Two Days National Conference
on
Advances in Biochemistry & Biotechnology for Nutritional Security in the Era of Climate Change

February 27th-28th, 2026

SOUVENIR & ABSTRACT

Dr. Rajendra Prasad Central Agricultural University
Pusa, Samastipur-848125 Bihar

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College of Basic Sciences & Humanities
Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar
In collaboration with
Society for Plant Biochemistry and Biotechnology, ICAR-IARI, New Delhi
and
Division of Biochemistry, ICAR-IARI, New Delhi

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and
Division of Biochemistry, ICAR-IARI, New Delhi

सत्यमेव जयते
डॉ. एम. एल. जाट
सचिव (डेयर) एवं महानिदेशक (भाकृअनुप)
Dr. M. L. Jat
SECRETARY (DARE) & DIRECTOR GENERAL (ICAR)

भारत सरकार
कृषि अनुसंधान और शिक्षा विभाग एवं
भारतीय कृषि अनुसंधान परिषद,
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MESSAGE

Ensuring food and nutritional security under increasing climate variability remains a key national priority. Recent advances in genomics, molecular breeding, metabolomics, genome editing, and integrative analytical approaches have strengthened the identification and deployment of traits related to yield stability, nutritional enhancement, and climate resilience. The integration of these approaches into research and development programmes is essential for translating scientific knowledge into practical outcomes.

Besides other disciplines, biochemistry and biotechnology have contributed significantly to agricultural research by improving our understanding of nutrient metabolism, stress responses, and biological interactions, thereby supporting enhanced productivity, resource-use efficiency, and sustainability of agricultural systems.

In this context organizing National Conference on "**Advances in Biochemistry & Biotechnology for Nutritional Security in the Era of Climate Change**" by Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur (Bihar) in collaboration with the ICAR–Indian Agricultural Research Institute, New Delhi, under the aegis of the Society for Plant Biochemistry and Biotechnology (SPBB) is a welcome step.

I am confident that the deliberations of the conference will contribute meaningfully to strengthening agricultural research and scientific collaboration. I extend my best wishes to the organizers and participants for the successful conduct of the conference.

(M. L. Jat)

Dated the 17th February, 2026
New Delhi

भाकृअनुप
ICAR
डॉ. देवेन्द्र कुमार यादव
उप महानिदेशक (फसल विज्ञान)
Dr. Devendra Kumar Yadava
Deputy Director General (Crop Science)

भारतीय कृषि अनुसंधान परिषद
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Department of Agricultural Research & Education
Ministry of Agriculture and Farmers Welfare
Govt. of India, Krishi Bhawan, New Delhi-110001

MESSAGE

Recent advances in molecular breeding, genomics, metabolomics, genome editing, and related biotechnological tools have significantly strengthened crop improvement programmes. These approaches facilitate precise identification and effective deployment of useful traits and support the development of climate-resilient and nutritionally improved crop varieties. Translating such scientific knowledge into field-relevant and farmer-oriented outcomes remains an important objective of agricultural research.

It gives me an immense pleasure that the Society for Plant Biochemistry and Biotechnology (SPBB) is organizing a National Conference on "Advances in Biochemistry & Biotechnology for Nutritional Security in the Era of Climate Change" at the College of Basic Sciences & Humanities, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur (Bihar), in collaboration with the Division of Biochemistry, ICAR-Indian Agricultural Research Institute, New Delhi. The conference provides a valuable platform for scientific interaction, knowledge sharing, and interdisciplinary exchange among researchers. I am confident that the deliberations of the conference will contribute to strengthening agricultural research, refining crop improvement strategies, and supporting evidence-based technology development.

I wish the conference every success and hope it leads to meaningful scientific and practical outcomes.

देवेन्द्र कुमार यादव

(D. K. Yadava)

Dated: February 9, 2026
Place: New Delhi

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Dr. Rajendra Prasad Central Agricultural University
Pusa, Samastipur (Bihar) - 848 125

Date : 17/02/2026

Message

Dr. Rajendra Prasad Central Agricultural University, Pusa, occupies a distinguished place in the history of agricultural education and research in India. As the birthplace of organized agricultural research in the country, the University has consistently contributed to scientific advancement, innovation, and sustainable agricultural development through its integrated efforts in teaching, research, and extension.

It gives me immense pleasure to share that the **National Conference on "Advances in Biochemistry & Biotechnology for Nutritional Security in the Era of Climate Change"** is being organized during **26–27 February, 2026** at the **College of Basic Sciences & Humanities, RPCAU, Pusa**, in collaboration with the **Division of Biochemistry, ICAR–Indian Agricultural Research Institute, New Delhi**, under the aegis of the **Society for Plant Biochemistry and Biotechnology (SPBB)**. The theme of the conference is highly relevant in the present agricultural scenario, where ensuring nutritional security and building climate resilience have emerged as major challenges.

Biochemistry and biotechnology play a pivotal role in understanding plant metabolism, nutrient utilization, and stress tolerance. Recent advances in these disciplines have significantly strengthened crop improvement programmes, enhanced nutritional quality, and supported the development of climate-resilient agricultural technologies.

It is particularly meaningful that this conference is being held at Pusa, the cradle of agricultural research in India. The rich legacy of this historic campus continues to inspire excellence, innovation, and scientific leadership in agricultural research.

The conference will provide an important platform for scientific interaction and exchange of ideas among researchers, academicians, and young scientists. The research contributions documented in this souvenir will serve as a valuable reference and knowledge resource for the scientific community.

I am confident that the deliberations of the conference will contribute significantly to advancing agricultural research and innovation. I extend my best wishes to the organizers and participants for the successful conduct of the conference.

(P. S. Pandey)

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SOCIETY FOR PLANT BIOCHEMISTRY AND BIOTECHNOLOGY

(REGISTERED UNDER SOCIETIES REGISTRATION ACT XXI OF 1860)

Prof. T. R. Sharma
President, SPBB
&
National Professor-BP Pal Chair, ICAR-NIPB, New Delhi
Former Deputy Director General (Crop Science), ICAR

Message

The Society for Plant Biochemistry and Biotechnology (SPBB) has been consistently working towards promoting research and scientific exchange in the areas of plant molecular biology biochemistry, biotechnology, and allied disciplines. In this context, the National Conference on "Advances in Biochemistry & Biotechnology for Nutritional Security in the Era of Climate Change" being organized at the College of Basic Sciences & Humanities, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur (Bihar), in collaboration with the Division of Biochemistry, ICAR-Indian Agricultural Research Institute, New Delhi, reflects the Society's commitment to addressing contemporary challenges in agriculture.

Biochemistry and biotechnology play a crucial role in understanding the plant metabolism, nutrient dynamics, stress tolerance, and biological interactions that influence crop productivity and nutritional quality. Advances in these fields have strengthened the crop improvement programmes and supported the development of climate-resilient and resource-efficient agricultural technologies.

From a crop science perspective, integration of biochemical and biotechnological approaches with conventional breeding has enhanced the efficiency and precision of gene cloning & characterization, trait identification and deployment. Such approaches are increasingly important for improving nutrient use efficiency, stress tolerance, yield stability, post-harvest processing and value addition under the changing climatic conditions.

The conference provides an effective platform for interaction among biochemists, biotechnologists, plant breeders, physiologists, and allied scientists. The scientific contributions compiled in this volume reflect ongoing research efforts in the crop improvement, nutrition, stress biology, molecular diagnostics and biotechnological applications, and will serve as a valuable reference for researchers, students and other stakeholders.

The scientific deliberations of the conference are expected to strengthen interdisciplinary research and contribute to improved understanding relevant to sustainable and nutrition-secure agriculture. I extend my best wishes to the organizers and participants for the smooth and successful conduct of the conference.

(T. R. Sharma)

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COLLEGE OF BASIC SCIENCES AND HUMANITIES
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Date: February 17, 2026

Message

Warm greetings are extended to all delegates, scientists, academicians, and research scholars participating in the National Conference on "Advances in Biochemistry & Biotechnology for Nutritional Security in the Era of Climate Change", being organized at the College of Basic Sciences & Humanities, Dr. Rajendra Prasad Central Agricultural University (RPCAU), Pusa, Samastipur (Bihar), in collaboration with the Division of Biochemistry, ICAR-Indian Agricultural Research Institute, New Delhi, under the aegis of the Society for Plant Biochemistry and Biotechnology (SPBB).

The theme of the conference is highly relevant in the present agricultural scenario, where ensuring nutritional security and sustainability under changing climatic conditions has emerged as a major scientific challenge. Advances in biochemistry and biotechnology provide important tools for understanding plant metabolism, nutrient dynamics, stress responses, and biological interactions, thereby supporting crop improvement and sustainable agricultural practices.

The conference has been carefully planned to provide a common platform for scientists, academicians, researchers, and students working in biochemistry, biotechnology, crop science, and allied disciplines. Emphasis has been placed on creating opportunities for meaningful scientific exchange, discussion of recent research findings, and interaction across disciplinary boundaries.

The technical sessions, invited lectures, and oral and poster presentations are expected to encourage focused discussions on emerging concepts, methodologies, and applications relevant to nutritional security and climate-resilient agriculture. Such interactions are essential for strengthening interdisciplinary understanding and for identifying future research directions.

Sincere thanks are due to all dignitaries, speakers, advisory committee members, and participants for their valuable support and active involvement. I also acknowledge the dedicated efforts of the organizing committee, faculty members, and supporting staff whose commitment has made the planning and organization of this conference possible. Best wishes are extended for the successful conduct of the conference and productive scientific deliberations.

(Amaresh Chandra)
Convener

21/02/2026

Message from the Organizing Secretary

It gives me immense pleasure to present this Abstract-cum-Souvenir Book of the National Conference. On behalf of the Organizing Committee, I extend a warm welcome to all distinguished speakers, researchers, academicians, students, industry experts, and delegates who have graciously joined us for this significant academic gathering. This conference has been envisioned as a vibrant platform to deliberate on contemporary advancements, emerging challenges, and innovative solutions in the concerned field. The overwhelming response in the form of high-quality research abstracts from diverse institutions across the country reflects the growing scientific engagement and commitment toward knowledge generation and dissemination. The Abstract-cum-Souvenir Book stands as a testimony to the scholarly contributions of researchers who are striving to address pressing scientific and societal issues. The compilation showcases original research findings, novel methodologies, and transformative ideas that will undoubtedly stimulate meaningful discussions and future collaborations.

I sincerely appreciate the dedicated efforts of the members of the organizing committee, advisory board, reviewers, volunteers, and supporting staff whose meticulous planning and coordination have made this event possible. I also extend my gratitude to our sponsors and collaborating institutions for their valuable support. I am confident that the deliberations and interactions during this conference will foster academic excellence, strengthen professional networks, and inspire young minds to pursue research with renewed enthusiasm. Wishing the conference great success and all participants a rewarding and enriching experience.

With warm regards,

Jyo 21/02/2026

(Jyostnarani Pradhan)
Organizing Secretary
National Conference
CBSH, RPCAU

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ABOUT THE UNIVERSITY

Dr. Rajendra Prasad Central Agricultural University (RPCAU), Pusa

Dr. Rajendra Prasad Central Agricultural University (RPCAU), Pusa was established on 7 October 2016 through the conversion of Rajendra Agricultural University (RAU), Pusa — a state agricultural university founded in 1970 by the Government of Bihar. The institution is located at a historically significant site where organized agricultural research and education in India first began. The origin of agricultural research at Pusa dates back to 1905, when the Agricultural Research Institute and College was established by the British Government in response to recurring food shortages in the country. Today, the university undertakes teaching, research, and extension activities in agriculture and allied sciences across the nation, with special emphasis on the State of Bihar.

Historical Perspective

The name "Pusa" holds a distinguished place in global agricultural history. The region's legacy dates back to 5 July 1784, when a stud farm was established at Poosah (Pusa) by the East India Company to breed cavalry horses under the supervision of Lieutenant Major Fraser. Later, the site was converted into a tobacco experimental farm and was leased to British tobacco companies between 1877 and 1897 for research aimed at supporting cigarette manufacturing in the United Kingdom.

Historically, the region formed part of the Tirhut Estate under the Darbhanga Raj. Following the British victories at the Battle of Plassey (1757) and the Battle of Buxar (1764), and the Treaty of Allahabad (1765), the imperial government acquired land near the right bank of the Burhi Gandak River. Agricultural activities evolved gradually, including model farming initiatives and experimental agricultural research.

Pusa became a landmark for agricultural research in pre-independence India when the Imperial Agricultural Research Institute (IARI) was established on 1 April 1905. The institute received generous support from Mr. Henry Phipps, whose donation facilitated the construction of the Phipps Laboratory and other infrastructure, including the Navlakha Building. The institution underwent several name changes before becoming the Indian Agricultural Research Institute (IARI) after India's independence. Following the devastating earthquake of 15 January 1934, the institute was relocated to New Delhi in 1936.

Contrary to popular belief, the original "Pusa" refers to the location in Samastipur, Bihar, which predates the institute's relocation. The region has historical references in ancient Indian texts, and the name existed long before contributions made by philanthropists.

Academic Structure

RPCAU comprises eight constituent colleges:

- Tirhut College of Agriculture (TCA), Dholi (Muzaffarpur)
- Post Graduate College of Agriculture (PGCA), Pusa (Samastipur)
- College of Agricultural Engineering & Technology (CAE&T), Pusa
- College of Community Science (CCS), Pusa
- College of Basic Sciences and Humanities (CBS&H), Pusa
- College of Fisheries (CoF), Dholi
- Pt. Deen Dayal Upadhyay College of Horticulture and Forestry (PDUCH&F), Piprakothi
- School of Agribusiness & Rural Management (SAB&RM), Pusa

The university offers undergraduate programmes in multiple disciplines including Agriculture, Horticulture, Agricultural Engineering, Community Science, Fisheries, Biotechnology, Forestry, and Food Technology. In addition, postgraduate programmes are offered in 28 subjects and doctoral programmes in 16 disciplines. Certificate courses and postgraduate diploma programmes have been introduced in alignment with the National Education Policy to enhance industry readiness.

RPCAU operates across three campuses — Pusa, Dholi, and Piprakothi — along with 18 Krishi Vigyan Kendras (KVKs) and four research stations spread over approximately 2063 acres of biodiverse land.

Research Activities

The university has made significant contributions to agricultural research, including the release of multiple crop varieties such as rice, wheat, sugarcane, pulses, maize, millet, coriander, and mushroom through CVRC/SVRC systems. Research activities are supported by numerous national and international projects, advanced research centres, and centres of excellence focusing on water management, climate change, food processing, embryo transfer technology, mushroom technology, indigenous cattle conservation, and agro-waste utilization.

RPCAU has successfully developed innovative technologies including herbal products, banana fibre textiles, mosquito repellents from turmeric leaves, and value-added agricultural products. The university has also implemented sustainable waste management initiatives, including converting temple floral waste into vermicompost, contributing to environmental sustainability and revenue generation.

Extension Activities

The university actively promotes agricultural development through its Directorate of Extension and KVK network. Extension programmes include farmer training, field demonstrations, on-farm trials, seed village development, and technology dissemination. These initiatives aim to enhance food security, reduce poverty, and promote sustainable agricultural practices.

Achievements

RPCAU has received several national recognitions, including top rankings among government universities and awards for excellence in higher education and green campus initiatives. The university continues to expand its research capabilities, including the establishment of advanced laboratories such as 5G innovation facilities. Students have achieved notable success in national examinations such as ICAR/CSIR NET and have secured high placement rates in professional programmes.

Vision

To enhance professional competency and promote excellence in agricultural education, research, and entrepreneurship through ethical practices, addressing regional, national, and global challenges.

Mission

- Promote high-quality experiential learning and integrated approaches linking soil, plants, animals, and society.
- Foster innovation-driven education, research, and entrepreneurship.
- Support sustainable food production through advanced research interventions.
- Enhance climate resilience in agriculture, particularly in Eastern India.

Goals

- Strengthen education, research, and extension to develop skilled human resources.
- Undertake strategic and applied research to enhance productivity and quality.
- Improve nutritional security and quality of life through sustainable agriculture.
- Provide integrated outreach linking scientific innovation with farming communities.

About the College of Basic Sciences and Humanities

The College of Basic Sciences and Humanities (CBS&H), established on 16 October 1981, is a constituent college of Dr. Rajendra Prasad Central Agricultural University (RPCAU), Pusa (Samastipur), Bihar. Agriculture being the backbone of Bihar's economy, with more than 80 percent of the population dependent on it for livelihood, the university was originally established as Rajendra Agricultural University on 3 December 1970 to promote agricultural development through education, research, and rapid transfer of improved technologies related to crop production and animal husbandry. The college was founded to provide a strong foundation in basic sciences and humanities to support agricultural education and to transform traditional subsistence farming into a modern science- and technology-driven production system.

Initially comprising seven departments, the college has been restructured and currently includes four departments: Agricultural Biotechnology and Molecular Biology, Botany with Plant Physiology and Biochemistry, Microbiology, and Statistics and Computer Applications. The college aims to impart high-quality education in basic sciences through sustainable and equitable approaches, develop dynamic curricula aligned with evolving scientific knowledge, promote teaching, research, and extension activities, and foster collaborations at intra- and inter-university levels.

Its mission is to strengthen academic and research activities through advanced teaching programmes and modern laboratory facilities to generate skilled human resources capable of addressing agricultural and environmental challenges. The vision of the college is to create a multidisciplinary institutional framework integrating biological sciences, statistics, computational biology, mathematics, physics, and language studies to address emerging challenges in food and nutritional security and agricultural sustainability. Strategically, the college emphasizes innovation-driven teaching aligned with NEP 2020, interdisciplinary collaboration, capacity building in scientific research, and enhancement of language and communication skills to prepare students for global engagement.

Academic programmes are offered at undergraduate, postgraduate, and doctoral levels, including DBT-supported programmes and opportunities for in-service candidates. The college fosters diversity by attracting students and faculty from various regions of India, contributing to a vibrant academic environment. Facilities include fourteen well-equipped laboratories for practical training, lecture theatres and departmental classrooms, smart classrooms with interactive technology, conference halls, and a well-maintained college library supported by the University Central Library. The ARIS Cell manages institutional internet connectivity, and round-the-clock Wi-Fi access is available.

Research activities focus on key thrust areas across departments, including molecular breeding, gene editing, and climate-resilient crop development in biotechnology; biofertilizers, microbial technologies, and germplasm conservation in microbiology; abiotic stress physiology, nutrient use efficiency, metabolomics, and post-harvest biochemistry in plant physiology and biochemistry; and artificial intelligence, big data analytics, machine learning, and genomic modelling in statistics and computer applications. In addition, the college actively engages in outreach and capacity-building programmes to strengthen scientific knowledge dissemination and agricultural innovation.

About the Society for Plant Biochemistry and Biotechnology (SPBB)

The Society for Plant Biochemistry and Biotechnology was established in May, 1991 with its Headquarters at Division of Biochemistry, ICAR - Indian Agricultural Research Institute, New Delhi, and registered under the Societies Registration Act of XXI of 1860 on 15th November, 1991. The aims and objectives for which the society was established are as under:

i. To advance Plant Biochemistry, Molecular Biology, Molecular Genetics and Biotechnology research in India.
ii. To provide forum to Plant Biochemists, Molecular Biologists, Molecular Geneticists and Biotechnologists for exchange of scientific knowledge.
iii. To foster high standards in teaching and research in the areas of Plant Biochemistry, Molecular Biology, Molecular Genetics and Biotechnology.
iv. To collect, collate and disseminate information on various aspects of Plant Biochemical, Molecular Biology, Molecular Genetics and Biotechnological research.
v. To work in association and cooperation with other National Societies/ Associations having similar objectives.
vi. To publish a journal covering Plant Biochemistry, Molecular Biology, Molecular Genetics and Biotechnology research.
vii. To do and perform all other acts, matters and things which may assist in, conduce to or be necessary for the fulfillment of the objectives and aims of the Society.

At present, SPBB has 1092 life Members including Ph.D. scholars, 03 Student/ordinary members (Year- 2026) and 5 Institutional Members. It has 24 foreign members from 12 different countries. The members are from the disciplines of Biochemistry, Biotechnology and Molecular Biology, Plant Physiology, Genetics, Microbiology, Molecular Genetics, and Mycology and Plant Pathology.

