DEPARTMENT OF PLANT SCIENCES
University of Hyderabad
Decoding Plantae..

प्रतिष्ठित संस्थान
INSTITUTION OF EMINENCE
राष्ट्रीय अपेक्षाएँ, वैश्विक मानक
National Needs, Global Standards
हैदराबाद विश्वविद्यालय
UNIVERSITY OF HYDERABAD

हैदराबाद विश्वविद्यालय
University of Hyderabad

Anusandhan
National
Research
Foundation

National Conference on

ADVANCES IN PLANT AND ENVIRONMENT INTERACTIONS

FEBRUARY 25 - 27 | 2026

National Conference on
Advances in Plant and Environment Interactions (APEI 2026)
&
17th Plant Sciences Colloquium

February 25-27, 2026

BOOK OF ABSTRACTS

Department of Plant Sciences

School of Life Sciences

University of Hyderabad

Telangana

About the Department of Plant Sciences

The Silver Jubilee Department of Plant Sciences is internationally recognized for its excellence in teaching and research. The strength of the Department lies in the exceptional academic and research profiles of its faculty, who have successfully secured extramural funding from a wide range of national and international agencies. Over the years, the Department has carried out prestigious international projects, including grants from the European Union, UGC-ISF (Indo-Israel), DST-JSPS, Indo- Bulgaria, Indo-German, and Indo-Russia collaborations. Additionally, it has been supported by institutional grants such as UGC-SAP (DRS), DST-FIST (Level II, twice), and DST-FIST (Level C), which have significantly enhanced its research capabilities.

These funding initiatives have enabled the establishment of state-of-the-art facilities, including a common instrumentation facility for high-end equipment, growth chambers, and a Repository of Tomato Genomics Resources. The Department also hosts a DBT Centre of Excellence for Genome Editing in Tomato and, since 2022, has been home to the DBT SAHAJ National Facility. Its advanced infrastructure supports cutting-edge research in plant sciences and microbiology, as reflected in the Department's impressive publication record and its contributions to institutional metrics such as QS World Rankings, NIRF, and NAAC.

As part of the School of Life Sciences, the Department benefits from additional support provided by the School and the University, including grants from UPE that facilitate research across various scientific domains. Faculty members engage in both fundamental and translational research, collaborating with industries and start-ups to address real-world challenges. Many faculty members have held prestigious administrative roles, such as Vice-Chancellors, and serve on high-level committees and taskforces of governmental agencies. Several Professors have been elected as Fellows of esteemed academies such as IASc, INSA, NASI, NAAS, and TWAS, while younger faculty have earned accolades such as the INSA and NASI Young Scientist Awards.

Currently, the Department offers two postgraduate programs—M.Sc. in Plant Biology and Biotechnology and M.Sc. in Molecular Microbiology—along with two Ph.D. programs in Plant Sciences and Microbiology. These programs are supported by four well-equipped classrooms and three dedicated teaching laboratories. The Department also hosts postdoctoral fellows funded through prestigious programs such as NPDF, CSIR-SRA, DBT-RA, UGC-DSK-PDF, and INSPIRE, creating a vibrant research ecosystem.

In addition to its teaching and research endeavors, the Department actively organizes national and international conferences, workshops, invited lectures, and outreach activities to foster knowledge dissemination and collaboration. Its commitment to excellence continues to drive innovation, making the Department a cornerstone of plant sciences and microbiology at the University of Hyderabad.

About the Conference

Plant biology and biotechnology are pivotal in addressing some of the most pressing global challenges, including food security, climate change, and sustainable agriculture. Recent breakthroughs in genomics, molecular biology, and biotechnology have transformed our understanding of plant systems, offering innovative solutions for crop improvement, enhanced disease resistance, and environmental sustainability.

The National Conference on Advances in Plant and Environmental Interactions (APEI 2026) is a premier gathering designed to showcase these advancements and foster meaningful dialogue among leading experts. This event brings together distinguished scientists to share their groundbreaking research and transformative insights, with the goal of inspiring novel approaches to address global agricultural and environmental issues.

APEI 2026 is designed as a dynamic platform for interdisciplinary collaboration and knowledge exchange. By highlighting the latest trends and challenges in plant sciences, the conference aims to catalyze innovative solutions. Additionally, the event strongly emphasizes nurturing young researchers, offering them the opportunity to engage with thought leaders and shape the future of plant biology and biotechnology.

With its blend of cutting-edge science, national expertise, and a focus on mentorship and collaboration, APEI 2026 promises to be an inspiring and impactful milestone in advancing plant sciences for the betterment of humanity.

About the Plant Sciences Colloquium

The Department of Plant Sciences has a long-standing tradition of organizing the Plant Sciences Colloquium, an annual event initiated in 2008 to showcase the Department's exceptional research achievements. This platform enables Ph.D. scholars to present their work, assess their progress, and refine their research through constructive discussions, valuable suggestions, and innovative ideas. To maintain the highest quality of research and foster a competitive spirit among its scholars, the Department has instituted a system where every Ph.D. student must present their research as an oral presentation and a poster presentation during their tenure. The colloquium is coordinated by one or two faculty members, while distinguished scientists from leading universities and institutes are invited to deliver keynote addresses and lead talks. These experts also evaluate the students' research, selecting the best oral and poster presentations alongside an appointed committee.

The event also serves as a valuable training ground for students in event management. Research scholars take on significant roles in organizing the colloquium, serving as Chairpersons and Co-Chairpersons under the guidance of faculty coordinators. To recognize and encourage high-quality research, the Department awards certificates and cash prizes to students who publish papers in journals with an impact factor of 4.0 or higher during the year. Additionally, the Department has instituted the Mahesh Award, in memory of the late G. Mahesh Kumar, a promising Ph.D. scholar of Prof. Appa Rao Podile, who tragically passed away in a road accident. This award, funded by contributions from Prof. Podile and his research team, is presented to the scholar whose research paper achieves the highest impact factor during the year. Only original research articles are considered for this prestigious award, with selections made by a designated committee.

In addition to the colloquium, the Department recognizes academic excellence in the M.Sc. Plant Biology and Biotechnology and M.Sc. Molecular Microbiology programs by awarding medals and certificates to students securing the highest rank in each semester:

Prof. Panchanan Maheshwari Award for securing the first rank in the 1st semester
Prof. Sipra Guha Mukherjee Award for securing the first rank in the 2nd semester
Prof. Toppur Seethapathy Sadasivan Award for securing the first rank in the 3rd semester
Prof. Birbal Sahni Award for securing the first rank in the 4th semester

To nurture creativity by merging science and art, the Department has introduced a Petri-Art Competition. M.Sc. and Ph.D. students participate by crafting artistic patterns on agar plates. A faculty committee evaluates the entries and awards prizes to the top three.

The Plant Sciences Colloquium exemplifies the Department's dedication to fostering excellence in research, academic performance, and creative expression. This initiative empowers students to excel in their academic and professional endeavors.

Department of Plant Sciences, School of Life Sciences
University of Hyderabad, Telangana

National Conference on
Advances in Plant and Environmental Interactions (APEI-2026)
&
17th Plant Sciences Colloquium

(February 25-27, 2026)

Day 1 | February 25, 2026

INAUGURAL SESSION

Venue: SLS Auditorium

09:30 – 10:00	**Welcome Address** **Ragiba Makandar,** Professor & Head, Dept. of Plant Sciences, University of Hyderabad, Hyderabad **Remarks of the Dean** **Anand Kumar Kondapi,** Dean, School of Life Sciences, University of Hyderabad, Hyderabad **Presidential Address** **Basuthkar Jagadeeshwar Rao,** Vice-Chancellor, University of Hyderabad, Hyderabad

Inaugural Talks

Chair: Appa Rao Podile | **Co-Chair:** S. Rajagopal

10:00 – 10:30	**Plenary Talk I: Mechanisms of Rhizocompetence in plant growth promoting rhizobacteria** **Anil Kumar Tripathi,** IISER-Mohali
10:30 – 11:00	**Plenary Talk II: Hidden Regulators: miRNA-encoded and complementary peptides in plant growth and stress resilience** **Prabodh Kumar Trivedi,** CSIR-CIMAP
11:00 – 11:03	**Vote of Thanks** **Sribash Roy,** Organizing Secretary - I, APEI-2026, University of Hyderabad, Hyderabad

~ Group Photo & High Tea ~

SESSION I: Developmental Biology

Chair: Rameshwar Sharma | **Co-Chair:** Yelam Sreenivasulu

11:30 – 12.00	**Keynote Lecture: Plant meiosis, gametogenesis, and flowering plant evolution** **Imran Siddiqi,** CSIR-CCMB, Hyderabad
12:00 – 12:25	**Invited Lecture I: Mitochondrial retrograde signaling in plants: Involvement of voltage-dependent anion channel, ROS and calcium in stress signaling** **Girdhar K. Pandey,** University of Delhi South Campus, New Delhi
12:25 – 12:50	**Invited Lecture II: The E3 ubiquitin ligases RDUF1 and RDUF2 control photosensory hypocotyl growth via inhibiting PIF3 and PIF4 activity in *Arabidopsis*** **Sreeramaiah N. Gangappar**, IISER, Kolkata
12:50 – 1:00	**Colloquium Presentation I: Manipulating folate degradation appears to be a promising approach to enhance folate levels in tomato fruits.** **Juvaria Raouf** (20LPPH03), University of Hyderabad, Hyderabad

LUNCH | Ground Floor - SLS

SESSION II: Plant-Environment Interaction

Chair: A. S. Raghavendra | **Co-Chair:** Irfan A Ghazi

14:00 – 14:30	**Keynote Lecture: Demystifying proteogenomic landscape and organellar odyssey empowering multi-host resistance in fungal disease** **Subhra Chakraborty,** BRIC-NIPGR, New Delhi

14:30 – 14:55	**Invited Lecture I: Bacterial cell walls** **Manjula Reddy,** CSIR-CCMB, Hyderabad
14:55 – 15:20	**Invited Lecture II: How mycorrhizal fungi help chickpea fight combined drought and dry root rot?** **Senthil-Kumar Muthappa,** BRIC-NIPGR, New Delhi.
15:20 – 15:45	**Invited Lecture III: Elucidation of the biosynthetic pathway of C3-epimeric triterpenoids in Boswellia** **Sumit Ghosh,** CSIR-CIMAP, Lucknow
15:45 – 16:10	**Invited Lecture IV: Delineate signaling cascades essential for root nodule symbiosis in crop legumes** **Swarup Roy Choudhury,** IISER-Tirupati
	~ Tea Break ~
	SESSION II: Plant-Environment Interaction *(continues)*
	Chair: G. Padmaja | **Co-Chair:** Jogi Madhuprakash
16:30 – 16:55	**Invited Lecture V: Development of durable resistance to bacterial blight disease in rice** **Hitendra Kumar Patel,** CSIR-CCMB, Hyderabad
16:55 – 17:20	**Invited Lecture VI: Plant antiviral response emerges from dsRBD dynamics and not just the structure** **Mandar V Deshmukh,** CSIR-CCMB, Hyderabad
17:20 – 17:30	**Colloquium Presentation I: Analyzing the effect of the azole fungicide tebuconazole on the fungal pathogen, *Fusarium graminearum*** **Sristishila Baruah** (21LPPH11), University of Hyderabad, Hyderabad
17:30 – 17:40	**Colloquium Presentation II: Identifying the genetic components altered by phytoplasma infection in sesame (*Sesamum indicum* L.)** **Arya Ramachandran** (21LPPH12), University of Hyderabad, Hyderabad
	~ Tea Break ~
17:40 – 19:15	**POSTER PRESENTATIONS & EVALUATION @ SLS Lobby**
	~ Dinner | Ground Floor - SLS ~

End of Day 1

	Day 2 | February 26, 2026
	Venue: SLS Seminar Hall
	SESSION III: Genomics and Epigenomics
	Chair: Alok Krishna Sinha | **Co-Chair:** Santosh R. Kanade
09:30 – 10:00	**Keynote Lecture: Mitogen Activated Protein Kinase: Orchestrating plant growth and adaptation** **Alok Krishna Sinha,** BRIC-NIPGR, New Delhi
10:00 – 10:25	**Invited Lecture I: The interplay between histone acetylation and methylation regulates cotton fiber development** **Samir V Sawant,** CSIR-NBRI, Lucknow
10:25 – 10:50	**Invited Lecture II: Role of climate in species distribution and role of reproductive factors in plant species diversity in the Indian tropics** **Vinita Gowda,** IISER-Bhopal
10:50 – 11:10	**Oral Presentation I: MYB4 Homeostasis as a Regulatory Node in Seedling Development: Roles of ARA4, HY5, and CAM7** **Siddhartha Dutta,** Sister Nivedita University, Kolkata
11:10 – 11:30	**Oral Presentation II: Engineering Lignocellulosic Biomass in *Sorghum bicolor* through CRISPR/Cas9 Editing of *CCoAOMT* and *COMT* genes** **S. Prasant,** Osmania University, Hyderabad
	~ Tea Break ~
	SESSION IV: Microbiology and Phycology
	Chair: Ch Venkata Ramana | **Co-Chair:** K. Gopinath
11:50 – 12:20	**Keynote Lecture: Unravelling the enigmatic plant-pathogen interactions in sugarcane employing "omics" toolbox - a way towards engineering disease-resilient sugarcane** **Amalraj Ramesh Sundar,** ICAR-SBI, Coimbatore

12:20 – 12:40	**Oral Presentation I: MPK3 mediated phosphorylation of WRKY48 down regulates CIPK6 expression during *Pseudomonas syringae* pv. *tomato* challenge in Arabidopsis** **Nidhi Singh,** BRIC-NIPGR, New Delhi,
12:40 – 12:50	**Colloquium Presentation I: Ureolytic bacterial diversity associated with calcifying seaweeds *Jania sp.* and *Halimeda sp.*** **Sushmita Mallick** (21LPPH02), University of Hyderabad, Hyderabad
12:50 – 1:00	**Colloquium Presentation II: Bacterial endophytes from wild millets and their role in plant growth promotion** **Sethu Kalyani** (21LPPH10), University of Hyderabad, Hyderabad
LUNCH | Ground Floor - SLS	
SESSION V: Student Colloquium	
Chair: Jogi Madhuprakash | **Co-Chair:** S. Siddharthan	
14:00 – 14:10	**Colloquium Presentation I: Comprehensive genome sequence analysis provides insights into the pathogenicity of Indian *Xanthomonas oryzae* pv. *oryzae* strains** **Komal Bhati** (21LPPH01), University of Hyderabad, Hyderabad
14:10 – 14:20	**Colloquium Presentation II: Ecological and genomic insights into seaweed-associated Verrucomicrobiota from the Gulf of Mannar** **Ramudu** (21LPPH08), University of Hyderabad, Hyderabad
14:20 – 14.30	**Colloquium Presentation III: Decoding the rasāyana basis of ayurvedically important indigenous rice bran cultivars through integrated metabolomics and network-pharmacology studies** **Komaragiri Rajesh Babu** (21LPPH06), University of Hyderabad, Hyderabad
14.30 – 14:40	**Colloquium Presentation IV: When does *Pseudomonas paraeruginosa* become a predator? A multi-omics approach in understanding the predatory mechanism(s)** **Hari Naga Papa Rao** (22LMPH01), University of Hyderabad, Hyderabad
14:40 – 14:50	**Colloquium Presentation V: Investigating the reversible induction of photosynthetic complexes in *Chlamydomonas reinhardtii* under salt stress** **Namrata Dubey** (22LPPH06), University of Hyderabad, Hyderabad
14:50- 15:00	**Colloquium Presentation VI: Dynamic Regulation of Pectin Methylesterification Controls Cell Wall Plasticity Under Cadmium Hormesis** **Manish Yadav** (20LPPH07), University of Hyderabad, Hyderabad
15:00 – 15:10	**Colloquium Presentation VII: Targeting NSm-interacting host susceptibility genes in tomato for engineering resistance to Groundnut Bud Necrosis Virus** **Appus MV** (20LPPH16), University of Hyderabad, Hyderabad
~ Tea Break ~	
SESSION VI: Molecular Breeding/Genomics	
Chair: Ragiba Makandar | **Co-Chair:** Vadivelmurugan I	
15:20 – 15:50	**Keynote Lecture: Making Rice Climate Resilient** **Raman Meenakshi Sundaram,** ICAR-IIRR, Hyderabad
15:50 – 16:15	**Invited Lecture I: Technology-integrated breeding pipelines for hybrid seed product development** **Thimmaraju Rudrappa,** Kaveri Seeds, Hyderabad
16:15 – 16:40	**Oral Presentation I: Title Fabrication of Biosensors for Food toxins and Adulterant detection** **Gajjala Sumana,** CSIR-NPL, New Delhi.
16:40 – 17:00	**Oral Presentation II: Functional Screening of Phosphate-Solubilizing Rhizobacteria Associated with Finger Millet from Pachaimalai Region, Tamil Nadu** **Subha Vairavel,** Bharathidasan University
17:15 – 18:15	**POSTER PRESENTATIONS & EVALUATION @ SLS Lobby**
~ Dinner | Ground Floor - SLS ~	

