra Pradesh being a major producer in India, primarily by small-scale farmers. The crop is susceptible to numerous plant pathogens, with viral diseases posing significant challenges. Among the 36 viruses reported in tomatoes globally, tospoviruses are particularly destructive, causing yield losses of up to 100%. Tospovirus infections have been recorded in various crops, including chili, brinjal, cowpea, potato, and peanut, across India. Groundnut Bud Necrosis Virus (GBNV-To), a member of the *Tospovirus* genus within the *Bunyaviridae* family, is a major virus affecting peanuts and tomatoes in India. It is transmitted by melon thrips (*Thrips palmi*) in a propagative manner. The complete nucleotide sequence of the coat protein (CP) gene of GBNV-To infecting tomatoes in Andhra Pradesh was determined, revealing an open reading frame of 831 bases encoding a coat protein of 276 amino acids. Sequence analysis showed over 94% homology with other GBNV isolates infecting different hosts in India. The study concluded that the GBNV-To isolate from tomato in Andhra Pradesh is the same strain of GBNV already prevalent in India. Understanding its genetic composition aids in managing this destructive virus.

Keywords: Tomato, Groundnut bud necrosis virus, variability, coat protein, gene analysis.

PP-10

Detection and Diagnosis of Plant Diseases: An Overview of Current Prospective Methods

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Abstract

Plant diseases and pests are major threats to global food security and environmental sustainability. Early and accurate detection of plant pathogens is critical for curbing disease spread and implementing effective management strategies. Traditional diagnostic methods, while cost-effective and informative, often rely on visual inspections that are slow, subjective, and less reliable for disease control. Integrating molecular and morphological approaches can enhance diagnostic accuracy and efficiency. Advancements in molecular and biosensing technologies have revolutionized pathogen detection, offering unmatched sensitivity, specificity, and speed. Emerging tools like microfluidics, lateral flow assays, and smartphone-based biosensors have improved portability and field applicability, enabling real-time and multiplex pathogen detection. Techniques such as loop-mediated isothermal amplification and CRISPR-based diagnostics facilitate rapid on-site detection, while DNA microarrays enable high-throughput identification of multiple pathogens simultaneously. Ongoing research focuses on optimizing these platforms to improve efficiency, reduce costs, and support timely decision-making. The widespread adoption of advanced molecular diagnostics has minimized crop losses, reduced reliance on chemical inputs, and promoted sustainable agricultural practices. These technologies hold great promise for building resilient agricultural systems, improving crop yields, and contributing to global food security. Continued advancements and accessibility will be pivotal in mitigating the impacts of biotic stresses on crop productivity.

Keywords: Plant disease detection, pathogen diagnostics, molecular methods, CRISPR technology, integrated biosensing approaches.

PP-11

Molecular and Morphological Characterization of Leafhoppers as Vectors of Redgram Phytoplasma in Andhra Pradesh

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Abstract

Phytoplasmas are obligate, pathogenic bacteria that are primarily transmitted by phloem-feeding insects of the order Hemiptera. A study was conducted to identify the potential vectors for phytoplasma associated with phyllody and little leaf diseases of red gram. Insects were collected from the infected fields at SV Agricultural College Farm, Tirupati by using yellow sticky traps at weekly intervals and were preserved. Three major collected leafhopper species were identified as *Hishimonus phycitis*, *Empoasca* sp. and *Empoascanara* sp. by microscopic observation based on morphological characters. The DNA was extracted from each species and nested PCR assay was performed with P1/P7 and R16F2n/R16R2 primers. Among the three species, only *H. phycitis* yielded the expected amplification product in both the initial PCR and nested PCR, producing ~1.25 kb amplicon. Further analysis of *H. phycitis* DNA with *rp* gene-specific primers resulted in 1300bp and 1200bp amplicons in first and nested rounds, respectively. The amplicons of partial sequences of ~1.2 kb 16S rRNA and ~1.3 kb of *rp* gene were cloned, sequenced and submitted to the GenBank database. A BLAST similarity search analysis revealed that the partial 16S rRNA and *rp* gene sequences of *H. phycitis* showed 99.57% to 100% similarity with strains identified under 16SrII group. Phylogenetic analysis of 16S rRNA and *rp* gene sequences and virtual RFLP analysis of F2nR2 region of 16S rRNA gene confirmed that the phytoplasma strain in leafhopper belongs to16Sr II-D sub-group, consistent with the strain known to infect red gram, *Ca*. Phytoplasma citri. To verify the identity of the phytoplasma-positive leafhopper, a PCR assay targeting the *COX1* gene with universal invertebrate primers was performed, further confirming the species as *Hishimonas phycitis*.

Keywords: Phytoplasma, *Hishimonas phycitis, Empoasca* sp., *Empoascanara* sp., nested PCR, *Ca*. phytoplasma citri, *COX1* gene.

PP-12

Artificial Intelligence-Enabled Plant Health Mechanization for Precision Agriculture

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Abstract

The escalating global population necessitates transformative approaches to agriculture, emphasizing sustainability and efficiency. This study investigates the integration of Artificial Intelligence (AI) into plant health management, presenting an in-depth analysis of its potential to revolutionize crop cultivation for future food security. Employing advanced AI technologies, including machine learning algorithms, computer vision, and sensor networks, this research focuses on the development of intelligent monitoring systems for real-time assessment and response to dynamic crop requirements. Key components of this AI-driven plant health mechanization include high-resolution cameras and sophisticated sensors for continuous monitoring. AI algorithms analyze the collected data to detect subtle changes in plant physiology, identify potential diseases, and assess nutrient deficiencies. Proactive monitoring enables early intervention, minimizing crop loss, and reducing the dependence on conventional pesticides and fertilizers. Beyond monitoring, AI-driven mechanization extends to precision farming equipment guided by sophisticated algorithms. These systems perform tasks such as precise irrigation, targeted fertilization, and selective pest control. The data-centric nature of AI-driven plant health mechanization is a central theme, leveraging vast datasets for pattern recognition, issue prediction, and cultivation optimization. Increased yield, resource efficiency, and reduced environmental impact underscore the potential of this paradigm to redefine the future of global food production. In conclusion, this paper presents a scientific exploration of the transformative potential of AI-driven plant health mechanization. By integrating intelligent monitoring, precision farming, and data-driven decision-making, agriculture is poised for a new era characterized by heightened productivity, reduced environmental footprint, and enhanced resilience in the face of global food security challenges.

Keywords: Artificial intelligence, plant health, agriculture, machine learning algorithms, intelligent monitoring systems, data-driven decision-making, precision agriculture.

PP-13

Morphological and Molecular Variability in *Colletotrichum* spp

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Abstract

The single spore isolation of different samples (*i.e.* soybean pod blight, brinjal fruit rot, anthracnose of chilli, bell pepper, mung bean, French bean and cowpea, leaf spot of turmeric, anthracnose of dragon fruit and pigeon pea) were collected from different locations of Raipur and identified on the basis of *in vitro* studies. Morphological variability studies of 10 isolates of *Colletotrichum* spp., revealed that among the 10 isolates, significantly higher (40.47 mm) radial growth was recorded in French bean isolate (C3). Conidial length and breadth of *Colletotrichum* spp. ranged between 15.95-27.00 X 2.50-4.84 µm, maximum average conidial length of 27.00 µm was recorded in mung bean isolate (C6). The beans isolate exhibited (4.84 µm) maximum conidial width. In all nine isolates, conidia were falcate in shape but bean isolate conidia were rod in shape. Setae size varied from 140.75 -249.21 X 4.31-5.96 µm, higher setal length (249.21 µm) was recorded in chilli isolate (C5). Similarly, the width of setae also differed in different isolates of *Colletotrichum* spp. and maximum (5.96 µm) was recorded in turmeric isolate (C2) and appressoria found single or in loose groups, medium to dark brown, smooth-walled, clavate, ovate, pear shaped or irregular outline. Genetic variability and multilocus DNA sequence analysis of 10 *Colletotrichum* spp. isolates from different hosts studied through gene marker. DNA sequence comparisons by three genes (ITS- 18S-26S, 28 rDNA and ITS- rDNA) verified species identity of *C.truncatum*, *C. dematium, C. acutatum C.*

lindemuthianum, C. gloeosporiodes and *C. capsici*. The correlation between morphological and molecular-based clustering demonstrated the genetic relationships among the isolates and species of *Colletotrichum* and indicated that ITS rDNA sequence data were potentially useful in taxonomic species determination.

Keywords: *Colletotrichum*, variability, ITS marker, appressorium.

PP-14

Biosensor Based E- Nose Technology for the Early Detection of Plant Pathogens

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Abstract

Plant diseases pose a significant threat to global agricultural productivity, causing crop yield losses ranging from 20% to 40% annually. Plants usually get infected by different plant pathogens such as bacteria, fungi, and viruses. To continue to feed the growing population and protect the global ecosystems, the surveillance and management of the spread of these pests and diseases are crucial. Traditional disease detection methods are often time-consuming, labour-intensive, and require sophisticated laboratory facilities. Emerging technologies, such as biosensors and electronic nose (E-nose) systems, can be adopted for rapid, sensitive, and cost-effective detection of plant pathogens. Plants usually produce a wide range of VOCs in the tissues and provide functional information about the plant's growth, defense, and its health status, which allows for the possibility of using non-invasive techniques to monitor the plants. Electronic nose technology is a chemical detection system that has recently been applied for the detection of several plant diseases and pests. It is designed to mimic human olfaction through an array of gas sensors coupled with pattern recognition components, which detects the volatile organic compounds (VOCs) released during pathogen infection. This technology demonstrates remarkable success in detecting major plant pathogens, including *Botrytis cinerea*, *Fusarium* species, *Ralstonia solanacearum* and various plant viruses. Recent integration of nanomaterials and advanced data analysis methods has further enhanced system sensitivity and reliability. With the advantages including instant monitoring capabilities, precise pathogen identification, and field applicability. E-nose technology represents a promising advancement toward efficient and sustainable agricultural disease management practices. This convergence of biosensor technology with synthetic biology opens new frontiers in developing portable detection devices, potentially transforming global approaches to plant health monitoring and food security.

Keywords: Biosensor, E-nose, emerging technologies, nanomaterials, VOC's.

PP-15

Morphological Characterization of *Magnaporthe oryzae* Isolates Collected from Major Rice Growing Areas of Telangana

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Abstract

Rice is a staple food for a significant portion of the global population. Both biotic and abiotic factors contribute to losses in rice production, with rice blast disease caused by *Magnaporthe oryzae,* being a major threat. This disease often leads to substantial yield reductions, with some outbreaks resulting in losses of 50% or more, posing a serious challenge to global food security. Despite the implementation of various management strategies, blast epidemics continue to cause devastating impacts on rice production. This highlights the need for improved and region-specific disease management approaches. The present study was aimed to characterize the variability among blast pathogenic isolates, which is crucial for understanding the pathogen's behavior that directly impacts rice production. Leaf blast samples were collected from various rice-growing areas of Warangal and Hanamkonda districts such as Atmakur, Maheshwaram, Theegarajupalle, Lohitha, Kamalapur, Damera, Hasanparthy and Regional Agricultural Research Staion, Warangal. The radial growth, conidial size, color, texture, and sporulation of different isolates on various culture media such as Potato dextrose agar (PDA), Oatmeal agar (OMA), PDA+Rice leaf extract, and OMA+Rice leaf extract were examined. Of these, OMA supplemented with rice leaf extract was found to be the most effective for promoting radial growth, conidial size, and sporulation of the pathogen. Among the eight isolates studied, the Maheshwaram isolate (M-2) showed the highest radial growth, larger conidial size, and enhanced sporulation. These findings highlight the importance of understanding isolate-specific variability to develop targeted disease management strategies. By addressing pathogenic diversity, this study enables more effective and sustainable control of rice blast disease, supporting rice production and global food security. Additionally, the insights gained contribute to improved disease management, rice breeding, and sustainable agricultural practices.

Keywords: Rice, *Magnaporthe oryzae*, blast, morphological variability, culture media, growth.

PP-16

Mating-Type Analysis in Rice False smut *Villosiclava virens* Populations Based on PCR-Based Approach

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Abstract

Rice false smut disease caused by *Ustilaginoidea virens* (Cooke) Takahashi (teleomorph *Villosiclava virens* (Nakata) E. Tanaka & C. Tanaka is a destructive fungal disease of rice crop. The disease has gained national importance because of its effect on grain yield and quality. The individual rice grain infected by the fungus, transforms it to a powder form and the grain looks like an enlarged size ball known as smut ball. Fifty-two *U. virens* isolates collected from different zones *viz*., Western Zone, Eastern Zone, Central Zone and Southern Zone of different parts of rice growing regions were selected for the study. DNA of the respective isolates was isolated using modified CTAB method and all the *U. virens* isolates were confirmed with the specific ITS primer US1-5/US3-3 with the amplified product size of 380bp. The PCR assay was standardized for *V. virens* idiomorph-specific primers to identify the mating type genes *viz*., MAT-1-1 and MAT-1-2. The genomic DNA of all 52 strains was subjected to PCR. The primer pair MAT-1-1F/MAT-1-1R amplifies 185bp of the MAT-1-1 idiomorphs and MAT-1-2F/MAT-1-2 primer pair amplifies 285bp of the MAT-1-2 idiomorphs. Among the 52 *V. virens* isolates collected, 34 (65.38%) isolates contained MAT1-1-1 idiomorphs and classified as MAT1-1-1 heterothallic mating type, 47 isolates (90.38%) had the MAT1-2-1 idiomorph and were classified as MAT1-2-1 heterothallic mating type, and 29 isolates (55.77%) contained both MAT1-1-1 and MAT1-2-1 idiomorphs and were classified as the homothallic mating type. Among the collected isolates, all the isolates from southern zone showed the presence of MAT1-2-1 idiomorph.

Keywords: False smut, idiomorph, mating type.

THEME 2:

Biosecurity, Epidemiology and Climate Change of Plant Disease Epidemics

PP-17

Survey on Fusarium Stalk Rot Disease of Maize in Andhra Pradesh

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Abstract

Fusarium is considered as a devastating fungal menace and is one of the most prevalent fungi on maize, particularly in Andhra Pradesh. It causes Fusarium stalk rot on plants, which is considered as a major threat to maize production, accompanied by small losses to total wipeout of the crop. This disease is more prevalent in area where water stress occurs after flowering stage of the crop. Owing to its soil borne infection pathway, fungicidal control of Fusarium stalk rot is not effective. Maize is affected by several biotic as well as abiotic stresses. Among all diseases, fungal diseases play an important role and causes major yield losses. Of late, Fusarium stalk rot caused by *Fusarium verticillioides* is becoming major threat to maize cultivation in Andhra Pradesh. A survey was carried out during *Rabi* 2021 and 2022*,* in order to study the incidence of *Fusarium* stalk rot in major maize growing districts, *viz*., Srikakulam, Vizianagaram, Kurnool, Guntur and Eluru and Kakinada districts. The results revealed that highest disease incidence was observed in Srikakulam (20.43%) followed by Eluru (15.45%) and Kurnool (13.04%). The pathogen was isolated from the infected stem showing typical symptoms of the disease by tissue segment method on potato dextrose agar medium (PDA). The pathogen was identified as *Fusarium verticillioides* on the basis of morphological and Molecular markers.

Keywords: Maize, disease severity, survey, *Fusarium* stalk rot.

PP-18

Occurrence of Chickpea Collar Rot Caused by *Sclerotium rolfsii* in Telangana

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Abstract

Chickpea is one of the major grain legumes grown after dry beans and dry peas globally. A survey was conducted during *Rabi* 2021-22 to obtain collar rot disease severity in respect to soil type, cultivar used, previous crop grown and practicing of seed treatment in major chickpea regions of Telangana *viz.,* Northern Telangana, southern Telangana regions and few parts of Central Telangana zones. Only 29% of farmers are practicing the seed treatment with fungicide and majority of the farmers practicing Soybean-chickpea, Maize-chickpea and Tobacco-chickpea cropping system. Collar rot caused by *Sclerotium rolfsii* Sacc was found only in Adilabad, Nizamabad, Jogulamba-Gadwal and Jagtial districts of Telangana and the maximum disease incidence recorded 10, 14.5, 9 and 8 per cent, respectively. Out of four districts, in three districts farmers are practicing Soybean-chickpea cropping pattern except in Jogulamba-Gadwal district, where they are following Tobacco-chickpea cropping system. The results indicated that minimum disease incidence (8%) was recorded from Polasa village of Adilabad district and highest incidence (15%) recorded from Boregoan Village of Nizamabad District.

Keywords: Chickpea, survey, collar rot, PDI.

PP-19

Assessment of *Rabi* soybean diseases in Telangana

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Abstract

Soybean, *Glycine max* (L.) Merill, known as "Golden bean" grown extensively throughout the world. Soybean primarily a *Kharif* crop and farmers face seed shortages due to poor germination.

To bridge this gap, Government of Telangana promotes *Rabi* soybean. Roving surveys were carried out across soybean-growing districts *viz.*, Adilabad, Nizamabad, Kamareddy, and Jagtial to record the incidence of soybean diseases during *rabi*, 2023-24 in Telangana state. A total of 25 fields were surveyed covering 10 mandals in 4 districts. JS 335, ASB 22, KDS 726, JS 9305 and MAUS 612 are mostly grown varieties during *Rabi* season. The *Rabi* soybean is affected by diseases like Alternaria leaf spot, yellow mosaic disease (YMD), dry root rot, anthracnose, powdery mildew and Sudden Death Syndrome. The mean disease incidence of Alternaria leaf spot ((27.16%), YMD (38.5%), dry root rot (15.4%), anthracnose (6.4%), powdery mildew (2.8%) and SDS (1.6%). Among the districts surveyed, ALS (37.9 %), YMD (51.3 %), dry root rot (25.4 %), anthracnose (9.7%) were recorded highest in jagtial district and powdery mildew (8.98%) and SDS (2.93%) were recorded highest in Nizamabad while Lowest incidence of ALS (8.6 %), YMD (20.5%), powdery mildew (0.24%) were recorded in Adilabad district where as dry root rot (7.65 %), anthracnose (2.57%) and SDS (0.51%) were recorded in Kamareddy district.

Keywords: Soyabean, Alternaria, anthracnose, powdery mildew.

PP-20

Assessment of Rice blast disease Incidence in different Agro-climatic zones of Andhra Pradesh, India

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Abstract

Rice blast (*Pyricularia oryzae*) causes significant loss to rice production, and is a major threat to global food security. A roving survey was conducted in eleven rice growing districts of Andhra Pradesh with different agroclimatic zones to assess blast disease incidence during *Kharif* and *Rabi* 2023. Percent disease incidence was calculated as the proportion of plants showing symptoms, out of the total number of plants. The disease incidence varied in different agroclimatic zones of Andhra Pradesh. The highest mean blast incidence 56.71% was recorded in Kavali mandal of Sri Potti Sriramulu Nellore district which is in the Southern zone and the lowest incidence 7.92% was noticed in Owk mandal of Nandyal district which is in the scare rainfall zone. Blast incidence was highly varied among the cultivars compared to the locations. The highest mean disease incidence was observed in cultivar MTU-7029 (56.86%) followed by BPT-5204 (49.04%) whereas the lowest mean incidence was recorded in NDLR-8 (6.21%).

Keywords: Agroclimatic zones, Disease survey, Percent disease incidence, Rice blast.

PP-21

Survey for the occurrence of maize turcicum leaf blight in guntur district of Andhra Pradesh

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Abstract

Turcicum leaf blight (TLB) of maize (syn. Northern leaf blight) caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs, is an important foliar disease of maize worldwide. Presently the survey was taken up to assess the disease severity of TLB in major maize growing areas of Guntur district of Andhra Pradesh during *rabi*, 2019-2020. Maize Turcicum leaf blight was prevalent in all the surveyed areas of Guntur district with a mean PDI of 29.03. Among the three surveyed mandals, Chebrole recorded the highest PDI of 30.41 which is followed by Bapatla (29.86 PDI) while the least PDI (26.84) was recorded from Duggirala mandal. Amongst the six villages (2 per each mandal) surveyed, highest PDI (30.83) was recorded from Chebrole village of Chebrole mandal which was succeeded by Bapatla village of Bapatla mandal (30.28) and least PDI (26.39) was recorded in Perlapudi village of Duggirala mandal.

Keywords: Maize, Turcicum leaf blight, percent disease index

PP-22

Disease Outbreaks in Chickpea Due to Climate Change in S P S R Nellore District of Andhra Pradesh

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Abstract

Plant disease outbreaks pose significant risks to global food security and environmental sustainability worldwide and result in the loss of productivity and biodiversity, which exhibitnegative impact on the environmental and socio-economic conditions of farming community. One of the major concerns with potential climate change is that the frequency of extreme weather events including cold and heat waves, droughts, heavy precipitation, flooding and storms. These extreme weather events may also affect the prevalence of plant pathogens and related crop disease risk. Climate change further increases outbreak risks by altering pathogen evolution and host–pathogen interactions and facilitating the emergence of new pathogenic strains. Diseases of chickpea, *viz*., Colletotrichum blight, rust, and Sclerotinia blight are caused by fungi *Colletotrichum ciceri, Uromyces ciceris-arietini* and *Sclerotinia sclerotiorum*, respectively. Among these, Colletotrichum blight used to be the minor disease or incidence was not observed in chickpea growing areas of Nellore district for the past one decade. During *Rabi* 2022-23, yield losses from blight reached up to 100% in susceptible cultivars under favourable conditions. Pathogen, *C. ciceri* infection and disease development are favored at temperature between 15°C- 30°C with optimum at 20°C, relative humidity 90% and leaf wetness period for at least 6-10 h. Similarly, weather parameters namely average temperature 17.3°C -22.4°C, average relative humidity 90-95%, rainfall 420.9 mm and rainy days 11 were recorded in chickpea growing mandals during November, 2022. These weather parameters favored the Colletotrichum blight incidence in Chejerla mandal with 23.3-45.3%, Kaluvoi with 43.3-67.4%, Kaligiri mandal with 35.6-47.5%, Vinjamuru mandal with 28.9-50.2 per cent during *Rabi* 2022-23. Changing disease scenario due to climate change has highlighted the need for future studies on such models, which can predict the severity of important pathogens of major crops in real-field conditions. Simultaneously, disease management strategies should be reoriented in changing conditions with amalgamation of new strategies for sustainable food production.

Keywords: Colletotrichum blight, weather, temperature, rainfall, chickpea, climate change.

PP-23

Effect of Date of Pruning on the Severity of Anthracnose Disease on Rejuvenated Mango cv. Amrapali

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Abstract

The effect of rejuvenation times on mango cv. Amrapali under sub-Himalayan Terai region of West Bengal; the plants were headed back at 150 cm above from the ground level with six different pruning times at the instructional farm, Department of Pomology and Post-Harvest Technology, Faculty of Horticulture, Uttar Banga Krishi Vishvavidyalaya, Pundibari, West Bengal. The different times of rejuvenation were considered as the treatments to find out the severity of anthracnose (*Colletotrichum gloeosporioides*) disease of mango under natural field condition without any control measures during 2019-20 and 2020-21. The maximum severity of anthracnose (37.03%) was recorded with the plants of Amarapli pruned during 15th January, where as it was minimum (28.61%) with the plants pruned during 1st December. The mean percent disease index (PDI %) for severity (January to November) of anthracnose was recorded highest with the plants pruned during 15th January and lowest with the plants pruned during 1st December.

Keywords: Anthracnose, amrapali, mango, rejuvenation, Sub-Himalayan Terai region.