The Society had the honour of being led by distinguished scientists/academicians as Presidents : Dr. S. Ramachandran, then the Secretary, DBT (1992-1994); Dr. R.S. Paroda, then the Secretary, DARE & Director General, ICAR (1995-2000); Prof. V.L. Chopra, then the Secretary, DARE &Director General, ICAR (2000-2005); Dr. S. L. Mehta, former Deputy Director General (Education), ICAR and Vice Chancellor, MPUAT, Udaipur (2006 –2024); Prof. T.R. Sharma, National Professor-BP Pal Chair, ICAR-NIPB & former Deputy Director General (Crop Science), ICAR, New Delhi (2024 to till date).

As its main activity, the Society is publishing the 'Journal of Plant Biochemistry and Biotechnology' (JPBB) since January 1992. Initially, the Journal was published biannually, but since

January 2013, four issues per year are being published due heavy pressure of a large number of MS received from India and abroad. The latest Thompson Reuter 'Impact Factor' 2025 of the Journal is 1.5. It has been our endeavour to timely publish the Journal while maintaining its standard and constantly improving its quality. The members of the Society receive the Journal online, free of cost. Based on the quality/impact factor of the Journal, the Society has been graded and put in category 'A' by the Indian Council of Agricultural Research.

The Journal publishes review articles, research papers, short communications and commentaries in the areas of plant biochemistry, plant molecular biology, microbial and molecular genetics, DNA finger printing, micropropagation, and plant biotechnology including plant genetic engineering, new molecular tools and techniques, genomics and bioinformatics.

The Journal is being Abstracted/Indexed in : Science Citation Index Expanded (SciSearch), Journal Citation Reports/Science Edition, SCOPUS, Chemical Abstracts Service (CAS), Google Scholar, CSA,CAB International, Biological Abstracts, BIOSIS, CAB Abstracts, Elsevier Biobase, Food Science and Technology Abstracts, Global Health, Indian Science Abstracts, OCLC, SCImago, Summon byProQuest (http://www.springer.com/ life+sciences/journal/13562).

Earlier, the Journal received a rare distinction of being covered in Institute of Scientific Information (ISI)'s Electronic Library Project. From Volume 20 - Issue 1(Jan - June, 2011), the Journal is being co-published by the Society and Springer Nature India Private Limited.

Since its inception, the Society has organized the following National Symposia/Seminars and International Conferences:

I. The first National Symposium on the “Role of Plant Biochemistry and Biotechnology in Improving Crop Productivity” at the Indian Agricultural Research Institute, New Delhi from November 18-19, 1991.

II. The second National Symposium on the “Developments in Plant Molecular Biology & Genetic Engineering” at the Tamil Nadu Agricultural University, Coimbatore from December 29-31, 1993.

III. The third National Symposium on the “Role of Plant Biotechnology in Improving Agriculture- challenges and opportunities, and Physiological & Biochemical Basis of Crop Yield” at the University of Rajasthan, Jaipur from March 23-25, 1995. This Symposium was co-sponsored by the Society for Plant Physiology & Biochemistry.

IV. The fourth National Symposium on “Current Trends in Plant Biochemistry and Biotechnology” was organized at CCS Haryana Agricultural University, Hisar from February 23-25, 1996.

V. The fifth National Symposium on the “Role of Plant Biochemistry and Biotechnology in

Improving Crop Productivity" was organized at ICAR Research Complex for NEH Region, Barapani, Meghalaya from March 18-20, 1997.

VI. The sixth National Symposium on the "Role of Plant Biochemistry and Biotechnology in Improving Crop Productivity" was held at University of Agricultural Sciences, Bangalore from March 4-6, 1999.

VII. The seventh National Symposium on "Biotechnology for Sustainability in Agriculture" was held at GB Pant University of Agriculture and Technology, Pantnagar from April 27-29, 2000.

VIII. The eight National Symposium on the "Relevance of Plant Biochemistry and Biotechnology- Modern Trends" was held at The American College, Madurai (TN) from March 1-3, 2001.

IX. The ninth National Symposium on the "New Opportunities and Challenges for Improving Crop Productivity through Biotechnology" was organized at the Department of Biotechnology and Molecular Biology, CCS Haryana Agricultural University, Hisar from February 13-15, 2002.

X. The first "International Conference on Plant Biotechnology for Food Security : New Frontiers" was organized by the Society and the National Research Centre on Plant Biotechnology, in association with the Indian Agricultural Research Institute, New Delhi from Feb 21-24,2012.

XI. The tenth National Conference on "Science of Omics for Agricultural Productivity: Future Perspectives" was organized at GBPUAT during 4-6 March, 2014.

XII. The eleventh National Symposium on "Germplasm to Genes: Harnessing Biotechnology for Food Security and Health" was organized by the Society and the National Research Centre on Plant Biotechnology during 09-11 August, 2015.

XIII. The twelth National Symposium on "Transgenic Crops in India: Progress and Challenges" was jointly organised at CCSHAU Hisar during 16-17 March, 2016.

XIV. The thirteenth National Symposium on "Connecting Innovations in Plant Biology for Food and Nutritional Security" at WTC, ICAR-IARI, New Delhi on 19.11.2018.

XV. The fourteenth National Conference on "Integrative Plant Biochemistry and Biotechnology" at ICAR- Indian Institute of Rice Research, Hyderabad, during 08-09 November, 2019.

XVI. The fifteenth National Virtual Conference on "Current Trends and Challenges in Plant Biochemistry and Biotechnology"during 20-21 November 2020 jointly organized by BITS-Pilani, Goa & SPBB, New Delhi.

XVII. The sixteenth National Symposium on "Emerging Innovations in Plant Molecules for Achieving Food and Nutritional Security" jointly organised by Navsari Agricultural University, Navsari& Div. of Biochemistry, ICAR-IARI under the aegis of the SPBB at Navsari in Hybrid mode during 22-23 September, 2022.

XVIII. The second, "International Conference on Biochemical and Biotechnological Approaches for Crop Improvement (IBBACI)" was organised by the Society in association with the Division of Biochemistry, ICAR-IARI, New Delhi, ICAR-NIPB, New Delhi and CSIR-NBRI, Lucknow during 30.10.2023 to 01.11.2023 at NASC Complex, New Delhi.

XIX. The seventeenth National Conference on "Emerging Innovations in Biochemistry and Biotechnology for Holistic Development of Agriculture" was organised by SPBB in collaboration with Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Jammu and the Division of Biochemistry, ICAR-IARI, New Delhi during 06-07 March, 2025 at SKUAST, Jammu.

Besides the Conferences/Symposia, in order to fulfil its mandate Society is involved in organising several workshops/training programmes, webinar and lecture series in different country zones on current science topics. For these activities proposals are invited every year.

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Dr. N. B. Das Memorial Lecture - 2026

Tribute to a Pioneer Legend and Great Visionary

(27th February, 2026)

Dr. N. B. Das (NalinBandhu Das) was born on June 1, 1908 in a family of jurists, educationists and physicians of Chittagong (now in Bangladesh). He graduated in 'Honours in Chemistry' from the Calcutta University. He then joined Bose Institute as researcher and later on served the Bengal Chemical and Pharmaceutical Works for a short term. In 1930s, on being awarded 'The Lady Tata Memorial Scholarship', he proceeded to Germany for higher studies. He was awarded the Doctorate degree for his fundamental research on the biochemistry of enzymes. His Ph.D. research has been extensively cited in the text books of enzymology.

He had the privilege of working with two Nobel Laureates. Initially he was with Prof. Hans von Euler at the Biochemical Institute, University of Stockholm, Sweden. Here he worked extensively on the purification and characterization of enzymes involved in amino acid metabolism in animal system, especially with respect to cofactors/coenzymes, and on the role of ATP in the conversion of DPN to TPN. Later on, he moved to the Institute of Medical Chemistry, University of Szeged, Hungary as 'The Lady Tata Memorial Scholar', to work with Nobel Laureate Prof. Albert Szent-Gyorgyi, to whom he considered his Guru. He carried out extensive studies on the inhibition of the succinic and lactic-malic dehydrogenases. His research work is widely cited in research papers and books.

After working for nearly 12 years in renowned laboratories abroad, Dr. Das returned back to India on the call given by Prof. P. C. Mahalanobis, the father of modern statistics in India. Patriotic feeling brought Dr Das home to use science and technology for the welfare of people. On his return, he joined the mother campus of Indian Veterinary Research Institute (then Imperial Institute of Veterinary Research) at Mukteswar to work on cattle vaccines and sera. Subsequently, in the year 1949, he joined the Division of Soil Science and Agricultural Chemistry at IARI as the first Biochemist where he established a Biochemistry Laboratory. This was the beginning of introducing and emphasizing the role of biochemistry in agriculture, especially with respect to the quality of food crops. Dr. Das was the first to study the nutritive quality of crops as influenced by variety, manures and fertilizers. From these studies, the first major recommendation that foliar application of urea and micro-nutrient elements enhances crop yield, was made in early 1950s.

Recognizing the importance of Agricultural Biochemistry in improving agriculture, a small Biochemistry Section in the Division of Soil Science and Agricultural Chemistry was transformed into the full-fledged Division of Biochemistry in November 1966, and its founding father Dr. N.B. Das was made the first Head of the Division. Biochemical research and education was tailored to meet the new challenges of Indian agriculture. New Post-Graduate courses were designed to impart skills in new technologies that aimed at studying intermediary metabolism, molecular biology, enzymology and nutrition. The first batch of M.Sc. and Ph.D. students was admitted in the academic year 1967-68.

In the formative years, the major emphasis was given on the biochemical and biological evaluation of nutritional value of newly developed varieties of food grains, effect of plant nutrients on nutritional value as well as yield of food grains, biochemical studies in nitrogen fixing bacteria, and utilization of agro-industrial wastes for the production of lysine as well as enzymes like cellulase and amylase. Under his leadership one of the finest facilities for doing outstanding research in plant biochemistry was built. The technique of PAGE was introduced for the characterization of soluble proteins and iso-enzymes. Dr. Das guided a number of M.Sc. and Ph.D. students from India and neighboring countries, who later went on to hold various responsible positions within and outside India.

After his superannuation in the year 1970, in recognition of his valuable contributions in the field of biochemistry and his distinct position as a biochemist in the country, he was made Emeritus Scientist by the ICAR.

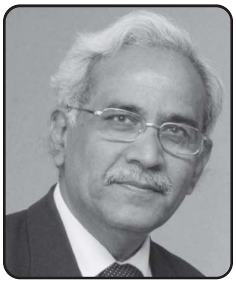
Dr. N.B. Das was not only a renowned and most respected biochemist, but also an unassuming, quiet and noble gentleman, and his smiling face was characteristic of him. He personified what is best in Indian culture. His commitment to excellence in science was total. This great scientist left for his heavenly abode on 17th November, 1971. The Society for Plant Biochemistry and Biotechnology decided to organize 'Dr. N.B. Das Memorial Lecture' to perpetuate his memory.

Till 2025, seven (07) Dr. N. B. Das Memorial Lectures have been delivered by renowned distinguished academicians of the country - **Dr. M. S. Naik**, then the Head, Division of Biochemistry, ICAR-IARI, New Delhi; **Dr. P. V. Sane**, then the Director, National Botanical Research Institute, Lucknow; **Dr. H. K. Das**, Former Dean, Jawaharlal Nehru University, New Delhi; **Prof. G. Padmanaban**, then the President, National Academy of Sciences, India; **Dr. T. Mohapatra**, then the Secretary, DARE and Director General, ICAR; **Prof. Rajeev Varshney**, Professor, Murdoch University, Australia, and **Prof. S. L. Mehta**, Former Vice-chancellor, MPUAT, Udaipur.

For the year 2026, the society feel honoured to confer this Award on another great luminary in the field of Plant Molecular Biology, Genomics and Biotechnology- **Prof.Akhilesh Kumar Tyagi**, Former Director, NIPGR, New Delhi

Dr. N. B. Das Memorial Lecture - 2026

Prof.Akhilesh Kumar Tyagi



Prof.Akhilesh Kumar Tyagi is an eminent plant molecular biologist and genomics scientist whose pioneering work has significantly advanced plant biotechnology and crop improvement research in India. Born on 15 May 1956 in district Bulandshahr, India, Prof. Tyagi obtained his Ph.D. from the University of Delhi in 1983, followed by advanced research training in Germany focusing on photosynthesis-related nuclear and chloroplastic genes.

Prof. Tyagi served as Professor and later Senior Professor in the Department of Plant Molecular Biology, University of Delhi South Campus, and has held several major leadership positions including Director of the Interdisciplinary Centre for Plant Genomics and Director of the National Institute of Plant Genome Research, New Delhi. He also served as Executive Director (In-charge) of the National Agri-Food Biotechnology Institute, Mohali, and President of the National Academy of Sciences, India.

His research contributions span plant genomics, molecular physiology, stress biology, reproductive biology, and genetic enhancement of crops. Prof. Tyagi has led several landmark national initiatives including the Indian participation in rice and tomato genome sequencing projects and major functional genomics programmes. These efforts have played a foundational role in establishing high-throughput genomics research in India and identifying novel genes associated with yield and stress tolerance.

Over the course of his career, Prof. Tyagi has authored more than 300 high-impact publications and supervised a large number of postgraduate, doctoral, and postdoctoral researchers. He has delivered hundreds of invited lectures at national/international level and contributed extensively to scientific capacity building and human resource development in plant science.

In addition to his research leadership, Prof. Tyagi has served on several national policy and advisory bodies, including DBT, DST,UGC task forces and program advisory committees, and on editorial boards of leading journals in plant biology and genomics.

Prof. Tyagi is a Fellow of the Indian National Science Academy, National Academy of Sciences, India, Indian Academy of Sciences, National Academy of Agricultural Sciences, and The World Academy of Sciences. His numerous honours include the J. C. Bose National Fellowship, National Bioscience Award, BirbalSahni Medal, Shri Om Prakash Bhasin Award for Science and Technology, and several prestigious memorial lecture awards.

Through his sustained scientific leadership and pioneering research, Prof.Akhilesh K. Tyagi has made outstanding contributions to plant genomics, biotechnology, and agricultural innovation in India and globally.

Dr N.B. Das Memorial Lecture, SPBB

Water-deficit response: Role of rice A20/AN1 zinc-finger stress-associated protein (SAP) genes

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ABSTRACT

Development and growth of rice are severely affected by water-deficit resulting in significant yield loss. We have analysed response of rice for the same at transcriptome level. Analysis of data from our investigation along with information in data base on various water-deficit stress conditions imposed in one reproductive and six vegetative stages of rice development has helped identify 7682 differentially expressed genes. Out of their encoded proteins, 17% have been predicted to be nuclear localized with high level of confidence. Detailed analysis for transcription factors and metabolic pathway genes identified potential key components of stress response. The A20/AN1 zinc-finger containing stress-associated protein (SAP) gene family has been found to be closely related to stress response in rice and other plants. Overexpression of these genes during water-deficit confers tolerance in homologous and heterologous transgenic systems, including protection against yield loss. The target genes influenced by their overexpression show significant overlap in addition to the specific complement. Using protein interaction approaches, its members have been found to interact with proteasomal pathway proteins (OsRAD23, polyubiquitin) and regulators of stress signaling ((OsMBP1.2, OsDRIP2, OsSCP and OsAMTR1). Within the protein, A20 domain was found to be important for such interactions. These multiple interactions may result in altered gene expression and physiological state responsible for stress tolerant phenotype. However, SAP gene family has undergone sub-functionalization and OsSAP7 overexpression imparts sensitivity to stress. Such investigations should help unravel molecular basis of gene action and water-deficit stress tolerance.

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ABSTRACTS AND EXTENDED SUMMARY

Theme A
Climate-Resilient Crops for Nutritional Security

Abstract No: A1

Harnessing natural variation to optimize rice photosynthetic efficiency: A genomic perspective

Aashish Ranjan
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ABSTRACT

Optimizing photosynthetic efficiency of staple crop plants, such as rice, holds enormous potential for sustainable crop yield increases.Desirable manipulations in leaf developmental and physiological features holds enormous potential for increasing photosynthetic efficiency, as leaves are the prime site of photosynthesis. The natural genetic variation in leaf photosynthesis and underlying attributes is an overlooked and untapped resource. The genus Oryza, including cultivated rice and wild relatives, offers tremendous genetic variability to explore photosynthetic differences and underlying attributes. Investigation of the variations in photosynthesis across multiple wild and cultivated rice accessions identified several photosynthetically efficient wild rice accessions. Leaf morphological traits, such as wider and thicker leaves, and anatomical features, such as mesophyll features and chloroplast surface area exposed to intercellular space, contribute to higher photosynthetic efficiency in wild rice accessions.Moreover, large-scale field phenotyping exhibited remarkable variation in leaf photosynthesis and related leaf physiological and developmental traits among cultivated Indian rice accessions. While comparative transcriptomics involving wild and cultivated rice identified genetic regulators of rice leaf size and transition from development to photosynthesis, GWAS with cultivated landraces identified thegenetic loci regulating the photosynthetic efficiency. We identified a genetic loci on chromosome 1, strongly enriched in photosynthetic genes and regulators, that significantly associated with photosynthesis rate as well as associated physiological traits. SNP variations in the photosynthetic genes in the region formed distinct haplogroups with contrasting photosynthetic traits. We further identified and genetically validated the transcriptional regulators of the genes in the delineated region contributing to the photosynthetic efficiency. The identified genes and regulators are being targeted for increasing photosynthetic efficiency of cultivated rice varieties.

Abstract No: A2

Response of growth and yield of Rabi maize under future climate: an assessment using DSSAT modelling

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ABSTRACT

Bihar, the third largest maize-growing state in India, has significant potential for Rabi maize cultivation due to its high productivity and growing demand for food, fodder, and industrial uses. The present study calibrated and validated the DSSAT CERES-Maize model (v.4.8.5) using field experiments conducted at RPCAU, Pusa, across multiple sowing dates from late October to early December for varieties Shaktiman 4 and Shaktiman 5. The model demonstrated satisfactory performance, with good agreement between simulated and observed phenology and yield, and Shaktiman 4 exhibiting superior kernel filling characteristics. Sensitivity analysis indicated that Rabi maize is more responsive to changes in maximum temperature than minimum temperature, with moderate warming enhancing yield and shortening crop duration. Climate projections (2030–2099) under SSP2-4.5 and SSP5-8.5 scenarios revealed significant increases in both maximum temperature and minimum temperature, with stronger warming trends under SSP5-8.5, particularly during the latter half of the century. Significant upward trend was found for temperature, while rainfall and solar radiation showed high inter-annual variability with no consistent long-term trend. Results depicted that elevated thermal condition would lead to earlier maturity in Rabi maize due to faster phenological development. Average crop duration is found to be around 142 days. Projected dry matter production is expected to increase in both scenarios, though gains may stabilize or slightly decline under high-emission conditions after mid-century. Grain yield is projected to increase by an average of about 8% over the baseline, with higher gains during Phase 2 (2065–2099) due to favorable thermal conditions. Correlation analysis revealed that temperature variables positively influence yield and dry matter accumulation, whereas rainfall plays a minimal role due to supplemental irrigation during the Rabi season.

Keywords: Winter maize, DSSAT, future climate, temperature variability, Bihar

Abstract No: A3

Decoding Aquaporin Function and Engineering Precision Traits: A Journey from Molecular Insights to Genome-Edited Crops

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ABSTRACT

Aquaporins play a central role in regulating water and solute transportacross plant membranes, influencing both stress tolerance and nutrient homeostasis. In our work, we first identified and characterized aquaporin across multiple plant species and elucidated their evolutionary pathin higher plants. We examined aquaporins across more than 1,000 diverse plant species and investigated their roles in nutrient uptake under both controlled growth conditions and field environments. This comparative and evolutionary analysis provided critical insights into solute specificity, functional aspects and divergence. This study particularly helped in defining the roles of distinct aquaporin subfamilies in basic molecular activities in different tissues and also under diverse environmental stress conditions. Building on this foundational knowledge, we conducted detailed molecular investigations of aquaporin transport mechanisms, with a particular focus on the silicon transporter in rice. Through structural and functional analyses, we identified two key pore-lining amino acids that enable dual transport of silicon and arsenic. Using targeted mutagenesis, we demonstrated that precise alteration of these residues can effectively reducearsenic transport while retaining optimal silicon uptake. This is an important breakthrough in ensuring both crop performance and food safety.Arsenic contamination in agriculturalfields and subsequently in the food chain is a rapidly increasing concern throughout the rice-growingareas worldwide. Exploringthese mechanistic insights of Aquaporin solute specificity, we are now advancing toward translational applications using genome editing technologies, with a special emphasis on prime editing to introduce the desired amino acid substitutions into elite rice varieties. Parallel efforts in tomato and mustard have further demonstrated the successful implementation of genome editing to enhance stress tolerance and nutritional quality.This presentation will provide an integrated overview of our journey from fundamental aquaporin research to field-oriented innovation, highlighting how mechanistic understanding of solute transport can be translated into next-generation crop improvement strategies aimed at climate resilience and nutritional security.