End of Day 2

Day 3 | February 27, 2026

Venue: SLS Seminar Hall

Mahesh Award Presentation	
Chair: Jerome Xavier Gunasekaran	
10:00 – 10:20	**Mahesh Award Lecture: Poly-3-hydroxy butyrate production and it's characterization from a new species, *Rhodobacter alkalitolerans* strain JA916^{T} in different growth conditions** **Mohammad Yusuf Zamal** (18LPPH09), University of Hyderabad, Hyderabad
SESSION VII: Plant Stress Adaption	
Chair: Swarup Roychoudhury | **Co-Chair:** Vadivelmurugan I	
10:20 – 10:40	**Oral Presentation I: Unveiling PUB E3 Ligases in Arabidopsis Pollen-Pistil Dialogue** **Sourabh Parmar,** IIT-Gandhinagar
10:40 – 11:00	**Oral Presentation II: Conserved synteny and tandem duplication events drive the expansion of intronless wound induced protein (WIP) gene family in chickpea and Medicago** **Aravind Kumar Konda,** ICAR-IIPR, Kanpur
11:00 – 11:20	**Oral Presentation III: Leaf ontogeny shapes primary and secondary metabolic responses to herbivory** **Anit Baidya**, Central University of Karnataka, Gulbarga
~ Tea Break ~	
VALEDICTORY SESSION	
11:40 – 11:45	**Opening Remarks** **Sribash Roy,** Organizing Secretary-I, APEI 2026, University of Hyderabad, Hyderabad
11:45 – 12:15	**Valedictory Address** **M. N. V. Prasad,** University of Hyderabad, Hyderabad
12:15 – 12:40	**Distribution of Prizes and Certificates**
12:40 – 12:45	**Vote of Thanks** **Vadivelmurugan I,** Organizing Secretary - II, APEI-2026, University of Hyderabad, Hyderabad, Telangana
~ Lunch & Departure ~	

End of the Program

Contents

Plenary Talks

Hidden Regulators: miRNA-Encoded and Complementary Peptides in Plant Growth and Stress Resilience

Prabodh Kumar Trivedi

CSIR-Central Institute of Medicinal and Aromatic Plants (CSIR-CIMAP), Lucknow, India.

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Abstract

Recent advances in plant molecular biology have profoundly reshaped our understanding of the regulatory architecture underlying gene expression, revealing multiple additional layers of post-transcriptional, translational, and epigenetic fine-tuning that orchestrate diverse biological processes. Among these emerging regulatory elements, small peptides, typically comprising fewer than 100 amino acids, have gained considerable attention as potent signaling molecules that modulate plant growth, development, cell-to-cell communication, and adaptive stress responses. These peptides are derived either from small open reading frames (sORFs) embedded within non-canonical transcripts or are generated through proteolytic processing of larger precursor proteins, underscoring their diverse biosynthetic origins and regulatory potential. A particularly intriguing and recently characterized class of regulatory molecules is primary microRNA-encoded peptides (miPEPs), which are translated from short open reading frames located within the primary transcripts (pri-miRNAs) of specific microRNAs. Accumulating evidence indicates that miPEPs play critical roles in plant developmental programs, metabolic regulation, and responses to biotic and abiotic stresses. Using an integrated experimental framework involving promoter–reporter assays, genetic overexpression lines, loss-of-function mutants, and molecular interaction analyses, we demonstrate that miPEPs, together with other classes of small peptides, constitute a highly sophisticated regulatory network governing multiple physiological and developmental pathways. Notably, miPEPs exhibit a unique auto-regulatory mode of action, wherein they directly associate with their cognate miRNA promoters, thereby establishing positive feedback loops that enhance miRNA transcription. This self-reinforcing regulatory circuit amplifies miRNA accumulation and fine-tunes downstream gene expression cascades, ultimately influencing key transcriptional and metabolic pathways. Such peptide-mediated promoter interactions reveal an unprecedented level of cross-talk between translational products and transcriptional control mechanisms in plants.

In addition to miPEPs, our recent work has identified a novel class of complementary peptides (cPEPs), which exert pleiotropic effects on plant physiology. These cPEPs markedly improve nutritional quality and metabolic output, while simultaneously conferring enhanced tolerance to environmental stresses, including nutrient limitation and abiotic/abiotic challenges. Collectively, these findings provide compelling mechanistic insights into the molecular basis of plant growth, environmental adaptability, and secondary metabolism, highlighting an intricate and previously underappreciated interplay between small peptide regulators and transcriptional networks. This work not only expands the conceptual framework of peptide-mediated gene regulation in plants but also underscores the transformative potential of peptide-based molecular strategies for crop improvement, nutritional enhancement, and the development of sustainable agricultural systems.

Keynote Lectures

Plant Meiosis, Gametogenesis, and Flowering Plant Evolution

Imran Siddiqi

CSIR-CCMB, Hyderabad, Telangana

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Abstract

Plants alternate between diploid sporophyte and haploid gametophyte generations. In mosses which retain features of ancestral land plants, the gametophyte is dominant and has an independent existence. However, in flowering plants the gametophyte has undergone evolutionary reduction to just a few cells enclosed within the sporophyte. The gametophyte is thought to retain genetic control of its development even after reduction. Our recent work based on analysis of the novel gene Arabidopsis *SHUKR* has shown that male gametophyte development in Arabidopsis, long considered to be autonomous, is also under genetic control of the sporophyte via a repressive mechanism that includes large-scale regulation of protein turnover. *SHUKR* acts as an inhibitor of male gametic gene expression. SHUKR is unrelated to proteins of known function and acts sporophytically in meiosis to control gametophyte development by negatively regulating expression of a large set of genes specific to post-meiotic gametogenesis. We show that *SHUKR* is rapidly evolving under positive selection suggesting that variation in control of protein turnover during male gametogenesis has played an important role in evolution within eudicots.

Demystifying proteogenomic landscape and organellar odyssey empowering multi-host resistance in fungal disease

Archana Sharma, Kanika Narula, Shobha Ghosh, Iqra Nafees Khan, Atreyee Sengupta, and **Subhra Chakraborty***

BRIC-National Institute of Plant Genome Research, Aruna Asaf Ali Marg, New Delhi-110067, India

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Abstract

Inter-connected loop of messages and counter-messages determine outcome of host-pathogen interaction. Multi-host pathogenicity across plant, animal and human is a major source of new infectious diseases; and the complex interaction renders multisector transdisciplinary approaches critical to address future food and health risks and challenges. *Fusarium oxysporum*, an ascomycetes fungus and multi-host pathogen causes vascular wilt in chickpea and fusariosis in worm and human. Although the precisely controlled innate immune response is governed by conserved cellular events in phylogenetically diverse hosts, underlying molecular mechanisms by which this process is regulated against multi-host pathogen remain unknown. To comprehend *Fusarium*-responsive multi-host pathogenicity, we have established the proteo-genomics landscape of a food legume, chickpea and worm in healthy and disease state. Further, with a quantitative organellar proteomics workflow combining integrated transcriptomics and metabolomics, we also demonstrated multilayered analyses at the resolution of organellar proteomics and phosphor-proteomic and their application to reveal new insight on the immune signature and pathogenesis during fusariosis. Most excitingly, network analysis identified significant functional modules pointing toward fusarium responsive common mechanism of remodelling, homeostasis and cell death response through divergent regulatory pathways across kingdom.

Mitogen Activated Protein Kinase: Orchestrating Plant Growth and Adaptation

Alok Krishna Sinha

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Abstract

Mitogen-activated protein kinase (MAPK) cascades play a crucial role in transducing environmental and developmental signals from the cell surface to the nucleus, enabling appropriate cellular reprogramming. These cascades consist of three key components: MAPKKKs (MAPK kinase kinases), which activate MAPKKs (MAPK kinases), and finally MAPKs, the terminal kinases in the cascade. In this presentation, the diverse roles of MAPKs in plant adaptation and growth will be explored. Specifically, their role during cell division in rice and thermomorphogenesis in *Arabidopsis* will be discussed. Notably, OsMPK3, a MAPK in rice, interacts specifically with the KRP3, an important component of cell-cycle and governs plant growth and yield. In *Arabidopsis*, the MPK4-PIF4-ARP6 module has been identified as a regulator of histone variant H2A.Z deposition, which controls hypocotyl cell elongation and helps plants adapt to elevated temperatures.

Unravelling the enigmatic plant pathogen interactions in sugarcane employing "*omics*" toolbox - a way towards engineering disease resilient sugarcane.

A. Ramesh Sundar[1]*. Kana Valiyaveettil Lakshana [1]N. M. R. Ashwin[2]., Dharmaraj Amalamol[1], A. Jeevalatha[1], R. Ramesh[1], P. Malathi[1] and R. Viswanathan[3]

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Abstract

Challenges in Indian Agricultural scenario involves biotic stress factors like insect pest and diseases, which is a significant production constraint. Adding to the complexity is the changing climatic conditions, which necessarily prompts us to reorient our research on climate resilient agriculture, so as to sustain our agricultural productivity in the global market. The stress-responsiveness of plants can be studied by analyzing changes in physiological and metabolic perturbations. Different domains of "Omics" namely Genomics, Transcriptomics, Proteomics and Metabolomics collectively contribute to decipher the functional genomics component in any plant-pathogen interaction. These tools of Omics offer new opportunities to address these challenges and generate a system-level understanding of metabolic interactions at the host-pathogen interface. Unwinding of whole genome sequences, followed by RNA and protein expression profiling added leverage to comprehensively determine how genes can contribute to complex phenotypes.

Sugarcane is one of the important commercial crops cultivated throughout the world mostly in countries with a tropical climate. Sugarcane is the primary source for manufacturing crystal sugar, which is a predominant commodity in the global food industry. Disease resistance in crop plants is an enigma to be unravelled, in spite of advances made in plant biology. Sugarcane by virtue of its genomic complexity proves to be enigmatic and so disease resistance remains yet to be deciphered. With the recent unwinding of the whole genome of sugarcane and with the emergence of robust molecular tools, a paradigm shift in the understanding of plant disease resistance in sugarcane is being witnessed recently.

Genomics research with the phenomenal upsurge to the next generation sequencing platforms has proven to be robust enough to decipher complete genetic information coding for useful traits of interest. Proteomics –a complementary tool to genomics is gaining substantial progress in many crop plants like Rice, Maize, Sorghum etc., besides having been well established in the model plant – *Arabidopsis*. There is an unprecedented acceleration in the pace with which this tool of "*omics*" is carrying forward progressively to address many unresolved issues in agricultural research. It is quite evident that Proteomics is a powerful tool in the post-genomic era and plays a key role in empowering systems biology in plants. The presentation will cover some of the interesting leads obtaining in deciphering disease resistance in sugarcane and the way forward to address emerging challenges for successful disease management in Sugarcane.

Making Rice Climate Resilient through Genomics-Assisted Breeding

Raman Meenakshi Sundaram[1], Laha GS[1], R Abdul Fiyaz[1], Jyothi Badri[1], Satendra Kumar Mangrauthia[1], Divya Balakrishnan[1], M.S. Anantha[1], C.N. Neeraja[1], M.B. Kalyani[1], M.S. Prasad[1], V. Prakasam[1], M.B.V.N. Kousik[1], E. Punniakoti[1], Hajira Shaik[1], Ramesh V Sonti[2], and Hitendra K Patel[2]

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Abstract

Rice is the primary staple for nearly half of India's population and a critical component of national food and nutritional security. However, rice production faces major challenges, including climate variability, shrinking natural resources, emerging pests and diseases, and plateauing yields. The present work highlights the development of climate-resilient rice varieties and hybrids through genomics-assisted breeding (GAB), integrating molecular mapping, candidate gene discovery, and precision trait introgression to accelerate varietal improvement. Novel genes and quantitative trait loci (QTLs) for resistance to major biotic stresses such as bacterial blight, blast, sheath blight, gall midge, and nematodes have been identified from diverse genetic resources and wild relatives. These genomic insights have enabled the development of Improved Samba Mahsuri (ISM) and a series of value-added derivatives (DRR Dhan series) combining multiple traits such as disease resistance, salinity tolerance, submergence tolerance, low soil phosphorus tolerance, high grain zinc, strong culm, and enhanced yield. Several of these varieties are widely adopted across India, contributing to yield gains, input savings, and enhanced farmer income. Climate-resilient varieties now occupy a significant share of the rice-growing area and have played an important role in stabilizing production under erratic monsoon conditions. Emerging approaches such as haplotype-based breeding, speed breeding, gene editing, and artificial intelligence are further accelerating the development of designer genotypes with superior trait combinations. Our word clearly demonstrates that genomics effectively complements conventional breeding, enabling rapid and cost-effective delivery of climate-resilient, high-quality rice cultivars.

Invited Lectures

Mitochondrial retrograde signaling in plants: Involvement of voltage-dependent anion channel, ROS, and calcium in stress signaling

Girdhar K. Pandey

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Abstract

Adverse environmental conditions, such as salinity, drought, and extreme temperature fluctuations, cause significant losses in agricultural productivity worldwide. Moreover, degrading environmental conditions are the major cause for a steep decline in average yields for many key crop plants. Several of these abiotic stresses lead to the generation of reactive oxygen species (ROS), which cause oxidative stress and hamper overall plant growth and development, and, hence, crop productivity.