PP-24

Epidemiology of Rhizome Rot Disease of Ginger Caused by *Pythium aphanidermatum* and *Fusarium oxysporum* f. sp. *zingiberi*

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Abstract

Ginger, *Zingiber officinale,* is a significant herbaceous perennial rhizomatous spice crop. It belongs to the family, Zingiberaceae. India is a leading country in the world in terms of area and production. The rhizome rot of ginger, caused by *Pythium aphanidermatum* and *Fusarium oxysporum* f. sp *zingiberi,* is a severe problem for the cultivation of ginger and is very sensitive to water logged conditions in the field. Moisture, along with other environmental factors, significantly impacts the emergence and spread of the disease. The disease was first appeared on 27th August 2023 (35th meteorological week) when cumulative rainfall was 639.8 mm, relative humidity was 71.3%, and maximum and minimum temperatures were 33.15°C and 25.75°C, respectively. After first appearance of the disease, it gradually increased and reached its peak (73.6%) on 21 January 2024 during (3rd meteorological week) when cumulative rainfall and relative humidity were 886.1 mm and 85.7%, respectively and maximum and minimum temperatures were 13.2°C and 6.5°C, respectively, and then disease remained in a stagnant phase till harvest of the crop. The disease was more progressive during the month of September to mid-December. Highest infection rate of rhizome rot of ginger (0.049) was recorded in 37-38th Standard meteorological week.

Keywords: Correlation analysis, cumulative rainfall, disease incidence, epidemiology, relative humidity, rhizome rot, rate of infection.

PP-25

Occurrence of Major Foliar Fungal Pathogens in Chrysanthemum

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Abstract

Chrysanthemum morifolium (Ramat) is a commercial flower crop, gaining more popularity as cut, loose flower and potted plant, with its regular demand throughout the year. It is difficult to get good quality exportable blooms in this crop, majorly due to the incidence of many diseases. The objective of the present study was to identify pathogenic fungi of economically important *C. morifolium* based on morphological characterization and molecular characterization of the pathogens. Microscopic studies of infected samples from open field and shade net condition showed the association of ten fungal genera *viz., Alternaria* sp., *Fusarium* sp., *Septoria* sp., *Colletotrichum* sp., *Lasiodiplodia* sp., *Curvularia* sp., *Nigrospora* sp., *Botrytis* sp., *Phoma* sp. and *Stemphyllium* sp. and were initially identified based on macro and micromorphological characteristics. After isolation and identification, the per cent occurrence of the eight recorded fungal genera as follows *Alternaria* sp. Recorded the highest with 31.25% followed by *Fusarium* sp.(26.15%), *Colletotrichum* sp. (10.85%), *Lasiodiplodia* sp. (10.25%) and least being *Aspergillus* sp. (7.25%), *Curvularia* sp. (5.25%), *Rhizopus* sp. (4.55%), *Nigrospora* sp. (3.25%). Among the isolated fungi, *Rhizopus* sp., *Fusarium* sp., and *Aspergillus* sp. are fast growing; *Alternaria* sp, *Lasiodiplodia* sp, and *Colletotrichum* sp., were moderate growing, whereas *Curvularia* sp., and *Nigrospora* sp. are slow growing. Pathogenicity tests were conducted with all the isolated fungi, Koch's postulates could be proved in case of *Alternaria* sp., *Colletotrichum* sp., *Lasiodiplodia* sp. and were considered as predominant pathogens. The identity of homology searches for rDNA sequences of the said predominant pathogens was further determined up to the species level by comparing DNA sequences and phylogenetic analyses. Comparative nucleotide sequence analysis through BLAST program of National Centre for Biotechnological Information (NCBI) showed 98.16% similarity with *Alternaria alternata*, 99% similarity with *Colletotrichum gloeosporioides*, and 99.21% similarity with *Lasiodiplodia theobromae*. The gene sequences were submitted to NCBI and obtained the accession numbers.

Keywords: Chrysanthemum, microscopic studies, *Alternaria* sp., *Colletotrichum* sp., *Lasiodiploidia* sp., pathogenicity tests, rDNA sequences.

PP-26

Prevalence of Dieback of Neem in Nagarkurnool District of Telangana

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Abstract

Neem, *Azadirachta indica*, commonly known as Indian lilac or Margosa, is a medicinal tree native to India and belonging to the family Meliaceae. Its fruits, seeds, leaves, stems, and bark contain diverse phytochemicals with antifeedant, antibacterial, antifungal, and biopesticide properties, making it valuable in traditional medicine. However, neem trees in Telangana have recently been severely affected by dieback disease caused by *Phomopsis azadirachtae*, posing a significant threat to their health. To assess the disease incidence, a survey was conducted in Nagarkurnool district, Telangana, during October 2023, when the disease was at its peak. Infected plants displayed symptoms such as twig blight and inflorescence blight. Disease incidence ranged from 46% to 75%, with the highest recorded in Venkatapur village and the lowest in Gangaram village. Correlation analysis between disease incidence and weather parameters revealed a positive correlation with relative humidity and rainfall, while temperature and evaporation had a negative correlation. This study highlights the relationship between weather conditions and neem dieback development, providing essential insights for future research. Understanding these dynamics is crucial for devising effective management strategies to mitigate the impact of this disease on neem trees in Telangana.

Keywords: Neem, dieback, survey, *Phomopsis azadirachtae,* symptoms.

PP-27

Incidence of Powdery Mildew in Ridge Gourd

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Abstract

Incidence of powdery mildew in Ridge gourd studied the parents are Arka Sumeet, Konkan Harita, Jaipur Long, Saloni-5 and NRG-9 parents and along with three crosses F_3 progeny of the incidence of powdery mildew was found in almost all the parents. The highest incidence of powdery mildew was recorded in parent Arka Sumeet, Jaipur Long, Saloni-5 and NRG- 9 (22.5 percent), whereas the least incidence of powdery mildew was recorded in parent Konkan Harita (20 percent) and F_3 progenies (18.00 percent) of cross-I Arka Sumeet x Konkan Harita. Cross-II Arka Sumeet x Jaipur Long F_3 progenies (14.50 percent). Cross-3 Saloni-5 x NRG- 9 F3 progenies (10.90 percent).

Keywords: Ridge gourd, powdery mildew, progenies

PP-28

Influence of Weather Parameters on the Incidence of Stem Rot Disease in Groundnut across Major Growing Regions of Telangana

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Abstract

Groundnut, *Arachis hypogaea* L. is an important oilseed crop and the economic production of groundnut is constrained by soil-borne diseases. Stem rot, caused by the necrotrophic fungus *Sclerotium rolfsii*, is the most common soil-borne disease in groundnut. A roving survey was conducted in major groundnut growing areas of Telangana during *Kharif* 2019 and *Rabi* 2019-20 to collect preliminary data on the incidence level and pattern of prevalence of stem rot disease. The Warangal district has the highest incidence of stem rot, while the lowest incidence was found in Wanaparthy and Nagarkurnool districts. During *Kharif* 2019, disease incidence was positively correlated with weather parameters, *viz*., temperature, relative humidity and rainfall, whereas evaporation showed negative correlation. During *Rabi* 2019-20, temperature, relative humidity and evaporation showed positive correlation and rainfall showed negative correlation. This study provided an elementary idea about the per cent disease incidence and paved the path for developing ecosystem specific management strategy to reduce impact of soil borne diseases of groundnut in different districts of Telangana.

Keywords: Disease incidence, groundnut, temperature, relative humidity, *Sclerotium rolfsii*

PP-29

Influence of Weather Factors on Disease Severity of Rice Blast Caused by *Pyricularia grisea* (Sacc.) Causing Rice Blast *in-vivo*

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Abstract

During *Kharif* 2020-21and 2021-22, the PDI showed significantly positive correlation with minimum temperature and evening relative humidity. Step down regression analysis revealed that the minimum temperature, morning and evening relative humidity accounted for 70.07 per cent of variation (R^2=0.70) in PDI. Based on pooled analysis of two seasons, the prediction model for *Kharif* was arrived as $Y=107.67327-4.10070_{\text{min. temp}} + 0.26864_{\text{morn. RH}} + 0.14116_{\text{even. RH.}}$ During *Rabi* 2020-21 and 2021-22, the correlation studies revealed that the PDI showed significant negative correlation with maximum temperature and significantly positive correlation with minimum temperature and evening relative humidity. Step down regression analysis revealed that the minimum temperature alone accounted for 45.0 per cent of variation (R^2=0.45) in PDI. These parameter in combination with evening relative humidity accounted for 53.00 per cent variation (R^2= 0.53) in severity. Based on pooled analysis of two seasons, the prediction model for *Rabi* was arrived as $Y= 92.95310 - 4.02740_{\text{min. temp}} + 0.43790_{\text{even. RH}}$.

Keywords: Rice, blast, incidence, PDI.

PP-30

Influence of Weather Parameters on Powdery Mildew Disease of Sunflower

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Abstract

An experiment was conducted at RARS, Nandyal, during rabi 2021-22 to study the influence of weather parameters on powdery mildew disease of sunflower using the susceptible hybrid KBSH-44. The crop was sown on four different dates: November I FN, November II FN, December I FN, and December II FN. Results showed that the lowest disease severity (PDI: 10.5%) was observed in the fourth sowing date (December II FN), while the highest severity (PDI: 36.6%) was recorded in the first sowing date (November I FN). Disease initiation occurred earlier in the first sowing (January, flowering stage) compared to the fourth sowing (February, star bud stage). Correlation studies revealed that PDI was positively correlated with maximum temperature (0.36) and temperature range at a 1% significance level, as well as with mean temperature and wind velocity (0.34) at a 5% significance level. Conversely, PDI showed a negative correlation with evening relative humidity (-0.3) and relative humidity range. These findings highlight the role of weather factors in influencing disease severity, aligning partially with earlier studies by Karuna et al. (2016). The study concludes that to minimize powdery mildew severity and associated yield losses, sowing sunflower in the second fortnight of December is recommended during the rabi season.

Keywords: Sunflower, powdery mildew, *Golovinomyces cichoracearum*, weather parameters, date of sowing, disease severity, PDI.

THEME 3:

Host Plant Resistance and Molecular Approaches of Disease Management

PP-31

Development of Early Duration, High Yielding Chickpea Culture with Resistance to *Fusarium* wilt and Dry Root Rot

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Abstract

Chickpea, *Cicer arietinum* is a vital *Rabi* pulse crop in Telangana, occupying an area of 3.3 lakh acres. The introduction of high-yielding, short-duration varieties (100-105 days) like JG-11 and JAKI-9218 has contributed to increase in chickpea cultivation in the state since the 1990s. However, many of the currently cultivated chickpea varieties have become susceptible to diseases like *Fusarium* wilt and dry root rot, leading to significant yield losses of over 20%. This has forced farmers to explore other cropping systems. To make chickpea a more profitable crop for farmers, it is crucial to develop varieties that are both high-yielding (8-10 quintals per acre) and resistant to *Fusarium* wilt and dry root rot. In viewof the severity of the disease in the region and the need of resistant varieties, research efforts at the Agricultural Research Station (ARS), Adilabad, PJTAU, Telangana, have focused on developing high-yielding chickpea genotypes with disease resistance. One such promising genotype identified is ADBG-1 (P-201924), and was tested in All India Coordinated Research Project (AICRP) trials (IVT Rainfed) during 2018-19. ADBG-1 demonstrated impressive performance with an average yield of 1897 kg/ha across 9 locations in the Western Central Zone (WCZ) and 2018 kg/ha across 4 locations in the South Zone. Additionally, ADBG-1 exhibited excellent resistance to *Fusarium* wilt, showing no incidence in one location (Rahuri), and a low incidence (1.43%) in Badnapur. At four other locations (Junagadh, Indore, Jabalpur, and Kalaburagi), the genotype displayed moderately resistant reactions (below 20% incidence). Furthermore, it showed moderate resistance (19.32%) against Dry root rot and strong resistance (4.49%) to collar rot disease at Jabalpur location. Given its high yield potential, early maturity (100 days maturity) and resistance to key diseases, ADBG-1 presents a promising option for farmers with limited resources, particularly those with scarce irrigation. Its development can help improve chickpea productivity, contributing to better livelihoods for farmers in Telangana and other similar regions.

Keywords: Chickpea, *Fusarium* wilt, Dry root rot, ADBG-1.

PP-32

Castor Germplasm Screening for Resistance against Wilt, *Fusarium oxysporum* f.sp. *ricini*

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Abstract

Castor, *Ricinus communis* L., is an important non-edible oilseed crop majorly grown in arid and semi-arid regions of the world. The castor oil has huge value worldwide due to its industrial uses. Many biotic and abiotic factors are involved in low production and productivity of castor crop. Castor wilt, *Fusarium oxysporum* f. sp. *ricini,* is one of the major biotic factors causing yield losses up to 80%. The disease is soilborne in nature and difficult to control inspite of using all available management practices. Host plant resistance is the best alternative for the wilt management in castor crop. The present study was carried out at Regional Agricultural Research Station, Professor Jayashankar Telangana State Agricultural University, Palem during *Kharif* 2020 to identify the resistant germplasm against castor wilt disease. In all, 35 castor germplasm accessions supplied by ICAR - Indian Institute of Oilseeds Research were evaluated against *Fusarium* wilt pathogen under wilt sick plot and the inoculum load was maintained at 2×10^3 cfu/g of soil. The Standard checks, 48-1 (Jwala) (Resistant) and JI-35 (Susceptible) were sown after every five germplasm accessions and each entry was sown in a single row and wilt incidence was recorded at monthly intervals up to 150 days after sowing. Among 35 germplasm accessions, four accessions *i.e.,* RG-3860, RG-3961, RG-3963 and RG-3994 showed immune reaction against *Fusarium* wilt with zero per cent incidence and 13 lines *i.e.,* RG -3843, RG -3885, RG- 3887, RG- 3930-12, RG -3932, RG -3934, RG -3940, RG -3943-1, RG -3951-1, RG -3953-1, RG -3965-1, RG -3966 and RG -3967 have shown resistant reaction with less than 20 per cent wilt incidence. Remaining germplasm accessions have shown susceptible reaction to wilt disease and the incidence in standard checks JI-35 (susceptible) and 48-1(Jwala) (Resistant) was 100 and zero per cent, respectively.

Keywords: Castor, germplasm accessions, wilt, resistance.

PP-33

Screening of Advanced Red Gram Breeding Material Against *Fusarium* Wilt

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Abstract

Red gram is an important dry land crop of Telangana state. In Southern Telangana zone, red gram occupies about 1.50-1.80 lakh ha. of area annually under rainfed conditions. Though good number of varieties were released from Agricultural University in collaboration with ICRISAT, they belong to long and medium duration maturity groups and mature between 160-180 days. In spite of having promising varieties, the productivity of red gram is not exceeding 600-800 kg/ha due to several constraints such as, moisture stress at critical crop growth stages and incidence of wilt disease. This is mainly because of cultivation of long/medium duration varieties which are susceptible to wilt. Cultivation of early or mid-early maturing varieties which can complete their crop growth period within 150 days and resistance to wilt disease will be the best option to get good yields. Thus, keeping this in view, utilizing the advance generation breeding material of early maturing red gram, research was initiated in the year 2014 at Regional Agricultural Research Station, Palem. PRG-434, a pedigree selection from the cross LRG-41 x TTB-7 has been evolved under this programme. In observation varietal trial, PRG-434 recorded a yield potential of 1819.00 kg/ha which is 5.3% superior over the best check Asha (1727 kg/ha) during *Kharif*, 2022. This culture has also recorded yield of 1350.38 kg/ha which is 11.8% superior over the best check PRG-158 (1207.9 kg/ha) under rainfed situations by maturing in 140-145 days in preliminary varietal trial during *Kharif*, 2023. It has medium bold sized seeds and suitable for dal milling. This advanced entry along with other test entries was screened in wilt sick plot in *Kharif*, 2023 at ARS, Tandur along with resistant and susceptible checks *viz*., ICPL-87119, ICP 2376, respectively and was recorded as moderately resistant (23.16%) for wilt disease.

Keywords: Red gram, fusarium wilt, screening.

PP-34

Evaluation of Sugarcane Germplasm for Resistance Against Yellow Leaf Disease and Molecular Confirmation Through RT-PCR and transmission by Aphid Vector

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Abstract

Sugarcane yellow leaf virus (SCYLV) is a viral disease affecting sugarcane and at present has attained epidemic proportions, seriously affecting sugarcane production in the country. The SCYLV has a negative effect on sugarcane yield and yield contributing parameters. Initial spread of the virus occurs through infected seed cane and secondarily by aphid vector majorly., *Melaphis sacchari*. Managing SCYLV is difficult due to its vector-borne nature and transmission through infected seed cane. However, integrated management strategies including cultural, chemical, biological, and other conventional strategies including identification of sources of resistance and breeding for disease resistance needs to be adopted. In the absence of disease resistant varieties for cultivation, virus-free tissue culture seedlings derived through meristem culture are recommended to manage yellow leaf in sugarcane. Further, host resistance has not been exploited in the crop due to lack of information on resistance to yellow leaf disease in the germplasm and the parents. Hence, a study was undertaken to screen available germplasm at Agricultural Research Station, Perumallapalle to identify sugarcane genotypes having resistance to Yellow Leaf Disease (YLD). A total of 130 sugarcane genotypes were assessed for YLD severity based on 0-5 grade and out of them, five genotypes recorded '0' grade without any YLD symptoms till the harvest. The five genotypes were subjected to molecular analysis of SCYLV using the primer set SCYLV-613F and 613R. Only one genotype ie., 97R167 showed negative amplification while the other genotypes showed faint band indicating the presence of virus. The genotype 97R 167 was further evaluated through artificial inoculation studies using the viruliferous aphid vector, *melanaphis sachhari* followed by molecular analysis by RT-PCR for confirmation of resistance and was identified to be resistant against YLD.

Keywords: Sugarcane, Yellow leaf virus, host resistance, aphid.

PP-35

Influence of Phytochemicals on Sclerotia and Ooze Formation and its Maturity against Stem Rot Fungus *Sclerotium rolfsii* in Groundnut

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Abstract

Groundnut is one of the most important food and cash crops of ourcountry.Stem rot caused by Sclerotium rolfsii Sacc. is an important disease in groundnut causing up to 10-25% yield losses extending up to 80% in severe cases. The study evaluated the effect of three phytochemicals (Piperine, Reserpine, β-sitosterol) on sclerotia and ooze formation under *in vitro* conditions. All the three phytochemicals were effective in inhibiting the sclerotial formation, maturity of sclerotia and number of sclerotia. The phytochemical β-Sitosterol (29 days) was the most effective in inhibiting the sclerotial formation followed by reserpine (28 days) and ethyl protocatechuate (27 days) at a concentration of 2000 ppm. However, there was no significant difference among these three compounds in inhibiting the sclerotial development. Reserpine was the most effective in inhibiting the number of sclerotia formed at 1000 ppm (181), 1500 ppm (48) and 2000 ppm (30) compared to the control (358).The results revealed that increase in concentration of phytochemical caused maximum inhibition of both sclerotial development and number of sclerotia formed under *in vitro* conditions.

Keywords: Groundnut, phytochemicals, Sclerotium rolfsii.

PP-36

Evaluation of Advanced Sorghum Breeding Lines for Grain Mold Resistance

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Abstract

Sorghum is the fifth most important cereal crop for millions of people. Grain mold is an important biotic stress with yield losses reaching up to 100% in highly susceptible cultivars. Several qualitative traits like panicle shape and compactness, grain hardness, presence or absence of a pigmented testa, photoperiod sensitivity, glume coverage, production of phenols, antifungal proteins and other secondary metabolites affect grain mold resistance. Sorghum cultivars with white grain pericarp are more vulnerable to grain mold than those with brown and red grain pericarp. Among the several approaches to manage the sorghum grain mold, host-plant resistance is the most effective and economical option. During *Kharif* 2022, 45 sorghum advanced breeding lines along with two checks, *viz.,* resistant B58586 and susceptible Bulk Y lines were evaluated for grain mold disease incidence on grain mold field grade (GMFG) and grain mold threshed grade (GMTG) scales of 1-9. Seven lines of Palem, *viz.,* PSV 303 (2.7 and 3.0), PSV 312 x 402 (2.7 and 3.0), PSV 312x407 (.8 and 3.8), PSV 313x316 (3.5 and 4.2), PSV 313x6002 (2.5 and 2.7), PSV319x407 (2.6 and 2.9), PSV 407x6002 (3.4 and 4.0) were resistant with <3.6 for GMFG and 4.3 for GMTG compared to the incidence of 6.3 and 6.8, respectively in the susceptible check Bulky Y.

Keywords: Sorghum, breeding lines, grain mold, host plant resistance

PP-37

Development of High Yielding Local Suitable Rice Cultivars Possessing High Yield with Durable Resistance to Blast (*Pi5)* and Bacterial Leaf Blight (*Xa21*).

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Abstract

Rice is the predominant crop in Telangana state, prone to various diseases and pests. In this context, there is a need to develop varieties having resistance to biotic stresses. The present study aims to develop high yielding rice varieties with durable resistant to blast and bacterial leaf blight. For this, a cross was made between RP 5973-20-9-8-24-12-3 (MTU1010 NIL-219A) x Akshaydhan (RP6132) and the breeding material was forwarded to F7 generation through Marker assisted pedigree breeding and was evaluated and screened for Blast and BLB resistance in uniform blast nursery and glass house respectively at RARS, Jagtial during *Rabi* 2019-20. A total number of 48 entries were screened for blast (Uniform Blast Nursery) and BLB (artificial inoculation for in Glass house) out of which, 4 entries (JGL 41640, JGL 41657, JGL 41667 and JGL 41706) were shown resistant reaction to bacterial leaf blight and blast. Breeding material of (NIL of MTU1010 (*Pup1) x* NIL of *Akshayadhan (Xa21* and *Pi54)* at F8 generation (*Pup1, Xa21* and *Pi54)* was screened for BLB at Regional Agricultural Research Station during *Kharif* 2020. Among the screened entries, 10 entries (JGL 41640, JGL 41657, JGL 41660, JGL 41666, JGL 41667, JGL 41671, JGL 41678, JGL 41681, JGL 41686, JGL 41706) were shown resistant reaction to bacterial leaf blight. It was shown that Marker Assisted selection (MAS) was successfully implemented in developing the high yielding varieties with durable resistance to BLB and blast, which could serve as good donors for the future-breeding program and after testing in station trails and may be released as new varieties.

Keywords: Rice, marker assisted breeding, blast and BLB

PP-38

Evaluation of Recombinant Inbred Lines of Mungbean, *Vigna radiata* for Yellow mosaic virus Resistance

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Abstract

In the present investigation, 128 F_6 Recombinant inbred lines (RILs) of mungbean (MGG-295 X WGG-42) were screened against Mungbean yellow mosaic virus resistance. The disease screening was done using 0-5 disease rating scale.The RILs were grouped based on the reaction of MYMV present in rows (F_6 Lines) and complete reaction of MYMV by its expression. The disease intensity was recorded by observing the per cent infected plants to the total number of plants based on a rating scale. Disease incidence was assessed by calculating the percentage of infected plants relative to the total number of plants. These Recombinant inbred lines would be utilized as donors to develop MYMV resistant lines and can also be used for further artificial screening studies like agroinoculation, forced feeding method. Additionally, resistant genotypes demonstrated robust agronomic performance, indicating their potential in breeding programs to develop YMV-resistant cultivars.

Keywords: Screening, greengram, resistant, mungbean, yellow mosaic disease, recombinant inbred line.