Keywords: Winter maize, DSSAT, future climate, temperature variability, Bihar

Abstract No: A4

Concept and Application of AI in Biotechnology for Nutritional Security and Climate Smart Agriculture

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ABSTRACT

Global agriculture faces the dual challenge of feeding a rapidly growing population while coping with climate variability, land degradation, and declining nutritional quality of crops. Traditional breeding and management approaches are often too slow and resource-intensive to address complex, multigenic traits such as nutritional enhancement, stress resilience, and yield stability under fluctuating environments. Artificial Intelligence (AI), integrated with modern biotechnology, offers a transformative framework for data-driven agriculture by enabling predictive, adaptive, and scalable solutions across genomics, crop improvement, and agro-ecosystem management. In this context, AI functions not merely as an analytical tool but as a decision-support paradigm capable of integrating heterogeneous biological datasets including genomics, transcriptomics, proteomics, metabolomics, phenomics, and environmental variables.

At the molecular level, AI accelerates gene discovery and functional annotation through deep learning–based sequence analysis, protein structure prediction, and regulatory network inference. Machine learning models such as convolutional neural networks (CNNs), transformers, and graph neural networks (GNNs) are increasingly used to identify genes controlling micronutrient accumulation, anti-nutritional factors, and stress tolerance traits. AI-assisted genome editing further enhances biotechnology interventions by predicting optimal CRISPR targets, minimizing off-target effects, and simulating phenotypic outcomes prior to experimental validation. These capabilities enable rapid development of biofortified crops enriched with iron, zinc, provitamin-A, essential amino acids, and health-promoting metabolites, directly contributing to nutritional security.

AI also revolutionizes breeding through genomic selection and predictive phenotyping. By learning genotype–environment–management (G×E×M) interactions from large breeding datasets, AI models can forecast yield and nutritional performance across diverse agro-climatic zones. High-throughput phenotyping using drones, hyperspectral imaging, and computer vision allows non-destructive assessment of plant health, nutrient status, and stress response in real time. Integrating these observations with genomic predictions enables accelerated development of climate-resilient cultivars capable of maintaining productivity under drought, salinity, heat, and emerging pest pressures. Such climate-smart crops reduce dependence on chemical inputs and support sustainable intensification.

Beyond crop genetics, AI-enabled biotechnology supports climate-smart agriculture through

microbiome engineering and precision management. Machine learning models analyze soil metagenomes to identify beneficial microbial consortia that enhance nutrient uptake, nitrogen fixation, and stress tolerance. Predictive models also guide application of biofertilizers, biostimulants, and biopesticides by matching microbial functions with crop developmental stages and environmental conditions.

In summary, the convergence of AI and biotechnology establishes a holistic framework for sustainable agricultural transformation. By linking molecular design, intelligent breeding, microbial engineering, and precision farming, AI enables simultaneous improvement of productivity, nutritional quality, and environmental resilience. This integrative paradigm represents a key pathway toward achieving nutritional security and climate-smart agriculture in the era of data-intensive biological science.

Keywords: Artificial Intelligence; Agricultural Biotechnology; Climate-Smart Agriculture; Genomic Selection; Genome Editing; CRISPR; Multi-omics Integration; Biofortification;

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Abstract No: A5

Physiological, Biochemical, and Molecular Dissection of Low-Light Tolerance in Rice: From Signalling Pathways to Yield Stability

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ABSTRACT

Low-light (LL) stress during the *Kharif* season, largely driven by persistent cloud cover and atmospheric dimming, reduces photosynthetically active radiation (PAR) by ~40–60%, resulting in substantial yield losses in rice. To elucidate the mechanisms conferring LL resilience, we employed an integrated systems-level framework combining physiological, biochemical, and molecular analyses in contrasting rice genotypes. Physiological assessments demonstrated that LL-tolerant genotypes effectively suppress excessive shade-avoidance responses and maintain higher photosynthetic efficiency, thereby supporting stable growth under reduced irradiance. Biochemical analyses identified Sedoheptulose-1,7-bisphosphatase (SBPase) as a key metabolic stabilizer, with sustained enzyme activity strongly correlating with biomass maintenance and final yield under LL conditions. At the molecular level, Phytochrome A (PhyA) was identified as the primary LL sensor; disruption of its signaling cascade led to down-regulation of *OsPIL1* and *Lhcb* genes, impairing light harvesting and electron transport. We further delineated a "Light-Auxin–Starch" regulatory continuum, wherein LL-mediated repression of *OsYUC11* reduced spikelet indole-3-acetic acid (IAA) levels, consequently lowering AGPase and sucrose synthase activities and constraining grain filling. LL-tolerant genotypes also displayed distinctive epigenomic signatures, including altered DNA methylation landscapes and shifts in regulatory miRNAs, collectively contributing to enhanced LL tolerance. To improve phenotypic discrimination under variable light environments, we developed a Combined Stress Tolerance and Stability Index (CSTSI), which increased selection robustness across fluctuating irradiance regimes. Additionally, bi-parental and genome-wide association mapping approaches using a panel of 192 diverse rice genotypes uncovered multiple novel QTLs and stable QTL hotspots harboring 12 key hub genes (e.g., *OsAUX1, OsSBDCP1, OsNPF5.16,* etc.) associated with photosynthesis, hormone signaling, starch biosynthesis, and stress adaptation. Superior haplotypes linked to enhanced grain number, spikelet fertility, biomass, and grain yield, along with their donor genotypes, were also identified. Collectively, these findings provide mechanistic insights and actionable physiological, biochemical and molecular targets for breeding shade-tolerant, high-yielding, and climate-resilient rice cultivars.

Abstract No: A6

Ubiquitin proteasome system (UPS) modulatedheat stress tolerance in wheat

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ABSTRACT

Rising temperatures and climate change has greatly affected wheat production and productivity. Ubiquitination is intricately involved as a central regulatory pathway enabling plants to sense, respond and cope with heat-induced proteotoxicity. UPS is a post-translational modification process which target damaged proteins for degradation, modulates signalling components and coordinates multiple stress-responsive pathways.SKP1 (S-phase kinase protein1) is an essential regulatory component of SCF (Skp1-cullin-F-box) E3 ubiquitin ligases involved in maintenance of cellular protein homeostasis through ubiquitin mediated proteasome system .To assess the functional role of SKP1under terminal heat stress (THS) in wheat,genetic variability analysis was carried out in a panel of 25 contrasting germplasm through extensive phenotyping and transcript profiling of *TaSKP1-6B-4* during anthesis under ambient and THS in field experiments for two consecutive years.Whole genome wide search of SKP1 gene family identified 95 SKP1 genes which were structurally characterized. Grain yield, leaf senescence and other agronomic-morpho-physiological parameters combined with transcript profiling, cvHD2967, was found to be the best positively responsive to THS which by pedigree was not heat tolerant. Further analysis of role of UPS was also analysed after seed priming with two plant hormones. The results document regulatory involvement of SKP1/UPS in wheat climate resilience.

Abstract No: A7

Designing rice to sustain foodsecurity in warmer future climate

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ABSTRACT

Recent climate change trends are characterized by concurrent increases in atmospheric CO_2concentration, air temperature, and the frequency and severity of drought events. While elevated CO_2can exert variable effects on crop yield and quality, rising temperature and water limitation remain the most severe constraints on agricultural productivity worldwide. Rice (*Oryza sativa* L.), the most important cereal crop for human nutrition, feeds more than four billion people, predominantly in Asia and Africa, where it constitutes a major proportion of daily caloric intake and thus plays a central role in global food security. Although rising CO_2levels have the potential to stimulate photosynthesis and biomass accumulation in rice, both heat and drought stress markedly reduce yield stability, particularly under reproductive-stage stress. Projections of future climates indicate a CO_2-rich atmosphere accompanied by more frequent heat waves and prolonged drought spells, underscoring the urgent need to develop rice cultivars capable of sustaining productivity under warmer and drier conditions.

Dissecting the physiological, biochemical, and carbon balance-related mechanisms underlying rice responses to elevated temperature, with particular emphasis on distinguishing the effects of high day temperature and high night temperature (HNT), which are increasingly recognized as distinct but equally important components of climate warming. Through extensive field- and chamber-based experiments using diverse rice germplasm, including elite cultivars, landraces, and stress-tolerant donors, we have characterized the stage-specific sensitivity of rice to heat stress and identified key traits governing yield stability under warming conditions. We have demonstrated that high day temperature predominantly affects reproductive development by disrupting pollen viability, spikelet fertility, and seed set, thereby limiting sink establishment. In contrast, HNT imposes its major effects during the post-flowering and grain-filling phases, where yield losses arise not from impaired sink formation but from altered source-sink dynamics, reduced assimilate transport to developing grain, and increased respiratory carbon losses (maintenance respiration). This clear functional separation between day and night temperature effects has important implications for trait-based breeding strategies, as it highlights the need to target distinct physiological processes for improving tolerance to different thermal stress regimes.

Maintenance (dark) respiration as a critical determinant of yield performance under HNT. Elevated night temperature consistently increased respiratory carbon expenditure, particularly during the post-flowering period when assimilate demand by developing grains is high. This augmented maintenance respiration, associated with processes such as cellular repair, ion transport, and metabolic

homeostasis, substantially reduced the pool of carbon available for grain filling. Across genotypes, higher dark respiration rates under HNT were strongly associated with lower total biomass accumulation and reduced grain yield, indicating that respiratory efficiency is a key driver of heat resilience. Importantly, substantial genetic variation was observed in both the magnitude and temperature sensitivity of night respiration, suggesting that respiration is a selectable trait rather than a fixed physiological constraint. Genotypes maintaining lower respiration rates or exhibiting a smaller increase in respiration under HNT were better able to sustain biomass production and grain yield, primarily through maintenance of a more favourable carbon balance. On the other hand, the impact of HNT on source-sink dynamics revealed that elevated night temperature disrupts carbon allocation at multiple levels. At the source, HNT reduced starch synthesis and assimilate reserves in leaves, limiting the availability of translocatable carbohydrates during grain filling. Conversely, at the sink, HNT weakened sink strength by impairing the activity of key enzymes involved in sucrose unloading and starch biosynthesis within developing grains, including cell wall invertase, sucrose synthase, and starch synthase. Concurrently, increased activity of starch-degrading enzymes such as α-amylase under HNT promoted premature starch breakdown in the endosperm, further reducing grain weight and quality. These coordinated alterations in source metabolism, phloem transport, and sink enzymatic capacity collectively constrained carbon flux to the grain, thereby amplifying yield losses under warmer nights. Together, these findings established source-sink dysregulation and enhanced respiration as two tightly linked physiological processes underlying HNT-induced yield decline in rice.

Under HNT, many genotypes exhibited a marked reduction in net carbon gain due to the combined effects of suppressed photosynthesis and elevated respiration, resulting in a negative carbon balance particularly during the grain-filling period. This imbalance directly translated into reduced biomass and grain weight. Importantly, genotypes capable of maintaining a higher A/R□ ratio under HNT consistently showed superior yield stability, highlighting carbon balance as a unifying framework for understanding temperature resilience. These findings shifted the focus from single-process traits to whole-plant carbon economics, emphasizing that yield stability under warming conditions depends not only on stress avoidance or tolerance mechanisms but also on the efficiency with which plants acquire, conserve, and allocate carbon.A major advancement arising from this work is the integration of elevated CO_2responsiveness into the framework of heat stress tolerance. Recognizing that future climates will be characterized not only by higher temperatures but also by increased atmospheric CO_2concentration, rising CO_2 could benefit C_3 plants due to higher saturation point as compared to C4 plants. By screening diverse rice genotypes for phenotypic plasticity forCO_2responsiveness we could identify that CO_2-responsive genotypes exhibited enhanced photosynthetic rates, increased biomass accumulation, and improved grain yield components under elevated CO_2, and elevated CO_2combined with HNT. The compensation of carbon loss under HNT resulted in maintenance of a more positive carbon balance, improved A/R□ ratios, and reduced yield penalties in CO_2-responsive genotypes. These results provided experimental evidence supporting the hypothesis that CO_2responsiveness can function as a buffering mechanism against heat-induced respiratory losses, particularly under warm night conditions.

Integrating physiological traits such as respiration efficiency and CO_2 responsiveness with genomic and molecular insights offers new opportunities to identify candidate genes and pathways for targeted improvement. Efforts are increasingly focusing on high-throughput phenotyping, multi-omics technologies, genome editing tools and speed breeding platform to design rice genotypesresilient to stress combinations. Such strategies will be critical for sustaining rice yield and quality under future climate marked by warmer temperatures, limited water availability, and elevated atmospheric CO_2.

Abstract No: A8

Identification of cold stress responsive genes and miRNAs in Bitter Gourd

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ABSTRACT

Cold stress is a major abiotic constraint that significantly affects the growth, productivity, and geographical distribution of many horticultural crops, including bitter gourd (*Momordica charantia* L.). Despite its high nutritional and medicinal value, the molecular mechanisms underlying cold stress tolerance in bitter gourd remain poorly understood. In the present study, we investigated the transcriptomic and regulatory responses of bitter gourd under low-temperature stress to identify key genes and microRNAs associated with cold tolerance. Publicly available RNA-sequencing data were retrieved from the NCBI Sequence Read Archive and processed through a standard bioinformatics pipeline involving quality assessment, read trimming, genome alignment, and gene expression quantification. Differential expression analysis revealed a distinct set of cold-responsive genes involved in stress signaling, hormone regulation, antioxidant activity, and metabolic adjustment. Functional enrichment analysis highlighted the involvement of pathways related to abscisic acid signaling, reactive oxygen species scavenging, and transcriptional regulation under cold stress conditions. In addition, putative cold-responsive microRNAs were identified, suggesting a crucial role of post-transcriptional regulation in modulating stress-associated gene networks. The integrated analysis provides insights into the coordinated transcriptional and regulatory mechanisms that contribute to cold stress adaptation in bitter gourd. The candidate genes and miRNAs identified in this study offer valuable resources for future functional validation and may aid in the development of cold-tolerant bitter gourd cultivars through molecular breeding approaches.

Keywords: Cold Stress, Differentially Expressed Genes (DEGs), microRNA, Bitter Gourd

Abstract No: A9

Crop Modeling for Climate-Resilient and Nutritionally Secure Agricultural Production

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ABSTRACT

Climate change is increasingly threatening agricultural productivity and nutritional security through rising temperatures, altered rainfall patterns, and changing atmospheric CO_2 concentrations, particularly in rainfed and marginal regions. Crop simulation models provide an effective approach to quantify climate impacts on crop growth, phenology, yield, and resource-use efficiency, and to evaluate climate-resilient and nutrition-sensitive production strategies. By integrating climate, soil, crop, and management factors, widely used process-based models support informed decision-making under climate uncertainty. In this context, millets have emerged as climate-smart nutri-cereals due to their C_4 photosynthesis, short life cycle, efficient resource use, and strong tolerance to drought, heat, and poor soils. Using the DSSAT CERES-Millet model, the study evaluated the effects of sowing dates and varietal selection on pearl millet productivity under semi-arid conditions. The model demonstrated strong predictive performance, with a simulated grain yield of 3000.89 kg ha^{-1} closely matching the observed yield of 2989.56 kg ha^{-1}, indicating high simulation accuracy. Phenology, leaf area index, and grain yield were satisfactorily reproduced by the model. Optimized sowing windows, particularly mid-July planting, improved yield stability by enabling crops to escape terminal heat and moisture stress. Owing to their high content of protein, dietary fiber, iron, zinc, calcium, vitamins, and antioxidants, millets contribute significantly to nutritional security. Overall, the findings highlight the usefulness of crop simulation models as robust decision-support tools for promoting climate-resilient and nutritionally secure agricultural production systems.

Keywords: Climate change, Crop simulation models, Heat stress, Yield prediction, Decision-support systems

Abstract No: A10

Non-CG DNA hypomethylation promotes photosynthesis and nitrogen fixation in soybean

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ABSTRACT

Non-CG methylation plays a significant role in plant adaptation to environmental stress, such as mediating heat responses (hypocotyl elongation) and heavy metal tolerance. Hypomethylation can lead to improved agronomic traits such as larger seeds and increased photosynthesis, often by derepressing specific genes. The objective is to understand the impact of CRISPR/Cas9-mediated non-CG DNA hypomethylation on growth, seed quality, photosynthesis, and nitrogen fixation in soybean, and to identify key regulatory genes involved in these processes. CMT gene was targeted and 4 orthologs were chosen from phylogenetic tree analysis with *Arabidopsis.* Successful gene editing was confirmed by PCR amplification and sequencing. Quantification of DNA methylation levels by Whole genome bisulfite sequencing. Transcriptional level analysis to evaluate the effect on gene expression. The protein content of seeds are intensified. It is helpful in production of high yield soybean, epigenome engineering, modification of climate resilient crops, multiomics integration and studies can be done on biosafety evaluation.

Keywords : Hypomethylation, CRISPR/Cas9, PCR amplification, WGBS, epigenome, multiomics, biosafety.

Abstract No: A11

Reducing the Sugarcane Breeding Cycle through Simultaneous Evaluation of Seedling Ratoon and First Clonal Generation for Selection of High Brix and High Yielding Clones

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ABSTRACT

Sugarcane (*Saccharum spp.*) is a major commercial, industrial, and energy crop cultivated worldwide for its high sucrose content and economic importance. Varietal improvement in sugarcane involves hybridization followed by multi-stage clonal selection, a process that typically requires 9–11 years due to the crop's long growth cycle. Under changing climate scenarios, prolonged breeding cycles delay the deployment of stress-resilient and high-performing cultivars, highlighting the need for accelerated and efficient selection strategies. The present study aimed to simultaneously evaluate seedling ratoon and first clonal generation of sugarcane hybrids for the identification of high brix and high cane yielding genotypes, thereby reducing the breeding cycle and facilitating the recovery of desirable genotypes lost due to poor germination during clonal propagation. A total of 42 test genotypes along with three standard checks were planted in an augmented design under both seedling ratoon and first clonal generation during the planting season of 2024–25 at the breeding plots of the Sugarcane Research Institute, RPCAU, Pusa. Observations were recorded on twelve agro-morphological and quality traits, including number of shoots at 120 and 270 days after planting (DAP), brix (%) at mid-October, mid-November and mid-December, cane length, cane girth, number of millable canes, number of nodes per shoot, number of nodes in millable canes, single cane weight, and cane yield. Analysis of variance revealed significant mean sum of squares for all traits except cane girth in both generations, indicating substantial genetic variability among the genotypes. Mean performance analysis showed wide variation for cane yield, number of millable canes, single cane weight, and number of shoots at 120 DAP. Distributional analysis indicated positive skewness and leptokurtic behaviour for number of shoots at 120 and 270 DAP and cane yield in the seedling ratoon generation, whereas traits in the first clonal generation exhibited near-symmetrical distributions, suggesting stabilized trait expression under selection pressure. Based on combined performance for brix and cane yield across both generations, the genotypes CoX24003, CoX24007, CoX24011, CoX24017 and CoX24020 were identified as promising and advanced to the next stage of selection. The integrated evaluation approach enhances selection efficiency, reduces the sugarcane breeding cycle by one year, and supports the rapid development of climate-resilient, high-yielding sugarcane cultivars.

Keywords : Seedling ratoon, first clonal generation, augmented design, brix and cane yield.