Voltage-dependent anion channels (VDACs) are highly conserved β-barrel proteins in eukaryotes and regulate metabolite transport between mitochondria and cytoplasm. VDACs play an important role in regulating mitochondrial Ca^{2+} homeostasis. However, in plants, the relationship between VDACs and Ca^{2+} is not well elucidated. VDACs can also transport reactive oxygen species (ROS), such as the superoxide radical ($O_2^{\bullet-}$), from mitochondria to the cytosol. Both Ca^{2+} and ROS, in turn, modulate the permeability and conductance of VDACs and affect VDAC function. So, we have characterized the Arabidopsis VDAC proteins using *Δpor1* mutants to test their roles in responses to ROS and salt-stress-inducing agents. Using this system, we have demonstrated the role of Arabidopsis VDAC proteins in respiration, mitochondrial membrane potential (MMP), reactive oxygen species (ROS) homeostasis, and responses to oxidative and salt stress. Furthermore, we hypothesized that oxidative stress leads to the generation of Ca^{2+} signature, which is transduced downstream in the pathway by calcineurin B-like protein (CBL) -interacting protein kinase, CIPK and this in turn, phosphorylates VDAC3 at the mitochondria. The phosphorylated VDAC3 probably serves as a gateway for the passage of ROS from mitochondria to the cytosol and regulates the mitochondrial retrograde signaling (MRS) and cellular physiology. In conclusion, we report an important class of protein kinases, CIPKs, and their potential involvement with the outer mitochondrial membrane channel "VDAC" in regulating plant oxidative stress responses. This knowledge of Ca^{2+} signaling regulating VDAC would be very useful in devising genome editing technology to impart abiotic stress tolerance in crop plants in the near future.

The E3 ubiquitin ligases RDUF1 and RDUF2 control photosensory hypocotyl growth via inhibiting PIF3 and PIF4 activity in Arabidopsis

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Abstract

Light has a striking effect on plant growth and development. The two E3 ubiquitin ligases, RING DOMAIN OF UNKNOWN FUNCTION 1117 1 (RDUF1) and RDUF2, act as positive regulators of photomorphogenesis via forming a positive feedback loop with the master regulator, HY5. In this study, we uncovered an alternative pathway(s) by which RDUF1/RDUF2 promote seedling photomorphogenesis independent of the HY5 pathway. We report that RDUF1/RDUF2 repress PHYTOCHROME INTERACTING FACTOR 3 (PIF3) and PIF4. Our genetic analysis suggests that RDUF1 and RDUF2 are epistatic to both PIF3 and PIF4 in the photomorphogenic pathway, as the hypocotyl lengths of the *pif3pif4rduf1* and *pif3pif4rduf2* triple mutants were similar to those of the *pif3pif4* double mutants. Further, Y2H and BiFC assays demonstrated direct physical interactions between RDUF1 and RDUF2 with PIF3 and PIF4. Moreover, biochemical analysis revealed that RDUF1/RDUF2 destabilize PIF3 and PIF4 proteins by enhancing their ubiquitination and degradation. Alternatively, RTqPCR and DNA-protein interaction assays reveal that PIF3/PIF4 directly bind the Gbox LRE on the *RDUF1* and RDUF2 promoters and repress their gene expression. Collectively, this study uncovered PIF3/PIF4 as novel substrates of RDUF1/RDUF2 E3 ubiquitin ligases for degradation and thereby promote seedling photomorphogenesis in Arabidopsis.

Elucidation of the biosynthetic pathway of C3-epimeric triterpenoids in *Boswellia*

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Abstract

Plants produce a diverse array of specialized metabolites with therapeutic applications. Triterpenoids (C30 isoprenoid compounds) represent one of the most structurally and functionally diverse class of specialized metabolites. However, understanding triterpenoid biosynthetic pathways and biosynthetic enzymes remain largely incomplete. Our research group at CSIR-CIMAP employs integrative approach, combining transcriptomics, metabolomics, biochemical analyses, and pathway reconstruction to understand triterpenoid biosynthesis in medicinal herbs and trees. We have identified and biochemically characterized a suite of enzymes belonging to the oxidosqualene cyclase, cytochrome P450 monooxygenase, UDP-glycosyltransferase and acetyltransferase families, which catalyze crucial reactions towards triterpenoid scaffold generation and decoration leading to structural diversification of triterpenoids. My talk will cover recent work of our group in the medicinal tree *Boswellia serrata* towards the elucidation of the complex biosynthetic pathways of anti-inflammatory boswellic acids (BAs), which are a rare group of C3-epimeric triterpenoids. Understanding BA biosynthesis, particularly knowing if C3-epimerization occurs at the triterpenoid epoxidation/cyclization steps catalyzed by squalene epoxidase (SQE)/2,3-oxidosqualene cyclase (OSC) or at the later stage of scaffold modification, remains largely elusive. We identified SQEs and OSCs from *B. serrata* transcriptome, and functionally characterized them *in vitro*, *in planta* assays, and using yeast SQE/OSC mutants to know the involvement of SQEs/OSCs in BA biosynthesis. The results suggested that C3-epimeric triterpenoids are not the direct products of squalene epoxidation/2,3-oxidosqualene cyclization reactions, rather these compounds might form via epimerization at the later stage of triterpenoid scaffold modification, thus, establishing a critical step into BA biosynthetic pathway. Besides, we have characterized a BAHD acetyltransferase catalyzing scaffold-selective C3-O-acetylation of BAs.

Bacterial Cell Walls

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Abstract

Peptidoglycan, a defining feature of most bacterial cell walls is crucial for the integrity and morphology of bacteria. Initially identified as a target of beta-lactam antibiotics, peptidoglycan has become a subject of much interest for its biology, its potential for the discovery of novel antibiotic targets, and its role in infection. It is a polymer made up of several glycan strands cross-linked through short peptides and forms a large net-like scaffold that surrounds the bacterial cytosolic membrane. The significance of cross-link formation in peptidoglycan is known for decades as the beta-lactam antibiotics target the enzymes that catalyze this step. However, the importance of cross-link hydrolysis in peptidoglycan biology remained largely underappreciated. Recent studies from our lab have demonstrated the functions of cross-link cleavage in diverse physiological processes, including an indispensable role in peptidoglycan expansion during the cell cycle, thereby making cross-link cleaving enzymes an untapped target for novel drugs. Here, I will elaborate on the fundamental roles of cross-link specific peptidoglycan hydrolysis and its regulation in bacteria.

How mycorrhizal fungi help chickpea fight combined drought and dry root rot?

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Abstract

Dry root rot (DRR), a globally emerging disease of chickpea caused by *Macrophomina phaseolina*, intensifies under drought conditions. Tissue water status plays a crucial role in pathogen infection and disease development. Arbuscular mycorrhizal fungi (AMF) are known to alleviate drought and pathogen-induced stress, though the underlying mechanisms under combined stress remain largely unexplored.

To understand this interaction, we conducted rhizobox experiments combined with confocal microscopy and tissue osmotic potential analyses using deep-rooted donor and shallow-rooted receiver chickpea genotypes. In addition, multi-location field trials were performed in DRR-sick plots across 24 microenvironments, involving three pairs of donor and receiver plants. These studies aimed to elucidate the role of common mycorrhizal networks (CMNs) in water transfer, called bio-irrigation, in mitigating DRR under drought, with subsequent evaluation of disease severity and yield performance.

AMF colonization improved root water status, maintained cell turgor, and restricted the spread of *M. phaseolina* by reducing microsclerotia formation. This, in turn, enhanced stress tolerance and protected yield under combined drought and pathogen stress. Improved root hydration and sustained cell turgor likely reduced necrotic cell death and prolonged the biotrophic phase, thereby slowing disease progression. We are currently investigating whether AMF plays a role in recruiting beneficial microbes to provide protection against disease under challenging drought conditions, and, if so, how the rhizobiome shifts in pathogen hotspots toward a healthier soil state.

These findings underscore the vital role of donor plants in facilitating AMF-mediated protection in intercropping systems. The work provides new insights into sustainable, field-relevant strategies for managing combined abiotic and biotic stresses in chickpea.

Delineate signalling cascades essential for root nodule symbiosis in crop legumes

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Abstract

Leguminous plants have established a mechanism to accommodate a group of soil bacteria (rhizobia) within their roots by forming a specialized organ called root nodule, where the bacteria can reside and fix atmospheric nitrogen. Root nodule formation is precisely regulated by chemical signals between plants and microbes. The membrane-bound Lysin motif receptor-like kinases or LysM-RLKs receptors play crucial roles in the perception and further transmission of regulatory signals to control numerous developmental and metabolic events essential for nodulation. The compatible interaction between the host and symbiont is mediated by a series of signaling events, including recognition by Nod factor receptors, calcium spiking, phytohormone signaling and activation of several host and rhizobial genes. To understand the processes behind nodulation, we are investigating how receptor-mediated signals modulate the downstream signaling cascades in legumes. Using RNAi silencing, physiological and molecular analysis, we are dissecting the role of genes involved in nodule formation. The outcome of this work will significantly contribute to designing new strategies for improving root-nodule symbiosis and potentially advancing towards sustainable agriculture.

Development of durable resistance to bacterial blight disease in rice

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Abstract

Rice crop is affected by several biotic and abiotic stresses. Bacterial Blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most serious bacterial diseases of rice, which can result in up to 50% yield loss. Towards a molecular understanding of rice-*Xoo* interactions, we conducted a meta-analysis of transcriptomic data and identified a rice *flavone synthase* (*OsFNS*) gene. *OsFNS* is targeted by a type III effector protein of *Xoo* and is a susceptibility factor for *Xoo* in rice. We have further characterised the *OsFNS* gene through various functional assays and transgenic approaches. Currently, using functional genomics and genome editing, we are developing durable resistance to BB disease in rice. Using a forward genetics approach, we identified an induced-mutant line (BB42) derived from an elite rice cultivar (Samba Mahsuri) that exhibits broad-spectrum resistance to BB. Using gene-mapping approaches, *Mitogen-Activated Protein Kinase 6* (*OsMAPK6*) on rice chromosome 6 was identified as associated with BB resistance. The mutant line (BB42) and identified allele (*OsMAPK6*) is now being characterized in more detail. In a reverse genetics strategy, we used Targeting Induced Local Lesions In Genomes (TILLING) to identify rice lines with loss-of-function mutation in two previously characterised susceptibility factors of *Xoo viz., OsTFIIAγ1* and *Os11N3*. *xa5* and *xa13* are two of the commonly used BB resistant alleles. *Xoo* strains that break down *xa5* and *xa13* resistance genes use *OsTFIIAγ1* and *Os11N3* as alternate susceptibility factors, respectively. Further, we have generated two pyramided lines *viz., xa5* + *OsTFIIAγ1* and *xa13* + *Os11N3*. The double pyramided lines of *xa5* + *OsTFIIAγ1* and *xa13* + *Os11N3* exhibited enhanced resistance to multiple strains of *Xoo* for which the single resistance allele lines show susceptibility

Plant antiviral response emerges from dsRBD dynamics and not just the structure

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Abstract

The initiation of the RNA interference (RNAi) pathway requires the formation of a ternary complex comprising Dicer, a double-stranded RNA (dsRNA) initiator, and a dsRNA-binding protein (dsRBP). Structural investigations of dsRBPs and their interactions with various initiator dsRNAs have revealed that distinct species have evolved unique modes of dsRBP-dsRNA recognition. While a recent cryo-EM structure of human Dicer (hDicer) has led to a proposed model for ternary complex formation, this model does not fully explain the catalytic mechanism of Dicer or the stepwise assembly process of the complex. Despite strong sequence and domain architecture conservation among Dicers and dsRBPs, both plants and insects retain multiple isoforms of these proteins, each adapted to recognise specific dsRNA substrates.

Notably, dsRBPs with multiple dsRNA-binding domains exhibit highly conserved structures and evolutionary profiles, yet they differ significantly in their substrate recognition capabilities. In this study, we present structural data and NMR-based dynamic analyses to elucidate the molecular basis of differential dsRNA binding in representative organisms across the evolutionary spectrum, ranging from *C. elegans*, *D. melanogaster*, and *A. thaliana*.

The interplay between histone acetylation and methylation regulates cotton fiber development.

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Abstract

The epidermal cells of cotton ovules that commit to developing fibres provide an intriguing model for studying genetics and epigenetics. Inhibiting histone acetylase activity through treatment with Anacardic acid (AA), a p300/PCAF inhibitor, in *in vitro* ovule cultures promotes the development of cotton fibers. Transcriptome and ChIP-seq analyses have revealed that AA enhances fiber yield by increasing the expression of genes in the auxin pathway while suppressing the expression of cell cycle genes. Furthermore, foliar application of AA on developing flowers and bolls significantly improved cotton yield across multiple genotypes and locations. Multi-location AICRP trials conducted over two years confirmed a yield enhancement of 5-30% in cotton. Further, we have demonstrated that cotton histone deacetylase 5 (HDA5) plays a positive role in regulating cotton fibre development by regulating H3K9 deacetylation. Reduced expression of *GhHDA5* inhibits fiber initiation, resulting in decreased lint yield in its RNA interference (RNAi) lines*, via* alterations in reactive oxygen species homeostasis and elevated autophagic cell death in developing fibers. Further, the co-expression network analysis indicates that GhHDA5 functions as a multi-protein repressor complex, which includes other histone modifiers, such as HDACs and histone methyltransferases, as well as Heat Shock Proteins (HSPs). The expression analysis also revealed that several members of GhHSP70 and GhHSP90 were significantly expressed during the different stages of fiber development. Inhibition of HSP70 and HSP90 activity in *in vitro* ovule culture resulted in the retardation of fiber growth at early and later stages of fiber development, respectively. Suppression and overexpression lines of these Heat Shock Proteins (HSPs) showed decreased fiber growth at the initiation and elongation stages. ROS levels were found to be imbalanced in transgenic ovules due to alterations in HSP expression, leading to disruption of cellular homeostasis.

Additionally, expression and promoter analysis revealed that the histone methyltransferase gene *GhSUVH1* is expressed at a higher level at the initiation stage of cotton fiber development. GhSUVH1 regulates trimethylation of H3K9 mark. RNAi lines of *GhSUVH1* showed early flowering, more boll settings, and higher seed number, lint weight, and harvesting index than the overexpression lines and the control.

Our study provides a detailed view of epigenetic regulation involving histone modifications and modifiers, paving the way for the development of more resilient cotton varieties.

Role of climate in species distribution and role of reproductive factors in plant species diversity in the Indian tropics

Vinita Gowda, Sukhraj Kaur and Aleena Xavier

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Abstract

Biodiversity and community structure are known to be shaped by biotic processes such as competition and speciation, and by abiotic factors that can be climatic and/or edaphic. Today, using biodiversity surveys, ecological models, and new statistical methods, it is possible to test the dominance of either biotic or abiotic factors in shaping plant communities. In India, at least three biodiverse regions are identified - the Western Ghats, NE of India, and the Western and Central Himalayas. I will present results from two distinct studies that will emphasise the need to investigate both the distribution and the reproductive traits in determining species assemblages and the underlying speciation processes within a plant community. In the first study, we noted that climatic factors determined landscape-scale plant community assemblages. This also, in turn, shaped flowering phenology, plant-pollinator interactions, and reproductive success of plants within the study communities. In the second study, we noted that plant species with wide distribution ranges and adaptability to variable climates show variations in both their phenotypic and genotypic traits, which confuses our conventional definition of a taxon or a species. Our results show that taxonomic concepts of species and speciation processes may need to be reassessed for these widely distributed plant species, and we propose possible models for the same.

Technology Integrated Breeding Pipelines for Hybrid Seed Product Development

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Abstract

Commercial crop breeding pipelines are increasingly integrating advanced technologies to accelerate genetic gain while improving operational efficiency and product consistency. Modern programs combine Speed breeding, technologies such as rapid generation advancement, high-throughput phenotyping, and genome-wide genotyping with genomic selection to shorten breeding cycles and enhance selection accuracy. Early-stage marker-based prediction enables efficient resource allocation by prioritizing superior candidates before extensive field testing. Gene editing technologies complement these pipelines by enabling precise modification of high-value alleles for yield, stress tolerance, and quality traits while preserving elite genetic backgrounds. Integration of digital breeding platforms allows seamless management of phenotypic, genotypic, and environmental data, supporting continuous model refinement and evidence-based decision-making across breeding cycles. This presentation focuses on how together, these technology-integrated approaches increase selection intensity, reduce cycle time, and improve prediction reliability, resulting in sustained gains in breeding efficiency and faster delivery of competitive commercial varieties adapted to dynamic market and climate challenges.