PP-39

Management of Late Leaf Spot, *Phaeoisariopsis personata* Disease of Groundnut with Systemic Acquired Resistance Inducers

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Abstract

Late leaf spot disease of groundnut caused by the fungus *Phaeoisariopsis personata* is the most important constraint to groundnut production in almost all groundnut growing areas in India. This disease, due to its drastic reduction of photosynthetic tissues in plant foliar parts, leads to about 70% yield loss in susceptible cultivars. In the present investigation, greenhouse experiments were conducted to study the ability of systemic acquired resistance (SAR) inducers to protect groundnut plants from late leaf spot (LLS). Two different SAR inducers *viz.*, salicylic acid (SA) at three different concentrations of 4mM, 7mM, 10mM, and DL-β-amino-n-butyric acid (BABA) at three different concentrations of 5mM, 10mM and 15mM were used in this experiment. The results indicated that foliar sprays of all tested SAR inducers at different concentrations significantly reduced the incidence of late leaf spot compared to untreated control. DL-β-amino-n-butyric acid (BABA) @ 10mM significantly (*P* = 0.05) reduced LLS severity by 74.2% as compared to control whereas, salicylic acid (SA) @ 7Mm increased the pod yield and other growth parameters like shoot length, root length, no.of nodules and no.of gynophores significantly when compared to control.

Keywords: Late leaf spot, SAR inducers, salicylic acid, BABA, foliar spray

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PP-40

Marker Assisted Introgression of *AHAS* Gene, Conferring Herbicide Tolerance, into the Elite Rice Variety, DRR Dhan 44

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Abstract

Direct Seeded Rice (DSR) is rapidly followed in many rice growing in India due to its unique advantage of saving water and labor. It is reported that the incidence of brown spot, blast, bacterial leaf blight is more observed under DSR compared to transplanted method. Weeds are major hindrance to shift from conventional transplanted rice to DSR. *AHAS* gene which impart herbicide tolerance to cultivated rice will address the issue of weeds effectively under DSR. Therefore, this study aims to introgress *AHAS* gene (i.e. conferring tolerance to the herbicide, Imazethapyr) using Pusa 44-NIL as the donor parent and DRR Dhan 44 as the recurrent parent. A cross was made between DRR Dhan 44 X PUSA 44(NIL) in *Kharif* 2021, and a total of 45 F_1 plants were confirmed with gene specific marker for presence of herbicide tolerant *AHAS* gene in heterozygous condition. The true F_1 plants, identified through marker-assisted selection were selfed to generate F_2 plants. The F_2 plants that were positive and homozygous for the *AHAS* gene were identified with the gene-specific marker and advanced till F_5 generation through pedigree method of selection. During *Kharif* 2024, the F_5 plants were screened for their tolerance to Imazethapyr, along with grain yield and agro morphological attributes. A total of five lines possessing herbicide tolerance along with high yield and grain type similar to DRR Dhan 44 were identified and advanced for further evaluation in multi-location trials. This will enhance the adoption of DSR using improved lines.

Keywords: Direct seeded rice, weeds, marker assisted selection

PP-41

Effect of Moisture Deficit Stress and Nutrient Management on Aflatoxin Contamination of High Oleic and Normal Groundnut

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Abstract

Groundnut is a vital oilseed crop that serves as a key source of oil and protein for the majority of the population. However, pre-harvest aflatoxin contamination poses a significant challenge to groundnut production. A field experiment was conducted during *Rabi* 2022-23 and 2023-24 at ICRISAT, Patancheru, to assess the influence of moisture stress and nutrient management on pre-harvest aflatoxin contamination in high-oleic and normal groundnut varieties. The experiment utilized a split-plot design across two environments: non-stress conditions (irrigation at 1.0 E pan from 50 days after sowing to harvest) and stress conditions (irrigation at 0.5 E pan from 50 DAS to harvest). Four nutrient management treatments were applied: N_1 (NPK @ 30-40-50 kg ha^{-1}), N_2 (NPK + Gypsum @ 500 kg ha^{-1}), N_3 (NPK + Gypsum + Vermicompost @ 5 t ha^{-1}), and N_4 (NPK + Gypsum + Vermicompost + PGPR seed treatment @ 9 g kg^{-1}). These treatments were tested on three varieties: Girnar 4 (ICGV 15083), Girnar 5 (ICGV 15090), and Kadiri Lepakshi (K1812). Moisture stress significantly increased aflatoxin contamination in groundnut kernels in both the years. The contamination was substantially higher under stress conditions than in non-stress conditions. Nutrient management treatments did not significantly influence aflatoxin content under either stress or non-stress conditions. Among the varieties, Kadiri Lepakshi recorded the highest aflatoxin levels under stress and across environments, while Girnar 5 consistently exhibited lower aflatoxin content, comparable to Girnar 4. The combination of Kadiri Lepakshi under stress conditions recorded the highest aflatoxin levels across all treatments and environments. These findings highlight the exacerbating effect of moisture stress on aflatoxin contamination and the relative resistance of Girnar 5 under stress-prone conditions. Developing strategies to mitigate stress-induced aflatoxin contamination is crucial for ensuring groundnut safety and quality.

Keywords: Aflatoxin, peanut, nutrient management, high oleic variety.

PP-41a

Development of Blast-resistant versions of Swarna-Sub1, an elite rice variety using Marker-Assisted Gene Pyramiding

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Abstract

The rice variety Swarna-Sub1 is known for its tolerance to submergence, a critical trait for cultivation in flood-prone areas. However, this variety showed a significant decrease in yield in regions that were prone to the devastating blast disease caused by the fungus *Magnaporthe oryzae* (*Pyricularia oryzae*). To address this issue, we have employed a marker-assisted backcross breeding approach to pyramid three major blast resistance genes, namely Pi1, Pi2, and Pi54, into the Swarna-Sub1 genetic background. The strategy involved using the donor lines Swarna-LT (*Pyricularia oryzae*). To overcome this problem, three major blast resistance genes viz., Pi1, Pi2, and Pi54 were pyra mided through marker-assisted backcross breeding using donors, Swarna-LT (having *Pi1* & *Pi54*) and Swarna-A51 (having *Pi2*) to introduce the desired blast resistance genes. Foreground selection was carried out using molecular markers tightly linked to the three blast resistance genes, as well as the *Sub1* gene responsible for submergence tolerance, to ensure the retention of these important traits in the recurrent parent. Based on the comprehensive evaluation of disease resistance and agronomic performance, we have selected the best 25 plants from the two- and three-gene pyramided BC_3F_2 homozygous lines. These selected lines had a maximum of 93.5% recurrent parent genome and were further advanced to the BC_3F_5 generation. The stringent recurrent parent genome recovery analysis using SSR markers helped minimize the linkage drag, with the three-gene pyramided lines exhibiting a range from a minimum of 0.2 Mb to a maximum of 2 Mb. The two and three blast resistance genes pyramided lines, such as SS30-24-82, SS30-24-73, and SS30-24-46, demonstrated a high level of blast resistance and submergence tolerance. The successful integration of marker-assisted backcrossing and phenotypic selection strategies enabled the development of Swarna-Sub1 lines with multiple blast resistance genes, along with superior agronomic and grain quality traits. These lines hold immense potential as valuable genetic resources for the rice breeding program to address the challenges posed by blast disease and fluctuating water availability.

Keyword: Rice, blast- resistant, MAS, *Pyricularia oryzae*

PP-42

Field Evaluation of Maize Endophytes against Charcoal Rot of Maize Caused by *Macrophomina phaseolina*

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Abstract

Charcoal rot of maize, caused by *Macrophomina phaseolina* is one of the most devastating seed as well as soil borne fungal pathogens globally, including India and Telangana state leading to severe yield losses in maize crop. Disease management with fungicides was not successful due to complex soil borne nature of the pathogen. Under this scenario, the plant genotype colonizing mutualist endophytes showing biocontrol activity is the best option for managing the disease among other conventional approaches. Keeping this in view a study was conducted at Maize Research Centre, ARI, Rajendranagar to evaluate maize endophytes against charcoal rot of maize under field conditions. Endophytes were isolated from different maize genotypes and three potential endophytes *i.e.,* one fungal (ERF2), two bacterial (ESB9 and ESB17) endophytes were selected based on their performance in dual culture and plant growth promotion. Further, treatments were formulated with three potential endophytes (seed treatment + soil application) and their combinations under field conditions. All the treatments increased the yield significantly and reduced the incidence of charcoal rot along with enhanced plant growth. Among the nine treatments, the treatment T_5 involving (*Bacillus subtilis* ESB9 (T_2) + *Pseudomonas rettgeri* ESB 17 (T_3)) recorded highest yield of 8023.5 kg ha^{-1} with disease reduction of (53.7 %). Treatments T_4 and T_7 were also statistically on par with T_5 in terms of reduction in charcoal rot incidence (50.6 % and 46.5 %), enhanced grain yield (7901.4 and 7664.2 kg ha^{-1}). The combination of two endophytic bacterial isolates, *viz*., *B. subtilis* and *P. rettgeri* when applied both as seed treatment and soil application were effective in managing charcoal rot disease and improving the yield in maize. These potential endophytes have to be developed as bio-inoculants for improving plant growth and suppressing charcoal rot disease in maize.

Keywords: Charcoal rot, maize, endophytes, *Bacillus subtilis, Pseudomonas rettgeri.*

PP-43

Deciphering the Effects of Fusarium Dry Rot on Potato Tubers'Biochemical Properties using Titrations, GC-MS/MS and FTIRS pectroscopy

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Abstract

Fusarium dry rot (FDR),caused by more than 17 species within the *Fusarium* genus,is a major post-harvest disease affectingthe physiological and biochemical properties of potato tubers during storage. Infection primarily changes carbohydrate composition, affecting starch, amylose, amylopectin, reducing sugars, sucrose, and total soluble sugars. Notably, *Fusarium*-induced dry rot increases starch digestibility, raising the glycemic index and glycemic load, which may pose health risks for consumers. Therefore, there is an urgent need to analyse the impact of FDR disease on potato tubers. Keeping this in view, this study was conducted inthe Department of Plant Pathology at CCS Haryana Agricultural University, Hisar, during 2023-2024 to analyse the various physico-biochemical properties of potato before and after 30 days of infection of FDRusing titration methods, GC-MS/MS and FTIR spectroscopy. Fifty-three *Fusarium* isolates were isolated from major potato-growing regions of Haryana, followed by artificial inoculation on healthy tubers on Kufri Chipsona cultivar using cork-borer method. Biochemical changes were statistically assessed using Duncan's multiple range test. Results revealed that tubers infected with isolate PDR 5.4.2 led to the lowest starch content, while isolates PDR 5.4.1, PDR 7.2, and PDR 11.1.1 increased soluble sugar content. Tubers infected with isolates PDR 12.7 and PDR 6.1 resulted in elevated levels of reducing sugars, while PDR 3.3 showed the highest polyphenolic content and antioxidant activity in infected tubers. Additionally, volatile compounds responsible for off-flavors in infected potatoes were identified using GC-MS/MS and further confirmed by FTIR spectroscopy. These findings provide valuable insights for plant pathologists, nutritionists, food technologists, and potato growers, highlighting the nutritional and health impacts of *Fusarium* infection in stored potato tubers.

Keywords: Fusarium dry rot, potato tubers, carbohydrate composition, GC-MS/MS, FTIR spectroscopy, biochemical analysis.

PP-44

Validation of Yellow Mosaic Disease Resistance in Soybean using SSR Markers

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Abstract

Soybean (*Glycine max* (L.) Merr.) (2n=40) is a dicotyledonous and annual leguminous crop important for food and feed products. Yellow mosaic virus (YMV) is major viral disease of soybean resulting in economic loss to the tune of 30-50%. Initially, confined to the northwest plains of India, the sudden outbreak of YMV in central India during 2015 and subsequent spread to south India demonstrated its potential to spread to other soybean growing areas. Keeping this in view, the study was conducted to introgress YMD resistance in the genetic background of high-yielding soybean varieties as a management approach to YMV. Ten soybean advanced breeding lines along with two checks SL 958 (resistant) JS 335 (susceptible) were screened for yellow mosaic disease resistance during Summer, 2023 at Agricultural Research Station, Adilabad and Institute of Biotechnology, Hyderabad under field conditions and validated using SSR markers. Among 10 entries, SL 955, DS 3105, DS 3106, PS 1347, PS1670, NRC 128 showed resistance with yellow mosaic disease reaction of < 3 on 1-9 scale compared to the disease reaction of 9 on the susceptible check (JS 335). Genotyping advanced breeding lines using two simple sequence repeat (SSR) markers (Satt 322 and BARCOSOYSSR_02_0423) revealed that all the resistant genotypes SL 958, SL 955, DS 3105, DS 3106, PS 1347, PS1670 except NRC 128 carried the positive alleles for YMV disease resistance. The allele for susceptibility was found in the YMV susceptible genotypes NRC 37, NRC 157, JS 95-60, NRC 130 and JS 335. The study showed that SSR marker Satt 322 can be used to screen soybean germplasm to identify YMV resistant genotypes and that identified resistant lines can be used as donors in soybean breeding program for marker assisted selection.

Keywords: Soybean, YMV, SSR markers.

PP-45

Evaluation of Safflower Germplasm for Resistance to Wilt Caused by *Fusarium oxysporum* f. sp. *carthami*

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Abstract

Safflower, *Carthamus tinctorius,* is a significant oilseed crop renowned for its high-quality oil, particularly rich in oleic acid, which is widely used in the food and cosmetic industries. Despite its economic value, safflower production is severely impacted by various biotic stresses, with *Fusarium oxysporum* f. sp. *carthami* causing Fusarium wilt being one of the most destructive diseases. This soil-borne pathogen leads to severe yield losses, particularly in regions where the pathogen is endemic. The persistence of the pathogen in soil and the lack of effective chemical control measures make the management of Fusarium wilt particularly challenging. Therefore, the development of resistant safflower varieties is a key strategy to mitigate the disease and enhance safflower production. The present study was aimed to evaluate safflower germplasm for resistance to Fusarium wilt. A field experiment was conducted during the *Rabi* season of 2022-23, testing 33 elite safflower genotypes sourced from different centers of the All India Coordinated Research Project (AICRP) under ICAR-Indian Institute of Oilseeds Research, Hyderabad against Fusarium wilt in a uniform Fusarium wilt sick plot at Agricultural Research Station, Tandur, PJTAU. The experiment was carried out in a randomized block design with two replications. The inoculum load of *F. oxysporum* f. sp. *carthami* in the wilt sick plot was maintained at 5×10^5cfu/g of soil. Fusarium wilt susceptible genotype Nira, PBNS-12, and the resistant check TSF-1 were planted in every fifth row to assess the resistance levels. The results revealed that out of the 33 genotypes tested, ANG-21-1-4 was immune to the disease, showing no signs of wilt. Eight genotypes exhibited moderate resistance with 0-10% mortality, including SSF-18-70, AKS-356, PBNS-227, TSF-447, TSF-446, SSF-18-86, SSF-18-69, and SSF-18-86. Four genotypes (AKS-355, ANG-22-8-16, TSF-443, and ISF-300) showed tolerance with 11-20% mortality. Seventeen entries were classified as susceptible, while eleven entries were highly susceptible to Fusarium wilt disease. This study identified promising safflower genotypes with varying resistance levels, which can be utilized in future breeding programs to develop wilt-resistant safflower varieties, thereby enhancing sustainable oilseed production.

Keywords: Safflower, Fusarium wilt, disease, resistance.

PP-46

Screening and Identification of *Fusarium* Wilt Resistant Lines from the Advanced Breeding Material Developed through Genepool Concept in Castor

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Abstract

Castor (*Ricinus communis* L.), a monotypic species belongs to the family Euphorbiaceae. It is an important industrial cropowing to its oil which contains ricinoleic acid. *Fusarium* wilt caused by *Fusarium oxysporum* f. sp. *ricini* is a most destructive disease of castor and is both seed and soil borne. The wilt appears in all castor growing states of India causing significant yield losses up to 80%. Being a monotypic species, limited variability in castor was observed for yield contributing traits as well as for resistance to diseases and pests which has led to slow progress in castor breeding programmes. The genepool concept, refers to the use of diverse genetic material from different sources, including wild relatives, landraces, and elite cultivars, to create a broad base of genetic diversity for different traits was adopted in castor at RARS, Palem. Through this approach, new combinations of beneficial traits are generated, and resistance to diseases like *Fusarium* wilt can be introduced into elite castor cultivars by utilizing the material generated.In this study, elite castor lines *viz*., PCS-124, PCS-106, PCS-262, DCS-107, PCS-136 and PCS-309 with diverse genetic background were selected and random mating was done in isolation for three consecutive seasons *viz*., *kharif*, 2016, 2017& 2018 followed by selection and advancement of generations. The stabilized breeding material (inbred lines) derived from this genepool was screened for wilt resistance in wilt sick plot available at RARS, Palem. Nearly 25 lines were screened in two splits. Twelve lines were screened during *Kharif*, 2022 and thirteen were screened during *kharif*, 2023. Out of these, MGP-27, PPL-1004 and MGP-145 were recorded 0% wilt incidence indicating complete resistance to the disease. Whereas, PPL-1008, PCS-407, PCS-408 and PCS-372 showed resistance by recording less than 20% wilt incidence and PCS-406 and PCS-401 showed moderate resistance to the disease.Remaining lines were found susceptible up on screening under wilt sick plot conditions. The study has yielded, two pistillate and seven monoecious lines which were found resistant to *Fusarium* wilt. These lines can be utilized in crossing programmes to develop wilt resistant hybrids or if found superior in yield trials, the lines can be promoted as varieties.

Keywords: Castor, *Fusarium* wilt, genepool, inbred lines, variability.

PP-47

CRISPR-Mediated Genome Editing for Durable Resistance against Plant Viruses

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Abstract

Viral diseases in crops cause enormous losses throughout the world, both conventional and non-conventional approaches have been applied to develop plants resistant to viruses. As plant viruses evolve rapidly by recombination and mutation, the conventional strategy may fail to control these viruses. Durable resistance is required to overcome these challenges. The CRISPR (clustered regularly interspaced palindromic repeats)/CRISPR-associated 9 (CRISPR/Cas9) system has recently emerged as an efficient genome-editing tool for many eukaryotic species, including plants. This technology has some advantages over artificial microRNAs and RNAi for engineering virus resistance in plants by the disruption of essential viral or host gene instead of silencing those genes at the RNA level. Several studies have demonstrated the advantages of the CRISPR/Cas9 system to effectively confer resistance to DNA and RNA viruses in plants, either by directly targeting and cleaving the viral genome or by modifying the host genes. The CRISPR/Cas system requires a Cas endonuclease and a customized single guide RNA (sgRNA) complimentary to target DNA. CRSIPR/Cas9 and other CRISPR/Cas systems are applied for targeted mutagenesis, The rapid development of CRISPR technology is a definite milestone and has advantages over other systems. Plant viruses do not possess the ability to counter CRISPR-based immune defense originated from prokaryotes. Furthermore, by editing host factors and removing gene editing CRISPR machinery by backcross, virus-resistant transgene-free plants can be generated. Moreover, new CRISPR-based systems such as multiplexed CRISPR can also be used to develop broad spectrum resistance against different kinds of pathogens by targeting multiple pathogens or by transcriptional activation of plant dominant resistance gene(s), respectively.

Keywords: CRISPR/Cas, genome editing, plant viruses, immune defense, virus resistance.

PP-48

Application of plant resistance inducers (PRIs) to control stem and root rot disease incited by *Macrophomina phaseolina* in sesame (*Sesamum indicum)*

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Abstract

The efficiency of plant resistance inducers (PRIs) i.e. chitosan (CH), salicylic acid (SA) in controlling *Macrophomina phaseolina,* the causal agent of stem and root rot disease in sesame under *in vitro* conditions was evaluated. The treatments CH 1.0 g/l and CH 0.5 g/l + SA 2.5%caused the highest reduction in mycelia growth of *M.phaseolina* on potato dextrose agar compared to control. Under greenhouse conditions, CH 1.0 g/l + SA 5% was more effective compared to CH 1.0 g/l with disease incidence reduced to 70.4 and 67.4% respectively at pre=emergence stage of 10 days after sowing (DAS). At post-emergence stage of 40 DAS, the disease incidence reduced to 62.8 and 60.4% respectively. Meanwhile, the highest values of survival plants 79.4 and 77.8% were recorded with the same treatments. The study suggested that using plant resistance inducers in comparison with fungicides might be considered as an eco-friendly, safe, cheap and easily applied method for controlling such soil-borne plant pathogens considering the avoidance of environmental pollution and the side effects of fungicides application.

Keywords: Sesame, plant resistance inducers, chitosan, salicylic acid, stem and root rot disease.

PP-49

Genetic Analysis of Maize Germplasm for Resistance to Post Flowering Stalk Rot

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Abstract

In maize, diseases are one of the major constraints in realizing the yield potential. Among the different diseases reported in maize, post flowering stalk rot (PFSR) complex is one of the most serious, destructive and widespread groups of diseases in maize. The disease causes internal decay and discoloration of stalk tissue, directly reducing yield by blocking translocation of water, nutrient and can result in death and lodging of the plant during the cropping season. Yield losses range from 10 to 42% and can be as high as 100% in some maize growing areas. A set of maize inbred lines was evaluated at Agricultural Research Station, Karimnagar for charcoal rot during *Rabi,* 2021-22. Maize inbred lines KML-2, KML-4, KML-10, KML-11, KML-17, KML-26, KML-33 were identified as moderately resistant and inbred lines KML-14, KML-25 were identified as susceptible lines. The selected resistant and susceptible lines were crossed with two diverse tester lines LM-13 & LM-14 as testers following a Line x Tester design to study the gene action. The combining ability of the inbred lines was estimated and the lines were grouped based on heterotic group general and specific combining ability (HSGCA) for yield and disease. Evaluation of the hybrids developed from the crosses during *Kharif* 2022 revealed that the hybrids differed significantly ($p < 0.05$), as was the general combining ability (GCA) effects ($p < 0.01$), while specific combining ability (SCA) effects were found to be non-significant for disease. The Baker ratio, which shows the relative importance of GCA over SCA, was close to unity inferring a predominant additive gene effect towards resistance to disease.

Keywords: Combining ability, GCA, SCA, HSGCA, PFSR

PP-50

Gene Expression Analysis of Rice Tungro Disease and Vector Resistant Germplasm against Rice tungro virus

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Abstract

Rice, *Oryza sativa* L., is the most important staple food crop in the world, feeding more population than any other crop. It is an ideal model crop plant due to its small genome size, extensive genetic resources and ease of transformation with other cereal crops. Two different resistant genotypes *viz*., Vikramarya and Utri Merah were inoculated with Rice tungro virus and after 15 days of inoculation, gene expression studies were carried out using six qRT-PCR primers to understand Rice-RTV interaction. The present study pertaining to gene expressions in rice cv. Vikramarya revealed that all the six genes were upregulated *i.e.*, PORA, CAO1, SOD, PSAa and PSBa showed up-regulation with fold difference of 1.624505, 2.989698, 8.574188, 2.675855 and 2.657372, respectively in the virus inoculated plants. The plants were inoculated with non-viruliferous insects showed up-regulation of three genes *viz*., SOD, PSAa and PSBa with 6.773962, 2.639016 and 4.287094, respectively. Similarly, two genes *viz.,* PORA and CAO1 showed down regulation of genes with fold change of -1.31951 and -1.28343, respectively. These results revealed that the virus interacted with host proteins disturbed the gene expression of host cell resulted in the suppression of genes related to development and morphogenesis processes and the suppression of genes caused disease symptoms.

Keywords: Rice tungro virus, *Nephotettix virescens,* qRT- PCR.