Abstract No: A12

Marker-Assisted Development of Drought-Tolerant Rice Genotype of Manipur Using SSR Markers

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ABSTRACT

Rice is the staple food of Manipur, where productivity is severely affected by intermittent drought during reproductive and grain-filling stages. Breeding rice in rainfed situation requires characterization of Elite and Indigenous Rice Genotypes of Manipur for Drought Tolerance through Phenotyping and Marker Analysis. The creation of novel germplasm using various hybridization process by identifying various donors with appropriate background and abiotic stress tolerance to the well adopted local varieties susceptible to drought is the need of an hour. The local rice landrace Konjenjphou, though agronomically important, is highly susceptible to drought. The present study aimed to develop drought-tolerant rice genotypes adapted to Manipur by introgressing drought-responsive QTLs from the donor variety Sahbhagi Dhan into the recipient parent Konjenjphou through Marker-Assisted Selection (MAS). SSR markers **RM257** linked to major drought-tolerance QTL (qLR9.1, qHI9.1, qSF9.1 and qRWC9.1) present on chromosome 9, and **RM566** linked to qDTY9.1 present on chromosome 9 related to root traits were used. Both markers show clear difference between the bands therefore easily utilized for F1 confirmation, and subsequent selection based on MAS in segregating generations enabled efficient identification of drought-tolerant plants. The selected lines exhibited significantly improved spikelet fertility, RWC, proline content, and yield under stress compared to the recipient parent based on different morpho-physiological and biochemical traits. The study demonstrates that MAS is an efficient approach for improving drought tolerance in traditional rice cultivars of Manipur.

Abstract No: A13

Forecasting of Maize yield in Karnataka through Auto Regressive Integrated Moving Average (ARIMA) Models

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ABSTRACT

This research paper entitled "Forecasting of Maize yield in Karnataka through Auto Regressive Integrated Moving Average (ARIMA) Models" is based on the secondary data. Data was collected for the years 1990 to 2021 from the websites and Department of Economics and Statistics and India Agri. Stat. The different ARIMA models were used on the basis of Autocorrelation Function (ACF) and Partial autocorrelation Function (PACF) at various lags.TheARIMA models are fitted to the original time series data as well as the first difference data to check the stationarity. The possible ARIMA model are identified on the basis of significant coefficient of autoregressive and moving average components. Data for the year 1990 to 2019 were used for model building and rest two years data i.e. 2020 and 2021 were used for validation of yield forecast model of Maize. It was found that the ARIMA (2,0,1) model is best fitted for forecasting of Maize yield in Karnataka among all the other models namely ARIMA (0,0,1), ARIMA (1,0,0), ARIMA (1,0,1), ARIMA (0,1,1), ARIMA (1,1,1), ARIMA (0,1,2) and ARIMA (2,0,1). The parameters of all these models were computed and tested for their significance. Various statistics were also computed for selecting the adequacy, invertibility, stationarity, Diagnostic checks, % forecast error and parsimonious model with t-test and chi-square test. The low values of MAPE, MAE, RMSE, % forecast error and BIC are good inferences for forecasting of Mize yield in Bihar. Four years ahead forecasting from 2021 to 2024 for maize yield were calculated using ARIMA models. The four year ahead yield forecasting of maize in Karnataka for the year 2021,2022 ,2023 and 2024 are 357 kg/ha, 358 kg/ha, 355 kg/ha,358 kg/ha respectively. The ARIMA model for forecasting yield of Maize in Karnataka is as below:

$$\mathbf{Z_t – Z_{t-1} = 15.841 + 0.249(z_{t-1} - z_{t-2}) + 0.196(z_{t-2} - z_{t-3}) - 0.19(a_{t-1} - a_{t-2}) + at}$$

Keywords: Forecasting of Maize yield, ARIMA models, Box and Jenkins (1976),Time series

Abstract No: A14

Harnessing the Role of APETALA2/Ethylene-Responsive Transcription Factors in Microplastic Stress Tolerance in Millets

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ABSTRACT

Microplastics (MPs) are tiny plastic particles that can persist for hundreds of years in the environment. They are presently recognized as a pervasive environmental contaminant and an emerging form of abiotic stressor for agricultural systems. They can alter soil characteristics, nutrient availability, microbial diversity and impede plant growth and development. Millet is an extremely hardy and nutritious cereal crop capable of withstanding both biotic and abiotic stresses. Millet has been reported to be tolerant of heat, drought, cold, and salinity stress, due to several candidate genes, including NF-Y, Dof, WRKY, MYB, NAC, and HSP. However, very little research has been conducted on microplastic stress and the genes associated with its susceptibility or tolerance. In our laboratory, we have been investigating the molecular mechanisms underlying microplastic stress tolerance in millets, as well as the candidate genes involved. APETALA2/ethylene-responsive (AP2/ERF) transcription factors (TFs) regulate plant responses to stress by influencing hormone signalling pathways and interacting with specific genes. By binding to cis-regulatory elements in the promoters of target genes, these transcription factors coordinate responses to MP stress and control the expression of many genes, thereby ensuring tolerance to MP stress. Thus, the AP2/ERF TF has the potential to improve millet's tolerance to MP stress and other environmental factors. This will facilitate future research and development in millet and other crop improvement programs and contribute to achieving sustainable development goals.

Keywords: APETALA2, Abiotic stress, Microplastic, Millets, Transcription factors.

Abstract No: A15

Impact of Climate Resilient Agriculture for Ensuring Food Security: Sustainable Opportunities and Challenges for Marginal Farmers in Muzaffarpur, Bihar

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ABSTRACT

Climate Resilient Agriculture (CRA) effectively responds to climate change while contributing to sustainable productivity adapted to local hydro-meteorological conditions. CRA provides resilience to climate variability by enhancing agricultural viability through water exchange between surface and groundwater systems. In water-stressed countries such as India, where demand for water from agriculture, industry, and domestic use is increasing, CRA offers ways to address current and future food security challenges. The Climate Resilient Agriculture (CRA) programme was conducted by Krishi Vigyan Kendra, Turki, Muzaffarpur in two villages of Bihar, India. A survey conducted revealed that after the introduction and three years of continuation of the programme, maximum number of respondents (61.17%) were found to be in the category of higher adoption for CRA technologies due to the assured benefits in economic terms as well as for soil conservation and environmental protection and has made more and more farmers to adopt those technologies. Demonstrations were conducted in 205 acres in Kharif season and 245 acres in Rabi season. The B:C ratio of all Kharif crops were higher with CRA technology application (2.7 for paddy, 2.5 for maize. 1.9 for finger millet and 1.6 for sorghum) as compared to conventional practices (1.44 for paddy, 2.31 for maize. 1.56 for finger millet and 1.21 for sorghum). Crops demonstrated in Rabi season also showed that both the yield and B:C ratio (3.11 for wheat, 2.95 for lentil, 3.13 for chickpea, 2.83 for mustard and 3.70 for Rabi maize) were higher with the application of CRA technologies as compared to traditional ones (1.2 for wheat, 1.8 for lentil, 1.5 for chickpea, 1.9 for mustard and 1.77 for Rabi maize). This programme has open many new climate resilient options for the farmers to adopt in this scenario of changing climatic conditions. The climate resilient agriculture (CRA) technologies have been very successful especially in Rabi crops and increases the net profit of farmers by cutting down the cost of cultivation. However, the major challenges faced in the implementation of the programme was to convince farmers to come out from their traditional method of crop cultivation and adopt our technologies in the initial stages which were later reduced when the results started showing the impact.

Keywords: Climate Resilient crops, conventional practices, soil conservation, food security, climate variabilities.

Abstract No: A16

Assessment of nano fertilizers on Physiological Efficiency of Wheat

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ABSTRACT

Nano fertilizers are receiving considerable attention due to their enhanced nutrient use efficiency in plants and the increasing demand among farmers for sustainable crop production. Keeping this in view, the present study was undertaken to evaluate the effects of nano fertilizers on physiological and biochemical parameters of wheat. The field experiment was conducted during the rabi season of 2025–26 at the Research Farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar. The experiment comprised nine treatments with three replications and was laid out in a randomized block design (RBD). Observations on photosynthetic rate, SPAD chlorophyll index, water use efficiency, transpiration rate, and stomatal conductance were recorded at 40 days after sowing (DAS) i.e. 7 days after spraying. All the measured parameters showed significant variation among treatments. The maximum SPAD value was recorded in treatment T_2 (46.13), while the minimum was observed in T_1 (41.93). Water use efficiency was highest in T_6 (9.25 μmol CO_2 $mmol^{-1}$ H_2O) and lowest in T_2 (2.43 μmol CO_2 $mmol^{-1}$ H_2O). The photosynthetic rate was highest in T3 (24.39 μmol CO_2 m^{-2} s^{-1}), followed by T_6 (22.74 μmol CO_2 m^{-2} s^{-1}). The highest transpiration rate was recorded in T_6 (1.71 mmol H_2O m^{-2} s^{-1}), while the lowest was observed in T_1. Similarly, stomatal conductance was maximum in T_6 (135.3 mol H_2O m^{-2} s^{-1}), followed by T_5, T_2, and T_3. Overall, the results indicate that nano fertilizer application significantly improves physiological performance in wheat at 40 DAS.

Abstract No: A17

Biochemical Responses of rapeseed genotypes (*Brassica napus* L.) under saline stress conditions

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ABSTRACT

A field experiment was conducted during the rabi season of 2023 to investigate the molecular, genetic, and biochemical responses of rapeseed (Brassica napus L.) genotypes under saline stress conditions. The experiment was laid out in a Randomized Block Design at the Genetics and Plant Breeding Farm, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). Eleven rapeseed genotypes, namely TS-38 (check), TS-46, TS-67, TS-75-2ME, TS-75-2MM, TKM-20-1, TKM-20-2, Panchali, Bhawani, Tapeshwari, and PT-303, were evaluated for genetic variability, phenotypic and genotypic coefficients of variation (PCV and GCV), heritability (broad sense), genetic advance, correlation, path coefficient, and genetic divergence. Analysis of variance revealed highly significant differences among genotypes for all eleven characters, indicating the presence of substantial genetic variability under saline stress. High PCV and GCV were observed for grain yield, harvest index, spikelets number, biological yield per plant, and grains per panicle. High heritability coupled with high genetic advance as percent of mean was recorded for grain yield, spikelets number, biological yield per plant, grains per panicle, and harvest index, suggesting the predominance of additive gene action. Grain yield exhibited the highest genetic advance (26.02%), whereas days to 50% flowering showed the lowest. Grain yield showed significant and positive phenotypic correlation with harvest index, grains per panicle, and panicle-bearing tillers per plant. Path coefficient analysis revealed that harvest index exerted the highest positive direct effect on grain yield, followed by grains per panicle and panicle-bearing tillers per plant, while biological yield contributed the maximum positive indirect effect. Cluster analysis grouped the genotypes into four distinct clusters, with maximum inter-cluster distance observed between clusters II and I, indicating greater genetic divergence. Days to 50% flowering contributed most to genetic divergence, followed by spikelet fertility, harvest index, grain yield, and spikelets number. These findings highlight the potential of identified traits and diverse genotypes for selection and improvement of rapeseed under saline stress conditions.

Key Words : Crop improvement. stress tolerance,

Abstract No: A18

Morphological and Biochemical Mechanisms Associated with Heat Stress Tolerance in Maize (*Zea mays* L.)

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ABSTRACT

Maize (Zea mays L.), popularly known as the "Queen of Cereals," is one of the major cereal crops worldwide but is highly sensitive to high temperature stress, particularly during the reproductive stage. Heat stress adversely affects plant growth, physiological functions, and biochemical processes, ultimately leading to yield instability. The present study aimed to investigate the morphological, physiological, and biochemical responses of maize under heat stress during early reproductive development. Four contrasting sets of maize inbred lines were evaluated under field conditions at the Field Phenotyping Facility, CASCC, RPCAU, Pusa. The experiment consisted of two treatments: heat stress imposed during the early reproductive stage and a normal environment serving as control. Heat stress significantly affected plant growth, physiological traits, and biochemical activities, with notable variation among the inbred lines. UASBM6 recorded the highest plant height under both control (210 ± 7.93 cm) and heat stress (181 ± 4.00 cm) conditions, showing the greatest reduction due to stress, whereas UASBM35 showed the lowest plant height of 126 ± 6.11 cm (control) and 118.33 ± 1.20 cm (stress). Anthesis–silking interval (ASI) increased under heat stress, with the highest increase was observed in UASBM6 (11.66 ± 1.46 days) and the lowest in UASBM35 (6.33 ± 0.67 days). Biochemical analysis revealed a significant increase in antioxidant enzyme activities under heat stress. Catalase and peroxidase activities were markedly higher under heat stressed conditions, indicating enhanced scavenging of reactive oxygen species. UASBM6 exhibited the highest catalase (1718.89 ± 22.13 mmol g^{-1} FW min^{-1}) and peroxidase (23.07 ± 0.38 mmol g^{-1} FW min^{-1}) activities, while lower activities were recorded in UASBM35. Overall, the study highlights genotype-dependent physiological and biochemical responses contributing to heat stress tolerance in maize.

Keywords: Maize; Heat stress; Reproductive stage; Physiological traits; Biochemical responses and Antioxidant enzymes

Abstract No: A19

Climate resilient crops for nutritional security: Synergistic role of putrescine-doped ZnOnanoentities in droughtstressed rice

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ABSTRACT

Climate change-induced drought severely threatens rice (*Oryzasativa* L.), a staple crop important for nutritional security of over half the global population.While exogenous polyamines (PAs) have shown promise in enhancing drought stress (DS) tolerance in cereals, their integration with metallic nanoparticles for superior climate resilience remains underexplored. This study evaluates the synergistic efficacy of chemically synthesized putrescine (PUT)-doped zinc oxide nanoparticles (PUT-nZnO) in conferring DS tolerance to the drought-sensitive rice cultivar Swarna Sub1. We employed fourteen-day-old seedlings subjected to 12% polyethylene glycol-induced DS were foliarly treated with PUT alone or PUT-nZnO, and assessed for growth parameters, thermography, chloroplast ultrastructure, PA and ethylene signaling, cell viability, redox balance, and nuclear stability. Results demonstrated that PUT-nZnO markedly outperformed PUT alone by reinforcing membrane integrity, curtailing DNA degradation, reinstating ion homeostasis through enhanced ATP hydrolysis, preserving cellular structure and viability, modulating reactive oxygen species production, and augmenting antioxidative pathways.Additionally, elevated PA-oxidizing enzyme activity and optimized PA distribution promoted efficient chloroplastic energy transfer, with ultrastructural analysis confirming superior chloroplast integrity and downregulated ethylene signaling reducing programmed cell death. These findings establish PUT-nZnO as a biocompatible nano-enabled strategy for developing climate-resilient rice, thereby supporting stable yields of this nutritionally essential crop and advancing food and nutritional security in vulnerable agro-ecosystems facing escalating climatic adversities.

Keywords : Climate-resilient rice, Polyamine, Nanoparticle, Chloroplast, Redox biology

Abstract No: A20

Integrated nutrient sources and weed management practices influence yield performance, weed and economics of climate resilient finger millet crop

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ABSTRACT

Finger millet (Eleusine coracana) is a climate-resilient and nutritionally rich crop, yet its productivity is often limited due to inadequate nutrient and weed management practices. In this context, a field experiment was conducted during Kharif-2024 at Pusa Farm, RPCAU, Samastipur, Bihar. The experimental soil was calcareous sandy loam in nature with initial pH of 7.82, EC 0.29 dSm^{-1}, low organic carbon (0.45%), and available N, P_2O_5 and K_2O was 194.6, 16.9, and 115.4 kg ha^{-1}, respectively. Thes design was split plot with 3 replications. results showed that the weed-free treatment recorded the highest weed control efficiency (75.4%), which was statistically comparable to oxyfluorfen at 0.1 kg ha^{-1} (PE) followed by 2,4-D at 0.5 kg ha^{-1} (PoE) (72.4%). This herbicide combination also resulted in the lowest weed dry matter (105.3 g m^{-2}) and weed index (14.3%). Maximum N, P, and K uptake by grain and straw was observed under weed-free conditions, followed by oxyfluorfen (0.1 kg ha^{-1} PE) fb 2,4-D (0.5 kg ha^{-1} PoE), with nutrient uptake increases of 19.4% (N), 16.8% (P), and 18.7% (K) over the weedy check. Weed-free plots recorded the highest economic returns (gross return ₹1,24,415 ha^{-1}, net return ₹88,881 ha^{-1}, B:C ratio 2.61). Among herbicidal treatments, oxyfluorfen fb 2,4-D showed superior profitability (gross return ₹1,19,147 ha^{-1}; B:C ratio 2.34). Despite being a single-season study, the results indicate that 75% RDN through chemical fertilizers combined with 25% FYM, along with oxyfluorfen (0.1 kg ha^{-1} PE) followed by 2,4-D (0.5 kg ha^{-1} PoE), is an effective and sustainable option for improving finger millet productivity and profitability.

Abstract No: A21

Genome-wide Expression Profiling of Pathogenesis-related 1 Gene Family in response to Finger Millet Blast Infection

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ABSTRACT

Pathogenesis-related (PR) proteins constitute a crucial component of the plant innate immune system and play a significant role in defence against fungal pathogens. Finger millet (*Eleusine coracana* L.), an important climate-resilient cereal crop, is highly susceptible to blast disease, necessitating a deeper understanding of its molecular defence mechanisms. The present study focuses on the systematic characterisation of pathogenesis-related (PR) proteins in finger millet through an integrated *in silico* and biochemical approach. Genome-wide identification of PR proteins in finger millet was achieved by BLASTp and HMMER-based homology searches. A critical synthesis of existing literature was undertaken to contextualise PR protein classification and functional relevance in plant defence. Orthologous analysis, based on well-characterised*PR* gene sequences from *Arabidopsis thaliana* and *Oryza sativa*, enabled the identification of *PR1* genes in finger millet. Sequence conservation analysis of PR1 proteins revealed the preservation of key amino acid residues, suggesting functional conservation across species. Additionally, biochemical profiling of blast-infected finger millet genotypes indicated defence-associated responses consistent with the involvement of PR proteins in host resistance. Building upon these findings, the study is currently progressing towards experimental validation of the retrieved PR-related proteins in blast-infected finger millet genotypes to establish their expression patterns and functional significance during pathogen challenge. Overall, this work provides valuable insights into the conservation, biochemical relevance, and potential defensive role of PR proteins in finger millet, thereby contributing to the development of molecular strategies for enhancing blast resistance in this nutritionally important crop.

Keywords: Pathogenesis-related, Blast, Genome-wide identification, Biotic Stress

Abstract No: A22

An Entropy-Weighted Adaptive Capacity Index for Farmers under Climate Change in North Bihar

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ABSTRACT

Climate change threatens agricultural livelihoods in vulnerable regions such as North Bihar, India. This study constructs an Adaptive Capacity Index (ACI) for farm households using the Sustainable Livelihood Framework (SLF), integrating indicators across five livelihood capitals. Primary data were collected from selected districts of North Bihar. An entropy-weighted method was used to derive objective indicator weights. Distance to the agricultural office received the highest weight (0.17), followed by land ownership (0.11) and soil quality (0.10), underscoring the importance of institutional access and natural resources in shaping adaptive capacity. Based on the index, most farming households exhibited a moderate level of adaptive capacity, while only a small proportion attained a high level. Robustness of the index was assessed using bootstrap resampling. The smaller interquartile range (IQR) across resamples indicates consistent weighting and stability of the index. The findings highlight key constraints to farmers' adaptive capacity and demonstrate the usefulness of an SLF-based entropy-weighted index for identifying vulnerable households and guiding climate-resilient livelihood interventions in North Bihar.

Keywords: Adaptive capacity; Climate change; Sustainable Livelihood Framework; Entropy-weighted index; Bootstrap sensitivity analysis

Abstract No: A23

Evaluation of Frontline Demonstrations on Yield and Economics Analysis of Green gram in Muzaffarpur District of Bihar, India

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ABSTRACT

Front line demonstrations (FLDs) on the improved green gram variety IPM 205-7 were conducted at farmers' fields in Muzaffarpur district during the summer seasons of 2021–22 and 2022–23 to evaluate yield performance, technological gaps, and economic feasibility of improved cultivation practices. The demonstrated plots consistently recorded significantly higher grain yield compared to farmers' traditional practices. On a pooled two-year basis, the improved technology produced an average of 24.2% higher yield than the local check, indicating a clear yield advantage due to adoption of recommended practices. The extension gap between demonstrated technology and farmers' practices ranged from 200-220 kg ha^{-1}, with an average of 210 kg ha^{-1}, highlighting substantial scope for increasing green gram productivity through improved extension efforts. The yield enhancement under FLDs was mainly attributed to the use of an improved variety, balanced nutrient management, and scientific crop management practices. Although the demonstrated technology involved a slightly higher cost of cultivation, it resulted in higher economic returns, with an additional net return of ₹12,650 ha^{-1} and an average benefit–cost ratio of 2.8, confirming its economic viability. Variations in technology gap and technology index across years reflected differences in the adaptability and feasibility of recommended practices under varying agro-climatic conditions. Higher technology index values suggested the need to strengthen extension services for effective technology transfer. Economic returns varied across seasons due to changes in grain yield and minimum support price (MSP), with the highest gross return recorded during 2022–23. Overall, the FLDs proved effective in enhancing farmers' knowledge, skills, and adoption of improved green gram cultivation practices.