Oral Presentations

MYB4 Homeostasis as a Regulatory Node in Seedling Development: Roles of ARA4, HY5, and CAM7

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Abstract

Calmodulin7 (CAM7) is an important transcriptional regulator implicated in the control of early seedling development in *Arabidopsis thaliana*, particularly during light-mediated morphogenic transitions. CAM7 functions in concert with the bZIP transcription factor HY5 to promote photomorphogenesis across multiple wavelengths of light, thereby contributing to the fine-tuning of light signaling pathways. In the present study, we identify AtMYB4 as a novel CAM7-interacting partner through a yeast two-hybrid screening approach and demonstrate that AtMYB4 acts as a positive regulator of photomorphogenic growth. Biochemical and genetic analyses reveal that CAM7 and HY5 directly associate with the promoter region of *AtMYB4*, enhancing its transcription and thereby facilitating photomorphogenic development under diverse light conditions. In parallel, we identify ARA4 from the same yeast two-hybrid screen as a functionally contrasting component that serves as a negative regulator of photomorphogenesis, with its effects being particularly pronounced under white light conditions. Mutational and double-mutant analyses indicate that the altered hypocotyl elongation phenotypes observed in *atmyb4* and *ara4* mutants are partially or completely suppressed upon additional loss of CAM7 function, highlighting a complex genetic interplay among these components. Furthermore, interaction studies reveal that ARA4 genetically antagonizes AtMYB4, counteracting the elongated hypocotyl phenotype characteristic of the *atmyb4* mutant background. Transactivation assays further substantiate these findings by demonstrating that CAM7, in association with HY5, positively regulates *AtMYB4* promoter activity, whereas ARA4 exerts an inhibitory influence on *AtMYB4* expression. Collectively, these results delineate a regulatory module in which AtMYB4 homeostasis is governed by the coordinated and antagonistic actions of CAM7/HY5 and ARA4. This dynamic balance ensures appropriate photomorphogenic responses during early seedling establishment. Our study thus uncovers a previously uncharacterized regulatory network that integrates transcriptional activation and repression mechanisms to maintain developmental homeostasis in response to light cues, providing new insights into the molecular framework underlying seedling photomorphogenesis in plants.

Engineering Lignocellulosic Biomass in *Sorghum bicolor* through CRISPR/Cas9 Editing of *CCoAOMT* and *COMT* genes

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Abstract

Lignocellulosic biomass recalcitrance remains a major constraint for efficient bioethanol production, largely due to the presence and composition of lignin in plant cell walls. In *Sorghum bicolor*, a leading bioenergy and forage crop, caffeoyl-CoA O-methyltransferase (*CCoAOMT*) and caffeic acid O-methyltransferase (*COMT*) are key enzymes in the monolignol biosynthetic pathway that regulate lignin content and syringyl/guaiacyl (S/G) lignin composition. In this study, CRISPR/Cas9-mediated genome editing was employed to precisely modify *SbCCoAOMT* and *SbCOMT* genes with the aim of modulating lignocellulosic biomass quality. Single guide RNAs targeting coding regions were designed and introduced into Sorghum via *Agrobacterium*-mediated transformation. Molecular characterization confirmed targeted insertions and deletions, resulting in heritable loss-of-function mutations. Edited Sorghum lines exhibited a significant reduction (26-38%) in lignin deposition and an altered S/G ratio (62% increase), compared to wild-type plants, without severe penalties on plant growth and biomass yield. Moreover, edited lines showed a significant increment in cellulose and hemicellulose content, which may enhance the overall yield of bioethanol. The results demonstrate that targeted editing of *CCoAOMT* and *COMT* effectively reprograms lignin biosynthesis and improves the processability of *sorghum* biomass. This study highlights the potential of CRISPR/Cas9 genome editing as a precise and efficient strategy to engineer Sorghum with optimized lignocellulosic traits, contributing to the development of improved bioenergy crops for sustainable biorefinery applications.

Keywords: CRISPR/Cas9, *Sorghum bicolor*, Lignin, Lignocellulosic biomass, bioethanol.

MPK3 mediated phosphorylation of WRKY48 downregulates CIPK6 expression during *Pseudomonas syringae* pv. *tomato* challenge in Arabidopsis

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Abstract

WRKY transcription factor (TF) family are one of the key regulators of plant immune responses, functioning as both activators and suppressors depending on the pathogen encountered. Among these, WRKY48, a class IIC TF, functions as a negative regulator of pattern-triggered immunity (PTI) in *Arabidopsis thaliana*. Only a few negative regulators have been identified that control genes increasing plant susceptibility to pathogens. Our study explicates the regulatory mechanisms underlying the function of WRKY48, revealing its role in repressing the expression of *CIPK6*, a negative regulator of immune response in *Arabidopsis*, during *Pseudomonas syringae* DC3000 (*Pst*DC3000) infection. This suppression is mediated through MPK3-dependent phosphorylation of WRKY48. *In vitro* phosphorylation assays demonstrated that MPK3 primarily phosphorylates WRKY48 at serine residues S^{35} and S^{40}. The phosphorylated WRKY48 predominantly localizes to the nucleus, enhancing its DNA-binding affinity and trans-repressive activity at specific W-box motifs in the CIPK6 promoter. The bioinformatics analysis identified two WRKY-binding sites (P1 and P2) on the CIPK6 promoter and electrophoretic mobility shift assays confirms the preferential binding of WRKY48 to the P1 site. Unlike other WRKY TFs (WRKY28 and WRKY8) in the same subgroup, WRKY48 exhibited unique specificity, highlighting the distinct regulatory roles within the WRKY family. Functional studies demonstrated and support an epistatic model in which MPK3 acts upstream of WRKY48 to phosphorylate and activate it, thereby enhancing its ability to repress CIPK6 transcription during *Pst*DC3000 infection. In this regulatory module, MPK3 is epistatic to WRKY48 at the level of post-translational activation, while WRKY48 is epistatic to CIPK6 at the transcriptional level. This MPK3–WRKY48–CIPK6 signaling axis defines a phosphorylation-dependent transcriptional repression pathway that contributes to Arabidopsis immune responses.

Fabrication of Biosensors for Food toxins and Adulterant detection

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Abstract

For the management and prevention of many chronic and acute diseases, the rapid quantification of toxicity in food and feed products have become a significant concern. Technology advancements in the area of biosensors, bioelectronics, miniaturization techniques, and microfluidics have shown a significant impact than conventional methods which have given a boost to improve the sensing performance towards Environmental toxins detection. Efforts have been made to fabricate biosensors using various nanomaterials and transduction techniques for achieving higher detection range, limit of detection, shelf-life of the biosensor by integrating nanomaterials for various environmental toxins detection using electrical and optical transduction mechanism. The advanced developments for the sensor development at CSIR-NPL will be discussed in detail in the conference

Functional Screening of Phosphate-Solubilizing Rhizobacteria Associated with Finger Millet from Pachaimalai Region, Tamil Nadu

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Abstract

Finger Millets are climate-resilient and nutritionally superior crops; however, their productivity in arid and semi-arid regions is often constrained by low phosphorus (P) availability due to soil P fixation. In the present study, phosphate-solubilizing bacteria (PSB) were isolated and characterized from millet rhizosphere soils collected from the Pachaimalai hills region of Tiruchirappalli district, Tamil Nadu, India, with the aim of identifying efficient plant growth–promoting rhizobacteria (PGPR) for sustainable millet cultivation. Rhizosphere soil samples were processed using serial dilution and plating on Pikovskaya's agar to isolate PSB, and potent isolates were selected based on clear halo zone formation and phosphate solubilization efficiency. Selected isolates were further characterized through morphological, biochemical, and functional assays. Quantitative phosphate solubilization was evaluated under in vitro conditions, followed by comprehensive screening of PGPR traits including indole-3-acetic acid (IAA) production, siderophore secretion, hydrogen cyanide (HCN) production, exopolysaccharide (EPS) synthesis, and gibberellic acid production. Several PSB isolates exhibited significant phosphate solubilization along with multiple growth-promoting attributes, indicating their multifunctional role in enhancing nutrient availability and plant growth. The synergistic expression of P solubilization and PGPR activities suggests their potential to improve root architecture, nutrient uptake efficiency, and overall millet growth under nutrient-limited soil conditions. This study highlights the ecological significance of indigenous PSB from the Pachaimalai region and emphasizes the importance of region-specific strain selection for biofertilizer development. The identified PSB strains demonstrate strong potential as sustainable microbial inoculants to enhance phosphorus use efficiency and productivity of millets, contributing to eco-friendly and resilient agricultural practices.

Unveiling PUB E3 Ligases in Arabidopsis Pollen-Pistil Dialogue

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Abstract

Pollen-pistil interactions govern angiosperm fertility by determining successful fertilization and seed development, yet the molecular mechanisms controlling pollen-pistil compatibility remain poorly understood. Plant U-Box (PUB) E3 ubiquitin ligases have been implicated as modulators of self-incompatibility and broader reproductive processes in Brassicaceae species. In self-incompatible *Brassica*, the E3 ubiquitin ligase ARC1 (Plant U-Box ARM-Repeat-Containing protein) targets stigma compatibility factors essential for pollen germination and tube formation for proteasomal degradation. Notably, ARC1 is absent in self-compatible *Brassica* species but functionally conserved in self-incompatible *Arabidopsis lyrata,* suggesting that similar mechanisms may exist in other plant lineages. Heterologous expression of SCR, SRK, and ARC1 from *Arabidopsis lyrata* can induce self-incompatibility in otherwise self-compatible *Arabidopsis thaliana*, demonstrating functional portability of these reproductive regulators. *Arabidopsis thaliana* encodes 64 *PUB*s, with AtPUB17 identified as the closest homolog to *Brassica* ARC1. However, despite their evolutionary conservation, the specific roles of *PUB*s in self-compatible *Arabidopsis* reproduction remain unclear. Here, we comprehensively profile *PUB* gene expression across reproductive tissues (pollen and stigma), map their chromosomal distributions, and perform phylogenetic analyses to pinpoint candidate regulators of pollen–pistil interactions. Integration of expression and evolutionary data reveals *PUB* genes with distinct stigma and pollen-enriched expression patterns, nominating them for functional analysis. These *PUB* mutants were subjected to detailed phenotypic assays, including pollen tube growth dynamics and seed-set measurements under controlled pollination regimes. To evaluate functional conservation with *ARC1*, *AtPUB17* was expressed under the stigma-specific *SLR1* promoter, allowing direct evaluation of its role in pollen-pistil recognition. Our results identify a subset of pollen- and stigma-specific PUBs as key regulators of reproductive compatibility in *A. thaliana*, providing a framework to dissect ubiquitin-mediated control of fertilization in self-compatible crops.

Conserved synteny and tandem duplication events drive the expansion of intronless wound induced protein (WIP) gene family in chickpea and Medicago.

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Abstract

Wound-induced polypeptides (WIPs) are small, low–molecular weight proteins that have been linked to root nodule biology and pathogen-triggered immunity, yet their genome-wide organization and evolutionary history remain poorly understood in chickpea. Here, we performed a comparative genomics and pan-transcriptomic analysis of the WIP gene family in *Cicer arietinum*, using *Medicago truncatula* as a closely related legume reference and *Arabidopsis thaliana* as an outgroup. Hidden Markov Model–based searches of the PF12609 WIP domain, followed by domain confirmation and redundancy filtering, identified 10 intronless WIP genes in chickpea, compared with 18 in *Medicago* and 6 in *Arabidopsis*. Chromosomal mapping revealed strong clustering of WIP loci, with chickpea WIPs largely confined to two chromosomes, consistent with conserved gene organization across the three species. Collinearity and microsynteny analyses supported interspecific conservation between chickpea and *Medicago* (multiple collinear gene pairs), whereas no collinear WIP pairs were detected between chickpea and *Arabidopsis*, suggesting extensive rearrangements over deeper evolutionary time. Duplication analyses indicated that WIP family expansion in chickpea was driven predominantly by tandem duplication with limited segmental contribution, and Ka/Ks patterns were consistent with purifying selection acting on duplicated copies. Phylogenetic reconstruction, conserved motif patterns, and uniformly intronless gene structures further supported structural conservation despite diversification. Finally, transcriptome-based expression profiling across development and under *Fusarium oxysporum* challenge revealed both tissue-biased expression suggestive of partial neofunctionalization and inducible patterns consistent with conserved roles in nodulation and immune responses. Collectively, these results demonstrate that tandem duplication and conserved microsynteny have shaped WIP gene family expansion in legumes and provide a proof-of-concept for using gene-neighborhood conservation to infer orthology and functional conservation across species.

Leaf ontogeny shapes primary and secondary metabolic responses to herbivory

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Abstract

Herbivory is known to induce large shifts in plant metabolism, yet most metabolomic studies implicitly assume that these responses are comparable across leaf ages, despite long-standing evidence that leaf developmental stage fundamentally alters resource status, metabolic capacity, and defence value. Previous work on plant defence has largely inferred ontogenetic effects from trait-level measurements or pooled metabolomic datasets, leaving unresolved whether herbivore-induced changes in primary and secondary metabolism are developmentally conserved or stage specific. As a result, it remains unclear whether herbivory elicits a single metabolic response within a plant or distinct responses constrained by leaf ontogeny. To address this, we performed untargeted metabolomic profiling of young, intermediate, and mature leaves of the Fabaceae plant *Mucuna pruriens* under control and herbivory conditions, integrating multivariate discrimination, differential metabolite analysis, and pathway enrichment to resolve how herbivory-driven metabolic changes vary across leaf developmental stages.