PP-51

Development of Hybrids for resistance to Post Flowering Stalk Rot Tolerance and Yield in Maize

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Abstract

Globally, maize is highly valued for its multifarious use as food, feed, fodder and raw material for large number of industrial products. Post-flowering stalk rots (PFSR) are the most serious, destructive and widespread group of diseases in maize. development of PFSR resistant maize hybrids is a feasible alternative for cultivation of maize in disease prone areas.The present study was conductedat Agricultural Research Station, Karimnagar during *Kharif* 2020 and *Rabi* 2020-21 to identify potential single cross hybrids exhibiting high yields and PFSR tolerance. During *Rabi* 2018-19, 200 inbred lines of CIMMYT were inoculated with *Macrophomina phaseolina* by toothpick method. Fifty potential inbred lines with PFSR tolerance were identified, of which, 15 inbred lines were used as parents for hybridization during *Kharif* 2019 in line × tester design. Forty hybrids developed during *Kharif* 2020 were evaluated for PFSR tolerance along with the PFSR tolerant check KNMH -4010131. Further evaluation of these hybrids during *Rabi* 2020-21 identified the hybrid KNMH-419466 as a potential high-yielding hybrid with grain yield of 12,675 kg/ha and disease rating of 1 compared to the check Karimnagar Makka-1 (9,274 kg/ha). The high yielding PFSR tolerant maize hybrid KNMH-419466 has the potential to improve the production and productivity of maize in Telangana state.

Keywords: Maize, PFSR, stalk rots. post flowering, grain yield

PP-52

Biochemical Responses in Plants Related to Phytoplasma Infection

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Abstract

Phytoplasmas are wall-less prokaryotic bacteria that cause significant physiological and biochemical changes in infected plants, leading to symptoms like witches' broom, phyllody, stunting, yellowing, and abnormal floral structures. These infections affect hormonal, nutritional, and stress signaling pathways, disrupting plant growth and development. Phytoplasma infections induce anatomical changes, including damage to chloroplasts, vascular bundles, and sieve elements. Chloroplasts undergo degradation, with destruction of their outer and inner membranes, irregular grana arrangements, and damaged thylakoids. In some cells, chloroplasts are completely destroyed. Mitochondria also show structural abnormalities, including swelling and disruption of cristae. The infections lead to decreased photosynthesis and disrupt nutrient transport, causing carbohydrate accumulation in leaves. Increased production of reactive oxygen species (ROS) leads to oxidative stress, triggering the activation of ROS scavenging systems. Phytoplasma infection alters primary and secondary metabolites and protein levels, reflecting the plant's defense responses and affecting nutrient metabolism. These changes in gene expression and protein levels are associated with hormonal regulation and indicate that the plant's response to infection is induced rather than constitutive. Phytoplasma-induced biochemical alterations provide insight into the underlying mechanisms of plant defense and stress responses.

Keywords: Phytoplasma, phyllody, biochemical changes, stress signaling pathways, ROS.

THEME IV:
Microbiome, Biological Control and Integrated Disease Management

PP-53

Potential of Finger Millet Endophytes for Biocontrol and Plant Growth Promotion

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Abstract

Finger millet (*Eleusine coracana* (*L.*) *Gaertn.*) is highly nutritious crop rich in proteins, minerals, fiber, and vitamins. However, its production is significantly affected by various biotic and abiotic factors, with foot rot caused by *Sclerotium rolfsii* being a major threat, leading to yield losses of up to 50%. Conventional control methods, such as fungicides, are often economically and environmentally unsustainable. Endophytic bacteria have emerged as promising biocontrol agents due to their ability to suppress pathogens, promote plant growth, and degrade contaminants. The present study aimed to evaluate the antagonistic effects of bacterial endophytes against *S. rolfsii* to explore eco-friendly disease management strategies. Thirty bacterial isolates were isolated from finger millet growing areas of Telangana, Andhra Pradesh and Karnataka. These isolates were tested for their ability to inhibit the growth of *S. rolfsii* using the dual culture technique. Among them, three isolates FM-5H (*Bacillus* sp.), FM-1T (*Alcaligenes* sp.), and FM-4G (*Providencia* sp.) showed significant inhibition of mycelial growth by 66.00%, 65.19%, and 64.30%, respectively. Additionally, these isolates tested highly positive to plant growth promoting traits such as phosphate solubilization, IAA, ammonia, siderophore, and moderately positive to HCN production. The results suggest that these endophytes can effectively control foot rot disease and promote finger millet growth.

Keywords: Finger millet, foot rot, *Sclerotium rolfsii*, endophytic bacteria, bio-control.

PP-54

In vitro Broad Spectrum Antifungal Activity of Essential Oils from Plant Origin

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Abstract

Fungi are known to colonize variety of environments, the colonization in closed indoors are important for the occupants health. Though most of the filamentous forms are saprophytes, these will infest the different materials like fruits, vegetables, wood and leather. The sporulation and conidia formed from mycelia forms will persist in the indoors that could be potential risk for occupants. A study was carried on documentation of fungi from aeromycoflora of air-conditioned indoors. Fungal isolates of *A. spergillus niger*, *A. fumigatus*, *A. parasiticus*, *A. terreus*, *A. oryzae*, *A. versicolor*, *A. nidulans*, *Alternaria alternata*, *Penicillium citrinum*, *Fusarium oxysporum* and *Trichoderma viride* were tested for toxin production and allergy. Among the isolates of fungi, there were toxigenic, allergenic and pathogenic to immunocompromised patients. The anti-fungal efficacy of 20 essential oils of eucalyptus, mint, lavender, clove, nutmeg, turpentine, vetiver, cyperus, gingergrass, orange, geranium, cinnamon, camphor, lime, ylang-ylang, jasmine, sandalwood, rose, lemongrass was tested using poisoned food technique in single and combinations with amphotercin-B as positive control. The oils were classified into different classes based of their efficacy. These essential oils were found to be harmless with long history of use. The potency of essential oils proves to develop fumigants for indoors and reduce the incidence of harmful fungi from indoors.

Keywords: Skin prick tests, aflatoxins, *Aspergilli, Penicillium, Alternaria, Trichoderma.*

PP-55

Isolation and Evaluation of Forest Soil Microflora against Redgram Wilt Caused by *Fusarium udum*

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Abstract

Pigeonpea is an important legume crop in India which is affected by *Fusarium* wilt resulting in severe yield losses. The present study was carried out to develop an ecofriendly management strategy against *Fusarium udum* using forest soil microbes. A total of thirty six fungal isolates and forty two bacterial isolates were isolated, purified from the forest soils of Tirumala Kunta and Katkur reserve forest areas of Bhadradri Kothagudem district and observed for morphological and cultural characteristics. All the isolates were tested for efficacy under *in vitro* conditions, five isolates (one fungi and four bacteria) were observed showing the highest per cent inhibition of 73.77 (FSF10), 64.23 (FSB2), 63.56 (FSB4), 62.66 (FSB16), 66.00 (FSB30) against *F. udum.* Further, four bacterial isolates were evaluated for Plant Growth Promoting (PGP) traits like cellulase, ammonia, HCN, IAA and siderophore production test which showed positive results indicating the PGP activity of the isolates. Further, the five potential isolates were identified at molecular level as *Trichoderma erinaceum* (isolate FSF10), *Bacillus subtilis* (isolate FSB2), *B. tequilensis* (isolate FSB4), *B. subtilis* (isolate FSB16) and *Pseudomonas stutzeri* (isolate FSB30). This present investigation acknowledged the antagonist nature of FSM against *F. udum* which can be exploited as biocontrol agents for managing redgram wilt.

Keywords: Forest soil microbes, efficacy, molecular, *Fusarium udum,* redgram, PGP traits.

PP-56

Novel Compounds in the Interactions between Xanthomanas oryzae pv oryzae and Antagonistic Microbes

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Abstract

Rice, a staple food for over half the global population, suffers significant yield losses due to bacterial and fungal diseases. Among these, bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo), poses a major threat due to its widespread distribution and destructiveness under favorable conditions, particularly in irrigated and rain-fed Asian regions. Traditional reliance on chemical pesticides is being challenged by eco-friendly alternatives like biological control using beneficial microbes such as *Bacillus*, *Trichoderma*, and *Pseudomonas*. Xoo pathogenicity is governed by quorum sensing (QS), a bacterial communication process regulated by signaling molecules called autoinducers (AIs). Through QS, Xoo coordinates the production of virulence factors like extracellular polysaccharides (EPS), cell wall-degrading enzymes, siderophores, and Type III secretion effectors, which are critical for infection. The diffusible signal factor (DSF)-based QS system, involving *cis*-11-2-methyl-dodecenoic acid (DSF), modulates these virulence functions and facilitates cross-kingdom signaling with hosts. Soil microorganisms interact antagonistically or mutualistically, influencing pathogen suppression. Targeting Xoo's DSF-mediated QS using beneficial microbes offers a sustainable BLB management strategy, enhancing agricultural resilience and food security. Research on fungal-bacterial interactions and microbial antagonism, particularly involving *Pseudomonas*, *Bacillus*, and *Trichoderma*, may uncover novel compounds to suppress Xoo pathogenicity effectively.

Keywords: Bacillus, Trichoderma, Pseudomonas, bacterial leaf blight, quorum sensing.

PP-57

Prevalence and Management of Chilli Fruit Rot, *Colletotrichum capsici* in Khammam District of Telangana

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Abstract

Chilli, *Capsicum annuum,* is highly susceptible to fruit rot caused by *Colletotrichum capsici*, leading to significant yield losses in chilli cultivation. A roving survey was conducted between October and December 2021 for the fruit rot incidence in the *erstwhile* Khammam district of Telangana, encompassing various chilli cultivars, including highly pungent, medium pungent and low pungent varieties. The highest disease incidence (89.0%) was observed in Pinapaka village (Khammam), while Erraguntapadu village in Sathupally had the lowest incidence (10.0%). Koch's postulates were fulfilled to confirm the pathogenicity of *C. capsici via* artificial inoculation on mature red ripe fruits using the pin prick method. Among the 19 isolates tested, isolate *Cc*-3 showed the highest percentage of infected fruit area (86.0%), while isolate *Cc*-12 exhibited the least. *In vitro* evaluation of 14 different fungicides against *C. capsici* (isolate *Cc*-3) revealed varying efficacy, with tebuconazole 25.9% EC exhibiting the lowest EC50/ED50 value (18 $\mu g\ ml^{-1}$), followed by difenoconazole 25% EC (115 $\mu g\ ml^{-1}$), carbendazim 12% + mancozeb 63% WP (316 $\mu g\ ml^{-1}$) and highest was recorded in tebuconazole 50% + trifloxystobin 25% WG (3720$\mu g\ ml^{-1}$). The results indicate that tebuconazole and difenoconazole were the most effective fungicides for controlling *C. capsici*, suggesting their potential for disease management in chilli.

Keywords: Chilli, *Colletotrichum capsici*, disease incidence, Telangana.

PP-58

Identification of Endophytes for the Combined Management of *Macrophomina phaseolina* and *Spodoptera frugiperda* in Maize

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Abstract

Maize (*Zea Mays* L.) is an important food, feed and industrial crop across the world. The production and productivity of the crop is constrained by the incidence of *Macrophomina phaseolina* and *Spodoptera frugiperda*. The present study was conducted to identify endophytes for the combined management of both the pests in maize. In all, 63 bacterial and 53 fungal endophytes were isolated from various maize-growing regions of Telangana. *In vitro* evaluation using dual culture technique revealed that the isolates inhibited *M. phaseolina* with inhibition percentage ranging 33.3-87.7%. The isolates also showed *S. frugiperda* larval mortality percentage of 10 to 72%. Based on the plant growth promoting tests, three isolates, *viz*., ERB 26 (88.8%, 69%), ERB 31 (71%, 51%), and ESF 14 (77.7%, 58%), isolated from Maize Research Centre, Rajendranagar, Hyderabad, farmer's field, Nirmal district, and farmer's field, Khanapur, respectively were found to be the most effective against *M. phaseolina* and *S. frugiperda,* respectively. Currently, endophytes have been considered as one of the most suitable biocontrol agents due to better colonization and acclimatization potential. Besides conferring crop protection, endophytes also enhance the fitness of the host plants.

Keywords: Maize, endophytes, *Macrophomina phaseolina*, *Spodoptera frugiperda*, biocontrol, PGPR.

PP-59

RNA Based Biopesticides - A Novel Management Strategy against Cucumber mosaic virus in *Capsicum chinense* and Potato virus Y in *Solanum tuberosum*

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Abstract

Sustainable agriculture depends on methods and technologies that are both effective and environmentally friendly. RNA interference (RNAi) is a natural process in eukaryotes that reduces gene expression in a targeted way and can be adopted to control plant pathogens through topical applications. The theory suggests that externally applied double-stranded RNA (dsRNA) in plants may mimic the viral RNA intermediates involved in virus replication, activating gene silencing via the RNAi pathway. In this study, dsRNA coat protein molecules specific to CP gene of CMV and PVY were applied to control Cucumber mosaic virus in *Capsicum chinense* Jacq., and Potato virus Y in potatoes. The results indicated that application of dsRNA molecules along with virus sap on leaves, significantly suppressed symptom development. Consequently, RNA-based biopesticides are emerging as a promising alternative to chemical controls, allowing precise and specific targeting of pathogens. Using bioinformatics to design dsRNA sequences with minimal overlap with native plant genes is essential to reduce potential risks. With careful and thorough development, RNAi-based biopesticides hold great promise for transforming plant pathogen management in a safe and effective way.

Keywords: RNAi, biopesticides, CMV, PVY, *Capsicum chinense*, potato.

PP-60

Demonstration of Management of Wilt in Chili for Increased Yields and Higher Net Returns

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Abstract

Chilli (*Capsicum annuum*), a key commercial spice crop belonging to the Solanaceae family, is widely cultivated in tropical and subtropical regions. Unfortunately, the expected yields are not getting realized because of incidence of many foliar and soil borne fungal diseases. Fusarium wilt caused by *Fusarium oxysporum* f. sp. *capsici* is one of the most destructive diseases, which causes heavy yield loss in almost all chilli growing areas. By the time above ground symptoms are evident, the vascular system of the plant gets discoloured, particularly in the lower stem and roots. To overcome this problem, demonstrations were conducted for management of wilt in chilli through integrated disease management approaches such as crop rotation, raising and incorporation of green manure, soil application of 10 Kg neem seed kernel powder, application of *Trichoderma viride* @ 2 kg multiplied in 90 kg farm yard manure at the time of transplantation, application of *T. viride* in the rows after transplantation, restriction of flow of water from infected area to healthy plants, providing good drainage, recommended doses of fertilizer application, early identification of wilt affected plants and by adopting the recommended chemical measures, *viz*., drenching the plants with copper oxy chloride @ 3 g/l and copper hydroxide 2.5 g/l on rotation basis. The result of the study revealed that the demonstration plot recorded a yield of 43.37 q/ha as compared to the check plot (27.22 q/ha). The average percent disease incidence recorded in demonstration plot was 8.05%, while 15.90% recorded in check. The per cent increase of yield over control noticed in demonstration plot was 59.32%. Besides this, the demonstration plot gave higher gross returns, net returns with higher B: C ratio when compared to check.

Keywords: Chilli, wilt, *Trichoderma viride,* copper hydroxide.

PP-61

Assessment of Bioformulations against *Colletotrichum truncatum* and *Macrophomina phaseolina* in Soybean

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Abstract

Soybean (*Glycine max* L. Merill) is a vital oilseed legume with high nutritional value and diverse industrial applications. However, seed viability is significantly impacted by seed and soilborne infections, resulting in substantial production losses. Developing quality, disease-free seeds is critical, yet conventional synthetic chemicals pose environmental risks. Eco-friendly bioformulations offer a sustainable alternative without residual effects. A study at the Seed Research and Technology Centre, PJTSAU, Hyderabad, evaluated 12 bioformulations, including *Trichoderma viride*, *T. harzianum*, *T. viride* + *Pseudomonas fluorescens*, *T. harzianum* + *Bacillus subtilis*, neem oil, basil oil, chitosan, silicon-based chitosan, and gibberellic acid, against *Macrophomina phaseolina* and *Colletotrichum truncatum*. Using dual culture and poisoned food techniques, *T. viride* + *P. fluorescens* demonstrated maximum mycelial inhibition (88.16% and 62.00%), followed by *T. harzianum* + *B. subtilis* (88.01% and 53.64%). Basil oil at 5 ml/l showed 100% inhibition for both pathogens, outperforming other bioformulations. Silicon-based chitosan and gibberellic acid also showed significant inhibitory effects. The study concludes that consortial bioagents (*T. viride* + *P. fluorescens*, *T. harzianum* + *B. subtilis*) and basil oil are highly effective against soybean seedborne pathogens, highlighting the potential of bioformulations in sustainable seed management.

Keywords: Soybean, bioformulations, seedborne pathogens, *Trichoderma*

PP-62

In vitro and *in silico* analysis of potential bacterial species of *Bacillus* and *Pseudomonas* against *Macrophomina phaseolina*

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Abstract

Dry root rot caused by *Macrophomina phaseolina* is one of the most devastating diseases that cause severe yield loss in *Vigna mungo* cultivation. Plant growth-promoting rhizobacteria (PGPR) are extensively harnessed as biocontrol agents due to their effectiveness in combating a wide array of plant pathogens through a multifaceted approach. In this study, four potential rhizobacterial isolates (*Bacillus* spp. and *Pseudomonas* spp.) showed production of indole-3-acetic acid, siderophores, ammonia, hydrolytic enzymes, biofilms which are significant plant growth promoting (PGP) traits and they also inhibited *M. phaseolina* by dual plate method. Further, metabolites were extracted from all the four bacterial isolates and characterized using thin-layer chromatography (TLC) and Fourier-transform infrared spectroscopy (FTIR) and gas chromatography-mass spectrometry (GC/MS) analysis for the presence of secondary metabolites that would suppress *M. phaseolina*. Understanding the potential interactions of these bacterial bioagents with specific fungal target sites remains a significant challenge. Hence, we focused our study to understand the interaction of rhizobacteria against the virulent proteins of *M. phaseolina* using molecular docking. Furthermore, stability analysis and orientation studies of volatile compounds through molecular dynamics simulations demonstrated their efficacy under *in silico* conditions. The results of the same will be presented.

Keywords: *M. phaseolina*, volatiles, *Bacillus* spp., *Psuedomonas* spp., molecular dynamic simulation.

PP-63

Enhancing Seed Quality and Resilience of Chilli Crop Against Anthracnose through Seed Treatment with Endophytes

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Abstract

Chilli (*Capsicum annuum*), a vital agricultural and culinary crop, faces significant threats from anthracnose, a seed-borne disease caused by *Colletotrichum capsici*. This fungal pathogen can cause 50–80% yield losses, severely affecting fruit and seed quality, jeopardizing farmers' livelihoods, and threatening food security. Conventional management strategies include chemical fungicides and resistant varieties, but biocontrol methods offer sustainable and eco-friendly alternatives. Biocontrol agents, derived from natural organisms, minimize environmental harm, reduce chemical residues, and combat pathogen resistance through diverse inhibitory mechanisms while enhancing soil health and microbial diversity. While resistant varieties can be effective, their development is time-consuming and may not address all scenarios. Integrating biocontrol into agricultural practices ensures effective disease management and sustainability. This study aims to isolate endophytes from healthy chilli plants in anthracnose-affected fields across diverse regions. The isolates will be screened *in vitro* for efficacy against *C. capsici*. The most effective endophytes will be used to coat healthy chilli seeds, which will then be evaluated under *in vivo* and field conditions. The study seeks to identify superior endophytic treatments capable of enhancing chilli crop resilience, mitigating anthracnose impacts, and improving overall crop quality for sustainable production.

Keywords: Endophytes, chilli anthracnose, seed treatment, biocontrol, sustainability.

PP-64

Efficacy of Bio-formulations as Seed Dressers for the Management of Chilli Anthracnose

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Abstract

Chilli (*Capsicum annuum*) is highly susceptible to fruit rot/anthracnose caused by *Colletotrichum truncatum* (syn. *C. capsici*), with yield losses ranging from 10–89%, particularly in Telangana.

This study evaluated the efficacy of bioformulations, including chitin, *Bacillus subtilis*, yeast, seaweed extract, basil oil, and garlic extract, against a highly virulent pathogen isolate from cv. Armour. Azoxystrobin fungicide, pathogen, and healthy controls were used for comparison under *in vitro* conditions on farmer-grown cv. Teja S-13 seeds over zero, three, and five months after storage (MAS). Results showed significant variation in seed quality parameters over storage periods. At 5 MAS, chitin (T1, 10 g/kg) improved seed germination (11.58%, 20.73%), seedling vigor indices SVI-I (17.40%, 34.54%) and SVI-II (48.27%, 58.48%), and reduced seedling abnormality (20.00%, 35.48%) and seed infection (4.00%, 47.11%) compared to fungicide and pathogen controls. Yeast (T3, 5 g/kg) enhanced speed of germination (4.31%, 18.59%) and radicle emergence (14.02%, 19.26%), with an 11.59% increase in test weight. *B. subtilis* (T2, 10 g/kg) minimized electrolytic leakage by 5.28% and 33.83% against fungicide and pathogen controls. Field studies revealed basil oil (T5, 5 ml/kg) achieved maximum germination (84.25%) and minimal seedling mortality (13.75%) at 15 DAS, while chitin (T1) reduced anthracnose incidence (12.50%) at 45 DAS.

Keywords: *Colletotrichum truncatum, Bacillus subtilis,* basil oil, management, anthracnose

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PP-65

Evaluation of Native Biocontrol Agents against Fungal Soil Borne Diseases of Groundnut

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Abstract

Roving survey conducted during *Rabi* 2023-2024 in Bapatla and Prakasam districts of Andhra Pradesh has revealed the highest mean stem rot disease incidence was noticed in talluru mandal (7.79%) of Prakasam district. Whereas, highest mean collar rot incidence was observed in karlapalem (7.70%) of Bapatla district. Infected plant samples, healthy rhizosphere soil, and leaf samples were used for culturing soil borne pathogens *viz*., *Sclerotium rolfsii* and *Aspergillus niger* and native biocontrol agents *viz*., *Trichoderma*, *Pseudomonas,* Pink Pigmented Facultative Methylotrophs (PPFMs) on *Trichoderma* selective medium, Kings B and AMS media, respectively. Pathogens and biocontrol agents were further characterized for confirmation. The isolated and characterized biocontrol agents (fungal and bacterial) were tested against isolated soil borne pathogens *S. rolfsii* and *A. niger* under *in vitro* conditions by using dual culture technique. Maximum growth inhibition of *S. rolfsii* was recorded with KGT-3 *Trichoderma* isolate (67.22 %) while KGT-1*Trichoderma* isolate showed highest per cent of inhibition of *A. niger* (69.72%). Among *Pseudomonas* isolates tested against *S.rolfsii* and *A.niger*, highest inhibition was recorded with KGP-2 (65.56%) isolate and

KGP-3(62.22%). When methylotrophic isolates were tested against *S.rolfsii* and *A.niger*, maximum mycelial inhibition was obtained by KGM-1 with 63.06 per cent and KGM-3 with 63.61%.Fungicides *viz*., carbendazim25%+mancozeb50% WS, carboxin 37.5%+thiram 37.5% DS, tebuconazole 2% DS and copper oxychloride were evaluated against stem rot (*S.rolfsii*) and collar rot *(A.niger*) pathogens using poisoned food technique at recommended and half recommended concentrations in which complete inhibition (100%) of *S. rolfsii* was observed with carbendazim25% + mancozeb 50% WS and carboxin 37.5% + thiram37.5 % D S at both recommended and half the recommended dosages. While cent percent inhibition (100%) of mycelial growth of *A.niger* was observed with carboxin37.5%+thiram37.5% DS at recommended dosage and 95.93% inhibition at half recommended dosage. Molecular characterization was done for the potential biocontrol isolates of *Pseudomonas*, *Trichoderma* and *Methylobacteribum*. 16S-23S rRNA gene sequencing and their analysis through BLASTn search in NCBI database showed that the *Pseudomonas* isolate KGP-2 as *Pseudomonas fluoroscens,* while KGP-3 was identified as *P.areuginosa.* KGM-3 *Methylobacterium* isolate showed 86% similarity with *Methylobacterium* spp. and isolate KGM-1 had 84 % similarity with *Methylobacterium indicum.* Internal Transcribed spacer (ITS) region gene sequencing revealed that KGT-1 *Trichoderma* isolate was closely related to *Trichoderma harzianum*, whereas KGT-2 and KGT-3 were closest match with *Trichoderma* spp.