Keywords : Green gram, demonstration, gap analysis, economics, grain yields and production technology.

Abstract No: A24

Evaluation of Heterosis, Heterobeltiosis, and Genetic Variability in Maize Crosses

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ABSTRACT

The present study was undertaken to evaluate the extent of heterosis for yield and quality traits in maize. In the first experiment, six inbred lines were crossed with four testers using a line × tester mating design during kharif 2022. A total of 24 resultant hybrids, along with their parental lines and standard checks, were subsequently evaluated for heterotic performance during rabi 2022–23. Analysis of variance revealed significant differences among genotypes for all the traits studied, indicating the presence of substantial genetic variability. Estimates of standard heterosis varied widely among the crosses in the desirable direction, and several hybrids emerged as superior specific combinations. Heterosis for grain yield per plant was largely attributed to the combined expression of heterosis in key yield component traits. Among the evaluated hybrids, PFSR 132 × BML 6, PFSR 135 × BML 6, PFSR 70 × CML 286, PFSR 135 × CML 451, and PFSR 29 × BML 7 exhibited the highest levels of standard heterosis for grain yield per plant. These hybrids can be considered promising candidates for further evaluation and potential utilization in maize breeding programs aimed at yield enhancement.

Keywords : Maize, heterosis, hybrid vigour, standard heterosis, Grain yield, crop productivity

Abstract No: A25

Smart Fertilization for Nutritional Security: Precision Fertigation Strategies in Hybrid Brinjal

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ABSTRACT

Climate-resilient nutrient management strategies are crucial for enhancing crop productivity, profitability, and nutritional security under increasing resource constraints and climate variability. Precision fertilization through fertigation offers a sustainable approach to improve nutrient use efficiency while minimizing soil degradation and environmental losses. A field experiment was conducted at a farmer's field in Idikarai village, Coimbatore district, Tamil Nadu, to evaluate smart fertilization strategies using Tamil Nadu Agricultural University Water Soluble Fertilizer (TNAU-WSF, 19:19:19) in hybrid brinjal (Solanum melongena L.) cv. 'Lalita'. The experiment was laid out in a strip plot design with five main plot treatments comprising graded levels of STCR-based NPK (0, 25, 50, 75, and 100%) and five subplot treatments involving different rates and methods of TNAU-WSF application through fertigation and foliar spray. Results revealed that precision fertigation significantly enhanced growth, physiological efficiency, biochemical quality, nutrient uptake, soil fertility status, and fruit yield. The interaction treatment 100% STCR-NPK + TNAU-WSF @ 60 kg ha^{-1} recorded the highest yield (49.83 t ha^{-1}); however, it was statistically on par with 75% STCR-NPK + TNAU-WSF @ 60 kg ha^{-1}. Notably, the latter treatment achieved the highest benefit–cost ratio (4.09), demonstrating superior nutrient use efficiency with a 25% reduction in conventional fertilizer inputs. Progressive depletion of available soil N, P, and K from vegetative to harvest stages indicated effective nutrient uptake under fertigation. FTIR analysis confirmed the chemical stability and enhanced solubility of TNAU-WSF, supporting improved bioavailability during fertigation. The study highlights that smart fertilization through precision fertigation can enhance crop resilience, optimize fertilizer inputs, improve fruit quality, and ensure economic sustainability. The application of 75% STCR-NPK combined with TNAU-WSF @ 60 kg ha^{-1} emerges as a climate-smart, economically viable, and environmentally sound nutrient management strategy for sustainable brinjal production.

Abstract No: A26

Machine Learning Driven Prediction of Deletions and Duplications in Plant Genome

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ABSTRACT

Structural variations (CNVs), including deletions and duplications, represent a major source of large-scale variation in plant genomes (>1000bp) and are known to influence agronomically important traits. Accurate classification of CNV types remains challenging due to genome size, high repeat content, and heterogeneous sequencing coverage commonly observed in plant genomes. In this study, we present a Gradient Boosting-based machine learning framework for the prediction and classification of CNV types- deletions, duplications, and non-CNV regions in plant genomes. The proposed approach utilizes features derived from sequencing depth profiles, nucleotide composition, and coverage-related statistics that capture key characteristics of CNV regions. The model was trained using a high-confidence dataset comprising both experimentally validated and computationally curated CNVs, ensuring robustness across diverse genomic contexts. Performance evaluation was conducted across multiple CNV size ranges and varying training set sizes to assess model stability and generalization capability. The Gradient Boosting model demonstrated strong and consistent performance, achieving an overall classification accuracy of 89.27%, with precision, recall, and F1-score values of 89.3%, and a receiver operating characteristic area under the curve (AUC) of 0.9783. These results highlight the reliability of the proposed framework in distinguishing CNV types in complex plant genomes. This method focuses on accurately classifying CNV types from pre-identified genomic regions, thereby complementing existing CNV detection pipelines. The approach offers a scalable and efficient solution for CNV classification, with potential applications in plant genomics, breeding, and evolutionary studies.

Keywords : Machine Learning, Plant Genomics, Structural Variation, Deletion, Duplication

Abstract No: A27

Identification of Drought-Tolerant Finger Millet Genotypes at the Seedling Stage Using Integrated Phenotypic and Biochemical Traits

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ABSTRACT

The increasing frequency and severity of drought events under ongoing climate change pose a major threat to crop establishment and productivity, particularly in rainfed agroecosystems where finger millet (*Eleusine coracana* L.) is a key nutritionally rich cereal. Although finger millet is generally considered drought resilient, substantial genotypic, variation exists at the seedling stage, which remains inadequately characterised. Identifying drought-tolerant genotypes and understanding their physiological and molecular responses are therefore critical for improving climate resilience. In this study, drought tolerance in five finger millet genotypes was evaluated using an integrated morphological, biochemical, and molecular approach. The integrated analysis effectively discriminated genotypes based on their drought responses. Among the five genotypes, VL352 exhibited the highest level of drought tolerance, characterised by sustained seedling growth, enhanced root biomass, and a well-balanced antioxidant defence system. In contrast, RM1 and UdruMilliage were identified as drought sensitive, showing pronounced growth inhibition and oxidative imbalance, with excessive peroxidase activity particularly evident in UdruMilliage. GE444 and RAU-8 displayed moderate tolerance, with GE444 maintaining relatively better shoot growth and RAU-8 exhibiting improved root system exploration under stress. Based on Polyethylene-glycol (PEG)-induced drought tolerance, the genotypes were ranked as VL352 > RAU-8 > RM1 > GE444 >UdruMilliage. Furthermore, drought-responsive candidate genes were identified, and gene-specific primers were designed and synthesised. Ongoing work focuses on molecular validation of these genes under optimised PEG-induced drought stress with appropriate controls, aiming to elucidate the genetic basis of drought tolerance at the seedling stage in finger millet.

Keywords : Drought Response, Antioxidant defence, Climate resilient, Genetic expressivity

Abstract No: A28

Foxtail Millet: A Climate-Resilient Nutri-Cereal for Nutritional Security under Climate Change

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ABSTRACT

Foxtail millet (Setaria italica L.) is an important nutri-cereal known for its adaptability to diverse agro-climatic conditions and its potential role in ensuring nutritional security under climate change. With the increasing incidence of drought, heat stress, and declining soil fertility, the promotion of climate-resilient crops has become essential for sustainable agriculture. Foxtail millet is characterized by low water requirement, short duration, and tolerance to abiotic stresses, making it suitable for cultivation in rainfed and marginal environments. The crop is nutritionally rich, containing appreciable levels of dietary fiber, protein, minerals, and bioactive compounds, which contribute to addressing malnutrition and improving human health. In addition to its nutritional benefits, foxtail millet exhibits wide genetic variability, providing significant scope for crop improvement through selection and breeding approaches. The present review highlights the importance of foxtail millet as a climate-resilient crop and emphasizes its role in achieving nutritional security in the era of climate change. It also discusses the potential of foxtail millet in sustainable farming systems and its future prospects in crop improvement programs aimed at developing resilient and nutritionally superior cultivars.

Keywords : Foxtail millet, climate resilience, nutritional security, millets, sustainable agriculture

Abstract No: A29

Integrated biotechnological and AI innovations for crop improvement

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ABSTRACT

Crops provide food, clothing and other important products for the global population. To meet the demands of a growing population, substantial improvements are required in crop yield, quality and production sustainability. However, these goals are constrained by various environmental factors and limited genetic resources. Overcoming these limitations requires a paradigm shift in crop improvement by fully leveraging natural genetic diversity alongside biotechnological approaches such as genome editing and the heterologous expression of designed proteins, coupled with multimodal data integration. In this Review, we provide an in-depth analysis of integrated uses of omics technologies, genome editing, protein design and high- throughput phenotyping, in crop improvement, supported by artificial intelligence- enabled tools. We discuss the emerging applications and current challenges of these technologies in crop improvement. Finally, we present a perspective on how elite alleles generated through these technologies can be incorporated into the genomes of existing and de novo domesticated crops, aided by a proposed artificial intelligence model. We suggest that integrating these technologies with agricultural practices will lead to a new revolution in crop improvement, contributing to global food security in a sustainable manner. Guotian Li et.al (2025).

Key words: crop yield and quality, designed proteins, artificial intelligence, sustainable.

Abstract No: A30

Meta-QTL analysis for identification of candidate gene for waterlogging tolerance in pigeon pea

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ABSTRACT

Pigeon pea (*Cajanus cajan*) is an important grain legume cultivated in tropical and subtropical regions for its nutritional and agronomic importance. However, waterlogging stress is a major abiotic constraint limiting its productivity, particularly in low-lying rainfed areas. Exposure to excess soil moisture during germination and early vegetative stages causes hypoxia or anoxia, leading to physiological damage, reduced growth, and yield loss. Although certain pigeon pea genotypes exhibit tolerance to waterlogging through adaptive morphological and biochemical mechanisms, the genetic basis of this trait remains poorly characterized.The present study aims to elucidate the genetic architecture of waterlogging tolerance in pigeon pea through meta-QTL analysis and to identify potential candidate genes associated with this trait. Previously reported quantitative trait loci (QTLs) related to waterlogging tolerance were collected from published studies and integrated into a consensus genetic map using the LPmerge package in R-Studio. This approach enables the consolidation of QTL information across different genetic backgrounds and environments to identify stable genomic regions. A consensus linkage map covering multiple chromosomes was successfully constructed, providing a reliable framework for further meta-QTL analysis. These stable genomic regions are expected to harbor candidate genes involved in adaptive responses such as anaerobic metabolism, root modification, and antioxidant defense. The results offer valuable targets for marker-assisted selection and future functional genomics studies aimed at developing climate-resilient pigeon pea varieties.

Keywords: Waterlogging tolerance, Meta-QTL analysis, Consensus genetic map, Candidate genes, qRT-PCR

Abstract No: A31

Climate-Resilient Vegetable Cropping Systems and Fungal Diversity: Implications for Nutritional Security and Sustainable Agriculture in Madhepura

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ABSTRACT

Climate change has emerged as a major threat to global food and nutritional security by intensifying droughts, floods, heat stress, soil degradation, and the incidence of crop diseases. In this context, climate-resilient crops—including drought-tolerant, heat-resistant, flood-adaptive, and salinity-tolerant varieties—play a critical role in sustaining agricultural productivity under adverse environmental conditions. Hybrid and biofortified vegetable crops are particularly significant due to their high nutritional value and capacity to adapt to changing climatic scenarios. Vegetables are an indispensable component of the human diet, supplying essential vitamins, minerals, dietary fiber, antioxidants, and phytonutrients such as carotenoids, lutein, and lycopene that enhance immunity and reduce the risk of chronic diseases. Climate variability and environmental stress profoundly influence soil microbial communities, especially fungal populations, which can either promote plant growth through symbiotic associations or cause severe crop losses as pathogens. The present study investigates the fungal diversity associated with selected hybrid vegetable crop fields of Madhepura to understand their role in crop health, productivity, and nutritional quality under changing climatic conditions. The relevance of this study has increased in the post–COVID-19 period, where greater emphasis has been placed on nutritious and safe food production. Analyzing fungal diversity provides valuable insights into soil health, plant–microbe interactions, and disease dynamics within climate-resilient cropping systems. Integrating climate-resilient vegetable cultivation with an improved understanding of fungal diversity can contribute to sustainable disease management, enhanced ecosystem resilience, and stable nutritional output. Such integrated approaches are essential for supporting farmers' livelihoods and ensuring long-term food and nutritional security. Strengthening research efforts, policy support, and climate-smart agricultural practices will be key to developing resilient and sustainable food systems in the face of ongoing climate change.

Keywords: Climate-resilient crops, Fungal diversity, Hybrid vegetables, Nutritional security, Antioxidants, Plant pathology, Sustainable agriculture

Abstract No: A32

Morphological and molecular characterization of seedling-stage cold tolerance in rice (Oryza sativa L.) hybrids

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ABSTRACT

Low temperature is one of the most important abiotic constrains in rice cultivation. Rice plant growth and development are affected by cold stress from germination to reproductive stages. Twelve parents and thirty-two hybrids along with cold tolerant and susceptible check varieties were evaluated for cold tolerance at seedling stage. From the cold screening experiment, the hybrids viz., CMS 23A × IR 65514-5-2-19R-1, CMS 14A × IR 65483-14-1-1-4-13R, CMS 64A × IR 65514-5-2-19R-1 and CMS 64A × IR 63870-7-3-2-3-3R were found to be tolerant to cold stress whereas the hybrid, CMS 64A × JGL 29651 was moderately tolerant to cold stress. Molecular screening for confirmation of cold tolerance was performed using 13 SSR markers, resulting in the identification by three differentiating markers (RM85, RM341, and RM561). The identified tolerant genotypes were CMS 64B, CMS 69B, and IR 65514-5-2-1 19R-1, both for parents and hybrids viz., CMS 23A × IR 63870-7-3-2-3-3R, CMS 23A × IR 65514-5-2-1-19R-1, CMS 23A × JGL 27347, CMS 64A × IR 63870-7 3-2-3-3R, CMS 64A × IR 65483-14-1-1-4-13R, CMS 64A × IR 65514-5-2-1-19R 1, CMS 69A × JGL 21005 and CMS 69A × JGL 24444. The genotypes with cold tolerance in the seedling stage identified from this study and the SSR markers mentioned above could be useful for developing cold tolerant rice.

Keywords: Cold tolerance, Leaf discoloration score, Seedling stage, SPAD analysis, SSR markers, Rice hybrids.

Abstract No: A33

Molecular Characterization of ERF Genes for Waterlogging Tolerance in Foxtail Millet

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ABSTRACT

Waterlogging stress is a major abiotic constraint that adversely affects crop growth and productivity by creating hypoxic conditions in the root zone. Plants respond to such stress through complex molecular and biochemical mechanisms, among which Ethylene Responsive Factor (ERF) transcription factors play a central role in regulating hypoxia- and ethylene-mediated signaling pathways. Foxtail millet (Setaria italica), a climate-resilient and nutritionally important cereal, serves as an ideal model to investigate genetic determinants of waterlogging tolerance. The present study aimed to identify and molecularly characterize ERF genes associated with waterlogging tolerance in foxtail millet and to assess their potential role in stress adaptation. ERF genes were identified through genome-wide in silico analysis using conserved AP2/ERF domains. Identified genes were characterized for gene structure, conserved motifs, physicochemical properties, chromosomal localization, and phylogenetic relationships with ERF proteins from other cereal crops. Promoter regions were analyzed to identify stress-responsive cis-regulatory elements. Expression profiling of selected ERF genes was carried out using quantitative real-time PCR in waterlogging-tolerant and susceptible genotypes under controlled stress conditions. Additionally, genic simple sequence repeat (SSR) markers were mined from ERF gene sequences to develop functional molecular markers. Multiple ERF genes were identified and classified into distinct subfamilies. Promoter analysis revealed the presence of hypoxia-, ethylene-, and stress-responsive cis-elements. Expression analysis showed significant up-regulation of specific ERF genes in tolerant genotypes under waterlogging stress compared to susceptible ones. Several genic SSR markers derived from ERF genes exhibited polymorphism, indicating their potential application in marker-assisted breeding. Overall, this study provides valuable molecular insights into ERF-mediated waterlogging tolerance in foxtail millet and identifies promising candidate genes and markers for developing climate-resilient crop varieties.

Keywords: *Setaria italica,* ERF, PCR, Waterlogging, SSR, Hypoxia, Foxtail Millet

Abstract No: A34

Biochemical and molecular basis of parthenocarpy in cucurbitaceous vegetable crops under climate stress

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ABSTRACT

Climate change induced abiotic stresses such as elevated temperature, drought and erratic rainfall adversely affect pollination, fertilization, and fruit set in cucurbitaceous vegetables, resulting in significant yield losses. Parthenocarpy, the development of fruits without fertilization has emerged as an important adaptive trait to overcome climate induced pollination failure and ensure yield stability in cucurbits. The present study aims to elucidate the biochemical and molecular mechanisms regulating parthenocarpic fruit development in cucurbitaceous vegetables under climate stress conditions. Biochemical analyses indicate significant changes in endogenous phytohormone levels, particularly auxins and gibberellins, during early ovary growth in parthenocarpic genotypes compared to non-parthenocarpic ones. Enhanced carbohydrate metabolism and increased activity of enzymes associated with hormone biosynthesis support ovary enlargement and fruit initiation under stress. At the molecular level, differential expression of genes involved in auxin signalling (*ARFs* and *AUX/IAA*), gibberellin biosynthesis and stress responsive pathways has been reported in parthenocarpic cucurbits and related vegetable crops. These coordinated biochemical and molecular changes enable fruit development independent of fertilization. Parthenocarpy thus represents a climate resilient trait regulated by complex hormonal and gene networks. Understanding its biochemical and molecular basis will facilitate marker-assisted selection and biotechnological interventions for developing climate resilient, high-yielding cucurbit varieties. Exploitation of parthenocarpy can play a crucial role in ensuring sustainable vegetable production and nutritional security under changing climatic conditions.

Keywords: Parthenocarpy, cucurbits, climate resilience, abiotic stress, phytohormones, molecular markers

Abstract No: A35

NAC transcription factor–derived SSR marker characterization and genome-wide association analysis of seed longevity traits in *Allium cepa*

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ABSTRACT

Allium cepa is one of the most important vegetable crops in Asia; however, the rapid decline in seed viability poses a major constraint to maintaining a sustainable seed supply across planting seasons. To explore genomic regions potentially involved in the regulation of seed longevity in *A. cepa*, a total of 77 NAC transcription factor–derived simple sequence repeat (SSR) markers were developed from *Allium cepa* and *Allium sativum* NAC gene sequences. These NAC-derived SSRs were predominantly hexanucleotide repeats (81.8%) and exhibited high cross-transferability across Allium species, with a mean polymorphism information content (PIC) of 0.34 and a mean heterozygosity index of 0.45. In parallel, 30 previously reported *A. cepa* intron-length polymorphism (AcILP) markers were evaluated, of which 26 (86%) showed cross-transferability, with a mean heterozygosity index of 0.47 and a PIC value of 0.35.To identify molecular markers associated with seed longevity, genome-wide association studies (GWAS) were conducted using selected NAC-derived SSRs, AcILP markers, and genotyping-by-sequencing (GBS)–derived SNPs. Descriptive analysis of seed longevity traits revealed substantial variation in germination percentage and vigour indices among the tested *A. cepa* accessions. A significant association of SNP SCAJJJL010033730.1_40317 with both germination percentage and vigour index I indicated a possible pleiotropic effect linking seed germination and early seedling growth. Additionally, SNPs SCAJJJL010043805.1_135933, SCAJJJL010063632.1_30460, and SCAJJJL010052679.1_514690 were significantly associated with vigour index II. Functional annotation of genes proximal to these SNPs identified putative gag–pol and hypothetical proteins, suggesting a potential role in transcriptional regulation and stress adaptation mechanisms. This study represents the first report of SNPs associated with seed longevity in Allium, providing valuable genomic resources for the development of onion varieties with improved seed longevity.