We show that leaf ontogeny strongly structures baseline metabolism and fundamentally alters how herbivory reconfigures both primary and secondary metabolic pathways. Herbivory in young leaves predominantly affects primary metabolism, marked by shifts in sugars, organic acids, polyols, and amino acid–related pathways, indicating rapid metabolic reallocation rather than strong induction of specialised defences. Intermediate leaves exhibit the greatest metabolic responsiveness, with extensive and coordinated changes across central carbon metabolism, nitrogen metabolism, transport pathways, and multiple secondary metabolite biosynthetic routes, revealing high metabolic plasticity at this stage. In contrast, herbivory in mature leaves is characterised by pronounced repression of growth- and nitrogen-associated primary metabolites alongside selective activation of secondary metabolic pathways linked to defence, reflecting a transition toward defence-dominant metabolic regulation. Multivariate analyses revealed clear separation between control and herbivory treatments within each developmental stage, with limited overlap in herbivory-responsive metabolites across stages. Pathway-level analyses further showed that while similar metabolic pathways were involved across stages, the specific metabolites and regulatory directions differed, demonstrating ontogeny-dependent metabolic routing. Together, these results show that herbivory does not trigger a uniform metabolic response within a plant. Instead, leaf developmental stage strongly shapes how primary and secondary metabolism are reconfigured following herbivore attack. Our findings highlight leaf ontogeny as a key determinant of metabolic defence strategies and emphasise the importance of incorporating developmental context into studies of plant–herbivore interactions

Colloquium Presentations

Targeting NSm-interacting host susceptibility genes in tomato for engineering resistance to Groundnut Bud Necrosis Virus

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Abstract

Groundnut Bud Necrosis Virus (GBNV), a member of the genus Orthotospovirus, is a major constraint to tomato production in South and Southeast Asia, causing severe yield losses under field conditions. Viral movement proteins play a central role in host invasion by facilitating cell to-cell and systemic spread; however, the host factors exploited during this process remain poorly characterized.In this study, we investigated host susceptibility determinants associated with the viral movement protein NSm. The NSm protein was heterologously expressed and purified, and co-immunoprecipitation assays were performed using tomato total protein extracts to capture host interactors. Subsequent LC-MS/MS analysis identified multiple candidate host proteins potentially associated with intracellular trafficking, membrane remodeling, protein transport, and stress-responsive pathways, all of which are critical for viral transport and replication.Functional prioritization of candidate interactors was conducted using biological annotations, predicted subcellular localization, and relevance to viral movement mechanisms. Selected genes were targeted using CRISPR/Cas9-mediated genome editing to evaluate their potential role as susceptibility factors. Independent T0 edited lines have been generated and are currently undergoing molecular characterization for transgene integration and targeted mutagenesis.This integrative approach combining viral interactomics and genome editing provides a systematic framework for identifying host susceptibility genes that can be strategically disrupted to engineer durable resistance. The study highlights the potential of targeting host-assisted viral movement pathways as an alternative to conventional resistance breeding strategies, thereby contributing to the sustainable management of viral diseases in tomato. Keywords:Groundnut Bud Necrosis Virus, NSm movement protein, host-virus interaction, susceptibility genes, CRISPR/Cas9 genome editing, plant viral resistance

Analyzing the effect of the azole fungicide tebuconazole on the fungal pathogen, *Fusarium graminearum*

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Abstract

Fusarium graminearum is an ascomycete fungus causing Fusarium head blight (FHB) disease in wheat and barley. The FHB disease is controlled using chemical fungicides, particularly azole group of fungicides namely tebuconazole. However, reports suggest that *F. graminearum* is developing resistance to tebuconazole when applied to crop plants. Tebuconazole inhibits biosynthesis of ergosterol, a significant component of the fungal plasma membrane. The different mechanisms that *F. graminearum* uses to adapt itself to tebuconazole remains unknown. Therefore, it was aimed at identifying the mechanism of adaptation of *F. graminearum* to tebuconazole by allowing the fungus to grow at high concentration. Preliminary results revealed that fungal culturing in tebuconazole at high concentration (IC80) leads to its adaptation, resulting in insensitivity to tebuconazole. A transcriptome analysis led to detection of the genes involved in fungicide insensitivity. The gene ontology functional analysis showed enrichment for the terms transmembrane transport, plasma membrane, membrane and oxidoreductase activity. The KEGG pathway showed enrichment for metabolic pathways and biosynthesis of secondary metabolites. Genes related to secondary metabolites are selected for gene knockdown studies to validate their role in tebuconazole adaptation and the experiments are underway. These findings may help to develop targeted strategies to improve resistance to FHB disease.

Identifying the genetic components altered by phytoplasma infection in sesame

(*Sesamum indicum* L.)

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Abstract

Sesame (*Sesamum indicum L.*), commonly known as 'Queen of oil seeds' is an ancient oil seed crop belonging to the family Pedaliaceae. Phyllody is one of the most infectious diseases caused by the bacterium *Candidatus* Phytoplasma. Phytoplasma is an obligate plant pathogen that falls under class Mollicutes and resides in the host's phloem tissue. Since the damage rate by the disease is ranging from 60 to 100 percent, it is necessary to screen the plants for phytoplasma infection to identify the strain, group, and subgroup. Hence, we collected 275 leaf samples from IIOR, Rajendranagar, Hyderabad, in three consecutive kharif seasons from 2022 to 2024 and screened for phytoplasma infection. Genomic sequencing of two symptomatic samples from three consecutive kharif seasons, phylogenetic analysis using 16S rRNA and secA gene led to the identification the sesame phytoplasma as *Candidatus* Phytoplasma asteris that belongs to group 16Sr I and subgroup *B. Phytoplasma* releases effector molecules, which can hijack transcription mechanisms in the plants. Prelimary studies reveal that effector molecules interact with floral genes and result in their deformity, yet the mechanism remains unclear. This study focuses at identifying effector molecules using *in silico* analysis and gene expression studies, and the results are presented.

Ureolytic bacterial diversity associated with calcifying seaweeds *Jania sp.* and *Halimeda sp.*

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Abstract

Ureolytic bacteria play a pivotal role in microbially induced calcium carbonate precipitation (MICP), a sustainable and emerging technology for biocementation and eco-friendly construction applications. Urease-mediated hydrolysis of urea increases environmental pH and promotes calcium carbonate precipitation. This biomineralisation mechanism is being actively explored for applications in soil stabilisation, self-healing concrete, and sustainable infrastructure development. Natural calcifying ecosystems provide valuable ecological models for identifying efficient ureolytic microorganisms. Some marine macroalgae are characterised by calcium carbonate-rich thalli, which occupy specialised niches that may harbour ureolytic communities adapted to high-calcium microenvironments. In this study, we investigated the diversity of ureolytic bacteria associated with two calcareous macroalgae, Jania sp. And Halimeda sp., from the Gulf of Mannar, India, using 16S rRNA gene amplicon sequencing targeting the V3–V4 region. Taxonomic profiling revealed the relative abundance of bacterial phyla Bacillota, Pseudomonadota, Planctomycetota, Bacteroidota, Fusobacteriota, and Verrucomicrobiota. Upon enrichment in urea agar medium, genera such as Bacillus, Lysinibacillus, Sporosarcina, and Clostridium showed significant upregulation in both algal samples. To further validate ureolytic potential, in silico mining of the urease alpha subunit (ureC) gene from OrthoDB and NCBI databases confirmed the presence of urease genes in these genera. Ureolytic bacteria, including Bacillus sp., Priestia sp., Sporosarcina sp., and Streptomyces sp., were also isolated via culture-based assays and validated for the presence of urease genes. Additionally, the phenol-hypochlorite assay confirmed urease activity in native macroalgal samples. Collectively, these findings demonstrate that calcifying seaweeds harbour a diverse and functionally active ureolytic microbiota. Such algae-microbial consortia represent promising biological systems for advancing MICP-based biocementation and sustainable biomaterial innovations.

Bacterial endophytes from wild millets and their role in plant growth promotion

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Abstract

Millets, belonging to the Poaceae family, are among the earliest cultivated cereal crops and are nutritionally superior to major staples such as rice and wheat. Small millets are rich in proteins, dietary fiber, and essential minerals, offering health benefits including improved digestion and a low glycemic index, making them suitable for managing lifestyle-related diseases. However, millet productivity is constrained by various biotic and abiotic stresses, leading to increased reliance on agrochemicals to ensure food security for the growing population in India. Recently, plant health management strategies have shifted toward sustainable bio-based approaches, with endophytic microbes emerging as promising bio-agri-inputs. In the present study, a total of 147 endophytic bacterial isolates were obtained from seed accessions of little millet (*Panicum sumatrense* L.), foxtail millet (*Setaria italica* L.), and barnyard millet (*Echinochloa frumentacea* L.). Most isolates exhibited multiple *in vitro* plant growth-promoting (PGP) traits, including indole-3-acetic acid, ammonia, siderophore and hydrogen cyanide production, as well as solubilization of phosphate, potassium, and zinc. Based on 16S rRNA gene sequencing, the isolates were affiliated with 17 bacterial genera, including *Bacillus*, *Microbacterium, Achromobacter, Pseudomonas, Pantoea, Flavobacterium, Kasakonia, Cronobacter, Acinetobacter, Xanthomonas, Agrobacterium, Sphingomonas, Curtobacterium, Exiguobacterium, Halobacillus, Mesobacillus, Priestia*, and *Alkalihalobacillus*. *In vivo* screening demonstrated that bacterial consortia significantly enhanced plant growth compared to individual isolates. Analyses of stress-responsive genes, under biotic and abiotic stress conditions, identified two endophytic strains that strongly modulated stress-associated gene expression. The results revealed upregulation of genes related to phytohormone biosynthesis, nutrient acquisition, and stress tolerance mechanisms. Overall, this study provides a comprehensive functional and molecular characterization of millet seed endophytes and highlights the potential of selected endophytic bacterial strains and consortia as sustainable bioinoculants for improving millet growth and stress resilience.

Comprehensive genome sequence analysis provides insights into the pathogenicity of Indian *Xanthomonas oryzae* pv. *oryzae* strains

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Abstract

Xanthomonas oryzae pv. *oryzae* (*Xoo*) is a bacterial pathogen that causes bacterial blight (BB) disease in rice. Breeding efforts and resistant variety development are being hampered by evolution of highly virulent pathogen strains. While it poses a severe danger to global food security, understanding of its population dynamics and virulence evolution remains restricted. Despite being one of the world's major rice producers, India still lacks extensive comparative genomic data in this domain. To fill this gap, a complete genomic data of six hyper virulent strains (ADT, ASM, PNT-09-1-1, PUSA-1460-2, Ap-14-1 and IX-020) was generated using PacBio long read, single molecule real time (SMRT) sequencing method. The whole genome assembly revealed genome size ranging from 4.8 ~ 5.1 Mb, encoding 4094 ~ 5094 genes and average GC content of 63%. The average nucleotide identity (ANI) values between any two strain ranged from 97.1 ~ 99.9% %. All the six strains clustered tightly in terms of ANI, pan genome analysis and phylogenetic analysis while they were evolutionary distinct from other reference strains. Then, we performed genomic islands, prophage related gene analysis, secretion system, effector molecules and TALome analysis in these strains, which provided detailed comparison results of their presence and distinctive feature. Variations were observed among the presence of copy number of T2SS, T3SS and T3E. ASM and ADT showed presence of some unique gene sets and high genomic rearrangement was found in IX-020. Thus, this study not only provides complete whole genome of six highly virulent Indian *Xoo* strains but also emphasize on the differences in their genomic level through comparative genomics. Furthermore, these findings offered a theoretical foundation for investigating potential factors involved in genetic evolution and the pathogenic mechanism that causes bacterial blight disease.

Ecological and genomic insights into seaweed-associated Verrucomicrobiota from the Gulf of Mannar

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Abstract

Members of the phylum Verrucomicrobiota are increasingly recognized for their ecological versatility and capacity to degrade complex polysaccharides across diverse marine and freshwater ecosystems. In this study, we recovered eleven metagenome-assembled genomes (MAGs) affiliated with the orders Puniceicoccales and Verrucomicrobiales from seaweed-associated microbiomes in the Gulf of Mannar, India. Verrucomicrobiota constituted 0.6-2.9% of the total bacterial community across the analyzed algal samples, indicating their consistent presence but low abundance in these habitats. Five high-quality MAGs (JB022, JB024, JB025, JB027, JB023; completeness >90%, contamination <5%) were selected for detailed genomic and ecological characterization. Phylogenomic analyses revealed that these MAGs form distinct lineages within known Verrucomicrobiota families, expanding the known diversity of this phylum in marine algal ecosystems. Comparative genomic analysis showed that these genomes encode diverse biosynthetic gene clusters and a rich repertoire of carbohydrate-active enzymes (CAZymes) and sulfatases, suggesting adaptation to the degradation of sulfated polysaccharides typical of macroalgal substrates. These binned genomes also possess genes related to fermentative metabolism, nitrogen fixation, and partial denitrification, indicating metabolic versatility and potential contributions to nutrient cycling within algal holobionts. These findings reveal that seaweed-associated Verrucomicrobiota from the Gulf of Mannar represent phylogenomically distinct and functionally specialized lineages with ecological relevance in carbon and nitrogen cycling in coastal marine ecosystems. This study provides the first genomic insights into algal-associated Verrucomicrobiota from India, representing potential new taxa and underscores their potential roles in macroalgal polysaccharide degradation and holobiont functioning.

Decoding the rasāyana basis of ayurvedically important indigenous rice bran cultivars through integrated metabolomics and network-pharmacology studies

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Abstract

Rice bran derived from indigenous rice cultivars is a substantial source of phytochemicals with potential implications for gastrointestinal biology. This study evaluated rice bran from seven pigmented and two non-pigmented indigenous rice cultivars through comparative biochemical analysis, *in-vitro* bioactivity assessment, untargeted LC-MS-based metabolomics, and network pharmacology. Sequential extraction revealed a higher recovery of bioactive constituents in the acetone and methanol fractions, particularly in pigmented rice bran. The total phenolic, flavonoid, and tannin contents were consistently elevated in selected cultivars, with Karung Kavuni, Sivappu Kavuni, Njavara, Poonghar, and Palkuda Vazhai demonstrating superior phytochemical abundance compared to other samples. *In-vitro* bioactivity assessment indicated significant antioxidant and redox-modulatory potential, with DPPH and ABTS IC_{50} values in methanolic extracts reaching approximately 169–223 µg/mL and 323–375 µg/mL, respectively, for the most active cultivars. Antimicrobial screening against *Pseudomonas spp*. revealed dose-dependent inhibition, with maximum growth suppression (approximately 70–78%) observed at 400 µg/mL, notably in Poonghar, Palkuda Vazhai, Batukamma, and Kunaram Sannalu. Untargeted LC–MS analysis detected approximately 25,000 metabolic features, which were filtered to 2,676 reproducible metabolites. Multivariate analysis demonstrated clear metabolomic discrimination between pigmented and non- pigmented rice bran. Subsequent statistical prioritization identified 176 significant metabolites, from which 12 bioavailable compounds were selected based on their ADME properties. Network pharmacology analysis highlighted seven central targets (PIK3CA, SRC, EGFR, ERBB2, MET, KDR, and MTOR), with functional enrichment indicating the involvement of PI3K–Akt, ErbB signalling, focal adhesion, and metabolic regulation pathways relevant to gastrointestinal pathophysiology. Overall, this integrated analysis establishes a comparative biochemical and systems-level framework linking indigenous rice bran metabolite diversity with gastrointestinal pathway modulation, providing a rational basis for further mechanistic and translational studies.

When does *Pseudomonas paraeruginosa* become a predator? A multi-omics approach in understanding the predatory mechanism(s)

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Abstract

Bacterial predation is a fundamental yet underexplored ecological process that regulates microbial population dynamics, shapes community structure, and contributes to ecosystem stability, while offering significant potential for biotechnological and antimicrobial innovation. Although predator–prey interactions are well characterised in macroscopic systems, the diversity, ecological significance, and mechanistic basis of microbial predators remain poorly understood. Members of the genus *Pseudomonas* are widely recognised for their metabolic versatility, including xenobiotic biodegradation, environmental restoration, biosurfactant-mediated bioremediation, and the production of diverse bacteriostatic and bactericidal metabolites; however, predatory behaviour has not been previously reported for *Pseudomonas paraeruginosa*. In this study, we describe a serendipitous discovery of predatory activity in *P. paraeruginosa* JC876, isolated from the marine macroalga *Caulerpa scalpelliformis* collected from the Gulf of Mannar. Strain JC876 displayed pronounced predation against *Bacillus tequilensis*, evidenced by consistent prey clearance, providing the first indication of a predatory lifestyle in this species. Prey range analyses further revealed that strain JC876 can target multiple bacterial taxa, supporting a facultative, broad-spectrum mode of predation. Scanning electron microscopy confirmed an epibiotic predatory strategy characterised by close predator–prey association. In addition, in vitro prey enrichment followed by metagenomic analysis revealed an unexplored assemblage of epiphytic predatory bacteria associated with *Caulerpa* species, highlighting marine macroalgae as reservoirs of bacterial predators. Given the escalating global challenge posed by multidrug-resistant pathogens, the predatory capacity of strain JC876 underscores its potential application as a “living antibiotic” for biological control and microbiome modulation. Ongoing multi-omics investigations aim to elucidate the molecular determinants governing predator–prey interactions, thereby facilitating the future exploitation of *P. paraeruginosa* in sustainable antimicrobial and biotechnological applications.