Keywords: Groundnut diseases, native biocontrol agents, in vitro fungicides, evaluation

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PP-66

Evaluation of Mustard Germplasm for Resistance to Powdery Mildew (*Erysiphe cruciferarum*)

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Abstract

The oilseed sector forms a cornerstone of India's agricultural economy, positioning the country as the largest producer of oilseeds globally and a significant player in edible oil production and trade. Mustard, a key contributor, is predominantly a rainfed crop in India but faces challenges from various biotic and abiotic stresses, notably powdery mildew (*Erysiphe cruciferarum*). This fungal disease causes substantial yield losses, starting as small, scattered colonies on the older leaves and eventually covering the leaf surface under favorable conditions. The disease not only stunts growth but also destroys foliage, with *Brassica juncea* being the most severely affected among Brassica species. While chemical fungicides are commonly used for management, their environmental impact and economic unsustainability necessitate the identification of resistant germplasm. In this study, 50 mustard genotypes were screened for resistance to powdery mildew during the rabi season of 2020-21 at the Regional Agricultural Research Station, Polasa, Jagtial. The experiment followed a Randomized Block Design (RBD) with two replicates. Genotypes were evaluated under natural disease conditions, and resistance levels were classified based on disease scores. Of the genotypes tested, GM-3 and Swarna Jyothi exhibited resistant reactions with a disease score of 1. Nine genotypes, including Pusa Mahak and DRMR-601, showed moderate resistance (score-3). Fifteen genotypes displayed moderate sensitivity (score-5), while 16 genotypes were categorized as susceptible (score-7). Eight genotypes, including Varuna and Black Gold, showed high susceptibility (score-9). Notably, the moderately resistant check variety NRCHB-101 exhibited susceptibility due to favorable disease conditions during the crop growth period. The identification of resistant genotypes (GM-3 and Swarna Jyothi) and moderately resistant lines provides a foundation for breeding programs aimed at developing sustainable and disease-resistant mustard varieties.

Keywords: *Brassica juncea,* Indian mustard, *Erysiphe cruciferarum,* powdery mildew

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PP-67

Approaches and Advances to Manage Bacterial Leaf Blight to Enhance Rice Productivity

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Abstract

Rice (*Oryza sativa L.*) is the second most important food crop worldwide. Its productivity is significantly constrained by biotic and abiotic stresses, with bacterial leaf blight (BB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), being a major biotic threat. BB can cause yield losses ranging from 20-80%, with symptoms including water-soaked spots, pale yellow leaves, and linear yellowish-brown lesions. The disease thrives in warm, humid conditions, particularly in irrigated and wetland ecosystems. Management strategies for BB include chemical control, biological control, and host plant resistance. Among these, host plant resistance, governed by resistance (R) genes such as *Xa4*, *Xa21* and *xa13* offers an eco-friendly and sustainable solution. Also yield improvement remains a central goal in rice breeding programs, challenged by stagnation due to environmental stresses and suboptimal agronomic practices. It is a complex quantitative trait influenced by genetic and environmental factors, is determined by both direct traits (e.g., grain weight) and indirect traits (e.g., plant height, panicle length). Recent advances in molecular and conventional breeding have enabled the identification and utilization of yield-enhancing genes like *Gn1a*, *sd1*, and *GS3*, contributing to significant yield gains. Introgression of these genes through MAS helps in accelerated breeding. These advancements highlight the transformative potential of integrating molecular and conventional breeding approaches to unlock genetic yield potential and drive sustainable agricultural productivity.

Keywords: Rice, biotic stresses, bacterial leaf blight, R genes, *Xa4*, *Xa21*, *xa13,* yield improvement, yield-enhancing genes, *Gn1a, sd1* and *GS3* and marker assisted selection.

PP-68

Marker Assisted Breeding for Blast and Bacterial Leaf Blight Resistance in Rice

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Abstract

Rice is predominantly grown in Asia, which accounts for about 90% of global population. RNR 15048 (Telangana Sona) is one of the popular varieties grown in many parts of Telangana particularly during *Kharif* season. It is a short duration, high yielding, short slender rice variety but it is susceptible bacterial blight and blast diseases, which are endemic to many rice growing areas in India. MTU1010 NIL possessing major broad spectrum resistance genes against blast (*Pi54*) and bacterial leaf blight (*Xa21*) was used as donor to improve RNR15048, through marker assisted pedigree breeding combined with phenotype-based selection for agro-morphological traits specific for RNR15048. In the present investigation advanced breeding lines (F_4 generation) were screened through foreground selection for confirmation of presence of target trait specific genes *viz*., for blast (*Pi54*) and bacterial blight (*Xa21*). Foreground selection was carried out with co-dominant markers pTA248 and *Pi54*-MAS for checking the presence of *Pi54* and *Xa21,* respectively. Out of 50 advanced breeding lines, it was found that 45 lines possessing resistant allele of *Pi54* gene and resistant allele of *Xa21* gene. The same 50 advanced breeding lines were screened for BB resistance in the field and for blast in uniform blast nursery at ARI during *Rabi* 2023-24. Out of 50 lines screened for both BB and blast, 45 breeding lines were shown resistance to both blast and bacterial leaf blight diseases. Two

breeding lines exhibited good performance with high level of resistance to the diseases *viz*., blast and bacterial blight and possess high grain yield and grain quality better than RNR 15048. The results obtained in the present study indicated the success of marker assisted pedigree breeding coupled with phenotypic selection.

Keywords: RNR 15048, bacterial leaf blight, marker assisted breeding, *Xa21* and *Pi5*

PP-69

Screening of Maize Hybrids for Charcoal Rot Resistance

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Abstract

An investigation for "Identification of maize (*Zea mays* L.) hybrids with post flowering stalk rot resistance under high density planting system" was conducted at agricultural college, Polasa, Jagtial district, Telangana state with six lines and four testers which were crossed in Line × Tester mating system and generated 24 hybrids (*Kharif*, 2022). These 24 hybrids along with 10 parents and three checks: commercial check (DHM 117), susceptible check (Karimnagar macca-2) and resistant check (PFSR 3) were screened (*Rabi*, 2022-23) for charcoal rot resistance by artificial inoculation with toothpick method. Individual plants were inoculated by inserting toothpicks covered with fungal inoculum that were grown in laboratory at the second internode, at an angle of 450. The symptoms were recorded on 45th day after inoculation. Disease symptoms were scored on 1-9 scale given by Payak and Sharma (YEAR) at harvest by splitting the stalks of the inoculated plants longitudinally. The maize genotypes have been categorized as resistant, moderately resistant, moderately susceptible and highly susceptible genotypes. Among the evaluated parental inbreds and hybrid, the inbred line PFSR 135 and hybrid PFSR 51 × BML 6 were found to be highly resistant to charcoal rot with slight discoloration at the site of inoculation.

Keyword: Maize, charcoal rot, genotypes

PP-70

Development of Microcapsules with *Bacillus subtilis* Using Alginate for *Fusarium* Wilt Management in Chickpea

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Abstract

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *ciceris*, is a major disease affecting chickpea (*Cicer arietinum L.*) production globally. The use of biological control agents, such as *Bacillus subtilis*, offers an eco-friendly alternative to chemical treatments. However, the effectiveness of biocontrol agents is often hindered by environmental stress and short shelf life. This study aims to develop and evaluate alginate-based microcapsules for the encapsulation of *B. subtilis* to enhance its stability and efficacy against *Fusarium* wilt. In this study sodium alginate was used as the encapsulation matrix, cross-linked with calcium chloride to form stable microcapsules at different concentrations. Results showed that the alginate microcapsules effectively protected the bacteria, maintaining high viability under ambient storage. The sustained release of *B. subtilis* was observed over time, enabling prolonged activity against the pathogen. In greenhouse trials, plants treated with the encapsulated microcapsules exhibited significant reduction in disease incidence compared to unencapsulated treatments and control groups. Furthermore, treated plants demonstrated improved growth parameters, including increased shoot length, root length, and biomass. This study demonstrates the potential of alginate-based microcapsules to enhance the delivery, stability, and efficacy of *B. subtilis* for sustainable management of *Fusarium* wilt in chickpea. The approach offers a promising step towards integrating biocontrol strategies into agricultural practices, reducing reliance on chemical pesticides, and promoting sustainable crop production.

Keywords: Chickpea, *Fusarium* wilt, *Bacillus subtilis*, microcapsules, biocontrol

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PP-71

Integrated Disease Management of Stem and Root Rot, *Macrophomina phaseolina* in Sesame

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Abstract

In sesame, stem and root rot caused by *Macrophomina phaseolina* is one of the most important diseases causing significant yield losses of up to 25-30% each year, particularly in the turmeric fallows of Northern Telangana Zone. The objective of the study was to assess efficacy of the biocontrol and fungicide application for the management of *M. phaseolina.* The experiment was conducted during summer 2020 at RARS, Polasa, Jagtial. Seed treatment with *Trichoderma viride* @ 10 g/kg + furrow application of *T. viride* (2.5 kg/ha enriched in 100 kg of FYM) @ 250 kg/ha and foliar application of trifloxystrobin + tebuconozole @ 0.5 g/l at capsule initiation and second spray after 15 days interval resulted in lowest root rot disease incidence (19.2%) and maximum yield of 618 kg ha^{-1} followed by seed treatment with *T. viride* @ 10 g/kg + furrow application of *T. viride* (2.5 kg/ha enriched in 100 kg of FYM) @ 250 kg/ha and foliar application of Azoxystrobin @ 1 ml/l at capsule initiation and second spray after 15 days interval with 20.5 per cent disease root rot incidence.

Keywords: *Macrophomina phaseolina, Trichoderma viride,* trifloxystrobin + tebuconozole azoxystrobin and sesame

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PP-72

Integrated Disease Management of Dry Root Rot of Chickpea Caused by *Rhizoctonia bataticola* under Field Conditions

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Abstract

Dry root rot disease is one of the serious biotic constraints for chickpea production and is the most important and widespread soil borne disease, accounting for 10-35% losses in yields. A field study was conducted during two consecutive r*abi* seasons in systematic management approach integrating all the feasible disease management strategies. Different treatments, inclusive of effective fungicide (tebuconazole), talc based formulation of potential bioagent (CRT-4) applied as seed treatment along with castor cake @ 250 kg ha^{-1}, were evaluated. Results showed that the seed treatment with tebuconazole @ 1.25 g kg^{-1} + *Trichoderma* @ 10 g kg^{-1} seed and soil application of castor cake@ 250 kg ha^{-1} recorded lowest incidence of dry root rot (11.70%), highest root and shoot lengths of 10.14 cm and 28.09 cm, respectively, with a seed yield of 1581 kg ha^{-1} and with B:C ratio of 1.87. The next best treatment was seed treatment with

tebuconazole @ 1.25 g kg^{-1} + *Trichoderma* @ 10 g kg^{-1} seed and soil application of neem cake @ 500 kg ha^{-1} with disease incidence of 13.93 per cent, root and shoot lengths of 9.40 and 24.64 cm, seed yield of 1426 kg ha^{-1}and B:C ratio of 1.64 in comparison over control.

Keywords: Dry root rot, chickpea, tebuconazole, *Trichoderma.*

PP-73

Integrated Management of *Fusarium* Wilt in Maize: Enhancing Disease Control, Growth, and Yield through Bioagents and Organic Amendments

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Abstract

Maize, a globally important cereal crop, is susceptible to various diseases, with *Fusarium* wilt being one of the most damaging which impacting yield and quality. This study evaluated the effectiveness of bioagent *Trichoderma viride* (Tv-8) and organic amendments farmyard manure (FYM) and neem cake in managing Fusarium wilt and improving maize productivity. Out of the nine treatments tested, T7 (seed treatment with *T. viride* (10 g/kg), along with soil application of *Trichoderma*-enriched FYM (250 kg/ha) and neem cake (500 kg/ha)) was the most effective with a minimum wilt incidence of 12.9%. This was followed by the treatment T5 (seed treatment with *T. viride* (10 g/kg), along with soil application of *Trichoderma*-enriched FYM (250 kg/ha)) with wilt incidence of 29.1%. Both the treatments T5 and T7 significantly increased maize yield, with T7 yielding 6511.11 kg/ha (30.2% increase) and T5 yielding 6444.44 kg/ha (28.8% increase). T7 also resulted in higher cob weight (467.96 g, 29% higher than control) and taller stalks at 15 and 30 days after sowing. The results indicated that combining *T. viride* with organic amendments, such as FYM and neem cake, effectively controlled *Fusarium* wilt and improved maize growth and yield, offering a sustainable disease management strategy.

Keywords: *Fusarium* wilt, *Trichoderma viride*, organic amendments, maize yield.

PP-74

Antagonistic Nodule Endophytic Bacteria Effective against Stem Rot, Disease in Groundnut

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Abstract

Groundnut, *Arachis hypogaea,* is a globally significant oilseed crop, but its production is threatened by stem rot disease caused by *Sclerotium rolfsii*. In the present study, bacterial endophytes from groundnut root nodules were evaluated for eco-friendly management of stem rot disease. Groundnut plant samples with stem rot incidence ranging from 10% to 25%, with an average of 19% were collected from 12 fields in ten villages across Telangana in Nagarkurnool and Mahbubnagar districts during the *Rabi* 2023-24 season. Eight isolates of *S. rolfsii* were examined for colony morphology and sclerotial characteristics, which showed variability in color, type, growth, and sclerotial morphology such as arrangement, color, weight, and size. Pathogenicity tests on the Kadiri-6 groundnut variety confirmed the virulence of all isolates, with isolate GNSR1 identified as the most virulent showing 100% disease incidence. Twenty endophytic bacterial isolates from groundnut root nodules were characterized based on cultural, morphological, and biochemical traits, with a dominance of Gram-positive bacteria. *In vitro* screening using a dual culture assay identified GNEB 6 (71.40% inhibition), GNEB 13 (73.3% inhibition), and GNEB 16 (68.51% inhibition) as potential antagonists against *S. rolfsii*. Molecular characterization identified GNSR1 as *Agroathelia rolfsii*, while GNEB 6 and GNEB 13 were *Bacillus cereus* and GNEB 16 was *Bacillus subtilis*. Glasshouse tests showed that seed treatment with *B. subtilis* GNEB 16 significantly promoted plant growth, achieving 90% germination, 22.83 cm shoot length, 18.2 cm root length, and 77.2% disease control. The study describes the potential of nodule endophytic bacteria as biocontrol agents for sustainable stem rot management in groundnut while enhancing plant growth.

Keywords: Stem rot, *Agroathelia rolfsii*, *Bacillus cereus*, *Bacillus subtilis,* dual culture.

PP-75

Biological Control of Mango Powdery Mildew, *Oidium mangiferae* under Telangana Conditions: Efficacy of Eco-friendly Alternatives

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Abstract

Mango is a widely cultivated fruit crop in Telangana holding a leading position in terms of both area and production. Powdery mildew, a significant mango disease was first reported in India long before 1874. This disease caused by the fungus, *Oidium mangiferae,* is a major concern for mango growers worldwide. The fungus attacks the young tissues of various parts of mango tree, including the inflorescence, leaves and fruits. In severe cases, crop losses of up to 100% have been observed particularly when the disease spreads in epidemic form with blossom infection. The fungus can infect flowers and their stalks fail them to open or even drop from the panicle. While agrochemical treatments can manage the disease, their non-eco-friendly nature, high costs and potential side effects make it necessary to explore sustainable, low-cost and eco-friendly alternatives. A field experiment was conducted for three consecutive years from 2022 to 2024 to evaluate five biocontrol agents *viz., Trichoderma viride*, *Bacillus subtilis*, *Pseudomonas fluorescens*, *Verticillium lecanii* and *Trichoderma harzianum* for their effectiveness against mango powdery mildew at Fruit Research Station, Sri Konda Laxman Telangana Horticultural University, Sangareddy, Telangana. These agents were applied at three different concentrations (0.4%, 0.5% and 0.6%). Results showed that two applications of *B. subtilis* formulation provided maximum per cent disease control of 76.32% followed by *V. lecanii* at 72.07% at a 0.6% concentration. Among the bio-control agents tested, *P. fluorescens* proved to be the least effective at all the tested concentrations.

Keywords: Mango, powdery mildew, *Oidium mangiferae*, biological control agents

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PP-76

In-vitro evaluation of phylloplane bacterial isolates against Magnaporthe oryzae B.C. Couch causing rice blast

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Abstract

Rice (*Oryzae sativa*) is one of the leading food crops in the world and the most important staple food in Asia. Blast disease caused by *Magnaporthe oryzae* B.C. Couch is one of the most important fungal diseases of rice. In the present study, leaf samples for the study were collected from four major rice growing districts of Andhra Pradesh *viz*., Nellore, Tirupati, Bapatla and West Godavari. A total of 34 rice Phylloplane bacteria were isolated on HiCrome Bacillus Agar Base by leaf imprinting method. Among the 34 isolates, fourteen Gram +ve, rod shaped, creamy white to white colored bacterial isolates were selected for study on *in-vitro* antagonistic activity against *M. oryzae* by dual culture technique and paired plate technique. In the dual culture technique, two isolates i.e., PBT-22 and PWG-30 recorded significant inhibition in the growth of the rice blast pathogen (81.11%) at 15 days after inoculation. Whereas, in paired plate technique to study volatile metabolite production, PTB -22 isolate was found most effective against *M oryzae* recording highest inhibitory effect (85.88%) which is on par with PWG-27 (85.22%). The Promising bacterial isolates from the study with superior antagonistic ability *viz*., PBT-22 and PTP-12 were identified as *Bacillus altitudinis* and *Bacillus subtilis* respectively based on 16S rRNA sequencing.

Keywords: Rice blast, phylloplane bacteria, *Bacillus altitudinis*, *Bacillus subtilis.*

PP-77

Integrated Management of Chilli Fruit Rot using Biocontrol Agents, Plant Extracts and Fungicides

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Abstract

Chilli (*Capsicum annuum L.*) faces significant challenges from fungal diseases, with anthracnose (fruit rot) caused by *Colletotrichum* sp. being a major concern in India. In the present study, an attempt was made to evaluate seven bio-agents, botanicals and fungicides against *Colletotrichum* sp. under *in vitro* conditions. Results revealed that among the different fungicides, tebuconazole + trifloxystrobin, azoxystrobin + tebuconazole gave cent per cent inhibition of mycelial growth of the pathogen followed by thiophanate methyl + kasugamycin (84.58 %) while least inhibition was recorded in azoxystrobin (67.77%). Among the different bio-agents, *Trichoderma viride* (65.19%) was very effective in inhibiting the growth of pathogen and least inhibition was recorded in *Bacillus subtilis* 37.04 %) and among botanicals, Neem extract gave 43.88 per cent inhibition was very effective in inhibiting the mycelial growth whereas marigold was less effective in inhibiting the growth of pathogen (28.45 %). Field study was conducted during *Kharif* 2023 to know the efficacy of fungicides, botanicals and bio-agents under field condition. Among the different treatments evaluated tebuconazole + trifloxystrobin was very effective in management of fruit rot with a PDI of 27.00 per cent which was significantly lower than all other treatments followed by azoxystrobin + tebuconazole (32%) and highest PDI was recorded in plots treated with tulsi leaf extract (48%) when compared to control (60.67%). This study highlights the potential of fungicides, bio-agents, and botanicals in managing fruit rot in chilli and supports integrated disease management strategies.

Keywords: Chilli, fruit rot, IDM, *Colletotrichum*

PP-78

Biological Management of Wilt Disease of Chickpea

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Abstract

A total 22 *Trichoderma* isolates were obtained using *Trichoderma* specific media from 42 rhizosphere soil samples collected from healthy chickpea plants in wilt infected fields representing 7 districts, namely, Jagtial, Rajanna siricilla, Vikarabad, Adilabad, Warangal, Nizamabad and Nagarkarnul districts of Telangana during *yasangi*, 2020. Of the 22 isolates, based on colony colour, topography, conidia and conidiophore characters, 45.45% (10 isolates) were identified as *Trichoderma harzianum*, 27.27% (6 isolates) were *T. viride,* 18.18% (4 isolates) were *T. asperellum* and 9.09% (2 isolates) were *T. hamatum* species. In dual culture assay, *T. harzianum* isolate, Th-1 showed the highest of 87.7% reduction in growth of *Fusarium* isolated from wilt infected chickpea plants. The *T. harzianum* isolate, Th-1 was also evaluated against *Macrophomina phaseolina (I*=62.2%, 64.3%*)* isolated from sesame and soybean respectively, *Magnaporthe oryzae (I*=79.7%*)* isolated from rice and *Fusarium* isolated from soybean (I=80.6%) through dual culture assay. The 22 *Trichoderma* isolates were also characterized for the production of extracellular enzymes like Pectolytic activity, Amylolytic activity and Proteolytic activity. Of 22 isolates 10, 19 and 7 isolates were found positive for pectolytic, Amylolytic and proteolytic activity respectively. Further, the 22 isolates were characterized for Plant growth promoting activities like production of Indole Acetic Acid (IAA) and Phosphate solubilization. The isolate T-1 produced highest amount of 138.88 IAAµg/mL and isolate S-5 solubilized the highest amount of 190.10 µg/mL Phosphate. Based on the sequence obtained using ITS 1 and ITS4 primers, the Trichoderma isolate, Th-1 is identified as *Trichoderma harzianum.*

Keywords: Chickpea, biological control, wilt, *Trichoderma*

PP-79

Screening of Rejuvenated Mango Cultivars under Sub-Himalayan Terai Region of West Bengal against Anthracnose, *Colletotrichum gloeosporioides*

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Abstract

The severity of mango anthracnose disease on different mango varieties after the rejuvenation was assessed under sub-Himalyan Terai region of West Bengal. Rejuvenation of old and unproductive mango orchard have important role to rebuild canopies of fruit trees and it makes the plant manageable, easy for adoption of appropriate package of practices, improving vigour and yield. Five rejuvenated mango cultivars *viz*., Amrapali, Mallika, Himsagar, Fazli and Langra were selected to find out the severity of anthracnose, *Colletotrichum gloeosporioides* disease under natural field conditions without any control measures during 2019-20 and 2020-21 in the sub-Himalayan terai region of West Bengal. Maximum anthracnose severity was found in Mallika (62.69%) in the month of May, while minimum anthracnose severity was recorded in Himsagar (14.96%). Among the five cultivars studied, maximum average per cent disease Index (Avg. PDI) recorded in Mallika (50.83%), whereas minimum Avg. PDI noticed in Himsagar (19.96%). The mango cultivar Himsagar showed moderately resistant reaction and the cultivar Amrapali showed moderate susceptible reaction. Two cultivars Fazli and Langra showed susceptible reaction and cultivar Mallika exhibited highly susceptible reaction after the shoot emergence on rejuvenated plants under this agro-ecological system.