Keywords: Simple sequence repeat marker, NAC transcription factors, vigour index, marker-assisted selection, intron length polymorphic marker, seed longevity, GBS, GWAS

Abstract No: A36

Valorization of the Invasive Weed *Stachytarpheta jamaicensis* (L.) Vahl: Growth-Promoting Effects on Soybean (*Glycine max* L.)

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ABSTRACT

Stachytarpheta jamaicensis (L.) Vahl, an invasive weed species, is well recognized for its rich phytochemical profile, comprising flavonoids, phenolics, alkaloids, and terpenoids. This study investigates its potential as a natural biostimulant to enhance physiological, biochemical, and agronomic traits in soybean (*Glycine max* L.). *S. jamaicensis*extract (SjE) at concentrations of 10% and 25% were applied via soil drenching. The 10% SjE treatment significantly improved plant morphological attributes, including the number of leaves, shoot length, shoot fresh weight, root number, root length, and root fresh weight, compared to both the control and 25% SjE treatments. Photosynthetic pigment analysis revealed a 1.21-fold increase in chlorophyll a, 1.25-fold in chlorophyll b, and a 1.21-fold rise in total chlorophyll and carotenoids, indicating enhanced photosynthetic performance. Biochemical analyses further demonstrated significant increases in antioxidant enzyme activitiessuperoxide dismutase (2.02-fold), catalase (1.66-fold)and total phenolic content (1.68-fold), suggesting improved oxidative stress tolerance. These findings confirm that *S. jamaicensis* extract is an effective and sustainable biostimulant that can replace conventional chemical-based growth enhancers. Moreover, the repurposing of an invasive weed for agricultural benefit underscores a circular bioeconomy approach, aligning with sustainable and eco-friendly farming strategies. This study highlights the potential of *S. jamaicensis* in improving crop productivity and resilience through natural elicitor-based mechanisms.

Keywords: *Stachytarphetajamaicensis*, Soybean, Biostimulant, Growth Promotion, Sustainable Agriculture, Circular Bioeconomy.

Abstract No: A37

In Silico Characterization and Marker–Trait Association of BES1 Transcription Factors Conferring Fusarium Wilt Resistance in Chickpea (_Cicer arietinum_ L.)

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ABSTRACT

Chickpea (*Cicer arietinum* L.) is one of the most important pulse crops worldwide; however, its productivity is severely constrained by Fusarium wilt caused by *Fusarium oxysporum* f. sp. ciceris, leading to substantial yield losses. Brassinosteroids (BRs) are essential phytohormones regulating plant growth, development, and stress responses. BRI1-EMS-SUPPRESSOR 1 (BES1) transcription factors act as central regulators of BR signalling downstream of the BRI1 receptor, yet their role in chickpea biotic stress tolerance remains poorly understood. The present study aimed to perform a comprehensive in silico characterization of the BES1 transcription factor family in chickpea, identify biotic stress–responsive cis-regulatory elements in BES1 genes, and detect BES1 gene–specific single nucleotide polymorphisms (SNPs) associated with Fusarium wilt resistance through marker–trait association (MTA) analysis.A total of eight BES1 family members encoded by six BES1 genes were retrieved from the Plant Transcription Factor Database, and their corresponding coding sequences, gene IDs, and chromosomal locations were obtained from NCBI GenBank. Physicochemical properties of BES1 proteins were predicted using ProtParam. Promoter regions (1 kb upstream of the 5′ UTR) were analyzed for biotic stress–responsive cis-elements using the New PLACE database. BES1-specific SNPs were extracted from the CicerSeq database, and MTA analysis was conducted using disease incidence (DI%) data from 244 chickpea genotypes employing t-test and regression analysis, followed by validation using a General Linear Model in TASSEL.Chickpea BES1 proteins ranged from 316 to 703 amino acids in length with molecular weights between ~34 and 78 kDa. All BES1 proteins exhibited negative GRAVY values, indicating hydrophilic nature, and instability indices greater than 40. Promoter analysis identified five biotic stress–responsive cis-elements, among which GT1CONSENSUS was the most abundant across BES1 genes. In MTA analysis, SNP Ca8_7400723 within BES1 gene LOC101496832 showed a significant association with Fusarium wilt resistance ($R^2 = 0.07141$; $P = 9.26 \times 10^{-4}$). This study provides valuable insights into the structural, regulatory, and allelic diversity of chickpea BES1 genes and identifies a promising molecular marker for Fusarium wilt resistance, with potential applications in marker-assisted breeding.

Key words: Chickpea. Fusarium wilt, Brassinosteroids, Fusarium oxysporum, MTA, BES1

Abstract No: A38

Ethylene Signalling–Associated EIL Transcription Factors in Chickpea: Genome-Wide Characterization and Marker–Trait Association with Fusarium Wilt Resistance

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ABSTRACT

Chickpea (Cicer arietinum L.) is a globally important pulse crop whose productivity is markedly reduced by Fusarium wilt, a destructive disease caused by Fusarium oxysporum f. sp. ciceris. Among plant hormones, ethylene plays a pivotal role in regulating growth, development, and defense-related responses to biotic stress. The transcription factors Ethylene-Insensitive 3 (EIN3) and EIN3-Like (EIL) function as central components of the ethylene signaling pathway by modulating the expression of downstream ethylene-responsive factor genes. However, the genomic organization and potential contribution of EIL transcription factors to Fusarium wilt resistance in chickpea remain insufficiently explored. The present study aimed to perform an extensive in silico characterization of the EIL transcription factor family in chickpea, identify biotic stress–responsive cis-regulatory elements in their promoter regions, and detect EIL gene–specific single nucleotide polymorphisms (SNPs) associated with Fusarium wilt resistance through marker–trait association (MTA) analysis.A total of nine EIL genes were identified from the Plant Transcription Factor Database and further annotated using NCBI GenBank for chromosomal localization and coding sequence retrieval. Physicochemical properties of EIL proteins, including amino acid length, molecular weight, theoretical isoelectric point (pI), GRAVY, and instability index, were predicted using ProtParam. To elucidate transcriptional regulation, 1 kb upstream promoter regions (5′ UTR) were screened for biotic stress–responsive cis-elements using the New PLACE database. EIL-specific SNPs were retrieved from the CicerSeq database, and their association with Fusarium wilt resistance was evaluated using disease incidence (DI%) data from 244 chickpea genotypes. Statistical analyses were conducted using t-tests and regression in Microsoft Excel across whole and contrasting populations, followed by validation using a General Linear Model in TASSEL.The chickpea genome harbored nine EIL family proteins encoded by seven genes, with protein lengths ranging from 416 to 808 amino acids and molecular weights between ~47 and 90 kDa. All EIL proteins exhibited negative GRAVY values, indicating hydrophilic nature and predicted instability. Promoter analysis revealed multiple biotic stress–responsive cis-regulatory elements, suggesting transcriptional involvement of EIL genes during pathogen challenge. SNP mining identified 50 EIL-specific polymorphic SNPs, among which SNP Ca_7918992 within LOC101500668 showed a significant association with Fusarium wilt resistance across populations.These findings provide valuable insights into the structural, regulatory, and diversity of chickpea EIL genes and identify a promising SNP marker for enhancing Fusarium wilt resistance through marker-assisted breeding.

Key words: Ethylene, EIL, Chickpea, Fusarium Wilt, MTA

Abstract No: A39

Identification of indigenous bacterial wilt resistant eggplant accessions from south west coastal hotspot of India

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ABSTRACT

Eggplant (*Solanum melongena* L.) is a nutritionally important vegetable crop contributing significantly to nutritional security in India. However, its cultivation in high-rainfall south-west coastal regions is severely constrained by bacterial wilt caused by *Ralstonia solanacearum*, a destructive soil-borne pathogen with a wide host range and limited chemical control options. Harnessing resistance from indigenous germplasm represents a sustainable, climate-resilient strategy for disease management.The present study aimed to identify stable sources of bacterial wilt resistance from indigenous eggplant accessions conserved at the ICAR–National Bureau of Plant Genetic Resources (NBPGR), Regional Station, Kerala. A total of 101 accessions representing four *Solanum* species (*S. melongena, S. insanum, S. viarum,* and *S. violaceum*) and introgressed lines were evaluated under bacterial wilt sick-plot conditions during *Kharif,* 2022-23. Disease incidence was confirmed using the bacterial ooze test and recorded at weekly intervals and quantified using percent disease incidence (PDI). The accessions were classified into various resistance categories.Among the 101 accessions evaluated, 69 belonged to *S. melongena*. Of these, thirteen accessions exhibited high levels of resistance to bacterial wilt. These included modern cultivars Arka Keshav and Haritha (resistant check); primitive cultivars IC255756, IC624237, IC624240, and IC626119; and indigenous landraces IC256708, IC383695, IC421190, IC636521, IC636524, IC641518, and Vengeri.The identified resistant indigenous accessions provide valuable genetic resources for developing bacterial wilt–resistant hybrids and rootstocks, strengthening climate-resilient eggplant production systems and promoting sustainable utilization of native germplasm for nutritional security.

Keywords : *Ralstonia solanacearum, Solanum melongena,* indigenous germplasm, bacterial wilt, climate resilience

Abstract No: A40

SSR-Based Molecular Evaluation of Advanced Sub1-Introgressed Rice Lines derived from cross between Sabour Shree x Swarna-Sub1

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ABSTRACT

Rice is an important staple food crop worldwide. The productivity of rice is severely affected by several biotic and abiotic stresses. Focusing on abiotic factors, submergence due to recurrent flood in different regions of India such as Bihar, pose major threat to rice cultivation, with large area of lowland rice frequently affected during monsoon season. Under current climate change scenario, unpredictable flood has intensified yield losses in flood prone region. The *SUB1*quantitative trait locus (QTL) plays a crucial role in imparting submergence tolerance in rice by enhancing survival under complete inundation, thereby contributing to yield stability. The present study aimed to explore molecular characteristics of advanced Sub1 introgressed lines derived from crosses between Sabour Shree x Swarna-Sub1. Out of 50 SSR markers used, 27 showed polymorphism between two parental lines which were further utilizes for molecular evaluation of SUB1 introgressed lines. Molecular characterization using SSR markers, allowed for the assessment of genetic diversity among the advanced lines. The constructed dendrogram based on SSR markers revealed the genetic relationships and relatedness among the advanced Sub1 introgressed lines, forming four major clusters. The three advanced lines namely, BC_3F_4-SS-1and BC_3F_4-SS-10 are very closely related to Sabour Shree and also found better in terms of yield. The information obtained from molecular characterization provides valuable insights for further study related to adaptability under different agro-climatic zones of the Bihar.

Keywords: Introgressed lines, SUB1, Submergence, Rice, SSR

Abstract No: A41

Evaluating Heat Stress Adaptation in Linseed Through Physiological and Biochemical Traits

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ABSTRACT

Terminal heat stress (THS) poses a critical threat to linseed (Linum usitatissimum L.) productivity, particularly during the reproductive and seed-filling phases. This study evaluated the physiological, biochemical, and antioxidant responses of 36 selected linseed genotypes, identified from an initial screening of 124 genotypes, under optimum and late sown (heat-stressed) conditions over two consecutive seasons (2023-2024 & 2024-2025). Key physiological parameters, including chlorophyll content, relative water content (RWC), electrolyte leakage (EL%), malondialdehyde (MDA), and hydrogen peroxide (H_2O_2) levels, showed significant genotypic variation, reflecting differential oxidative stress responses. Tolerant genotypes such as RLU11, RLU10, and JLU11 maintained higher chlorophyll and RWC, with lower EL, MDA, and H_2O_2 under stress. Biochemical analyses revealed higher accumulation of proline, total phenolics, flavonoids, and tannins in tolerant genotypes, correlating with enhanced enzymatic (SOD, POD, CAT) and non-enzymatic antioxidant activity (FRAP, DPPH, ABTS). Moreover, oil content was better retained in heat-tolerant lines, while susceptible genotypes suffered sharp reductions. Principal component analysis confirmed that traits such as reduction in seed yield, antioxidant activity, and membrane stability parameters strongly contributed to variability under stress. The findings emphasize that membrane integrity, osmotic adjustment, and redox homeostasis are critical for heat resilience in linseed. This integrative approach provides valuable physiological and biochemical markers for selecting heat-tolerant genotypes and supports targeted breeding strategies to develop climate-resilient linseed cultivars.

Keywords:*Terminal heat stress, Linseed, Physiological characteristics, Biochemical characteristics, Oil content.*

Abstract No: A42

Heat Resilience in Wheat: Insights from Agronomic, Physiological, and Biochemical Traits

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ABSTRACT

Wheat, scientifically known as *Triticum aestivum* L., accounts for nearly thirty percent of global grain production and fifty percent of international grain trade, yet its productivity is significantly threatened by heat stress, particularly during the reproductive stage. Terminal heat stress, which occurs when temperatures rise during grain development, accelerates phenological events and impairs reproductive processes. This study evaluated 11 wheat genotypes under timely sown and late sown conditions during two consecutive seasons (2023 & 2024) to assess variation in agronomic, physiological, biochemical, and antioxidant traits associated with heat tolerance. Delayed sowing resulted in notable reductions in plant height, tiller number, days to anthesis, and pollen fertility.Physiological assessments revealed reduced chlorophyll content and relative water content, along with increased electrolyte leakage, malondialdehyde, and hydrogen peroxide in heat-stressed plants, indicating membrane injury and oxidative damage. Biochemical responses showed greater accumulation of proline, total phenolics, and flavonoids in comparatively tolerant genotypes, contributing to improved osmotic adjustment and stress mitigation. These compounds supported better antioxidant capacity and helped counteract oxidative stress in tolerant lines.These combined responses emphasise that membrane stability, osmotic regulation, and antioxidant defence play crucial roles in conferring heat resilience. The study underscores the potential of integrating agronomic and physiological biochemical markers to identify wheat genotypes with improved tolerance to terminal heat stress for future breeding programs.

Keywords: *Wheat, Terminal heat stress, Reproductive Biology, Physiological traits, Biochemical traits.*

Abstract No: A43

Mapping of Helminthosporium leaf blight resistantQTLs in oats

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ABSTRACT

Oat (*Avena sativa* L.) is an important winter cereal primarily cultivated in India as a forage crop, with emerging significance as a dual-purpose cereal for both human and animal nutrition. However, oat productivity is severely constrained by several biotic stresses, among which Helminthosporium leaf blight (HLB) is a major foliar disease capable of causing substantial yield losses under warm and humid conditions. Despite its economic importance, limited information is available on genetic resistance to HLB in oat, and resistant sources have not been adequately characterized or mapped. The present study aimed to identify resistant germplasm and map quantitative trait loci (QTLs) associated with HLB resistance. A diverse panel of 167 oat germplasm lines was evaluated for disease incidence and severity using a 1-9 rating scale. Most lines exhibited high susceptibility, while a few showed moderate resistance, with disease severity ranging from approximately 20 to 78 per cent. Based on contrasting disease responses, two parental lines were selected and hybridized to develop segregating populations. Disease screening of 140 F_2 plants revealed segregation fitting a complementary gene interaction, indicating the involvement of multiple genes governing resistance. Molecular characterization using 220 SSR markers identified 24 polymorphic markers between the parents, which were subsequently employed for genotyping and linkage map construction. QTL analysis using composite interval mapping detected disease resistance-associated QTLs on chromosomes 1 and 7. Although the population size and marker density may have limited the detection of minor QTLs, the identified genomic regions represent a significant step toward understanding the genetic basis of HLB resistance in oats. The findings provide valuable markers and resistant sources that can be effectively utilized in marker-assisted breeding programs to enhance disease resistance and reduce yield losses.

Key Words: Oats, HLB, QTL, Mapping

Abstract No: A44

Mushroom: A Resilient Crop for Nutritional and Economic Security

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ABSTRACT

Climate variability and resource degradation pose serious challenges to sustainable agricultural production and food security. In this context, mushrooms have emerged as climate-resilient crops with significant potential to enhance nutritional and economic security. Mushrooms are low in calories and fat yet rich in high-quality proteins containing essential amino acids such as lysine, leucine, and methionine, making them especially valuable for vegetarian and vegan diets. They also contain bioactive polysaccharides, including β-glucans and heteroglycans, known for their immunomodulatory, cholesterol-lowering, and anti-cancer properties. In addition, mushrooms provide unsaturated fatty acids, B-complex vitamins, vitamin D_2 (upon UV exposure), and essential minerals such as selenium, potassium, iron, and copper, contributing to dietary diversification and nutritional security.

Mushroom cultivation requires minimal land, water, and time and can be practiced year-round under diverse agro-climatic conditions. It efficiently utilizes agricultural and agro-industrial residues, converting low-value biomass into high-value nutritious food while reducing environmental pollution. Species such as *PleurotussppAgaricus*, *Calocybe*,*Hericium,Volvariella*, *Lentinula,Flammulina*exhibit wide adaptability to fluctuating environmental conditions.

Moreover, mushroom cultivation generates rapid income, employment, and entrepreneurial opportunities, particularly for small and marginal farmers, women, and rural youth. The spent mushroom substrate further enhances sustainability by serving as organic manure or soil conditioner. Therefore, integrating mushroom cultivation into existing farming systems can strengthen livelihood resilience and promote sustainable agriculture under changing climatic condition

Keywords: Mushroom, Climate, nutritional & economic security.

Abstract No: A45

Molecular, genetic and biochemical Responses of rice genotypes (*Oryza Sativa* L.) under salinity conditions"

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Theme: Crop improvement for drought, heat, andsalinity tolerance; genetic biofortification;promoting indigenous and orphan crops

ABSTRACT

A field experiment was counducted during the kharif season of 2023 to examine the **"Molecular, genetic and biochemical Responses of rice genotypes (*Oryza Sativa* L.) under salinity conditions"**. The field experiment was conducted in Randomized Block Design at Genetics & Plant breeding Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). The experiment consisted of 20 rice genotypes viz., IVT 101/5321, IVT 102/5308, IVT 103/5313, IVT 104/5301, IVT 105/5303, IVT 106/5320 (LC), IVT 107/5312, IVT 108/5314, IVT 109/5307, IVT 110/5319, IVT 111/5316, IVT 112/5302, IVT 114/5311, IVT 115/5306, IVT 116/5315, IVT 117/5305, IVT 118/5310, IVT119/5304, IVT 120/5309 and IVT 121/5317. Genetic variability, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability in broad sense and genetic advance in percent of mean were analyzed .The analysis of variance shows that mean sum of square due to treatment were highly significant for all eleven characters among 20 rice genotypes which is an indication that there is presence of sufficient variability among rice genotypes under saline condition. Tolerant varieties were IVT 112/5302, IVT 110/5319, IVT 102/5308, IVT 101/5321 and IVT 120/5309 as they gave higher yield.Higher magnitudes of phenotypic coefficient of variation were found for grain yield, harvest index, spikeletsnumber, biological yield per plant and grains/panicle. High estimates of heritability were observed for grain yield, spikelets number, biological yield per plant, grains/panicle, harvest index. Whereas medium estimates of heritability were observed for panicle bearing tillers per plant, test weight, spikelet fertility, plant height, panicle length, days to 50% flowering. Under saline condition grain yield (26.02%) showed highest value of genetic advance and days to 50% flowering (1.82%) showed lowest value of genetic advance. Grain yield showed highly

significant and positive phenotypic correlation with harvest index (0.640), grains/panicle (0.626) and panicle bearing tillers per plant (0.509). Harvest index showed maximum positive direct effect on grain yield followed by grains/panicle and panicle bearing tillers/plant.Grains/panicle showed maximum positive indirect effect on grain yield via biological yield/plant.Twenty rice genotypes under saline condition was grouped into four non-overlapping clusters.The highest intra cluster distance was recorded for cluster I followed by cluster II. The lowest intra cluster distance was observed for III. Maximum inter cluster distance was observed in case of cluster II and I followed by cluster IV and III.Under saline condition the maximum percent contribution in genetic divergence in rice genotypes was observed by days to 50% flowering followed by spikelet fertility, harvest index, grain yield and spikelets number. Other characters showed low values for contribution.SDS-PAGE dendrogram analysis it was concluded that there is minimum similarity between genotypes IVT 107/5312, IVT 114/5311, IVT 110/5319, IVT 118/5310, whereas maximum similarity between IVT 115/5306, IVT 101/5321, IVT 117/5305, IVT 121/5317, IVT 108/5314, IVT 109/5307 and IVT 112/5302. Nitrate reductase (NR) activity decreased in response to Nacl toxicity. The activity of nitrite reductase (NiR) decreased in response to salinity. The levels of NR and NiR in the salt sensitive cultivars were lower than those in the salt resistant varieties. The effect of salinity on nitrate reductase activity in rice plants showed that nitrogen assimilation is negatively impacted, and the impact was greater in salt-sensitive cultivars.Proline content abruptly increased in all rice genotypes in response to salinity. The maximum accumulation of proline was recorded in IVT 105/5303 and followed by IVT 110/5319 and IVT 111/5316 in treatment and least in IVT 118/5310 and IVT 120/5309. The maximum accumulation of total soluble sugar was recorded in IVT 106/5320 followed by IVT 104/5301, IVT 109/5307 and IVT 102/5308 and least in IVT 114/5311 followed by IVT 118/5310 and IVT 121/5317. PCR amplification with SSR primer RM 24 and RM 2 showed polymorphism. IVT 101/5321, IVT 102/5308, IVT 105/5303, IVT 110/5319, IVT 111/5316, IVT 114/5311, IVT 116/5315, IVT 118/5310 and IVT 121/5317 showed distinct banding pattern in RM 24 as well as bands IVT 105/5303, IVT 106/5320, IVT 108/5314, IVT 109/5307, IVT 110/5319, IVT 111/5316, IVT 112/5302, IVT 114/5311, IVT 115/5306, IVT 116/5315, IVT 117/5305, IVT 118/5310 and IVT 119/5304 showed distinct banding pattern in RM 2 whereas primers RM 493 and RM 242 showed monomorphism.