Investigating the reversible induction of photosynthetic complexes in *Chlamydomonas reinhardtii* under salt stress

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Abstract

The present study is aimed at understanding the role of cyclic electron transport on the acclimation and recovery of photosynthetic apparatus in wild-type and cyclic electron transport-deficient mutants of *Chlamydomonas reinhardtii* under salt stress. Salt is a major threat today due to global warming. High salt can affect photosynthesis and yield. Plants or algae are often exposed to various abiotic stresses, particularly salt. Therefore, the Proton Gradient Regulation 5 (PGR5) and Proton Gradient Regulation Like 1 (PGRL1) mutants grown in photoautotrophic conditions showed diminished growth and reduced chlorophyll fluorescence induction and OJIP transients, indicating reduced photochemical efficiency under salt stress. Increase in carotenoid content was more prominent in *pgr5* mutants when compared to wild type, presumably due to ROS generation under salt stress. The circular dichroism data showed that salt stress caused greater changes in pigment-pigment and pigment-protein interactions in mutant cells. Despite dynamic changes in the core proteins, the LHCs and antenna proteins of PSI and PSII were only slightly affected by salt stress. Further, changes in cell morphology and thylakoid membrane organization were also observed in high salt stress. Furthermore, the recovery studies indicated that the mutant cells were not recovered to their full potential upon transferring to the normal media, as evidenced in the wild-type cells. These results indicate that the partitioning of electrons in *pgr5* could be mediated through PSI remodelling by dissociating PSI–LHCI(–LHCII) super complexes. Our results showed that cyclic electron transport is critical for the acclimation of *C. reinhardtii* to high salt stress.

Dynamic Regulation of Pectin Methyl esterification Controls Cell Wall Plasticity Under Cadmium Hormesis

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Abstract

Hormesis is characterized by a biphasic, reverse U-shaped dose–response relationship, in which sub-toxic concentrations elicit adaptive and beneficial responses, whereas higher dose is toxic. This adaptive phenomenon is highly conserved across biological systems and is largely independent of the stressor, organism, or physiological process involved. In plants, heavy metals such as cadmium (Cd) are toxic at high concentrations, severely impairing growth and development, yet low doses can induce hormetic responses. The mechanistic basis of Cd-induced hormesis remains unclear. The plant cell wall is a dynamic matrix where homogalacturonan methylesterification controls the availability of negatively charged carboxyl groups, which co-ordinate Ca^{2+} to form cross-links that strengthen the wall. This process is regulated by pectin methylesterases (PMEs), while polygalacturonases (PGs) and pectate lyases (PLs) further modulate pectin remodeling. In present study we show that at hormetic level Cd subtly reprograms the enzymatic network to enhance structural plasticity without inducing toxicity. Tomato plants were grown for 10days in Hoagland's media and exposed to low Cd (1µM) and high (50µM) concentrations for the next five days and harvested on 5th day after treatment. Tissues were harvested and collected for the assays. Tissues crushed in liquid nitrogen were used for assays like MDA, Proline estimation, RNA Isolation, Transcriptome sequencing, and qRT-PCR. Samples were lyophilised, and different extraction methods were used to isolate Alcohol Insoluble Residue (Cell wall- AIR) for FTIR, XRF, and cell wall component estimation.Tomato plants exposed to low Cd showed enhanced growth, biomass, photosynthesis, and root density, with reduced proline and MDA, indicating a beneficial rather than toxic effect. Transcriptome and qRT-PCR analyses revealed differential expression of cell wall genes. AIR-based XRF showed that Ca^{2+} levels were altered in the control and hormesis conditions. FTIR analysis indicated a change in esterified pectin but stable Ca^{2+} cross-linking at low Cd, whereas high Cd caused de-esterification and Cd^{2+}-favored binding. Hormetic Cd significantly elevates uronic acid and modestly increases galacturonic acid without altering free sugars compared to control, indicating an adaptive wall reinforcement. This modulation may release methanol, which is observed to increase at hormetic levels. The results suggest that low-dose Cd induces controlled pectin remodeling and moderate Ca^{2+} reinforcement, promoting structural plasticity and growth. At higher doses, excessive metal accumulation shifts this balance toward rigidity and toxicity. Understanding these structural and molecular mechanisms may provide strategies to enhance crop resilience under adverse environmental conditions.

Manipulating folate degradation appears to be a promising approach to enhance folate levels in tomato fruits

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Abstract

Folate deficiency remains a major global health concern, particularly in populations dependent on staple cereals such as wheat, maize, and rice, which contain insufficient folate to meet the recommended daily allowance of 400 µg/day. While most biofortification strategies have focused on enhancing folate biosynthesis, our work highlights the complementary role of reducing folate degradation. Screening of natural accessions and mutant populations in our lab identified tomato lines with elevated fruit folate content, associated with reduced activity of folate-degrading enzymes. Molecular analyses revealed that reduction of gamma-glutamyl hydrolase activity is a key determinant of folate accumulation. To functionally validate this mechanism, we employed CRISPR/Cas9-mediated editing of gamma-glutamyl hydrolases in tomato. Characterization of the edited lines confirms that limiting degradation can enhance folate content. Our findings suggest that regulating folate degradation may be a viable strategy to enhance folate levels in tomato fruits.

Poster Abstracts

The Mitochondrial Tetrapyrrole Biosynthetic Pathway Regulates Gametophyte Development in *Arabidopsis thaliana*

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Abstract

In plants, the tetrapyrrole biosynthetic pathway begins with Glu via 5-aminolevulinate and is further modified by enzymes like uroporphyrinogen III decarboxylase, coproporphyrinogen III oxidase (CPO), and protoporphyrinogen IX oxidase (PPO) to porphyrin (Dailey, 1990; Grimm, 1998) in the cytoplasm. This enters the chloroplast and is converted to chlorophyll by Mg chelatase; if it enters the mitochondria, it is converted to heme by Fe chelatase. In animals, the tetrapyrrole biosynthesis pathway produces heme in mitochondria (Yin and Bauer, 2013), whereas reports on heme synthesis in plants are lacking. Researchers (Prathibha et al., 2017; Lermontova et al., 1997; Watanabe et al., 2001) demonstrated the existence of the mitochondrial tetrapyrrole biosynthesis pathway by analysing CPO and PPO mutants that caused seed sterility in Arabidopsis, tobacco, and spinach. This research aims to establish this pathway in Arabidopsis, by focusing on the uroporphyrinogen III decarboxylase (*UROD*) gene, which catalyses the first step of the pathway: the conversion of Uroporphyrinogen III to Coproporphyrinogen III. We are investigating the *UROD* gene (At3g14930) mutant in detail to assess its role in the mitochondrial tetrapyrrole biosynthetic pathway-mediated reproductive development. The *urod* mutant plant showed defects in gametophyte development, including nonviable pollen and unfused polar nuclei in the embryo sac, and subsequent seed development. Further, an attempt was made to identify possible interactions among pathway genes by generating and characterising double mutants of *urod* and *cpo.* This study highlights the mitochondrial tetrapyrrole biosynthesis pathway in gametophyte and seed development and sheds new light on tetrapyrrole/heme biosynthesis in plant mitochondria.

Key words: Uroporphyrinogen III decarboxylase , coproporphyrinogen III oxidase, female gametophyte, T-DNA insertion , Mitochondrial localisation

Taxonomic and functional diversity of seaweed-associated microbiomes in the Gulf of Mannar

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Abstract

Seaweeds in the Gulf of Mannar support a wide variety of distinct and complex microbial communities. By supporting functions like nutrition uptake, pathogen defense, and the synthesis of bioactive substances, these microbiomes are essential to the health and functionality of their hosts. Gaining knowledge about these organism's microbiomes can help one better understand the ecological connections in the Gulf of Mannar. With shotgun metagenomics, we may identify the functional roles of microorganisms in seaweed ecosystem in addition to cataloguing their diversity. Shotgun metagenomics was employed to analyze the microbiome associated with fifteen different marine seaweed samples. The reads analyzed suggested the presence of numerous taxa with varying abundance levels. For example, at Phylum-level, the abundance of reads belonging to *Bacteroidota*, *Planctomycetota*, *Spirochaetota* and *Verrucomicrobiota* were higher in the seaweed samples when compared to other phyla. This indicates that there might be some specific associations between these bacterial taxa and the seaweeds. The beta diversity indicates that each seaweed sample has a unique microbiome in terms of their composition and abundance. The metagenome is highly enriched in a number of CAZymes, suggesting a major role of the microbiome in complex carbon cycling. Apart from this, assembly and binning of these metagenomic reads yielded in about over hundreds of metagenome-assembled genomes (MAGs). Of these many MAGs represent novel taxa at species-level or higher. There were MAGs representing over twenty different phyla including the understudied phyla like *Gemmatimonadota*, *Chlamydiota*, *Fusobacteriota*, *Myxococcota*, *Spirochaetota*, *Planctomycetota* and *Verrucomicrobiota*. This study highlights the importance of studying these seaweed-associated microbiomes as they harbor a plethora of these understudied microorganisms.

Exploring Selective Endophytic Bacteria for Drought Stress Mitigation and Uranium Phytoremediation in Non-Host Plant Systems

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Abstract

The increasing global food demand, coupled with rapid urbanization and agricultural challenges, necessitates sustainable strategies to enhance crop productivity and environmental resilience. Beneficial endophytic bacteria offer a cost-effective approach to improve plant stress tolerance and facilitate phytoremediation. This study aimed to isolate, characterize, and evaluate selective endophytic bacteria from uranium-contaminated sites for their potential to confer drought tolerance and enhance uranium phytoremediation in non-host crop plants. Endophytic bacteria were isolated from *Prosopis juliflora* (Sw.) DC., *Ziziphus mauritiana*, and *Vitex negundo* L. growing in uranium mining areas. Isolates were screened for extracellular enzymatic activities (cellulase, amylase, pectinase, lipase), nitrogen fixation, ammonia production, phosphate solubilization, indole-3-acetic acid (IAA) production, and ACC deaminase activity. Among the isolates, PJ4 (*Bacillus amyloliquefaciens* M69), PJ6 (*Stenotrophomonas maltophilia* SaY2-b), and PJ12 (*Pseudomonas* sp. SG-08) exhibited superior enzymatic and plant growth-promoting (PGP) traits. Multivariate analyses (PCA and cluster analysis) confirmed these as the most potent endophytes. The selected isolates demonstrated osmotic stress tolerance up to 20% PEG 6000 and resistance to heavy metals AlCl, CoCl, FeCl, HgCl. Significant antifungal activity was observed against major phytopathogens. GUS labeling confirmed successful colonization of non-host crops (rice and peanut) in roots, stems, and leaves. Greenhouse experiments revealed that inoculation with individual strains and their consortium significantly enhanced growth, physiological, and biochemical traits under both irrigated and drought conditions. Consortium-inoculated plants showed superior performance, positively correlated with enhanced root architecture, proline accumulation, soluble sugars, and photosynthetic pigments. Phytoremediation studies demonstrated improved biomass and uranium accumulation in inoculated plants. Notably, *P. juliflora* exhibited higher root uranium accumulation (64 mg kg^{-1}, with a high root bioconcentration factor (BCF >1), low shoot BCF (<1), and translocation factor (TF <1), indicating strong phytostabilization potential. Overall, this study highlights the potential of selective endophytic bacteria, particularly consortium formulations, as sustainable bioinoculants for drought mitigation and microbe-assisted phytostabilization of uranium in non-host crops.

Saliva-Mediated Host Adaptation of Fall Armyworm: Implications for Pest Management in India

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Abstract

The fall armyworm (Spodoptera frugiperda J.E. Smith) is a highly destructive invasive pest that has rapidly spread across maize-growing regions of India, posing a serious threat to food and nutritional security. Its invasion success is attributed to its broad host range, high dispersal ability, and capacity to overcome host plant defenses. Among the key factors facilitating this adaptation is insect saliva, which contains a complex mixture of proteins that mediate plant–insect interactions. This study aims to elucidate the role of saliva-mediated host adaptation in fall armyworm under Indian agro-ecological conditions, with particular emphasis on maize-based cropping systems and associated tritrophic interactions.

Research Methodology: The study is based on insights derived from quantitative proteomic investigations of fall armyworm saliva. It examines the functional roles of salivary proteins involved in digestion, detoxification, immune defense, and modulation of host plant defense signaling. Special attention is given to biochemical interactions influencing jasmonic acid–dependent defense pathways and oxidative stress responses in host plants. Comparative analysis of salivary protein plasticity across different host plants, including maize, sorghum, and millets, is considered. The study also evaluates how salivary components affect herbivore-induced plant volatiles that regulate tritrophic interactions involving natural enemies.

Results and Conclusion: The study highlights that fall armyworm saliva contains diverse proteins such as glucose oxidase, peroxidases, heat shock proteins, detoxification enzymes, and immune-related proteins that play a crucial role in modulating host plant defense responses. These salivary proteins can suppress or fine-tune plant defense signaling, thereby enhancing larval feeding efficiency and survival. The salivary proteome exhibits notable plasticity in response to different host plants, enabling rapid adaptation to a wide range of crops cultivated in India. Furthermore, salivary components influence tritrophic interactions by modifying herbivore-induced plant volatile emissions, potentially reducing the effectiveness of natural biological control agents. The study concludes that understanding saliva-mediated molecular and biochemical mechanisms is essential for developing sustainable and ecologically sound pest management strategies. Such insights can aid in identifying novel targets for host plant resistance, improving biological control efficacy, and strengthening integrated pest management programs tailored to Indian agricultural systems.

Engineering pH-Responsive trans-Ferulic Acid/κ-Carrageenan Microbeads for Biodegradable and Sustainable Micronutrient Delivery in Agriculture

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Abstract

Micronutrient deficiencies in soils are a critical challenge in agriculture, particularly in acidic soil environments where nutrient availability is strongly limited by fixation, leaching, and altered metal speciation. These constraints contribute to inefficient nutrient uptake and reduced crop yields. Conventional micronutrient supplementation methods are often inefficient, environmentally harmful, and unsustainable, underscoring the need for smarter delivery systems tailored to soil pH conditions. In this study, we developed biodegradable, pH-responsive microbeads from κ-carrageenan (κ-CG) and trans-ferulic acid (TFA) for targeted micronutrient release. The κ-CG–TFA microbeads were synthesized via an eco-friendly process and optimized for size, morphology, stability, and nutrient retention. Characterization confirmed the successful incorporation of functional groups, while swelling, degradation, and release studies demonstrated efficient delivery of essential micronutrients (Mn^{2+}, Zn^{2+}, Cu^{2+}, and Fe^{3+}) under acidic conditions (pH 4.0), mimicking acidic soil environments. The inherent antioxidant activity of TFA conferred strong radical-scavenging capacity, further enhancing its functionality. Soil water and plant growth assays revealed that the microbeads improved micronutrient availability, significantly increased chlorophyll content and leaf area, promoted vigorous seedling growth, and caused no phytotoxic effects. Collectively, these findings establish κ-CG–TFA microbeads as a promising, eco-friendly platform for sustainable micronutrient delivery and stress reduction, thereby improving crop productivity in agriculture.