Keywords: Mango, anthracnose, severity, disease reaction, moderate resistant, susceptible

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PP-80

Assessment of Antifungal Activity of Native Potential Biocontrol Agents of Pigeonpea Rhizosphere against *Fusarium udum* in Telangana

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Abstract

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is one of the most important pulse crops of Telangana, which is infected by many pests and diseases. Among diseases, Fusarium wilt caused by *Fusarium udum* is the major disease causing 30-100 percent yield losses in pigeonpeaa. Though use of chemicals is a widely practiced approach to manage the disease, it is hazardous to human and environmental health. Therefore, it is important to assess the native potential biocontrol agents of the pigeonpea rhizosphere for their antifungal activity against *Fusarium udum* to develop effective and environmentally friendly methods to control the disease. A total of 42 rhizosphere soil samples were collected from different pigeonpea-growing areas of

Telangana State to isolate biocontrol agents. From the rhizosphere, 124 bacterial isolates and 81 fungal isolates were isolated. All the fungal and bacterial isolates were screened primarily for antagonism against *F. udum*. Among the ten *Trichoderma* isolates tested in dual culture, isolate S36RFI-42 recorded maximum inhibition of 87.15 percent over control. Among the 15 bacterial isolates tested in dual culture, isolate S14RBI-34 recorded maximum inhibition of 74.05 percent. Biochemical, morphological, and molecular characterization of potential biocontrol agents found that the potential fungal isolate S36RFI-42 is *Trichoderma viride* and the potential bacterial isolate S14RBI-34 is *Pseudomonas aeruginosa*. Further, they were used in pot culture studies to measure defense enzyme activity and soil, agronomic, and plant growth-promoting activity. They controlled the pathogen effectively and increased the plant growth-promoting activity. The present study revealed that the antifungal activity of native biocontrol agents, *viz*., *T. viride* and *P. aeruginosa*, isolated from the rhizosphere of pigeonpea, was effective in managing *Fusarium* wilt disease of pigeonpea.

Keywords: Wilt, pigeonpea, isolation, biocontrol agents, *Trichoderma viride*, *Pseudomonas aeruginosa,* rhizosphere.

PP-81

Exploration of Lactic Acid Bacteria for Potential Probiotic, Plant Growth Promoting and Biocontrol Attributes

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Abstract

Probiotic are defined as the micro-organisms which are beneficial in the human health. The aim of the study was to isolate lactic acid bacteria from fruit (Pomegranate, Jack fruit, Banana) and to evaluate their ability to inhibit the plant pathogenic bacteria. A total of 60 isolates were isolated and screened for microscopic and biochemical characters. *In vitro* evaluation was carried out against *Ralstonia solanacearum* and *Xanthomonas oryzae*. In the paper disc and well diffusion assay, the zone of inhibition ranged from 0.65 to 2.2 cm and in microplate method per cent inhibition ranged from 7.23 to 76.60 %. Based on the *in vitro* evaluation, ten effective isolates were selected. PCR amplification followed by 16sRNA sequencing results confirmed the isolates as LAB's belonging to *Lactiplantibacillus*, *Limosilactobacillus* and

Enterococcus genera. The isolates were characterized for probiotic properties and plant growth promoting rhizobacteria and bio-control attributes. All strains survived under gastric conditions with survival rate of 13.94 to 84.61 per cent and at 0.3 per cent bile salts. Effective isolates showed positive reaction for organic acid, indole acetic acid and gibberellic acid production. All strains were capable of phosphate solubilization with solubilization index (SI) of 2.32 to 2.97 and potash with SI of 2.29 to 3.4.

Keywords: Probiotics, fruits, PGPR, a pH tolerance.

PP-82

Unveiling the potential of microbial consortium to combat *Aspergillus niger* - Induced Collar Rot in Groundnut

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Abstract

Groundnut (*Arachis hypogaea* L.) is an important legume and oilseed crop widely cultivated in many countries, including India, but is prone to various microbial infections, with collar rot caused by *Aspergillus niger* being particularly detrimental to production. In the recent years, use of biological control agents for the management of diseases has been advocated widely. However, the narrow spectrum of activity exhibited by individual biocontrol agents can limit their effectiveness in managing plant diseases. Hence, it is hypothesized that a microbial consortium developed from the compatible biocontrol agents could potentially suppress the incidence of diseases with a synergistic effect on biocontrol and plant growth, surpassing the activity of individual microbial agents. Keeping this in view, the present study was taken up to evaluate the performance of three microbial consortia against collar rot disease of groundnut under *in vitro* and glasshouse conditions. A total of 13 treatments including three microbial consortia and individual biocontrol agents were imposed under *in vitro* (rolled paper towel method) and glasshouse (sick pot technique) conditions. Though, all the three microbial consortia (MC1, MC2 and MC3) developed using compatible potential isolates *viz., Trichoderma asperellum* (Tricho1 and Tricho2) and *Bacillus subtilis* (B3, S4KB5 and S8KB2) were promising in promoting plant growth, MC1 (*T. asperellum* Tricho1 + *B. subtilis* S4KB5 + *B. subtilis* S8KB2) showed highest germination percentage, shoot and root length, fresh weight, dry weight and vigour indices compared to other two consortia (MC2 and MC3) and individual biocontrol agents alone. Similarly under glasshouse conditions also, maximum disease reduction over control was recorded by MC1 (9.33%). Overall, the results clearly suggested the efficacy of microbial consortia in promoting plant growth and suppressing diseases compared to individual biocontrol agents, emphasizing the potential of microbial consortia in agricultural disease management.

Keywords: Bacillus, groundnut collar rot, microbial consortium and Trichoderma.

PP-83

Eficacy of Seed Treatment Fungicides against Major Seed and Soil-borne Pathogens

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Abstract

The agricultural sector plays a major role in the economy of India. Among the constraints affecting productivity of major cultivated crops, seed and soil-borne pathogens are the most important devastating pathogens occurring around the world causing significant economic losses. As they are seed and soil-borne in nature, seed treatment with fungicides is one of the effective method in controlling these pathogens. Keeping this in view, an *in vitro* study was conducted to evaluate the efficacy of six seed treatment fungicides *viz.,* captan, thiram, tebuconazole, carboxin + thiram, prochloraz + tebuconazole and thiophanate methyl + pyraclostrobin at different concentrations (100ppm, 250ppm, 500ppm, 1000ppm, 1500ppm and 2000ppm) against five prominent pathogens such as *Rhizoctonia solani* (rice sheath blight), *Macrophomina phaseolina* (maize charcoal rot), *Aspergillus niger* (groundnut collar rot), *Sclerotium rolfsii* (groundnut stem rot) and *Alternaria sesami* (sesame leaf blight) using poisoned food technique. Results indicated that carboxin + thiram and prochloraz + tebuconazole were the most effective fungicides in inhibiting mycelial growth of these pathogens, while captan and thiram were the least effective. Additionally, the per cent inhibition of mycelial growth was increased with increase in the concentration of fungicides. Implementation of these findings could enhance crop health and productivity, thereby contributing to the resilience and sustainability of India's agricultural sector. Further validation through field evaluations is recommended to ascertain the practical applicability of these seed treatment fungicides in real-world farming contexts.

Keywords: Fungicides, poisoned food technique and seed and soil-borne pathogens.

PP-84

Characterization of Rice Stem Rot Pathogen and Integrated Disease Management

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Abstract

A roving survey on incidence of stem rot of rice in major growing regions of Andhra Pradesh, Telangana and Tamil Nadu states of southern India. A total of 36 *Sclerotium oryzae* isolates were isolated from 60 diseased samples. Koch postulates were proved on susceptible rice cultivar Prabhat (MTU3626). Among the isolates, So15 has produced the highest mean per cent disease index (PDI) (39.51) with maximum AUDPC (489.52 units) and an infection rate of 0.065 units day^{-1}. *In vitro* evaluation of efficacy of six organic amendments (OAMs) against the virulent isolate of *S. oryzae* (So15) was carried out. Karanja cake has shown cent per cent mycelial growth inhibition followed by vermicompost (76.67%) and poultry manure (74.44%) at 5 per cent concentration. The bioefficacy of 12 fungicides was evaluated against the virulent isolate So15 in *in vitro* conditions. All fungicides at all five concentrations inhibited the mycelial growth when compared to control except validamycin 3% L at 250ppm. Among the fungicides tested, tebuconazole 250 EC (25.9% w/w) had completely (100%) inhibited the mycelial growth of the pathogen. A biointensive management study for control of stem rot was conducted in farmer's field at Kaikaram village, Unguturumandal of West Godavari district of Andhra Pradesh on susceptible cultivar MTU1121. Among the treatments, root dipping of seedlings with *Bacillus subtilis* strain BsIIRR (ON024393) at 10% + soil application of karanja cake @ 125 kg ha-1 + spraying of tebuconazole 250 EC (25.9% w/w) @ 1ml/L at 45 and 60 days of crop age (T7) recorded the lowest PDI (15.74) and the highest yield (6.26 t/ha) over all other treatments including control with B:C ratio of 1.76. Hence for the cost-effective management of stem rot, root dipping of seedlings with *B. subtilis* strain BsIIRR (ON024393) at 10% + soil application of karanja cake @ 125 kg ha-1 + spraying of tebuconazole 250 EC (25.9% w/w) @ 1ml/L at 45 and 60 days of crop age proved to be the best.

Keywords: Stem rot, organic amendment, biointensive management, paddy.

PP-85

Use of Biocontrol Agents, *Trichoderma viridae* and *Pseudomonas fluorescens* for Plant Disease Management

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Abstract

The increasing prevalence of soil-borne plant pathogens has driven the adoption of biological control agents (BCAs) as sustainable alternatives to chemical pesticides. Among the most effective BCAs, *Trichoderma viridae* and *Pseudomonas fluorescens* have demonstrated remarkable efficacy in managing plant diseases, enhancing growth, and promoting soil health. *T. viridae*, a potent mycoparasite, effectively combats pathogens like *Rhizoctonia solani*, *Macrophomina phaseolina*, and *Fusarium* spp. through mechanisms such as hyphal coiling, enzymatic lysis (β-1,3-glucanase, chitinase, protease, lipase), and nutrient competition. Its benefits include increased crop yield, improved germination, vigorous root and shoot growth, and enhanced nutrient uptake. Despite limitations like sensitivity to alkaline soils and slow growth under specific conditions, *T. viridae* provides long-term pathogen suppression when established in the rhizosphere. Recommended application methods include seed treatment, nursery soil application, and root drenching. *P. fluorescens*, a non-pathogenic bacterium, suppresses fungal pathogens and protects roots and seeds through secondary metabolites (phenazine-1-carboxylic acid, 2,4-diacetylphloroglucinol) and siderophore production, depriving pathogens of essential iron. It also induces systemic resistance through phytoalexin production and lignification. While effective in most crops, it is unsuitable for potato and lettuce due to hydrogen cyanide sensitivity. Application methods include seed treatment, root dips, soil applications, and foliar sprays. Production involves culturing *T. viridae* on potato dextrose agar, mass multiplication on sorghum grains, and talc-based formulation. *P. fluorescens* is grown in King's B medium, fermented, and formulated similarly. Quality control ensures microbial purity, spore viability, and optimal moisture content, with contamination monitored via Gram staining and spread plating. Effective marketing strategies are essential for widespread adoption. Field demonstrations, farmer education, and media campaigns build trust in BCAs' efficacy and environmental benefits. Collaborations with agricultural dealers, NGOs, and competitive pricing, including incentives like volume discounts, promote usage. *T. viridae* and *P. fluorescens* offer environmentally friendly, economically viable alternatives to synthetic pesticides. Their adoption enhances sustainable agriculture, improves soil health, reduces chemical dependency, and safeguards crop yields, benefiting both farmers and the environment.

Keywords: *Trichoderma viridae*, *Pseudomonas fluorescens*, biological control agents, soil-borne pathogens, biocontrol, plant disease management.

PP-86

Biopolymeric Derivates as an Innovative Approach for Sustainable Disease Management

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Abstract

Lignin derivatives which are obtained as byproduct in the paper and pulp industries, are majorly being used as adjuvant and dispersantin textile, food and pharmaceutical industries. It also posses antioxidant and antimicrobial properties, which can be explored in agriculture sector to develop sustainable disease management strategies. This study aims to investigate the compatibility of lignin derivatives with the biocontrol agents and its antifungal activity against fungi plant pathogens. This study was conducted at Plant Pathology Division, ICAR-Indian Institute of Oilseeds Research, Hyderabad. *In vitro* studies have been carried out by using completely randomized design. Different combinations of treatments were prepared using lignin derivative (LD) and chitosan. Compatibility of LD and chitosan with *Trichoderma harzianum* Th4d was tested using poisoned food technique and antifungal activity was assessed against foliar pathogens namely *Phaeoisariopsis personata* causing leaf spot of groundnut and *Golovinomyces cichoracearum* causing powdery mildew of sunflower, using spore germination technique. Significant difference was observed among the different treatments with respect to mycelial growth of *Trichoderma harzianum* Th4d. Initially slow growth of *T. harzianum* was observed, but after 7 days of incubationLD+chitosan exhibited 100% compatibility with full growth of *T. harzianum*. With respect to antifungal activity, combination of LD+chitosan+Th4d at the concentration of 0.10% showed significant inhibition of spore germination of *P. personata* and *G. cichoracearum* with 87.53 and 93.27%, respectively. These results suggest that lignin derivative integration with other biopolymers and biocontrol agents can be effectively used for the management of foliar plant pathogens.

Keywords: Lignin derivative, biocompatibility, antifungal activity.

PP-87

Seed Health and Quality Parameters of Soybean Treated with Green Synthesized ZnO and MgO Nanoparticles Against Seed-Borne *Fusarium oxysporum*

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Abstract

Soybean, a globally important legume crop has expanded in cultivation, but the prevalence of diseases has also increased. *Fusarium oxysporum* causing seed and seedling diseases, poses a potential threat to seed production in soybean. In this study, the effect of green synthesized neem-ZnO and neem-MgO nanoparticles, along with chemically synthesized ZnO and MgO nanoparticles, were evaluated for their ability to control soybean seed-borne *F. oxysporum* through seed treatment. The effect of these nanoparticles on seed health and quality was tested at different concentrations using blotter and rolled paper towel methods, respectively.In blotter test, neem-MgO and neem-ZnO nanoparticles significantly inhibited fungal growth on seedsin a concentration-dependent manner, with the lowest recovery (7.00-10.00%) at 2000 mg/kg compared to chemically synthesized nanoparticles. The rolled paper towel method showed that all nanoparticles improved seed quality parameters uch as germination percentage and seedling vigour indices with the highest improvement at 1500 mg/kg. However, at 2000 mg/kg, a decline in seed quality was observed likely due to phytotoxicity. Further, the uptake of neem-MgO and neem-ZnO nanoparticles by seed after seed treatment was confirmed by SEM analysis of 10-day-old seedlings. These results suggest that neem-ZnO and neem-MgO nanoparticles can be used as effective and eco-friendly alternatives to chemical treatments for managing soybean seed-borne *F.oxysporum.*

Keywords: Antifungal activity, *Fusarium oxysporum*, Green-synthesized nanoparticles, seed treatment, soybean.

PP-88

Evaluation of Plant Extracts and Biocontrol Agents against *Pyricularia grisea* (Sacc.) Causing Rice Blast *in-vivo*

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Abstract

Evaluation of plant extracts and biocontrol agents *in vivo* during *Kharif* 2021-22 indicated spraying with *Pseudomonas fluorescens* @ 0.4% resulted in the lowest leaf blast severity (28.6% PDS) followed by *Ocimum sanctum* @ 15% with 29.3% PDS. Spray with *P. fluorescens* resulted in highest rice grain yield (2264 kg ha^{-1}) followed by *O. sanctum* (2129 kg ha^{-1}). During *Rabi* 2021-22, spraying *P. fluorescens* 0.4% resulted in lowest leaf blast severity with 30.4% PDS followed by *O. sanctum* @ 15% with 36.9% PDS. Spray with *P. fluorescens* @ 0.4 % resulted in highest rice grain yield (2377 kg ha^{-1}) followed by *Ocimum sanctum* @ 15% (2168 kg ha^{-1}). From the pooled data of *in vivo* experiment on efficacy of plant extracts, lowest leaf blast severity was recorded with *P. fluorescens* @ 0.4% (29.5%) followed by *O.sanctum* @ 15% (33.1%). Significantly higher grain yields were recorded with *P. fluorescens* @ 0.4% (2173 kg ha^{-1}) and *Ocimum sanctum* @ 15% (2082 kg ha^{-1}) sprayed plots.

Keywords: Rice, blast, plant extracts, *P. fluorescens.*

PP-89

Optimizing Soil Health and Rice Productivity: Role of Native Bioagents in Managing Stem Rot Disease

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Abstract

Soil is vital for plant growth, providing water, nutrients, and support. Its properties are influenced by crop cultivation, microflora, nutrient addition, and water availability. Maintaining soil health is crucial for sustainable agriculture, with native bioagents offering a promising solution. This study evaluated the effects of *Trichoderma asperellum* (TAIK1), *Bacillus cabrialesii* (BIK3), *Pseudomonas putida* (PIK1), *Pseudomonas otitidis* (POPS1), and their consortium on soil health, plant growth, and stem rot disease caused by *Sclerotium oryzae* in rice.The bioagent consortium, applied via seed treatment or soil application, improved soil properties, including increases in pH (8.08 to 8.28), electrical conductivity (0.72 to 0.75 dS/m), organic carbon (0.57 to 0.68%), and nutrients like nitrogen (155 to 315 kg/ha), phosphorus (7.87 to 24.91 kg/ha), and potassium (121.29 to 249.42 kg/ha). Soil enzyme activities (urease, phosphatase, dehydrogenase) also increased. Treated plants showed a 39.16% increase in height, 30.29% more panicles, and a 41.36% higher grain yield, along with a 69.37% reduction in stem rot incidence.Improved soil health positively correlated with plant growth and negatively with disease severity. This sustainable approach enhances crop productivity, reduces reliance on chemical pesticides, and promotes environmentally friendly agricultural practices.

Keywords: *Trichoderma*, *Bacillus*, *Pseudomonas*, soil health, *Sclerotiumoryzae*, rice.

PP-90

Integrated Management Approach for Pod Borer Complex in Red gram: A Front Line Demonstration in Tandur

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Abstract

Redgram is main pulse crops grown in the Vikarabad district in Telangana. Pod borer complex is major constrain in redgram which include spotted pod borer (*Maruca vitrata*), gram pod borer (*Helocoverpa armigera*) and Pod fly (*Melanagromyza obtusa*). Pod borers usually occur during reproductive stage of the crop, which leads to the significant yield loss. DAATTC, Tandur conducted Front Line Demonstration on management of pod borer complex in redgram during the period 2021-22 and 2022-23 at five different locations in Vikarabad district. Management of pod borers with the aid of IPM package, which include pheromone traps installation @ 4/ acre, arrange bird perches @ 10/ acre, spray of azadirachtin 1500 ppm @ 5ml/l at bud initiation stage and flowering stage followed by need based sprayings with chlorantraniliprole 18.5% SC @ 0.3 ml/l or Emamectin benzoate 5% SG @ 0.4 g/l at pod formation stage. Monitoring of gram pod borer with pheromone traps resulted significant reduction in borer incidence by catching of male adults in traps. Spraying of azadirachtin during the initial pest stage was effectively reduced the pest incidence. Through the interventions implemented in demonstration fields showed notable reduction of borers incidence i.e. the spotted pod borer (11 %), gram pod borer (27%), and pod fly (19 %), this was lower in farmer practicing fields *viz.,* spotted pod borer (27%), gram pod borer (24%), and pod fly (29%).The cumulative yield of redgram for the two years was 1512 kg/ha in demonstration fields where as 1200 kg/ha in farmers practice. Gained high net returns Rs.59,800/- and cost benefit ratio 1:3.1 from demo fields compared to farmers practice was Rs.32,600/- with the 1:1.75 cost benefit ratio.

Keywords: FLD, IPM, pod borers, redgram, Tandur

PP-91

Evaluation of Fungicides against Neck Blast Pathogen, *Pyricularia oryzae* under *in vitro* Conditions

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Abstract

Rice is a staple food for over half the world's population. However, its production is significantly threatened by various biotic and abiotic stresses, particularly blast disease. Despite efforts to develop resistant cultivars, the rapid evolution of the blast pathogen has rendered many resistant varieties susceptible. Chemical control remains a critical strategy for managing this disease and minimizing yield losses. To identify effective fungicides for controlling rice blast, a study was conducted to evaluate the *in vitro* efficacy of ten different fungicide molecules against *Pyricularia oryzae*, the causal agent of the neck blast disease. The poison food technique was used to assess the fungicides' ability to inhibit fungal growth. Among the fungicides tested, tebuconazole 25.9% SC was the most effective, achieving 100% inhibition at 125 ppm, followed by trifloxystrobin 25% + tebuconazole 50% WG and azoxystrobin 11% + tebuconazole 18.3% SC, both of which showed high levels of inhibition. These two fungicides demonstrated comparable efficacy, with average inhibition rates of 92.96% and 95.93% at concentrations of 100 and 125 ppm, respectively. In contrast, azoxystrobin 23% SC was the least effective, with an inhibition rate of only 33.33% at 125 ppm. These findings highlight the potential of the listed fungicides as viable alternatives for managing rice blast disease, particularly following the ban on tricyclazole in basmati rice. Further research is needed to evaluate their efficacy under field conditions and to optimize their application strategies.

Keywords: Neck blast*, Pyricularia oryzae,* fungicides, poison food technique

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PP-92

Bacillus Species as Potential Biocontrol Agents Against Rice Pathogens

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Abstract

Rice is a staple food for over half of the global population, but it faces severe yield losses due to various bacterial and fungal diseases. Biological control using beneficial microorganisms like *Bacillus* species has emerged as an environmentally sustainable alternative to chemical pesticides. *Bacillus* strains, especially *B. subtilis*, *B. amyloliquefaciens*, and *B. velezensis*, demonstrate remarkable efficacy against rice pathogens including *Magnaporthe oryzae*, *Rhizoctonia solani*, and *Xanthomonas oryzae*. These beneficial bacteria synthesize an array of bioactive compounds through both ribosomal and non-ribosomal peptide synthetases (NRPS) and polyketide synthases (PKS). Notable compounds include lipopeptides such as surfactin, iturin, and fengycin, which exhibit direct antimicrobial activities. Additionally, *Bacillus* strains produce antimicrobial peptides (AMPs) like subtilin, bacillocin 490, mersacidin, bacilysin, and subtilomycin that contribute to their antagonistic properties against phytopathogens. Beyond direct antagonism, *Bacillus* species trigger induced systemic resistance (ISR) in rice plants, enhancing their defensive capabilities through the upregulation of pathogenesis-related proteins, phenolic compounds, and defense-related enzymes. Molecular studies reveal the activation of jasmonic acid and ethylene signaling pathways during this process. Some studies related to field trials demonstrate that *Bacillus* based biocontrol can reduce disease incidence by 44.6-85% while promoting plant growth and yield. This comprehensive understanding of *Bacillus* mediated biocontrol mechanisms provides a path for developing effective biological control strategies in sustainable rice cultivation, potentially reducing reliance on chemical pesticides while maintaining crop productivity and health.

Keywords: *Bacillus*, biocontrol, rice pathogens, lipopeptides, antimicrobial peptides, induced systemic resistance, sustainable agriculture.

PP-93

Management and Efficacy of Bacteriophage Formulations against *Xanthomonas oryzae* pv. *oryzae* Causing Bacterial Leaf Blight In Rice

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Abstract

This research investigated the potential of bacteriophages against bacterial leaf blight (BLB) in rice, a disease caused by *Xanthomonas oryzae pv. oryzae* (*Xoo*), which has been isolated from different rice-growing districts of Andhra Pradesh. Bacteriophage samples were collected from different paddy fields floodwater, BLB-infected leaf samples, pond water and sewage water and were assessed for phage activity by using the double agar assay method. Totally four isolates of bacteriophages were recovered by three successive single plaque isolations. Out of four, two bacteriophages Xoopv1 and Xoopv3 isolates exhibited significant lytic activity against *Xoo* bacterium and were further used. To enhance the stability and efficacy of the bacteriophages, they were formulated in different protectants with various combinations, *viz*., pregelatinized corn flour (0.5% and 0.25%), skim milk (0.75%), sucrose (0.5%), casecrete (0.5%), Trehalose (1%), Gelatin (1%), Gluten (1%), and copper nanoparticles. To assess the efficacy of these formulated bacteriophages, rice plants were artificially infected with *Xoo* bacteria. The plants were then treated with the phage formulations at six-day intervals, from 4 to 22 days of post-inoculation (Dpi). Among all days, the lowest disease severity was observed in the formulation of skim milk powder 0.75% + sucrose 0.5% with a value of 8.4% and was closely followed by the combination of casecrete 0.5% + pregelatinized corn flour 0.25% + sucrose 0.5% with a value of 8.9%, and the highest disease severity was recorded in the untreated control with a value of 44.92%. This study highlights the application of bacteriophages along with formulations of skim milk and casecrete, were proved to be very effective in reducing disease progression which can effectively mitigate the severity of bacterial leaf blight in rice.