Key Word : Crop improvement.salinity tolerance,

Abstract No: A46

Early Seedling Responses of Finger Millet Under Salinity Stress

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ABSTRACT

Finger millet (*Eleusine coracana* L.) is a nutritionally rich and climate-resilient cereal crop valued for its high mineral content and adaptability to marginal environments. However, increasing soil salinity under climate change poses a major constraint to seed germination and early seedling establishment, affecting crop productivity and nutritional security. Evaluation of germination rate and Seed Vigour Indices provides a reliable approach to assess salinity tolerance at early growth stages.The experiment was conducted under a completely randomized design with two treatments, and 3 replications under both control and salinity stress. Germination rate was recorded 15 days after sowing. Seed vigour Index I was calculated as germination percentage multiplied by seedling length, while Seed Vigour Index II was derived using germination percentage and seedling dry weight. Data were analyzed using analysis of variance. Salinity stress significantly reduced all seedling parameters. Germination rate declined from 66.69 % under control conditions to 55.64 % under salinity stress. Seed Vigour Index I decreased from 17701.43 to 7922.28, while Seed Vigour Index II reduced from 834.23 to 617.94 under saline conditions. Analysis of variance indicated highly significant treatment effects ($P < 0.05$). Correlation analysis revealed significant positive associations for Seed Vigour Index I ($r = 0.211$, $p = 0.001$), Seed Vigour Index II ($r = 0.244$, $p < 0.001$), and Germination Rate ($r = 0.316$, $p < 0.001$), with germination rate showing the strongest relationship. These findings highlight germination and vigour indices as effective screening tools for developing salt-tolerant, climate-resilient finger millet varieties to support nutritional security.

Keywords: Salinity, Germination rate , Seed Vigour Index I , Seed Vigour Index II.

Abstract No: A47

Salinity stress response of proso millet genotypes during germination and seedling stage

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ABSTRACT

Proso millet (*Panicum miliaceum* L.) is a short duration, allotetraploid crop (2n=4x=36) belonging to the family Poaceae, with an estimated genome size of 923 Mbp. It is known for its climate resilience, drought tolerance, nutritional content like highest protein content (12.5 g/100 g) among minor millets and represents an ideal choice for the present climate change scenario due to its minimal input requirements. Despite its climate resilient nature, salinity stress possesses detrimental effects on proso millet during the critical stages of seed germination and early seedling establishment. This study investigates 40 proso millet genotypes under salinity stress and the traits such as germination percentage at 12 days after sowing, Seedling Vigour Index I and Seedling Vigour Index II were recorded. The experiment was conducted in completely randomized design (CRD) with 3 replications each in stress and control.Correlation analysis established highly significant positive correlation between germination percentage with seedling vigour indices at 0.001 level. Analysis of variance revealed a significant reduction in trait values under salinity stress. Germination percentage declined from 73.75% under control to 57.50% under saline conditions, while Seedling Vigour Index I decreased from 1117.08 (control) to 617.14 (stress), and Seedling Vigour Index II from 16626.17 (control) to 7258.76 (stress), with treatment effects being highly significant ($p< 0.05$). These findings indicate that salinity stress significantly impairs initial seedling establishment. The high positive correlation between these traits suggests their reliability for screening under salinity stress at the germination stage for developing climate resilient and nutritionally secure proso millet varieties.

Keywords: Proso millet, Salinity stress, Germination percentage, Seedling Vigour Index

Abstract No: A48

Barnyard Millet: A Powerhouse of Bio actives for Modern Functional Foods

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ABSTRACT

Barnyard millet (*Echinochloa frumentacea*) is an underutilized minor millet gaining recognition as a promising functional food due to its exceptional nutritional and health-promoting properties. Belonging to the family Poaceae, this climate-resilient cereal is widely cultivated in Asia and Africa and is well adapted to low-input and stress-prone environments. The grain structure comprises bran, germ, and endosperm, contributing to its rich nutrient profile. Barnyard millet is gluten-free and characterized by high-quality protein, slowly digestible starch, and substantial dietary fiber. It is particularly valued for its micronutrient density, including iron, zinc, calcium, and phosphorus, along with significant levels of bioactive compounds such as polyphenols, flavonoids, tannins, alkaloids, chlorogenic acid, and gallic acid. These phytochemicals contribute to strong antioxidant, anti-inflammatory, anti-diabetic, anti-obesity, and potential anticancer activities.

Processing techniques such as dehulling, roasting, malting, germination, and fermentation enhance nutrient bioavailability while reducing anti-nutritional factors like phytic acid. Studies indicate that processed barnyard millet exhibits improved antioxidant capacity and functional properties, including favourable water and oil absorption capacity, swelling power, and bulk density, making it suitable for value-added product development. Its low glycaemic index and high Fiber content support glycemic control and gut health, thereby contributing to the prevention and management of chronic diseases.

Product development efforts have incorporated barnyard millet into bakery products, multigrain beverages, rusks, biscuits, and other functional foods without significantly compromising sensory quality. With growing global demand for naturally functional foods and increasing consumer awareness of health and sustainability, barnyard millet presents strong potential for enhancing food security and nutritional diversification. Overall, barnyard millet emerges as a nutrient-dense, bioactive-rich functional grain with significant applications in health-oriented food formulations and sustainable food systems.

Keywords: Climate resilient, gluten-free, food security, bioactive compounds, phytic acid, product development

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Abstract No: A49

Marker–Trait Association of Rice Blast Resistance for Climate-Resilient Production in the North Eastern Hill Region of India

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ABSTRACT

Rice blast is a major biotic constraint to rice productivity in the North Eastern Hill (NEH) region of India, causing yield losses of 40–46%. The NEH region is considered to be thecentre of diversity for both rice and *Magnaporthe grisea*, harbours highly variable pathogen populations that frequently overcome host resistance. This study aimed to identify effective blast resistance loci and associated molecular markers suitable for climate-resilient rice production under Meghalaya conditions.A mini core collection of 80 rice genotypes was evaluated across two seasons under upland and lowland (late, early and timely sown) ecosystems. Based on phenotypic screening, 43 contrasting genotypes were selected for marker–trait association analysis($P_{\alpha}<0.05$)using reported major gene-linked markers. Seven loci—**Pi54, Pi2, Pib, Pi2/9, Pi5, Pb1/qPbm, and Pi20(t)**—were significantly associated with blast resistance. **Pi5** and **Pi54** were consistently associated with leaf blast resistance, while **Pib** and **qPbm**showed association with neck blast resistance.

Under timely sown upland conditions, five markers (JJ803, RM224, RM7102, MRG4766, and 5083 Indel) were significantly associated with leaf blast resistance. Under late sown upland conditions, six markers (JJ803, RM224, RM7102, MRG4766, RM11715, and RM11787) showed significant association. Markers effective under early upland conditions were also associated under timely lowland conditions, indicating stability across ecosystems. Only one marker, 5083 Indel targeting gene qPbm11, showed significant association with neck blast resistance under both upland and lowland conditions.

Deployment of these stable resistance loci will contribute to the development of rice varieties with durable blast resistance, thereby strengthening climate-resilient rice production in the NEH region.

Keywords: Rice, blast resistance, marker–trait association, climate resilience, molecular markers, NEH region.

Abstract No: A50

High Temperature Induced Physiological Modulation In Lentil (*Lens culinaris*)

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ABSTRACT

An experiment was conducted here in the Department of Plant Physiology and Biochemistry, CBS&H, RPCAU, Pusa. Five genotypes (KLS-218, IBL-526, IPL-220, PSL-9, PUSA AGETI) of lentil *(Lens culinaris*) have been taken, in 3 dates of showing, in 3 replications, to observe the impacts of heat stress on physiology on the genotypes according to the changing climate. We performed techniques such as relative water content (RWC), membrane stability index (MSI), tissue temperature at grain filling stage and chlorophyll index for analysis of these varieties. It was found that the genotypes, with different dates of showing and their integrated effects showed some level of positive results like KLS-218, IPL-220 in photosynthetic activity, KLS-218, PSL-9 in membrane stability and KLS-218, IBL-526 in heat tolerance. But by changing the showing dates, there was a more positive impact on the varieties like IBL-526, KLS-218 in water holding capacity and cellular turgidity. KLS-218 was performed best out of all varieties in all above conditions.

KEY WORDS: Replications, Heat stress, Relative water content, Membrane stability index, Tissue temperature, Chlorophyll index, Photosynthetic activity, Heat tolerance, Cellular turgidity.

Theme B
Plant Metabolomics & System Biology

Abstract No: B1

Adaptive Resoponses to high CO_2 by Oil Seed Crop Plants *Brassica juncea* and *Brassica campestris* Grown in Free Air Carbon Dioxide Enrichment (FACE) Environment

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ABSTRACT

Adaptation of oil seed crop plants to climate change was studied in *Brassica juncea*, cv Pusa Jaikisan, and *Brassica campestris* cv Pusa Gold grown in free air carbon dioxide enrichment (FACE) (600 μmol mol^{-1}) (eCO_2) environment for three consecutive years. The eCO_2 plants had higher leaf area, biomass, and yield per plant as compared to ambient air-grown plants. The dark respiration increased in eCO_2 to support better crop growth. The light response curves of carbon assimilation demonstrated a 30%-40% increase in the light-saturated photosynthesis rate and higher quantum yield of carbon assimilation by leaves of eCO_2-plants mostly due to reduced photorespiration. The A-Ci curves demonstrated that the maximum carboxylation efficiency, Vcmax was not reduced in eCO_2 plants due to unaltered rubisco abundance. A decrease in stomatal conductance in eCO_2 reduced the transpiration rate and increased the water use efficiency. However, an increased leaf area index in eCO_2 would have offset the gains due to reduced transpiration. Proteomics and genomics profiling revealed an increase in the expression of proteins/genes involved in photosynthesis, nitrogen assimilation, ribosome biogenesis, signal transduction, antioxidative response and a decrease of those involved in photorespiration, amino acid metabolism, Fe-S cluster cofactor, and protein degradation as adaptation to eCO2. It is inferred that polyploid *Brassica* has intrinsic capacity to buffer photosynthesis against CO_2-induced downregulation when nitrogen supply and sink demand are sustained. The regulatory parameters identified here are promising targets for further research and marker-assisted breeding, genomic selection, or gene-editing approaches to improve yield potential under future eCO_2 regimes.

Sustained photosynthetic enhancement without Rubisco downregulation

A central uncertainty in predicting crop responses to eCO_2 is whether initial stimulation of photosynthesis is maintained or attenuated through biochemical acclimation. In many C_3 crops, prolonged exposure to eCO_2 leads to downregulation of Rubisco content and carboxylation capacity, particularly under nitrogen-limiting conditions, thereby reducing yield gains (Ainsworth & Long, 2021; Rogers et al., 2023). In contrast, our FACE-grown Brassica cultivars maintained elevated net assimilation rates across seasons, with no evidence of reduced Vcmax or Rubisco abundance. A–Ci analyses indicate that enhanced carbon gain was primarily driven by suppression of photorespiration rather than increases in electron transport capacity, consistent with theoretical predictions for C_3

metabolism under high CO_2. These results suggest that Brassica possesses intrinsic capacity to buffer photosynthetic machinery against CO_2-induced downregulation when nitrogen supply and sink demand are sufficient.

Carbon–nitrogen coordination as a determinant of CO_2 responsiveness

Increasing evidence indicates that sustained CO_2 responsiveness depends on the plant's ability to balance enhanced carbon assimilation with nitrogen acquisition and utilization. Disruption of this balance often leads to carbohydrate accumulation, feedback inhibition of photosynthesis, and reduced protein synthesis (Bloom et al., 2020; Medlyn et al., 2024). Transcriptomic and proteomic analyses in this study revealed coordinated upregulation of nitrogen assimilation pathways, ribosomal proteins, and translational machinery under eCO_2, suggesting that enhanced carbon availability was effectively channelled into growth-related metabolism. Maintenance of protein synthesis capacity likely underpins the absence of photosynthetic acclimation observed here and highlights carbon–nitrogen integration as a key target for breeding CO_2-resilient crops.

Metabolic reprogramming and redox homeostasis under elevated CO_2

Beyond photosynthesis, eCO_2 induced broad metabolic reprogramming, including increased respiratory activity and upregulation of redox-regulatory pathways. Elevated dark respiration under eCO_2, often interpreted as a cost, may instead reflect increased mitochondrial capacity supporting accelerated biosynthesis and growth, as reported in other high-yielding crop systems (Leakey et al., 2019). Concurrent upregulation of redox-associated proteins suggests active maintenance of cellular homeostasis under enhanced metabolic flux. Such coordinated regulation is increasingly recognised as essential for sustaining productivity under fluctuating and future climates.

Implications for oilseed biotechnology and climate-resilient breeding

From a biotechnological perspective, these findings identify several candidate processes underpinning long-term CO_2 responsiveness: (i) stability of photosynthetic protein complexes, (ii) efficient nitrogen assimilation and remobilisation, and (iii) maintenance of translational and redox capacity. Unlike short-term chamber studies, FACE-based multi-season validation strengthens the translational relevance of these mechanisms. Given the expanding genomic resources for Brassica species, the pathways and regulatory nodes identified here represent promising targets for marker-assisted selection, genomic selection, or gene-editing approaches aimed at improving yield stability under future CO_2 regimes.

Conclusions

In summary, this study demonstrates that Brassica oilseed crops can sustain enhanced photosynthesis and yield under elevated CO_2 through integrated physiological and molecular acclimation rather than transient stimulation. By linking field-based FACE data with multi-omics insights, we provide a mechanistic framework for understanding CO_2 responsiveness and identify actionable targets for crop biotechnology. These results support the strategic inclusion of CO_2 responsiveness and carbon–nitrogen coordination traits in breeding programmes aimed at climate-resilient oilseed production.

Abstract No: B2

Physiological and molecular response of colored wheat against nutrient deficiencies is linked to accumulation of distinct anthocyanins

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ABSTRACT

Anthocyanin-biofortified colored wheats provide enhanced nutritional value and antioxidant capacity, offering potential to alleviate malnutrition in vulnerable populations. This study examined the physiological, biochemical, and molecular responses of colored wheat genotypes—black (NABI MG-11), purple, blue, and white (PBW 621)—under phosphate (Pi) and iron (Fe) deficiencies, individually and in combination, at seedling and mature grain stages. Wheat seedlings were more sensitive to Fe than Pi deficiency, while combined Pi–Fe deficiency partially rescued root growth, particularly in black wheat, which showed smaller reductions in biomass, nutrients, and anthocyanin content.

Pi deficiency triggered changes in root morphology, biomass, micronutrient accumulation, and anthocyanin composition, following the adaptation trend white < blue < purple < black. Metabolomic and qRT-PCR analyses revealed stress-induced accumulation of distinct anthocyanins (cyanidin, delphinidin, and peonidin derivatives) and upregulation of genes related to phosphate transport and anthocyanin biosynthesis in black wheat. Overall, black wheat exhibited superior physiological and molecular adaptability, highlighting its potential for biofortification and sustainable cultivation under nutrient-deficient conditions.

Keywords : Colored grain, colored wheat, anthocyanins, phosphorous, transporters, deficiency, abiotic stress.

Abstract No: B3

Studying Precise Nitrogen Use Efficiency of Rice: A New Hydroponics System with Details Accounts Followed by GWAS to Identify Novel QTLs and Candidate Genes

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ABSTRACT

The efficient use of nitrogenous fertilizers in agriculture is critical for lowering nitrogen-induced pollution and reducing production costs. Although several studies have evaluated the performance of rice genotypes under nitrogen (N) stress, detailed protocols for screening these genotypes at both the seedling and maturity stages, without strict control of Nlevelsare limited, except in hydroponic systems. Though there are many hydroponics studies are reported in rice research, we did not get any account to grow rice till the maturity, specially under-N-stress. As the yield is the most important parameter under low-nitrogen, growing them till maturity is extremely important, and deciding the does at different stages of growth are equally important. A set up is necessary for the above purpose with materials required, spacing, and other growth condition. As we faced this challenges, we took up this task to develop the tecvhnology and here we present a detailed hydroponic protocol for growing both Indica and Aus type rice plants to full maturity under both N-stress and N-optimal conditions. The protocol outlines system requirements, experimental design, growth media, growing conditions, observed parameters, management practices, and troubleshooting guidelines. In addition to growth conditions, we describe standardized methods for recording observations throughout the plant growth cycle. To validate the protocol, initially two rice genotypes with contrasting nitrogen use efficiency (NUE), IR64 (Indica) and Nagina 22 (Aus), were grown to maturity under optimal and N-stress conditions. Significant differences ($p < 0.05$) between the genotypes were detected across multiple traits, including morphological characteristics and nitrogen uptake, from the seedling stage through maturity. We also assessed the role of aeration in the hydroponic system and found that non-aerated conditions were more suitable for rice cultivation. Overall, this protocol provides an efficient, cost-effective, and low-maintenance hydroponic system for studying nitrogen stress, enabling precise phenotyping and non-destructive root analysis.

Following this a genome-wide association study (GWAS) was conducted to identify novel quantitative trait loci (QTLs) and candidate genes associated with nitrogen use efficiency (NUE)related traits in rice using a diverse panel of 96 genotypes. Nitrogen is a critical nutrient for rice growth and yield; however, as usual, its excessive or inefficient use contributes to environmental pollution. Among cereal crops, rice inherently exhibits the lowest NUE. To elucidate the genetic basis of NUE, rice plants were grown to maturity under contrasting nitrogen regimes in the hydroponic system developed by us,

and subjected to GWAS. The association panel consisted of 96 genetically diverse genotypes, including landraces, improved varieties, and selected EMS-induced mutants differing in NUE, and was genotyped using 47,686 high-quality single nucleotide polymorphism (SNP) markers. Significant phenotypic variation was observed for all the nitrogen-responsive traits under both nitrogen conditions. The contrasting trait responses under different nitrogen regimes highlighted the need for regime-specific breeding strategies. Population structure analysis revealed two subpopulations with varying levels of admixture, while linkage disequilibrium analysis indicated an average LD decay of 108.4 kb. GWAS performed using three different algorithms - MLM, FarmCPU, and BLINK, which identified 568 significant marker–trait associations (MTAs) with -log10(p) values greater than 4 across traits and nitrogen conditions. Among these, 24 MTAs were consistently detected by all three algorithms, of which 13 were novel and encompassed 156 candidate genes within the corresponding LD blocks. Notable candidate genes underlying these novel MTAs included OsRNRS2, involved in chloroplast biosynthesis, and OsDREB1C, OsARF13, OsWAK16, OsAMT3, OsGLP, OsCAT9, and members of the OsAPx gene family, which are associated with nitrogen utilization and abiotic stress tolerance in rice. Additionally, candidate genes such as Osprx59, Osprx62, OsPSBS2, OsWAK14, OsWAK15, OsAMT3, OsNIN8, and OsHCT2 from MTAs with major allelic effects exhibited differential responses under nitrogen-deficient conditions. Collectively, these MTAs and candidate genes represent valuable genetic resources for the development of rice varieties with improved nitrogen use efficiency. This precise study was possible due to the newly developed Hydroponic system, and in near future the genes/QTLs will be utilized after functionally validating them.