Salt-Tolerant Endophytic Fungi from *Conocarpus erectus* and *Excoecaria agallocha*: Biodiversity and Screening for Industrial Enzymes and Plant Growth-Promoting Traits

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Abstract

Endophytic fungi inhabiting halotolerant plants represent a promising source of bioactive metabolites and industrially relevant enzymes adapted to saline stress. In the present study, endophytic fungi were isolated from the roots, stems, and leaves of two halotolerant plants, *Conocarpus erectus* L. growing in alkaline soils and *Excoecaria agallocha* L., growing in brackish water. Following surface sterilization, samples were macerated, serially diluted, and plated on Potato Dextrose Agar. Pure cultures were obtained through repeated sub-culturing based on distinct colony morphology. Salt tolerance of the isolates was screened using NaCl concentrations ranging from 1 M to 3 M. Genomic DNA was extracted using the CTAB method, and the Internal Transcribed Spacer (ITS) regions were amplified with ITS1 and ITS4 primers. Purified PCR products were subjected to Sanger sequencing. Bioinformatics analysis using the NCBI BLAST tool identified isolates from *E. agallocha* as *Rhizopus arrhizus* EL21, *Aspergillus tubingensis* ER51, *Aspergillus aflatoxiformis* ES52, and *Aspergillus quadrilineatus* (ES72, ES31). Isolates from *C. erectus* included *Aspergillus fasciculatus* (CR-3), *Aspergillus alabamensis* (CR-4), *Aspergillus fumigatus* (CR-5), *Aspergillus aflatoxiformans* (CR-6), and *Aspergillus oryzae* (CR-7). Hydrolytic enzyme profiling revealed strong strain-specific variability. High amylase activity was observed in *A. tubingensis* ER51 and isolate CR2, while *A. quadrilineatus* ES71 and *A. aflatoxiformans* CR6 showed minimal activity. *A. tubingensis* ER51 and *A. alabamensis* CR4 exhibited maximum cellulase activity, whereas *R. arrhizus* EL21 and isolate CR1 were the least active. Lipase production was highest in *R. arrhizus* EL21 and *A. oryzae* CR7, protease in *A. quadrilineatus* ES71 and *A. fumigatus* CR5, pectinase in *A. quadrilineatus* ES72 and isolate CR1, and chitinase in *A. quadrilineatus* ES72 and *A. fasciculatus* CR3. Oxidoreductase screening demonstrated elevated laccase activity in *A. quadrilineatus* ES72, *A. fumigatus* CR5, and isolate CR2, and higher lignin peroxidase activity in isolate ER52 and *A. oryzae* CR8. Siderophore production, a key plant growth-promoting trait, was highest in *R. arrhizus* EL21 and isolate CR2. These findings highlight halotolerant endophytic fungi as a potential resource for mitigating salinity stress in crop plants and for producing plant growth-promoting metabolites with significant biotechnological relevance under salt stress conditions.

Anticancer Potential of Rice Bran Metabolites: An In-Silico Network Pharmacology And Molecular Docking Approaches.

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Abstract

Rice bran derived from indigenous rice cultivars constitutes a substantial source of bioactive phytochemicals, including phenolic acids, flavonoids, sterols, and phytic acid, many of which have been linked to chemo-preventive effects. This study sought to systematically explore the anticancer potential of rice bran metabolites through an integrated in-silico approach, incorporating pharmacokinetic screening, target prediction, network pharmacology, and molecular docking. A comprehensive array of reported rice bran metabolites, such as ferulic acid, gallic acid, p-coumaric acid, phytic acid, γ- oryzanol constituents, and tocotrienols, was compiled from literature and metabolite databases. Drug-likeness and gastrointestinal absorption were assessed using Swiss ADME to identify bioactive candidates with favourable pharmacokinetic properties. Putative protein targets of selected compounds were predicted using Swiss Target Prediction, while cancer-associated genes were retrieved from GeneCards and related disease databases. Overlapping targets were utilized to construct compound-target and protein-protein interaction networks in Cytoscape. Functional enrichment analyses indicated that the predicted targets are primarily involved in key cancer-related pathways, including PI3K-Akt signalling, MAPK signalling, apoptosis regulation, and cell cycle control. Several hub genes commonly implicated in tumour progression, such as AKT1, TP53, EGFR, and CASP3, were identified as central nodes within the network. Molecular docking analysis demonstrated favourable binding interactions of selected metabolites with the active sites of these oncogenic proteins, suggesting potential multi-target modulation. Overall, this system-level investigation underscores the potential of rice bran metabolites as pleiotropic agents capable of modulating multiple cancer-associated pathways, supporting their promise as candidates for chemoprevention and therapeutic development. The findings provide a computational rationale for future experimental validation and functional studies.

Metabolic characterization of the pharmacological important plant *Cryptostegia grandiflora*: A potential key source for treatment of Alzheimer's disease

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Abstract

Cryptostegia species is known for its analgesic, antibacterial, anti-inflammatory, antioxidant, antiproliferative, antitumor, and antiviral properties. Our phytochemical analysis revealed substantial quantities of polyphenols, flavonoids, alkaloids, and anti-oxidant activity in *Cryptostegia grandiflora.* Total phenolic content (TPC) was highest in flower (206.60 ± 5.01mg GAE/g DW) and lowest in leaf (63.52 ±3.91 mg GAE/g DW). Like wise TPC, total flavenoid content (TFC) was highest in flower (40.56 ± 1.03 mg QE/g DW) but lowest in seed (16.34 ± 0.47 mg QE/g DW). Total antioxidant activity (TAA) was highest in the flower (245.04 ± 7.40 mg AAE/g DW) and lowest in leaf (109.85 ± 5.39 mg AAE/g DW). Free radical scavenging properties were evaluated using DPPH, ABTS, and reducing power determine by FRAP assays. The DPPH assay revealed strong scavenging ability in flower (i.e., 91.88 ± 1.56 %), and less in leaf (55.37±6.16 %). Likewise, ABTS assay of flower and seed showed 97.19 ± 1.48 % and 99.42 ± 0.30 % of inhibition when compared with leaf (64.87 ± 3.44% inhibition). Similarly, reducing power was more in flower (176.81±6.50 mg AAE/g dw) as compared to seed (157.09±5.84 mg AAE/g dw) and leaf (75.12±4.37mg AAE/g dw). The presence of phenolic, flavonoid, and alkaloid compounds in the methanolic extract was also complemented by a spectrum read using a UV-Vis spectrophotometer. FTIR analysis identified key functional groups, including alcohols, esters, carboxylic acids, and amines. Presently we are examining the metabolic composition of *Cryptostegia grandiflora* leaf through GC/MS, in which we identified around 179 compounds among which some are alkaloids and several amines and antioxidants, which showed significant binding with BACE1 protein. Further analysis of metabolic pathway and in-vivo pharmacological studies will add in-depth medicinal properties of *Cryptostegia grandiflora.*

Similarities and differences for iron uptake, transport, and storage pathways in major crops: a comparative genomics approach

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Abstract

Hidden hunger resulting from deficiency of vital nutrients in the diet affects more than two billion people worldwide. Increasing iron in food crops can provide a solution to the global iron deficiency problem.

Iron homeostasis is tightly regulated in plants. Iron is present in large quantities in the soil but is scarce in aerobic/alkaline soils. Plants have developed two mechanisms to absorb iron: Strategy I, which is based on reduction, and Strategy II, which is based on chelation. Rice has a combination of both mechanisms, but Arabidopsis follows Strategy I. However, little information is available on iron-rich crops such as sorghum, millet, soybean, and chickpea. The present study focuses on the conservation of iron uptake components in different plant species to understand the mechanisms of enhanced iron uptake. List of the genes that regulate iron uptake, translocation, and storage has been compiled. The crops selected for the study were determined by the iron content of the seeds and the accessibility of their complete genomic sequence. And the genomes/protein sequence data are downloaded from Phytozome. Comparative genomics analysis was carried out using OrthoFinder to group genes into orthogroups and identify conserved candidate genes associated with iron homeostasis across the selected genomes.

Orthogroups were used to determine whether pathway genes are present or absent. Gene expression studies were used to confirm the functionality of the candidates from the iron homeostasis pathway.Comparative genomic analysis revealed that all dicots retain conserved regulatory and downstream components of the Strategy I iron uptake pathway, while all monocots conserve those of Strategy II. This highlights the tightly regulated and conserved nature of iron uptake within the major crops of respective classes. However, further examination of the conservation of Strategy I and II components across those classes (monocots and dicots, respectively) showed partial overlap, indicating overlap between the two mechanisms, suggesting that iron uptake strategies are not strictly distinct, and such redundancy possibly helps the plants to adapt to diverse environmental conditions.

Taxonomic and genomic insights of few novel *Spirochaetales* members from Gulf of Mannar

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Abstract

Marine environment contains one of the largest and most divided microbiomes on the planet. It contains multiple specialized bacterial communities linked to distinct algae species, which are essential to the biogeochemical cycle. Advancements in sequencing technology and computational methodologies have enabled significant discoveries of previously unexplored members of marine algal-associated microbial diversity, including the, members of *Spirochaetales*, which are comparatively underreported in India. Shotgun metagenomic sequencing of few marine algal samples and enriched samples from the Gulf of Mannar, India, indicates that 1-2% of the total bacterial diversity comprises members of *Spirochaetales*. Nine Metagenome-assembled genomes (MAGs) from the *Sphaerochaetaceae* family and one MAG from the *Spirochaetaceae* family were obtained. The functional genomic investigation of the MAGs has shown signs indicative of phenotypic adaptations that facilitates their survival in algal-associated settings, such as the existence of carbohydrate-active enzymes, including galactosidase, fucosidase, and amylase, among members of the *Sphaerochaetaceae* family. The Biosynthetic gene clusters (BGCs) and antimicrobial resistance (AMR) genes confer a competitive advantage to these microorganisms by enabling them to evade detrimental circumstances in the ocean while cohabiting or flourishing with the marine algae. The phylogenomic analysis, OGRI values, comparative genomics and metabolic pathway analysis have demonstrated that MAGs are novel taxa within the order *Spirochaetales*. This resulted in the identification of new genus, which we propose as "*Candidatus* Marisalgaesphaerochaeta sargassi" gen. nov. sp. nov. The IMNGS data additionally indicated the occurrence of these members in various ecosystems. The identification of an increased number of non-spiral lineages has enhanced our comprehension of the evolutionary and functional intricacies of this order particularly association with the marine algae. These investigations suggest valuable insights into the ecology of these bacteria and their potential role in marine ecosystems, particularly in association with the algae.

Phytochemicals and Diabetes: Linking Plant Development to Therapy.

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Abstract

Diabetes mellitus is a chronic metabolic disorder characterized by impaired glucose regulation and associated complications. While conventional pharmacological interventions remain central to treatment, medicinal plants offer promising complementary strategies due to their diverse bioactive compounds and minimal side effects. Traditional systems of medicine have long utilized plants such as *Gymnema sylvestre* (gurmar), *Momordica charantia* (bitter melon), *Trigonella foenum-graecum* (fenugreek), and *Azadirachta indica* (neem) for glycemic control. Modern research validates their efficacy, demonstrating mechanisms including stimulation of insulin secretion, enhancement of glucose uptake, inhibition of intestinal glucose absorption, and reduction of oxidative stress. The developmental biology of these plants is closely tied to their therapeutic potential. Environmental factors such as soil nutrients, water availability, and climatic conditions influence the biosynthesis of phytochemicals like saponins, alkaloids, and flavonoids. For example, bitter melon fruits accumulate charantin and polypeptide-P under specific growth conditions, while fenugreek seeds produce 4 hydroxyisoleucine, a compound that improves insulin sensitivity. Understanding how developmental pathways intersect with environmental modulation is critical for optimizing phytochemical yield and therapeutic potency. Advances in molecular biology and bioinformatics have enabled the identification of gene clusters and metabolic pathways responsible for antidiabetic compounds. Integrative approaches combining transcriptomics, metabolomics, and environmental modeling reveal that stress conditions such as drought or nutrient limitation can enhance secondary metabolite production. This knowledge strengthens the scientific basis for plant-derived therapies and highlights the importance of sustainable cultivation practices. Medicinal plants represent a vital bridge between traditional knowledge and modern science. By elucidating the interplay between plant development, environmental cues, and phytochemical biosynthesis, this research underscores the translational potential of plant-based therapies in diabetes management. Such insights pave the way for accessible, sustainable, and effective interventions against metabolic disorders.

BHRIGU connects meiotic germline programming with paternal control of seed growth

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Abstract

The alternation of generations in flowering plants depends on precise coordination between meiosis, gametophyte development, and epigenetic regulation. While RNA-directed epigenetic mechanisms are known to regulate paternal genomic imprinting and endosperm development, how epigenetic states are established during meiosis and transmitted through the male germline remains unclear. This study aims to identify meiotic regulators that connect sporophytic epigenetic programming with paternal control of seed development. Loss-of-function mutants of *BHRIGU (BHR)* were characterized using cytological analyses of meiosis and post-meiotic pollen development. Gene expression patterns were examined to determine the temporal and spatial activity of *BHR*. Genetic crosses were performed to assess parent-of-origin effects on seed development and to evaluate interactions with known regulators of paternal imprinting. Seed size, ploidy status, and transmission patterns were quantitatively analyzed. Loss of *BHR* function results in complete male sterility due to post-meiotic microspore degeneration, despite normal meiotic progression and tetrad formation, indicating an essential role in the sporophyte-to-gametophyte transition. *BHR* expression is enriched in meiocytes, supporting a direct meiotic function. Notably, seeds derived from the limited functional pollen of *bhr* mutants are significantly larger than wild-type seeds. This large-seed phenotype is strictly paternally transmitted and independent of ploidy changes, resembling paternal genome excess in the endosperm. Genetic interaction analyses demonstrate that mutation of the paternally expressed genes *ADM2* and *PEG2* fully suppresses the seed size phenotype of *bhr*, linking BHR function to paternal imprinting pathways. Together, these findings identify *BHR* as a key meiotic regulator that establishes epigenetic states in the male germline required for balanced paternal contribution to seed development, revealing a previously unrecognized connection between meiotic epigenetic regulation and seed size determination.

Early stage expression of Cyclin-dependent kinase A (CDKA) Controls Symbiotic Cell Proliferation and Nodule Organogenesis in *Arachis hypogaea*

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Abstract

Plant growth and development, organ formation, and generational inheritance depend on cell division and the cell cycle, which are fundamental biological processes. In root nodule symbiosis, the initiation of nodule development begins with the reactivation and division of cortical cells; however, the mechanisms governing the cell cycle genes behind this process are not well understood. Our study investigated the role of Cyclin-Dependent Kinase A in the early stage of root nodule symbiosis in groundnut (*Arachis hypogaea*). The cell cycle inhibitor roscovitine showed a significant reduction in nodule primordia, mature nodules and restricted nodule enlargement, conveyed by downregulation of DNA synthesis genes, which decreased bacterial colonisation. Functional characterisation through CDKA knockdown and overexpression further confirmed its critical role in maintaining proper nodule number and nodule size by regulating DNA replication and bacterial colonisation. Tissue-specific expression analysis revealed high CDKA activity in early nodule primordia, root tips, and lateral roots, while its expression declined in mature nodules. Furthermore, genetic analysis demonstrated that CDKA acts downstream of NIN and NF-YC complex. Overall, we establish CDKA as a key regulator of nodule initiation and development, providing new insights into the cell cycle–mediated control of symbiotic organogenesis in groundnut. This work lays a strong foundation for elucidating the signaling network at an early stage during root nodule formation and symbiotic efficiency.