Keywords: Bacteriophages, double agar assay method, protectants, casecrete.

PP-94

Field Evaluation of Fungicides against Foot and Stem Rot of Mesta Incited by *Phytophthora parasitica* var. *sabdariffae*

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Abstract

Field trials were conducted at Agricultural Research Station, Amadalavalasa for four consecutive years during *Kharif* 2019, 2020, 2021 and 2022 to evaluate new fungicides against foot and stem rot incited by *Phytophthora parasitica* var. *sabdariffae* in roselle. The pooled result indicated that among the five different fungicides tested as seed dressing and foliar spray against *P. parasitica* var. *sabdariffae* in mesta during the four consecutive years, the seeds treated with metalaxyl MZ followed by spraying and drenching at 45 and 60 days after harvest (DAS) with metalaxyl MZ resulted in less disease incidence (13.8%) at the time of harvest. The next best treatments were dimethomorph + mancozeb (23.4%) and azoxystrobin (28.4%). Highest disease incidence was recorded in control plot (61.9%) along with the lowest fibre yield. The treatments metalaxyl MZ and dimethomorph + mancozeb have shown moderately susceptible reaction compared to control plot (high susceptible reaction). All the fungicidal treatments have shown moderately susceptible (MS) reaction compared to control plot (high susceptible reaction).

Keywords: Fungicides, foot and stem rot, *Phytophthora parasitica,* seed dressing, metalaxyl, fibre.

PP-95

Non-Conventional Approaches Using Homeopathic Drugs against Stem Rot Disease Caused by *Sclerotium rolfsii* in Groundnut

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Abstract

Agrohomeopathy is one of the sustainable approaches in agricultural research. Various scientific studies showed that potentised homeopathic drugs alter physiological activities of plants by affecting the rate of enzymatic activities, total sugar, protein and cholophyll contents in plants. In this study, three potential homeopathic drugs *viz*., *Chelidonium* @30C, *T. occidentalis* @ 200C, *Arnica montana* @30C were evaluated as seed treatment, foliar application and soil application under field conditions against stem rot of groundnut disease caused by *Sclerotium. rolfsii*. All the three homeopathic drugs reduced stem rot incidence in groundnut. with *Chelidonium*@30C and *Thuja occidentalis@200C* recordeding the least per cent disease incidence *i.e.,* 10.72 and 24.32 at 90 days compared to 100 per cent stem rot incidence in the inoculated control. The study demonstrated that homeopathic drugs can be effective alternative to chemical control in controlling the stem rot incidence in groundnut under field conditions.

Keywords: *Sclerotium rolfsii, Chelidonium*, *Thuja occidentalis*, *Arnica montana,* disease incidence.

PP-96

Antagonistic Activities of Microflora Isolated from Different Ecosystems against Groundnut Collar Rot and Stem Rot Pathogen

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Abstract

Groundnut collar rot and stem rot caused by *Aspergillus niger* van Tiegham and *Sclerotium rolfsii* Sacc. are important seed and soilborne diseases that is widely prevailing across groundnut farms, leading to serious economic losses. In this research, a total of 392 microbial isolates isolated from different sources were screened for their antagonistic activity against the test pathogens *S. rolfsii* and *A. niger* of groundnut of which 217 microbial isolates (39 fungal, 169 bacterial and 9 actinobacteria) showed antagonism against *S. rolfsii* and *A. niger.* The findings of this study provide valuable insights into microflora associated with the diversity.The study suggests that integrating biocontrol agents like *Trichoderma* and *Bacillus* species into groundnut farming could significantly mitigate the impacts of collar rot and stem rot diseases, offering a promising avenue for sustainable disease management in agriculture.

Keywords: collar rot, stem rot, sustainable, microflora, antagonism.

PP-97

In vitro and *in silico* Analysis of Potential Bacterial Species of *Bacillus* and *Pseudomonas* against *Macrophomina phaseolina*

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Abstract

Dry root rot caused by *Macrophomina phaseolina* is one of the most devastating diseases that cause severe yield loss in *Vigna mungo* cultivation. Plant growth-promoting rhizobacteria (PGPR) are extensively harnessed as biocontrol agents due to their effectiveness in combating a wide array of plant pathogens through a multifaceted approach. In this study, four potential rhizobacterial isolates (*Bacillus* spp. and *Pseudomonas* spp.) showed production of indole-3-acetic acid, siderophores, ammonia, hydrolytic enzymes, biofilms which are significant plant growth promoting (PGP) traits and they also inhibited *M. phaseolina* by dual plate method. Further, metabolites were extracted from all the four bacterial isolates and characterized using thin-layer chromatography (TLC) and Fourier-transform infrared spectroscopy (FTIR) and gas chromatography-mass spectrometry (GC/MS) analysis for the presence of secondary metabolites that would suppress *M. phaseolina*. Understanding the potential interactions of these bacterial bioagents with specific fungal target sites remains a significant challenge. Hence, we focused our study to understand the interaction of rhizobacteria against the virulent proteins of *M. phaseolina* using molecular docking. Furthermore, stability analysis and orientation studies of volatile compounds through molecular dynamics simulations demonstrated their efficacy under *in silico* conditions. The results of the same will be presented.

Keywords: *M. phaseolina*, volatiles, *Bacillus* spp., *Psuedomonas* spp., molecular dynamic simulation.

PP-98

In vitro Assessment of Biocontrol Agents for Controlling *Sclerotium rolfsii*

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Abstract

Groundnut (*Arachis hypogaea* L.) is a vital crop in Telangana, contributing significantly to the agricultural economy. Stem rot caused by *Sclerotium rolfsii*, is a a major disease which can lead to up to 50% yield loss. Since, the pathogen persist in the soil as resistant sclerotia, chemical control is both challenging and economically unfeasible. Alternative management strategies-such as biocontrol, offer a more sustainable and effective solution for long-term disease suppression. This study evaluated 31 biocontrol agents, including 13 fungal and 18 bacterial strains for their antifungal properties against *S. rolfsi* using the dual culture technique. All the biocontrol agents demonstrated significant inhibition of the *S. rolfsii* compared to the control. The strain, *Bacillus subtilis* FSB2 showed the highest inhibition at 60.37% followed by *Bacillus* sp. S9KB4 (56.60%) and *B. subtilis* S4KB5 (52.57%). Other notable *Bacillus* strains included *B. subtilis* 1 (51.11%) and *B. subtilis* FSB16 (50.74%). The minimum inhibition was observed in Actinomycetes strain AS3 (37.37%). In contrast, the highest inhibition among *Trichoderma* species was recorded by *T. asperellum* 5 (75.77%) followed by *T. asperellum* Ta_1 (74.03%) and *T. arenarium* (74.03%). Other effective strains included *T. harzianum* 4D (73.70%) and *T. viride* TV_2 (72.22%). The lowest inhibition was recorded by *T. viride* 1 (62.22%). Overall, both *Bacillus* and *Trichoderma* species exhibited significant inhibition against the pathogen. These biocontrol agents can be integrated into disease management strategies, providing an eco-friendly and effective solution for controlling *S. rolfsii*.

Keywords: Groundnut, *Sclerotium rolfsii*, biocontrol, Bacillus, dual culture, Trichoderma

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PP-99

Empowering Plant Protection: Engineered Inorganic Nanoparticles in the Fight against Plant Diseases

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Abstract

As the need for eco-friendly and sustainable approaches to plant disease management grows, scientists are turning to innovative solutions that promise effective control with minimal environmental impact. In the pursuit of sustainable pathogen management methods that protect the environment and support ecological balance, recent advancements have increasingly focused on the potential of nanotechnology. Nanomaterials, in particular, have shown great promise as components in the development of agents to counter phytopathogens. Among these, inorganic-based nanoparticles (INPs) stand out due to their non-toxic characteristics, hydrophilicity, biocompatibility, and remarkable stability compared to organic compounds. The evolution of drug delivery systems, aimed at maximizing effectiveness while minimizing side effects, has paralleled the development of new materials. With their unique properties, INPs are especially suited to targeting harmful microbes through various mechanisms. For example, they can adhere to microbial surfaces, leading to cell wall and membrane destabilization via metal ion release. Additionally, INPs can trigger toxicity in pathogens through the production of reactive oxygen species. Given the limited availability of new agrochemicals with innovative modes of action, it is essential to explore and precisely characterize INPs that demonstrate strong antimicrobial effects without causing phytotoxicity. Recent studies have made considerable progress in this field, examining various types of engineered INPs characterized by their distinct size, shape, composition, and surface properties. These nanoparticles display promising antimicrobial activity against a broad spectrum of pathogens, including bacteria, fungi, and viruses, making them a powerful alternative to conventional agrochemicals.

Keywords: Phytopathogens, inorganic based nanoparticles, phytotoxicity, disease management

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PP-100

Influence of Phytochemicals on Sclerotia and Ooze Formation, its Maturity against Stem Rot Fungus, *Sclerotium rolfsii* in Groundnut

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Abstract

Groundnut, known as the "King of Oilseeds," is a vital food and cash crop. However, its cultivation faces challenges from *Sclerotium rolfsii* Sacc., a soil-borne pathogen causing stem rot disease, which can lead to pod yield losses ranging from 10-25%, reaching up to 80% in severe cases. This study evaluated the efficacy of three phytochemicals—Piperine, Reserpine, and β-Sitosterol—against *S. rolfsii* under *in vitro* conditions, focusing on sclerotial initiation, ooze formation, sclerotial maturity, and the number of sclerotia formed. Results indicated a concentration-dependent inhibition of sclerotial formation by the phytochemicals. Among them, β-Sitosterol at 2000 ppm was most effective, delaying sclerotial initiation to 29 days, followed by Reserpine (28 days) and Ethyl Protocatechuate (27 days). However, no significant difference was observed among the three compounds in delaying sclerotial development at 2000 ppm. Reserpine proved most effective in reducing the number of sclerotial bodies, with

counts of 181, 48, and 30 at 1000 ppm, 1500 ppm, and 2000 ppm, respectively, compared to the control (358). The study concluded that increasing the concentration of phytochemicals significantly inhibited both sclerotial development and the number of sclerotia formed. Further β-Sitosterol and Reserpine could serve as effective alternatives for managing stem rot in groundnut, reducing the reliance on chemical fungicides and supporting sustainable agricultural practices.

Keywords: Groundnut, phytochemicals, *Sclerotium rolfsii.*

PP-101

Secondary Metabolites from Microbes for Plant Disease Management

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Abstract

Secondary metabolites are organic compounds not directly involved in the growth, development, or reproduction of organisms. In microbes, these metabolites often have ecological roles, such as defense mechanisms, competition, or communication. These compounds include antibiotics, antifungals, siderophores, phytohormones and volatile organic compounds (VOCs). They have shown potential in controlling a wide range of plant pathogens, including fungi, bacteria, viruses, and nematodes. Microbial secondary metabolites offer several advantages over traditional chemical pesticides. These properties make them highly suitable for integrated pest management (IPM) systems. For instance, antibiotics such as iturin and bacillomycin produced by *Bacillus* spp. exhibit strong antifungal activity against several phytopathogens, including *Botrytis cinerea* and *Fusarium* spp. Similarly, lipopeptides from *Pseudomonas* spp. have been effective against bacterial plant pathogens. Siderophores produced by rhizosphere microorganisms sequester iron, depriving pathogens of essential nutrients and thus inhibiting their growth. Research has also focused on the production of phytohormones like indole-3-acetic acid (IAA) and gibberellins by microbes, which can induce systemic resistance in plants making them more resilient to pathogens. Certain metabolites act as elicitors of plant immune responses which triggering SAR and ISR Overall, microbial secondary metabolites represent a promising avenue for the development of new, environmentally benign plant disease management strategies. Secondary metabolites are alternative to conventional chemical pesticides in plant disease management. Eco-friendly nature, make them valuable tools in sustainable agriculture. Ongoing research and technological advancements will enhance their efficacy and application in the field.

Keywords: Secondary metabolites, disease management, siderophore, microbial volatile organic compounds.

PP-102

Integrated Management Strategies for Mitigating Fusarium Leaf Spot: An Emerging Disease of Bael, *Aegle marmelos*

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Abstract

Bael (*Aegle marmelos* Correa.) is one of the most important medicinal and nutritional fruit belonging to the family Rutaceae, it is found all over India and adjoining countries. Like all other plants bael is also affected by various diseases. Fusarium leaf spot an emerging disease recently gained attention due to its increasing incidence in nurseries in eastern Uttar Pradesh, leading to significant foliar damage and reduced plant vigor. Keeping in view the importance of the bael plant and resulting losses from fusarium leaf spot disease caused by *Fusarium pallidoroseum*, the study was undertaken to generate information on the pathological studies and its management in *in-vitro* by following chemical fungicides, botanical extract and essential oils. Fourteen chemical fungicides, 24 botanical extracts and 10 essential oils at different concentrations were tested using poison food technique against *Fusarium pallidoroseum* under *in-vitro* condition. The data of radial mycelial growth (mm) and per cent inhibition were recorded 10 days after inoculation. Among the chemical fungicides propiconazole25% EC and tebuconazole 25.9% w/w at lower concentration (100 ppm) and tebuconazole 25%+trifloxystrobin 50% WG, hexaconazole 4%+zineb 68% WP, and thiophanate methyl 70 WP at higher concentration (500 ppm) completely inhibit the mycelial growth (100%) and superior over rest of the fungicides. Similarly, among the botanicals, Datura extract was the most effective with 19 per cent inhibition of mycelial growth at 5% per cent concentration followed by garlic, ginger, and onion extract. At 10% concentration Ginger extract with 27 per cent growth inhibition followed by datura, garlic, ratrani and neem leaf extract. Likewise, among essential oils tested clove oil, mint oil, eucalyptus oil, lemongrass oil and citronella oil completely inhibited the mycelial growth (100 %) followed by orange oil, basil oil and neem oil over control. Based on the present study, it can be concluded that fusarium leaf spot of bael can be managed effectively using above mentioned fungicides, botanicals and essential oils.

Keywords: *Aegle marmelos*, foliar infection, Fusarium leaf spot, nursery disease, pathogen management.

PP-103

Influence of Plant Microbiome on Plant Health

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Abstract

The plant microbiome plays a vital role in food security, nutrient balance, food safety, and environmental sustainability by acting as an interface between plant health and disease. Occupying various plant compartments, microbiomes influence plant health through interactions that either promote growth or induce systemic resistance, such as SAR (Systemic Acquired Resistance) and ISR (Induced Systemic Resistance). They also aid in mitigating abiotic and biotic stresses by modulating signaling pathways. Plants adapt their microbiomes using strategies like the "cry for help," attracting beneficial microbes during stress. Classic examples include symbiotic associations of AMF and Rhizobia in legumes. Advancements in technology have enabled plant microbiome engineering to enhance agricultural productivity and mitigate climate change impacts. Microbiome engineering, such as SYNCOMS (synthetic microbial communities), reduces microbial complexity while fostering stability and synergistic interactions. Tools like multi-omics, culturomics, and gene-editing technologies allow the development of tailored microbiomes to support sustainable agriculture. Modern agriculture faces challenges like climate change, soil infertility, and emerging plant diseases, exacerbated by global trade, pathogen evolution, and climate shifts. Current treatments often fall short, highlighting the need for innovative solutions. Harnessing plant-beneficial microbiomes offers a sustainable and long-lasting approach to improving disease resistance and crop productivity. These microbiomes enhance nutrient cycling, support plant growth under stress, and strengthen plants against pathogens by inducing SAR and ISR. The plant microbiome also adapts to environmental pressures, which can influence its diversity and functionality. By leveraging its potential, the plant microbiome provides eco-friendly disease management solutions, promoting sustainability in agriculture and paving the way for a new Green Revolution that benefits both the environment and humanity.

Keywords: Plant growth promotion, systemic acquired resistance, induced systemic resistance, SYNCOMS.

PP-104

Phylloplane Microbial Dynamics in Rice (*Oryza sativa* l.) under Drone Spraying of Pesticides

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Abstract

The phylloplane, defined as the surface of plant leaves, supports diverse non-pathogenic microorganisms including bacteria, fungi, and actinomycetes, that contribute to foliar pathogen suppression and overall plant health. However, pesticide applications have been shown to disrupt this delicate microbial balance, yet the effects of pesticides on non-pathogenic phylloplane microflora are underexplored. With the rise in the use of drone-based pesticide application, which offers higher precision and efficiency, there is an increasing need to assess its impact on the phylloplane microbial dynamics. This study aimed to evaluate and compare the effects of drone and conventional power sprayer pesticide applications on the phylloplane microbial populations of rice (*Oryza sativa*), focusing on key microbial groups and their ecological implications. Quantitative analysis revealed significant differences in microbial populations between drone and power sprayer treatments. Drone-based applications were associated with a reduction in total bacterial populations compared to power sprayer treatments. Specifically, *Pseudomonas* populations, known for their plant growth-promoting properties, fluctuated across treatments, with drone applications showing lower colony counts. Actinomycetes populations remained relatively stable across treatments, while fungal populations exhibited marked variability. Genera such as *Rhizopus* spp., *Aspergillus* spp., *Trichoderma* spp., and *Penicillium* spp. were differentially affected by pesticide treatments, with some showing increased abundance in certain drone-treated plots. Additionally, Gram positive bacterial populations exhibited resilience to pesticide application, increasing in abundance after treatment, whereas Gram negative bacteria demonstrated more variable responses.This study demonstrated that drone-based pesticide application induced significant shifts in phylloplane microbial communities, notably reducing bacterial populations while exerting variable effects on fungi and actinomycetes. These findings underscored the need for further research to clarify the ecological and plant health implications of drones on beneficial microbial dynamics in agriculture.

Keywords: Drone spraying, microbial ecology, phylloplane microflora, sustainable agriculture.

PP-105

Management of *Phaeophleospora* Leaf Spot of Sapota using Waste Decomposer

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Abstract

Sapota, *Manilkara achras,* is one of the most important fruit crops grown in Telangana. Leaf spot, caused by *Phaeophleospora indica,* is an important disease of sapota. Waste decomposer produced by National Center for Natural and Organic Farming, Ghaziabad was tested for its effectiveness against Phaeophleospora leaf spot for two seasons 2021-22 and 2022-23 at Horticultural Research Station, Konda Mallepally, Nalgonda district. Waste decomposer solution, one part diluted with 3 parts of water, was sprayed at fixed intervals of 10, 15, 20, 25, and 30 days along with control. Data pertaining to per cent leaves with lesions, average lesions per leaf and per cent disease severity (PDI) were recorded for two years. Pooled analysis of data recorded in both the years revealed that spraying of waste decomposer solution was effective in reducing the sapota leaf spot at all intervals of time. Least per cent infected leaves was observed when sprayed at 10 days (39.45 %) and 15 days interval (40.10%) followed by 20 days interval (53.50%). Treatments involving spray at 25 and 30 days interval were less effective (61.10 and 63.80 per cent of leaves infected) compared to treatments with 10, 15 and 20 days interval but were superior to control (70.40 per cent leaves infected). Average no. of lesions (16.50) per leaf was lowest in treatment with waste decomposer spray at 10 days interval followed by 15 days interval (19.30) compared to control (49.50). Percent disease severity PDI was also lowest in spray at 10 days and 15 days interval with PDI of 15.80 and 17.00, respectively compared control (PDI 42.00). Waste decomposer multiplied for one week in 200 l of water and 2 kg of jaggery and diluted 3 times with water can be effectively used to manage sapota leaf spot caused by *P. indica.*

Keywords: Sapota, leaf spot, *Phaeophleospora indica,* management, waste decomposer.

PP-106

Mutual Antagonistic Interaction between *Colletotrichum truncatum* and *Colletotrichum siamense* on Anthracnose Disease Severity in Dragon Fruit

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Abstract

Dragon fruit (*Selenicereus* sp.) is an important fruit crop native to Central and South America. In India, its cultivation is increasing to meet the growing demand driven by its high consumption rate. Stem and fruit anthracnose is one of the important diseases affecting its cultivation in major dragon fruit growing countries, including India. In the present study, two species, *Colletotrichum truncatum* and *Colletotrichum siamense*, were isolated from anthracnose disease samples collected from Aliabad village, Sangareddy district, Telangana, India. These two species were identified based on morphological (acervuli and conidial characters), cultural (colony morphology and color), and molecular (*ITS* and *ACT* gene sequences) characteristics. Pathogenicity assays were conducted by inoculating dragon fruit stems with individual and mixed inocula of both the species. The results confirmed that both *C. truncatum* and *C. siamense* are causative agents of stem anthracnose. Disease progression studies indicated that *C. truncatum* was more virulent as it could initiate symptom development within third day after inoculation (DAI) and disease progression was rapid leading to shot hole formation by 10DAI. Whereas, *C. siamense* caused feeble yellow discoloration of the inoculated region by 3 DAI, and developed shot hole formation after 25 DAI, indicating its lesser aggressiveness. Interestingly, when both *C. truncatum* and *C. siamense* were inoculated together, disease progression was delayed and limited to dark brown discoloration by the 15th day, indicating a reduced disease severity compared to individual infections. Further, the dual culture experiment was conducted to observe their behaviour when co inoculated in a Petri dish. In comparison to their monocultures, sporulation in *C. siamense* was completely inhibited in dual culture, while in *C. truncatum*, spore germination, growth, and sporulation were delayed. This suggests that both species experienced significant stress due to their competitive interactions, which clearly indicates that they are mutually antagonistic to each other. It was concluded that the mutual inhibitory action between *C. truncatum* and *C. siamense* apparently reduced the severity of anthracnose disease in dragon fruit.

Keywords: *Colletotrichum truncatum*, *Colletotrichum siamense*, antagonistic interaction, anthracnose, *Selenicereus undatus.*

PP-107

Sustainable Management of Sheath Blight in Rice: Evaluating the Efficacy of Botanical Extracts

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Abstract

Sheath blight, caused by the fungal pathogen *Rhizoctonia solani*, is a major threat to rice production, leading to significant yield and quality losses. This study evaluated the antifungal activity of six botanical extracts: *Datura stramonium* (Datura), *Polyalthia longifolia* (Ashoka), *Clerodendrum viscosum* (wild jasmine), *Eucalyptus globulus* (eucalyptus), *Chromolaena odorata* (Siam weed) and *Lantana camara* (wild sage), against *R. solani* under *in vitro* and *in vivo* conditions at two concentrations, 5% and 10%. Among the botanicals tested, *E. globulus* and *L. camara* demonstrated the highest inhibition of mycelial growth at 67.68% and 36.72%, respectively, while *E. globulus* recorded the lowest sheath blight disease intensity *in vivo* (27.42%). *In vitro* experiments were conducted using poisoned food techniques, and *in vivo* experiments followed a randomized block design (RBD) with three replications. Treatments involved three foliar applications of plant extracts at intervals of 15 days after symptom onset. Disease intensity was assessed using a 0-5 scale based on lesion coverage and plant damage. The preparation of plant extracts involved homogenization and incorporation into a potato dextrose agar (PDA) medium. The findings highlight the potential of *E. globulus* as an eco-friendly and effective botanical for managing sheath blight in rice. The results align with previous studies that underscore the role of plant-based biocides in integrated disease management strategies. The use of *E. globulus* and similar botanicals offers an environmentally sustainable alternative to conventional fungicides for controlling *R. solani* in rice cultivation.