Exogenous application dsRNA based antiviral therapy demonstrates improved immunity of papaya crop against viral infections

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Abstract

Papaya (*Carica papaya* L) of the family Caricaceae and is one of the most economically important fruit crops. It has enormous commercial importance because of its highly nutritive and medicinal value. Multiple pests are known to be the carrier of viruses and causes diseases to papaya, hence viral diseases are the most damaging to the plant. Of all the viral diseases, Papaya ring spot virus (PRSV) and Papaya Leaf Curl Virus (PaLCuV) are most important and devastating ones. Over the time, the incessant use of chemical pesticides leads to resistance in pest and further increase in dose that lead to more load to the environment. Hence, there is a need for alternative approaches that avoid the use of transgenes and resort immune response for plant protection. RNA interference (RNAi) has emerged as a powerful and sequence-specific antiviral defence mechanism in plants, offering a promising strategy to enhance papaya immunity against these viruses. They target conserved regions that acts as hotspots that have enough capacity to produce potential siRNA candidates that can confer a broad range of resistance across different viruses. RNAi operates through the generation of virus-derived double-stranded RNA, which is processed into small interfering RNAs (siRNAs) that guide the degradation or translational repression of viral RNA. In papaya, RNAi-based approaches targeting conserved viral genes such as coat protein, replication-associated protein, and suppressors of gene silencing have shown effective resistance against both DNA viruses like PaLCuV and RNA viruses such as PRSV. The strategy where direct or topical application of exogenous dsRNA molecules that have the potential to trigger RNAi. This would be a non-transgenic approach where *in vitro* produced dsRNA molecules derived from viruses is applied topically to the plant. By the topically applying dsRNA it can act as a type of vaccine, with the capacity of conferring protection against future viruses. In this study aims to propose a strategy that aims to demonstrate that the exogenous delivery of dsRNA through topical application has the potential to confer resistance against PaLCuV and PRSV. Designing/Synthesis and in vitro preparation/production dsRNA from specific regions of PRSV. Testing the efficacy of in vitro produced dsRNA molecules targeting genes of PRSV and PLCV by topical application on papaya plants. This would be a non-transgenic approach where *in vitro* produced dsRNA molecules derived from viruses is applied topically to the plant. By the topically applying dsRNA it can act as a type of vaccine, with the capacity of conferring protection against future viruses.

Identification and characterization of anthocyanin biosynthetic pathway genes in foxtail millet (*Setaria italica* L.)

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Abstract

Anthocyanins are bioactive flavonoid pigments that contribute to antioxidant activity and nutritional quality of cereal grains. Foxtail millet (*Setaria italica* L.), a climate-resilient and nutrient-rich crop suited to cultivation under suboptimal conditions, is increasingly recognized as a functional food; however, the genomic basis of anthocyanin biosynthesis in this species remains poorly understood. In this study, a genome-wide identification and comprehensive *in silico* characterization of anthocyanin biosynthetic pathway genes were performed in foxtail millet. A total of 111 genes representing all major enzymatic steps of the anthocyanin biosynthetic pathway were identified across 11 gene families. The identified genes were systematically characterized for conserved motifs, gene structure, predicted subcellular localization, and protein physicochemical properties. Promoter analysis revealed enrichment of cis-regulatory elements associated with light responsiveness, hormone signaling, and stress-related regulation, suggesting coordinated transcriptional control of anthocyanin biosynthesis. Comparative phylogenetic analysis demonstrated strong evolutionary conservation of these genes across plant species, along with lineage-specific diversification in foxtail millet. Furthermore, biochemical estimation of grain anthocyanin content in dark-coloured foxtail millet accessions supported the functional relevance of the identified biosynthetic framework, particularly for late-pathway genes. Overall, this study provides a genomic foundation for understanding anthocyanin metabolism in foxtail millet and identifies candidate genes for nutritional improvement and stress-adaptive breeding.

Biocompatible Glutathione-Coated CdS/ZnS Core–Shell Quantum Dots for Fluorescent Imaging and Targeted Sorting of Cancer Cells.

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Abstract

The purpose of this study was to develop and characterize glutathione (GSH)-coated CdS/ZnS core–shell quantum dots (QDs) with enhanced biocompatibility, stability, and fluorescence efficiency for application in cellular imaging and targeted cancer cell identification. The study aimed to reduce cytotoxicity associated with cadmium-based quantum dots while improving their potential use in bioimaging and flow cytometric sorting of circulating tumor cells (CTCs). CdS/ZnS core–shell quantum dots were synthesized using a one-pot high-temperature method. Surface modification was carried out through ligand exchange with DL-cysteine to render the nanoparticles water-soluble. Further functionalization was achieved using EDC/NHS-mediated conjugation of glutathione to enhance stability and biocompatibility. Characterization techniques included Transmission Electron Microscopy (TEM), X-Ray Diffraction (XRD), Dynamic Light Scattering (DLS), UV-Visible Spectroscopy, Fluorescence Spectroscopy, and Fourier Transform Infrared Spectroscopy (FTIR). Cytotoxicity was evaluated using the MTT assay on MCF-7 and HeLa cell lines. Cellular uptake was assessed through confocal laser scanning microscopy. Targeted labeling and sorting were performed using EpCAM antibody conjugation followed by flow cytometry analysis. The synthesized GSH-coated CdS/ZnS quantum dots exhibited a hydrodynamic diameter of approximately 20 nm and strong blue fluorescence emission at 455 nm with a quantum yield of 39%. FTIR analysis confirmed successful surface functionalization. MTT assay results demonstrated high cell viability (>90%) at concentrations up to 10 μg/mL, indicating minimal cytotoxicity. Confocal microscopy confirmed efficient cellular uptake in MCF-7 and HeLa cells. EpCAM-conjugated QDs enabled specific targeting and successful flow cytometric sorting of circulating tumor cells. In conclusion, the developed GSH-coated quantum dots represent a stable, low-toxicity, and efficient alternative to conventional fluorophores for cellular imaging, molecular targeting, and cancer cell detection applications

Chlorpyrifos-Induced Changes in Growth and Photosynthetic Pigments of Eggplant (*Solanum melongena* L.) Seedlings

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Abstract

Vegetables are a crucial component of the human diet, providing essential minerals and vitamins that promote overall health and well-being. They play a vital role in preventing chronic diseases and maintaining optimal health. Eggplant (*Solanum melongena* L.), native to India, is widely cultivated across Asia. India ranks second globally in eggplant production, with 0.66 million hectares under cultivation and an annual production of 12.4 million tonnes. However, eggplant crops are highly susceptible to pests, prompting farmers to rely heavily on chemical pesticides. This excessive use of pesticides can adversely affect plant growth, leading to reduced crop productivity. Moreover, the overuse of pesticides can also contaminate soil, water, and air, posing a threat to human health and the environment. To investigate this issue, a study examined the impact of varying doses (0-1.5 mM) of Chlorpyrifos on *Solanum melongena* L. seedlings. Chlorpyrifos is a widely used organophosphate insecticide, and its effects on plant growth and development are not well understood. The study monitored root and shoot length, fresh and dry mass, and photosynthetic pigments (Chlorophyll *a*, Chlorophyll *b*, and carotenoids). Results showed a significant decline in growth with increasing Chlorpyrifos doses. The seedlings exposed to higher concentrations of Chlorpyrifos exhibited reduced root and shoot length, and decreased fresh and dry mass. Photosynthetic pigment content followed a similar pattern, with Chlorophyll *b* being the most affected. The decrease in photosynthetic pigments can lead to reduced photosynthesis, ultimately affecting plant growth and productivity.

Keywords: Chlorpyrifos; Fresh and dry mass; Photosynthetic pigment; *Solanum melongena* L.

Ethylene response factor (ERF.D7) enhances tomato seedlings' growth and morpho-physiological traits under drought and salinity stress

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Abstract

Recent climate change has led to various abiotic stresses, including drought and salt stress. Early response of both stresses has been considered primarily identical and could cause physiological water scarcity in plants. One of the most widely cultivated vegetable crops is tomato (*Solanum lycopersicum* L), which requires high water throughout its growing season. To improve the stress tolerance capacity, we target a gene called Ethylene response factor (ERF.D7). Our result indicating that CRISPR-Cas9 mediated editing of *slerf.d7* gene plays a positive role under abiotic stress conditions in tomato. As the *slerf.d7^{CR}* mutant showed better growth, lower MDA and ROS than WT. Subsequent transcripts analysis of *SlERF.D7* gene revealed its downregulation under salt and drought. Surprisingly, the results showed that the mutant seedlings perform better under stress, as they accumulate less MG and achieve higher biomass. At the same time under non-stress conditions, mutant lines showed higher photosynthetic activity compared to WT. While the details molecular understanding of *slerf.d7^{CR}* mutant under stress lines remains unknown but our morphological and physiological result indicating that *slerf.d7^{CR}* gene could be a potent candidate gene for better stress management and crop production, especially for horticultural species.

Identification and functional validation of the component proteins of two-component high affinity nitrate transport system of wheat

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Abstract

Nitrate is one of the predominant sources of nitrogen for crops grown in aerobic soil; however, its distribution and concentration in the soil fluctuate with time and space, and it is often limited to the crop rhizosphere. To cope with such heterogeneity, plants have two major types of nitrate transporters: high- and low-affinity nitrate transport systems, operating at low and optimal nitrate availability, respectively. Wheat is one of the most important cereal crops, providing one-fifth of the global population's protein and calorie requirements. However, wheat has poor nitrogen use efficiency, i.e., 30-40%, implying 60-70% of applied nitrogen is lost to the environment, consequently posing environmental and economic concerns. The high-affinity nitrate transport system (HATS) encoded by *the NRT2* family of genes may serve as a target for improving wheat's nitrogen use efficiency because of its affinity for nitrate, even when it is available sub-optimally, i.e., in the µM range. Most of the HATS require an additional accessory protein, a member of the NAR2 family (Nitrate Assimilation Related 2), thereby forming a two-component high-affinity transport system with specific partners, NRT2 and NAR2 family member. The present study aims to identify the component proteins of a two-component high-affinity nitrate transport system operating in wheat root tissues. Here we report the identification and functional validation of a root-specific high-affinity nitrate transporter gene, i.e., *TaNRT2.1-B6*, from wheat and its NAR2 component partner proteins, employing PCA-based protein-protein interaction approaches, e.g., Split-Ubiquitin and Bimolecular Fluorescence Complementation assay, and further validation in two model systems, *Xenopus laevis* oocytes and complementation in *Arabidopsis thaliana* mutant. Our study demonstrated that TaNRT2.1-B6 can interact with three different TaNAR2 proteins through its cytosolic domain. The present study will help strategize ways to improve wheat's NUE by employing these component proteins.

Keywords: Wheat, NRT2, NAR2, High-affinity nitrate transporter, Nitrate Assimilation Related 2

Improving the growth and development of monocot and dicot plants using cryo-milled nano-DAP

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Abstract

Phosphorus (P), a non-substitutable macronutrient, is essential for energy metabolism, nucleic acids and membrane integrity in biological systems for growth and development. However, due to its high reactivity with cations and very slow movement in the soil solution, P gets rapidly fixed in soil while the plant accessible inorganic phosphate (Pi) remains one of the least bioavailable nutrients for plants in the rhizosphere. In modern agriculture, chemical phosphate fertilizers are routinely applied to crop fields to mitigate soil P deficiency globally. While the use of chemical P fertilizers increased crop productivity and ensured food security over the course of history, the overall uptake potential of such fertilisers by plants remains very poor and demands the development of improved fertilizer formulations with higher agronomic use efficiency.

Hence, the strategy of preparing nano-fertilizers, subsequent characterization and validation of its functionality was conceptualized and demonstrated with great success. Within this context, a novel processing strategy (cryo-milling) is demonstrated to prepare nano-diammonium phosphate (n-DAP) on a kg-scale without altering DAP's chemical bonding structure from commercial granular DAP (c-DAP). Cryo-milling procuded n- DAP with particle size ~5000 times smaller but specific surface area ~14000 times greater than that of c-DAP and at >50% lower input than c-DAP, enhanced the growth, development and yield of tested plants due to improved bioavailability of Pi even for a far lower input than c-DAP.

Keywords: Phosphorus, orthophosphate (Pi), nano-fertilizers, cryo-milling, diammonium phosphate

Enduring Stress: Stress-driven responses of *Fusarium graminearum* to long-term tebuconazole exposure

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Abstract

Fusarium graminearum (*Fg*) is the causal agent of fusarium head blight (FHB) disease in wheat, and one of the most efficient methods of controlling it is using chemical fungicides. Tebuconazole is the most commonly used fungicide. However, some reports suggest that *Fg* in the fields is becoming resistant to the fungicide. Tebuconazole inhibits ergosterol biosynthesis, a significant component of the fungal plasma membrane. The various mechanisms that *Fg* uses to become tebuconazole-resistant are still unexplored. In this study, we are trying to find answers to how *Fg* adapts to growing in high concentrations of tebuconazole. *Fg* was allowed to adapt to growing in a high concentration of tebuconazole; fungicide sensitivity and plant virulence studies were conducted to check if it shows resistance against it. A transcriptome study was performed to identify genes that are responsible for the adaptation of *Fg* to tebuconazole. A comparative fungicide sensitivity assay revealed that at lower concentrations, WT showed increase in mycelial growth, while at higher concentrations, the adapted *Fg* showed relatively higher level of mycelial growth. The virulence assay revealed that in the absence of tebuconazole, WT is more virulent. In the presence of tebuconazole, the adapted *Fg* was found to be more virulent. Transcriptome study revealed that genes involved in transmembrane transport and ergosterol biosynthesis were significantly upregulated. This study reveals the key genes that may be contributing to the adaptation of *Fg* in high tebuconazole conditions. These findings may aid in developing targeted strategies to mitigate tebuconazole resistance and improve FHB management in wheat.

Keywords: *Fusarium graminearum*, Stress, Tebuconazole, Adaptation, Transcriptome

Screening and classification of phytoplasma from *Sesamum indicum* L. in three consecutive kharif seasons within Telangana, India

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Abstract

Sesamum indicum L., commonly known as 'Queen of oil seeds' is an ancient oil seed crop. Since it is not mandated to any international research institute, the same is considered an 'orphan crop.' Sesame belongs to the family Pedaliaceae and is cultivated in latitudes between 40°N and 40°S over the tropics and subtropics of Asia and Africa. The crop is exposed to a variety of biotic and abiotic stress. Phyllody is one of the most infectious diseases affecting sesame, caused by the bacterium *Candidatus* Phytoplasma. Phytoplasma is an obligate plant pathogen that falls under class Mollicutes and resides in the host's phloem tissue. Since the damage rate by the disease is ranging from 60 to 100 percent, it is necessary to screen the plants for phytoplasma infection to identify the strain, group, and subgroup. The study comprised screening of 275 plant samples from IIOR, Rajendranagar, Hyderabad grown in three consecutive kharif seasons from 2022 to 2024. Genomic sequencing of two infected samples from three consecutive kharif seasons were used to identify the strain, group, and subgroup of phytoplasma. The strain under the study is observed as *Candidatus* Phytoplasma asteris belongs to group 16Sr 1 and subgroup B. Phytoplasma has effector molecules, which can hijack transcription mechanisms in the plants. Prelimary studies reveal that these effector molecules interact with floral genes and result in their deformity, but the mechanism is yet unclear. This study focuses on the ecological aspects of phytoplasma infection and its effector localization within plant cells. Further, the study highlights identification of effector molecules using *in silico* analysis and gene expression studies.

Keywords: Sesame, Phytoplasma, Phyllody

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