Keywords: *Rhizoctonia solani*, sheath blight, botanicals, rice, eco-friendly management.

MJ NARASIMHAN MERIT ACADEMIC AWARD-IPS CENTRAL ZONE

MJN-01

First Report of Indigenous *Bacillus thuringiensis* Exhibiting Lipopeptide-Mediated Antifungal Activity against *Rhizoctonia solani*

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Abstract

Biopesticides offer a safer alternative to chemical pesticides, among them Bacillus thuringiensis Berliner is the widely used bioinsecticide, with 90% of the biopesticide global market share. Although B. thuringiensis pesticidal proteins are well-documented for insecticidal activity, its antifungal potential remains underexplored. Hence in this study, an indigenous B. thuringiensis strain, NBAIR BtBrahmina, was isolated from the cadaver of Brahmina coriacea and characterized morphologically, biochemically, and molecularly. Crude lipopeptides were isolated from NBAIR BtBrahmina by acid precipitation method, and tested for inhibition of Rhizoctonia solani using the poison food technique, which showed 100% inhibition at a concentration of 50 µL crude lipopeptide/mL potato dextrose agar. To identify the virulence factors responsible for the antagonistic activity of NBAIR BtBrahmina, hybrid de novo whole genome sequencing was performed, which revealed biosynthetic gene clusters (BGCs) with similarity to petrobactin (100%), bacillibactin (85%), zwittermicin A (81%), thurincin H (70%), and fengycin (40%), along with six novel BGCs. Further MALDI-TOF MS analysis was performed to identify antifungal secondary metabolites, which confirmed the presence of lipopeptides with m/z ratio corresponding to fengycin and thulomycin, along with novel peaks. Additionally, the genome revealed a 6,776,894 bp circular chromosome, eight plasmids, 15 prophages, 23 genomic islands, insertion sequences, and three CRISPR regions, indicating significant genetic exchange and adaptability. This study is the first to report lipopeptide-mediated antifungal activity of an indigenous B. thuringiensis strain against R. solani, highlighting its potential for broad-spectrum biocontrol applications, reduced crop protection costs, and sustainable agricultural practices. Despite its century-long use as a bioinsecticide, B. thuringiensis has been underutilized as a biocontrol agent against phytopathogens. The study showed the antagonistic potential of the B. thuringiensis NBAIR BtBrahmina in the inhibition of R. solani and genomic insights highlighted the role of lipopeptides in the antifungal potential of the strain. Furthermore, it lays the foundation for future characterization of novel antifungal compounds in B. thuringiensis.

Keywords: Biopesticides, NBAIR BtBrahmina, MALDI-TOF MS analysis.

MJN-02

Bacillus and Trichoderma as Biological Mastery of the Ascendant Gummy Stem Blight in Andhra Pradesh and Telangana

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Abstract

Gummy stem blight caused by *Stagonosporopsis cucurbitacearum* (anamorph)/ *Didymella bryoniae* (telomorph) stands out as a significant menace to cucurbits, posing a severe risk to both yield and quality. Its mean severity in Andhra Pradesh and Telangana ranged from 9.6% to 23% causing up to 50% of yield loss in ridge gourd. Microbial agents belonging to the genus Bacillus and Trichoderma were recognized for their role as potential biocontrol agents against various phytopathogens through the production of diverse bioactive compounds. This study evaluated the effectiveness of 8APSO and 1TS strains of genus Bacillus and TRI-3 strain of genus Trichoderma in suppressing the disease in ridge gourd. Dual culture assay demonstrated significant antifungal activity of the strains against *S. cucurbitacearum.* 1TS and 8APSO were identified as Bacillus amyloliquefaciens, Bacillus subtilis, respectively and TRI-3 as *Trichoderma asperellum* upon subjecting to molecular identification. In greenhouse experiment, various combinations of Bacillus and Trichoderma strains were tested against the pathogen. Among these, combined application of three strains exhibited a significant disease suppression (76.05%). These findings highlighted the significance of strains *Bacillus* sp. (8APSO, 1TS) and Trichoderma isolate (TRI-3) as promising biocontrol agents for devising integrated disease management for gummy stem blight in ridge gourd.

Keywords: *Stagonosporopsis cucurbitacearum*, *Didymella bryoniae* Bacillus, Trichoderma, biological control.

MJN-03

Role of Plant Growth Promoting Rhizobacteria in Enhancing the Resistance in Tomato against *Fusarium oxysporum f. sp lycopersici*

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Abstract

Fusarium wilt of tomato is a devastating disease caused by the soil-borne fungus, Fusarium oxysporum f. sp. lycopersici. It poses a significant threat to tomato cultivation worldwide, leading to yield losses of 30% to 40%, which can escalate to 80% if climatic conditions are favourable for the fungal growth. Plant growth-promoting rhizobacteria (PGPR), which have significant potential to combat various pathogens play a crucial role by colonizing the plant's root system, thereby enhancing growth and yield. These rhizobacteria, with their biocontrol properties, offer an alternative to the high doses of fungicides typically used to deter pathogens and reduce disease severity through various mechanisms. In the present investigation, three rhizobacterial isolates were selected based on their in vitro antagonistic activity against the Fusarium wilt pathogen, using the dual culture technique. The in vivo studies of these rhizobacteria against the pathogen revealed that they can suppress the Fusarium wilt pathogen by enhancing various defence mechanisms like increase intotal phenol (18 mg catechol/100g of fresh weight), flavonoids (19 mg rutin/100g of fresh weight), polyphenol oxidase (0.152 units) and peroxidase (0.413 units) activity, after 48 hours of inoculation. The molecular characterization of these rhizobacteria showed that they belong to different strains of Pseudomonas and Bacillus. The biochemical analysis of the selected isolates showed that they produced significant levels of indole acetic acid (IAA), ammonia, siderophore, phosphorus and also enhance the growth promoting activities like increased shoot length, root length, fresh and dry weight in the tomato plants.

Keywords: PGPR, wilt, *Fusarium oxysporum,* biocontrol, tomato.

MJN-04

Population Dynamics of *Xanthomonas oryzae* pv. *oryzae* and CRISPR-cas9 Mediated SWEET Gene Editing for Bacterial Leaf Blight Resistance in Rice

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Abstract

Rice, *Oryza sativa*, is the most important staple commodity, providing food for nearly half the global population. The bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most destructive diseases afflicting rice fields. Seventy-four isolates were obtained as pure cultures and subjected to leaf clip inoculation, confirming their pathogenicity on TN-1 rice plants in a glass house. Typical BLB symptoms were observed as early as the 3rd day post-inoculation. The morphological and pathogenicity characteristics of 74 isolates from various rice-growing regions in India were used to differentiate them. The pathogenicity assay determined that all isolates were virulent on the susceptible variety TN-1, with the KPXoo19 isolate producing significantly more lesion length, xanthomonadin, and exopolysaccharide. Molecular confirmation using 16S rRNA sequencing identified 39 isolates as *X. oryzae* pv. *oryzae* and 35 as *Pantoea ananitis*. The latter was reported as a rice pathogen for the first time in Karnataka, India. Pathotype analysis with 22 near-isogenic lines (NILs) identified nine distinct pathotypes within 39 Xoo isolates, with pathotypes IV and VIII being the most prevalent (36%). The resistance genes Xa21, xa13, and xa8 exhibited broad spectrum resistance against these diverse pathotypes. Pathotype analysis classified 35 P. ananitis isolates into five major pathotypes and the resistance genes xa13, Xa21, and Xa11 were effective against these diverse pathotypes. Multi Locus Sequence Typing (MLST) analysis of 33 *Xoo* isolates revealed a high degree of genetic diversity while the isolate, KPXoo8, displayed distinct genetic characteristics. Gene-specific diversity analysis indicated varying degrees of genetic variation among housekeeping genes, with dnaK (Chaperone protein) showing the most variability. Genome-wide association analyses using various models identified SNPs associated with bacterial blight resistance linked to candidate SWEET genes namely, OsSWEET2b, OsSWEET 11 and OsSWEET 15. Using plants expressing Os SWEET11 : 13-gRNA and Os SWEET 14 - gRNA the Os SWEET 11, OsSWEET 13 and Os SWEET 14 genes were characterised using the CRISPR Cas 9 gene editing technology. Gene editing was confirmed in the transgenic plant, IR-64 revealed significant changes in the SWEET genes, particularly a decrease in the expression of Os SWEET14, Os SWEET11 and Os SWEET13 by 5- fold, 1.5-fold and 3-fold, respectively.

Keywords: 16S rRNA sequencing, Multi Locus Sequence Typing (MLST) analysis, bacterial leaf blight, rice.

MJN-05

Development of Microbial Consortium for Management of Fusarium wilt of Banana Caused by *Fusarium oxysporum* f.sp. *cubense* Tropical Race 4

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Abstract

Banana is a globally important crop which supports livelihood of millions of people. Production and productivity of banana is affected by many biotic and abiotic factors. Among the biotic constraints, Fusarium wilt of banana incited by a soil-borne fungi *i.e.*, *Fusarium oxysporum* f.sp. *cubense* race TR4 is a devasting threat to banana industry. In the present study, an effort was made to develop microbial consortia for the management of Fusarium wilt of banana caused by *Fusarium oxysporum* f.sp. *cubense* race TR4. The pathogen and total 09 biocontrol agents (05-fungal and 04-bacterial) were procured from Fruit Pathology Laboratory and Biocontrol Laboratory, Department of Plant Pathology and Nematology, RPCAU, Pusa. All the

BCAs possessed promising antagonistic potential against FoC TR4 (>65% PI), and have been molecularly identified. The fungal and bacterial BCAs were combined together and total 24 test consortial combinations were prepared. Upon *in vitro* evaluation of compatibility among the constituent BCAs in each consortial combinations, 09 consortial combinations were screened based on ≤1% inhibition of fungal constituent BCA in each combination. For conducting glass house experiment, 09 screened consortial combinations, 09 individual BCAs, 01 negative check (only pathogen, no BCA treatment) and 01 check (no pathogen, no BCA treatment) were selected for *in planta* evaluation of the consortial combinations. Observations were recorded for the development of external and internal symptoms of the disease by using disease score scale. Percent disease index (PDI) was calculated based on internal symptoms. The highest value of PDI was recorded for negative check (100%) followed by consortium *T. harzianum* (F5) + *T. asperellum* (F1) (80% PDI), the combinations *Bacillus subtilis* (B1) + *T. asperellum* (F2) and *B. velezensis strain2* (E2) + *T. harzianum* (F5) (60 % PDI) and individual *T. asperellum* (F3) (40% PDI), whereas remaining treatments check had shown no disease incidence (0 PDI). The plant vigour index (PVI) was highest for check (5514) followed by combination of E1+F2 (5070) and F5+F3 (4691). Also, PVI was significantly promising in combination *T. harzianum* (F5) + *T. asperellum* (F1) (2848), individual *T. asperellum* (F4) (2731) and combination *B. velezensis strain2* (E2) + *T. asperellum* (F2) (2726). *In vitro* evaluation of compatibility of BCAs with effective fungicides like Tebuconazole 50%+Trifloxystrobin 25%WG (Nativo) and Propiconazole 25%EC (Tilt) at concentrations 50, 100, 150, 250, and 500ppm, highlighted incompatibility of all the fungal BCAs (05) and compatibility of all bacterial BCAs (04). Similar pattern was observed while calculating *in vitro* compatibility of screened consortial combinations with the fungicide where all the constituent fungal BCAs were completely inhibited while all the constituent bacterial BCAs in the consortial combinations showed considerably good growth. The study revealed that consortium *B. velezensis strain1* (E1) + *T. asperellum* (F2) was the most promising combination exhibiting 0 PDI and highest PVI (3336) under *in planta* experiment, and should be taken forward for further study. Consortia (*T. harzianum* (F5) + *T. asperellum* (F3) and *B. velezensis strain2* (E2) + *T. asperellum* (F2)) were also found effective in managing the disease under *in planta* conditions and could also be selected for further study under *in vivo* conditions.

Keywords: Banana, Fusarium, microbial consortium.

MJN-06

Development of a Broad-Spectrum Microbial Consortium and Fungicide Combination against Major Seed and Soil-Borne Diseases

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Abstract

Telangana, a prominent state in India, heavily relies on agriculture as a vital part of its economy. Among the various crops cultivated, rice, maize, pigeonpea, chickpea, groundnut and sesame are of major importance. The productivity of these crops is limited by various biotic and abiotic constraints, including seed and soil borne diseases caused by fungal pathogens, resulting in significant yield losses. Though chemical fungicides have been developed for their disease management, their frequent and indiscriminate use has adverse effects on the environment and can lead to fungicide resistance. To address this challenge, the present research was formulated to develop an effective broad-spectrum microbial consortium and fungicide combination for the management of eight seed and soil borne diseases. A total of 15 biocontrol isolates (six fungal and nine bacterial) were evaluated for their antifungal activities against eight major seed and soil borne pathogens *viz., Rhizoctonia solani, Fusarium verticillioides, Macrophomina phaseolina, Fusarium udum, Fusarium oxysporum* f. sp. *ciceris, Sclerotium rolfsii, Aspergillus niger* and *Alternaria sesami* under *in vitro* conditions. Further, these biocontrol isolates were assessed for various plant growth-promoting traits and top five potential biocontrol isolates were selected to form three microbial consortia. Six fungicides were evaluated at different concentrations against the eight seed and soil borne pathogens and five potential biocontrol isolates. The three microbial consortia and most effective fungicide were evaluated for plant growth-promotion under *in vitro* using rolled paper towel method against two diseases *viz.,* collar rot of groundnut and wilt of chickpea. The combination of most effective microbial consortium and fungicide was further evaluated against groundnut collar rot and chickpea wilt under glasshouse conditions. Among the 15 biocontrol isolates, *Trichoderma asperellum* (isolate Tricho1 and Tricho2) and *Bacillus subtilis* (isolate B3, S4KB5 and S8KB2) were most effective in inhibiting the eight pathogens and also showed plant-growth promoting traits. Further, compatibility test among these isolates resulted in three microbial consortia namely, MC1 (Tricho1 + S4KB5 + S8KB2), MC2 (Tricho2 + S8KB2 + B3) and MC3 (S4KB5 + S8KB2 + B3). Overall, among the six fungicides tested at different concentrations against eight pathogens and five biocontrol isolates, carboxin 37.5% + thiram 37.5% DS showed the highest efficiency in inhibiting the pathogens and was the most compatible with the biocontrol isolates using poisoned food technique. In the rolled paper towel method, MC1 (Tricho1 + S4KB5 + S8KB2) recorded highest germination percentage, shoot length, root length and vigour indices in both groundnut and chickpea. Further, evaluation studies under glasshouse conditions revealed that MC1 combined with fungicide carboxin 37.5% + thiram 37.5% DS recorded lowest disease incidence of collar rot (21.00%) and wilt (26.00%) and significantly improved plant growth (germination %, shoot length, root length and vigour indices) compared to individual treatments in both groundnut and chickpea, respectively. The study demonstrated the potential ability of biocontrol isolates which were, collected and maintained in the Department of Plant Pathology, College of Agriculture, Rajendranagar, in managing eight major seed and soil borne pathogens. Further, the microbial consortia of *T. asperellum* isolate Tricho1 + *B. subtilis* strain S4KB5 + *B. subtilis* strain S8KB2 in combination with the fungicide carboxin 37.5% + thiram 37.5% DS was effective in managing collar rot and wilt in groundnut and chickpea, respectively. This environmentally friendly method could serve as a sustainable approach to reduce the yield losses caused due to diseases and enhance crop productivity.

Keywords: Seed and soil borne diseases, groundnut, Chickpea, Bioagents, consortium.

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Rapid Detection of Tobacco streak virus in Sunflower Using Crude Sap-Based RT-RPA Assay

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Abstract

Sunflower (*Helianthus annuus* L.) holds a prominent position in global agriculture as one of the most crucial oilseed crops. Sunflower necrosis disease (SND), caused by Tobacco streak virus (TSV), is an economically important disease of sunflower. Rapid and highly accurate TSV diagnosis is crucial for SND management. The current research was focused on the development of the reverse transcription-recombinase polymerase amplification (RT-RPA), an isothermal amplification assay for the quick and efficient detection of TSV using crude leaf sap of infected/suspected plants, lysed in 1M Tris extraction buffer (pH-7.5), as a template. Using the developed assay, the reaction mixture was incubated at 38 °C for 30 minutes for reliable identification of TSV in crude leaf sap. The developed assay was specific to the TSV and detects up to 10^{-8}, 10^{-10} and 10^{-13} dilutions of crude sap, cDNA, and plasmid template, respectively. The detection threshold limit of TSV by RPA assay was up to thousands of times more sensitive (cDNA and plasmid used as template) than reverse transcription polymerase chain reaction (RT-PCR). Using the developed RT-RPA assay, TSV was detected in 23 field samples including 4 asymptomatic samples of sunflower germplasm accessions grown at ICAR-NBPGR Regional Station, Hyderabad during the *Kharif* 2024. One of the key advantages of this assay is that it does not require any purification or isolation of the viral RNA. The assay eliminates the need for extensive sample preparation and specialized laboratory equipment, providing a quick and economical solution for detecting the virus in infected plants. This makes it a highly practical approach for field detection and large-scale monitoring of TSV, allowing for timely intervention and disease management. The assay's applicability and ease of use allowed for quick on-site diagnosis of the virus using field samples and in quarantine stations.

The TSV suspected sunflower samples were collected from ICAR-NBPGR, Regional Station, Hyderabad, RNA extraction was performed by using TSV-CPF and TSV-CPR primers which yielded the desired amplicon size of 900 bp. The RT-RPA assay was standardized for crude sap of infected samples by using different types of extraction buffers, *i.e.*, phosphate buffer, NaOH buffer, 50 mM-NaOH: 25 mM-EDTA (1:1), C-TAB buffer, Trizol reagent, Tris buffer (pH 7.5, 1M), at different incubation periods (5, 10,15, 20, 25, 30, 35, 40, 45 minutes) and incubation temperature conditions (35, 36, 37, 38, 39, 40, 41, 42, and 43ºC). Among the buffers used, Tris buffer has consistently produced the desired amplicon size of 270 bp, with an optimal incubation temperature of 38 °C and incubation time of 30 minutes. Comparative experiments with RT-PCR and RT-RPA show that RT-RPA can detect virus at 10^{-8}, 10^{-12}, 10^{-13} dilutions in crude sap, cDNA and plasmid, respectively. The detection threshold limit of TSV by RT-RPA assay was 1000 times more sensitive than that of RT-PCR. TSV was detected in 23 field samples including 4 asymptomatic samples of sunflower germplasm accessions grown at ICAR-NBPGR Regional Station, Hyderabad during the *Kharif* 2024.

In this study, we successfully detected the Tobacco streak virus in sunflower for the first time using a crude sap-based RT-RPA assay. The assay eliminates the need for extensive sample preparation and specialized laboratory equipment, providing a quick and economical solution for detecting the virus in infected plants. To enhance sensitivity further, a CRISPR/Cas-12-based on-site detection method for TSV should be implemented, enabling even more precise detection in field conditions. This combination of RT-RPA with CRISPR/Cas-12 has the potential to provide a reliable tool for TSV diagnostics in diverse agricultural settings.

Keywords: Sunflower necrosis disease, Tobacco streak virus, on-site diagnostics, crude sap, Reverse transcriptase recombinase polymerase amplification assay

Aims and Objects of DSPP

i) To promote knowledge-sharing among plant pathologists, scientists, students and industry for the advancement of plant pathology and related sciences.

ii) To encourage academic and research discussions and disseminate new scientific findings, developments and technologies in plant pathology.

iii) To organize seminars, workshops, and conferences that provide a platform for exchange of ideas and research outcomes related to plant pathology, pest management and crop disease control.

iv) To collaborate with academic institutions and industries to address local and wider agricultural challenges.


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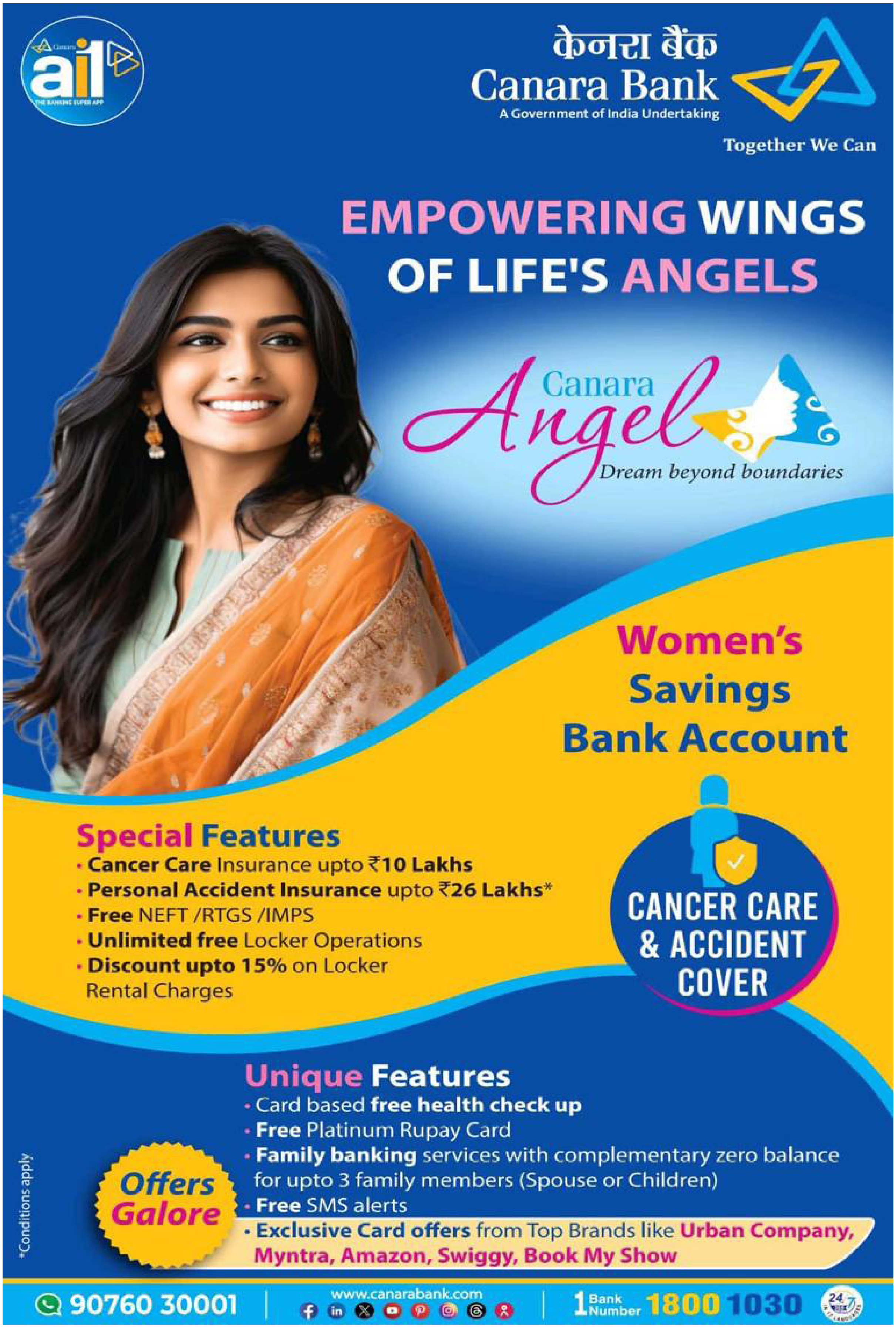

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