Abstract No: B4

Impact of post-anthesis high night temperature on starch and protein metabolism in developing grains of late sown wheat

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ABSTRACT

Late sowing of bread wheat (*Triticumaestivum* L.) imperils the grain development phase of the crop as it exposes it to short or long term episodes of high (day/night) temperature resulting in a significant loss in yield and quality of the crop. A study was conducted to evaluate the impact of post-anthesis high night temperature (HNT) (~2.6 °C above ambient) on yield and its components, flour quality, sucrose, starch and storage protein metabolism in developing grains of wheat ear. We hypothesized that genotypes with low heat susceptibility index maintain stability in above parameters under HNT. We selected four contrasting genotypes (HI 1544, HI 1563, HD 2864 and HD 2932) based on their HSI and maturity (early and late) duration. The increased grain growth rate under HNT in both grain (superior and inferior) types was associated with higher activity of sucrose synthase and invertases at 5 and 15 days after anthesis (DAA). The significant reduction in starch and amylopectin content at 20 DAA under HNT may influence pasting properties of the flour thus affecting on biscuit and cookie making quality. The accumulation of gliadin (α, β, γ) and glutenin (High-Low molecular weight) subfractions showed differential response across genotypes under HNT. An increased total protein, gliadin to glutenin ratio, falling number and reduced sedimentation volume under HNT can affect dough properties. Our study elucidates the effect of HNT on yield, starch and protein composition and consequently the flour quality.

Keywords: High night temperature, wheat, starch, protein.

Abstract No: B5

Dynamics of seed reserve utilization and NADPH Oxidase activity during the germination of Indian mustard (*Brassica juncea*) and its implications on seed vigour

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ABSTRACT

Indian quality mustard varieties are the new type of resources developed for their low levels of erucic acid (<2%) and glucosinolate (<30 μmole/g defatted meal) contents. These nutritionally enriched quality mustards are poor in seed vigour than the conventional type. Reactive oxygen species (ROS) are now known to play important role in seed physiology. NADPH oxidase enzyme 'deliberately' produces ROS during seed germination which play important role in seed germination. Reserve mobilization is essential to support the growth of embryo during germination and post germination growth. The present study was aimed to know the differential vigour response and the ROS dependency for reserve mobilization and utilization during seed germination in Indian mustard mediated by NADPH oxidase. Conventional genotypes have a significantly higher seedling vigour indices, whereas significantly lower seed vigour indices along with maximum electrical conductivity were observed in double-zero types. The NADPH oxidase activity was found to have a strong association with germination and post germination seedling growth mediated through intrinsic burst in superoxide radical production. The inhibition in NADPH oxidase activity by application of DPI reduced the normal growth of seedlings and thereby reduced the seed vigour indices. Among the seed reserves, starch utilization started immediately after imbibition which showed a positive correlation with speed of germination. Inhibition in NADPH oxidase activity also resulted in lesser utilization of all the primary seed reserves. Lipid content was significantly high in the conventional type however, the utilization was maximum in double zero type which also showed a strong association with lower seed vigour in double zero type of Indian mustard. The study as a whole elucidated the role of NADPH oxidase and comparative report on seed reserve utilization during seed germination which will be helpful to understand the germination behaviour of different types of Indian mustard.

Keywords: Indian mustard, seed vigour indices, seed reserve content, reserve utilization, NADPH oxidase

Abstract No: B6

Development and Commercialization of India's First 64K SNP Genotyping Chip for Climate-Resilient Grain Amaranth Breeding

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ABSTRACT

Grain amaranth (*Amaranthus hypochondriacus*), a climate-resilient pseudocereal with exceptional nutritional value, holds immense potential for addressing global food and nutritional security in the era of climate change. However, amaranth breeding has been significantly constrained by the lack of high-throughput genomic tools essential for accelerated genetic improvement under climate stress conditions. This study presents the development, validation, and successful commercialization of India's first 64K SNP genotyping chip (AmahySNP) for grain amaranth. The chip was designed using Affymetrix Axiom technology based on a high-quality reference genome of Amaranthus hypochondriacus and contains 64,273 high-quality SNP markers with 99.7% validation accuracy, distributed across genic (55.17%) and non-genic (44.83%) regions. The chip was comprehensively validated across 384 diverse amaranth accessions and employed for population structure analysis, genetic diversity assessment, and genome-wide association studies (GWAS). A representative core collection of 112 accessions was identified from 917 germplasm accessions, representing 12% of the total diversity. GWAS identified 13 novel loci associated with days to flowering, a critical trait for climate adaptation, with seven located within annotated genes. The chip reduces genotyping costs by 90% compared to whole-genome sequencing and significantly accelerates breeding cycles. This

collaborative research between BRIC-CDFD and ICAR-NBPGR demonstrates successful translation of genomic research into a practical breeding tool. The technology has been officially certified by ICAR (Certificate No. ICAR-CS-NBPGR-Product-2025-013, dated 16th July 2025) and granted Indian patent protection (Patent No. 580208, filed 04/05/2023, granted 09/02/2026) for 20 years, ensuring intellectual property rights and facilitating technology transfer to industry partners. The commercialized 64K SNP chip enables rapid development of climate-resilient, nutrient-dense amaranth varieties with enhanced nutritional profiles. This achievement directly supports national nutritional security and sustainable agriculture goals. The technology represents a significant milestone in translating genomic innovation into real-world agricultural solutions for climate-resilient food systems and farmer prosperity.

Keywords : Grain amaranth, SNP genotyping, GWAS, molecular breeding, climate resilience, nutritional security, genomic selection, patent

Abstract No: B7

GC-MS Based Metabolomic Analysis of *Trichoderma asperellum* and *Bacillus velezensis* against *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (Foc TR4)

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ABSTRACT

Fusarium wilt caused by *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (Foc TR4) is one of the most destructive diseases threatening global banana production. The persistence of the pathogen in soil and the limited effectiveness of chemical control measures have intensified the need for environmentally safe and sustainable disease management strategies. Biological control using antagonistic microorganisms has emerged as a sustainable alternative to chemical management, yet the underlying metabolic interactions remain insufficiently understood. The metabolomic interactions of *Trichoderma asperellum* and *Bacillus velezensis*in suppressing Foc TR4, with an emphasis on identifying key bioactive compounds involved in pathogen inhibition. By using untargeted metabolomics approaches based on gas chromatography-mass spectrometry (GC-MS), metabolic profiles were generated from mono and co-cultures of *T. asperellum* and *B. velezensis*in the presence and absence of the pathogen. The GC-MS peak profiles revealed a diverse array of metabolites associated with antagonistic activity during microbial interactions. Co-cultivation of these antagonistic microorganisms and Foc TR4 resulted in the production of antifungal compounds like ester, dipeptides and ether which inhibits the growth of the pathogen. Key metabolites putatively identified included Pyrrolo[1,2-a] pyrazine-1,4-dione, hexahydro- from *B. velezensis*, along with 5-Hydroxymethylfurfural associated with *T. asperellum*. In addition to direct pathogen suppression, these microorganisms enhance plant growth promotion and reducing yield losses caused by Fusarium wilt. The above findings suggest that the application of these biocontrol agents exhibits direct antifungal effect on pathogen's metabolism. Overall, this study provides insights into the metabolomic basis of microbial relationship. Understanding the complex metabolic interactions among *T. asperellum*, *B. velezensis*andFoc TR4 offer a scientific foundation for developing effective metabolite-based biocontrol formulations.

Keywords: Banana, Foc TR4, GC-MS, Metabolomics, Biological control

Abstract No: B8

Genetic and Environmental Regulation of Anthocyanin Biosynthesis in Winged Bean (*Psophocarpus tetragonolobus* L.)

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Objectives:

1. To identify the gene(s) responsible for anthocyanin content in winged bean
2. To analyse the expression pattern of the gene(s) responsible for anthocyanin content in a diverse set of germplasm using qRT-PCR

ABSTRACT

The winged bean (*Psophocarpus tetragonolobus* L.) is a nutrient-rich yet underutilized legume with protein and oil contents comparable to those of soybean. Some genotypes exhibit distinct anthocyanin pigmentation in various plant parts, which helps the plant cope with biotic and abiotic stresses. These anthocyanin pigments have traditionally been used as natural food colorants and are also potential pharmaceutical ingredients, offering various health benefits to humans and animals. This study aimed to identify and quantify major anthocyanins in different tissues of winged bean, analyze their developmental and temperature-dependent accumulation patterns, identify candidate biosynthetic genes, and validate their expression under low-temperature conditions using RT-qPCR. Ultra-Performance Liquid Chromatography (UPLC) analysis revealed the presence of delphinidin-3-glucoside and cyanidin-3-glucoside as the two major anthocyanins in winged bean, with their contents increasing in leaves and pods- particularly in mature leaves and young pods- under declining temperature conditions. Candidate gene mining within QTL-mapped genomic regions identified two putative regulators of anthocyanin biosynthesis: PT04_g20719 (*AP2 ethylene-responsive transcription factor BBM2*) and PT04_g20862 (*gibberellin 3-beta-dioxygenase 4*). RT-qPCR analysis confirmed their differential expression, with significantly higher transcript levels in the high-anthocyanin-accumulating genotype WB Purple-3 compared to WB CR-2 in tissues harvested in November, a period characterized by cold climatic conditions. These findings suggest that anthocyanin biosynthesis in winged bean is strongly influenced by temperature and regulated by hormone signaling. This insight provides a valuable foundation for breeding programs aimed at enhancing anthocyanin accumulation in winged bean for increased industrial and nutraceutical value.

Abstract No: B9

Morphological and Developmental Characterization and Putative Molecular Mechanism for Paired Spikelet Formation in a Common Wheat Mutant PS90

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ABSTRACT

The wheat spike architecture plays a crucial role in determining grain yield. This study characterizes an EMS-induced wheat mutant, PS 90, which exhibits secondary spikelets under primary spikelets at most rachis nodes. Microscopic analysis revealed that secondary spikelets initiate later than primary ones, indicating a distinct regulatory mechanism. Plant hormones such as auxin, gibberellin and cytokinin regulate meristem maintenance and organ formation, with auxin playing key role in organ initiation and differentiation. This study examines the expression of genes involved in auxin transport *(PIN1),* biosynthesis *(YUC4),* and signalling*(ARF5, IAA8, LFY)*, alongside regulators of paired spikelet formation, including photoperiod-responsive *(PPD),Teosinte Branched 1(TB1)*, *Flowering Locus T(FT1)*, and gibberellin metabolism *(GA20-OX)*. A combined approach integrating bioinformatics, gene expression profiling, and morphological analysis was used to explore the mechanism underlying paired spikelet formation. Functional enrichment analysis and qRT-PCR identified key regulatory pathways and gene interaction. Expression analysis in paired spikelet mutants showed upregulation of *GA20-OX, YUC4, AUX1, ARF5*, and *LFY,* while *PIN1* and *IAA8* were downregulated. Additionally, *TB1* and *PPD-B1* were upregulated, whereas *FT1* was downregulated. These findings suggest a coordinated genetic regulation of paired spikelet formation. By unravelling the molecular mechanism controlling this trait, this study provides for breeding high-yielding, resilient wheat varieties with improved productivity and sustainability.

Keywords : Paired spikelets, Scanning electron microscope, Auxin metabolism genes, Expression analysis, Real-time PCR

Abstract No: B10

Biochemical and Metabolic Studies of Wheat (*Triticum aestivum* L.) in Response to Salinity under Laboratory and Field Condition

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ABSTRACT

Wheat (*Triticum aestivum* L.) productivity is severely affected by salinity stress, which disrupts growth, metabolism, and yield. The present study evaluates the biochemical and metabolic responses of different wheat genotypes to salinity under laboratory and field conditions to identify salt-tolerant genotypes. aimed to evaluate salinity stress tolerance in ten wheat genotypes, namely Kharchia-65, KRL-3-4, FLW-16, PBW-757, DBW-252, FLW-2, FLW-1, DBW-11, HD-2851, and FLW-5. Salinity stress was imposed at four levels (25 mM, 50 mM, 75 mM, and 100 mM), along with a control treatment, under laboratory and field conditions at the Instructional Farm of Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya. Genetic variation was observed in germination percentage, with a drastic reduction in genotypes FLW-5 and FLW-16 under stress, while Kharchia-65 and KRL 3-4 showed better performance. Seedling shoot length significantly decreased in FLW-1 and FLW-2, and root length in DBW-11 under stress, whereas Kharchia-65 and DBW-252 performed better. Both fresh and dry weights of shoots and roots were significantly reduced in FLW-16, DBW-11, FLW-1, and HD-2851 under stress, with Kharchia-65 and KRL 3-4 showing resilience. Plant height saw a drastic reduction in HD-2851 and FLW-5, while Kharchia-65 and KRL 3-4 maintained better heights. Tiller number significantly reduced in FLW-16, FLW-2, and FLW-1, with Kharchia-65 and KRL 3-4 less affected. Spikelet length drastically reduced in DBW-252, FLW-5, and FLW-2, with Kharchia-65 and KRL 3-4 performing better. Salinity stress at the reproductive stage severely reduced yield, especially in FLW-1, while HD-2851, Kharchia-65, and KRL 3-4 were less affected. Catalase and peroxidase activities increased under stress, with Kharchia showing the highest increments. Nitrate and nitrite reductase activities decreased, most notably in DBW-252 and KRL 3-4, respectively. Proline levels increased significantly, especially in Kharchia-65 and KRL 3-4, while protein and total soluble sugar levels decreased, with HD-2851 and FLW-5 showing the highest reductions, respectively. High DNA concentration was found in HD-2851, and Kharchia-65 exhibited high similarity with DBW-11 in SDS-PAGE analysis. These findings highlight the differential response of wheat genotypes to salinity stress, with Kharchia-65 and KRL 3-4 consistently showing better performance across various parameters, providing insights for selecting and breeding wheat varieties with enhanced salinity tolerance.

Keywords: Salinity stress, Wheat genotypes, Salt tolerance, Antioxidant enzymes, Proline accumulation, Yield attributes

Abstract No: B11

Multi-Omics–Driven Strategies for Improving Pollen Fertility under Heat Stress in Maize (*Zea mays* L.)

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ABSTRACT

Exposure of crops to high temperatures due to climate change poses a serious threat to global food security by adversely affecting crop growth, reproduction, and yield stability. Maize is one of the world's major cereal crops, is particularly susceptible to heat stress, especially during the reproductive stage. Heat stress during this critical phase severely impairs pollen development, viability, and fertilization success, ultimately leading to significant yield losses. Consequently, the development of climate-resilient maize cultivars has become an essential goal of sustainable agriculture. Heat stress disrupts key physiological, metabolic, and molecular processes associated with pollen fertility, including carbohydrate metabolism, lipid homeostasis, reactive oxygen species (ROS) balance, hormonal regulation, and protein stability. Pollen grains are highly sensitive to elevated temperatures, with microsporogenesis and anthesis representing the most heat-sensitive stages. Recent advances in multi-omics technologies encompassing genomics, transcriptomics, proteomics, metabolomics, and epigenomics—have enabled comprehensive dissection of these complex heat stress responses. Integrative multi-omics approaches have uncovered critical regulatory networks involving heat shock proteins, transcription factors, antioxidant defence systems, hormone signalling pathways, and metabolic enzymes that collectively govern reproductive heat resilience in maize. Moreover, the identification of heat-responsive genes, quantitative trait loci (QTLs), and molecular markers through multi-omics analyses provides valuable resources for modern crop improvement. These insights can be effectively translated into breeding programs via marker-assisted selection, genomic selection, and genome-editing tools such as CRISPR/Cas systems. Strengthening pollen fertility and reproductive stability under high-temperature stress represents a promising avenue for enhancing maize resilience. This review highlights how integrating multi-omics insights with advanced breeding and biotechnological interventions offers a robust framework for developing climate-resilient maize cultivars, thereby contributing to sustainable crop productivity under future climate change scenarios.

Keywords: Climate change; Heat stress; Maize; Pollen fertility; Reproductive heat resilience; Multi-omics; Crop improvement

Abstract No: B12

Integrative Mechanisms of Waterlogging Tolerance in Little Millet (*Panicum sumatrense*): From Physiological Resilience to Yield Stability

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ABSTRACT

Waterlogging is a critical abiotic stress threatening crop productivity in monsoon-dependent agriculture. Little millet (*Panicum sumatrense*), a climate-resilient nutri-cereal, exhibits genotypic variability in tolerance; however, its physiological and biochemical mechanisms are not fully elucidated. This study investigated three contrasting genotypes—OBN P-2528 (tolerant), OBN P-2546 (moderately tolerant), and OBN P-2558 (susceptible)—selected from 51 accessions screened under controlled greenhouse conditions. Seedlings were exposed to 30 days of waterlogging stress, and responses were assessed across growth traits, leaf pigments, relative water content (RWC), membrane stability index (MSI), oxidative damage indices, osmolyte accumulation, protein and phenolic content, gas exchange parameters, antioxidant enzyme activity (SOD, POD), non-enzymatic antioxidant capacity (DPPH, FRAP), alcohol dehydrogenase (ADH) activity, root traits, and yield components. The tolerant genotype OBN P-2528 sustained minimal reductions in seedling growth (–17.23%), root volume (–22.22%), and chlorophyll a (–18.06%), while maintaining higher RWC and MSI. It exhibited enhanced antioxidative defence (SOD +11.8%, POD +24.5%), elevated non-enzymatic antioxidant activity, and greater proline (+63.77%) and phenolic accumulation, limiting lipid peroxidation and electrolyte leakage. Root plasticity through aerenchyma formation (21.91%) and higher ADH activity supported oxygen diffusion and metabolic adjustment. Photosynthesis, stomatal conductance, and transpiration were better sustained, translating to <20% yield loss, compared with >50% losses in OBN P-2558. These findings highlight that waterlogging tolerance in little millet is an integrated trait combining photosynthetic stability, osmotic adjustment, antioxidant defence, and root anatomical plasticity, providing physiological markers and a tolerant genotype for breeding climate-resilient millet cultivars.

Keywords : Little millet, waterlogging tolerance, antioxidant defence, osmolytes, ADH, root plasticity, yield resilience

Abstract No: B13

Deep Learning Based Framework for Predicting Protein–Protein Interactions in Rice

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ABSTRACT

Rice (*Oryza sativa*) is one of the world's most important food crops; however, its protein–protein interaction (PPI) network remains incompletely explored due to the limitations of experimental approaches. Computational prediction strategies provide an effective complementary solution, enabling large-scale and rapid exploration of interactomes. Leveraging recent advances in deep learning and natural language processing, we introduce RCNNricePPI, an integrated deep learning framework designed to predict rice PPIs directly from protein sequence information. The proposed method utilizes a Siamese recurrent convolutional neural network (RCNN) architecture combined with word2vec-based sequence embeddings, allowing the model to capture both local and long-range sequence features relevant to protein interactions. High-quality training and testing datasets were constructed through rigorous preprocessing and filtering procedures, including carefully curated positive and negative interaction samples, ensuring robust and reliable model performance. RCNNricePPI web server demonstrates strong predictive capability and represents a significant contribution to computational interactomics in rice. By facilitating the identification of molecular interactions underlying key biological processes, this framework serves as a valuable resource for the plant biology and bioinformatics communities.

Keywords: Rice, Protein–Protein interactions, RCNN, word2vec, Deep Learning.

Abstract No: B14

Root Plasticity and Xylem Modifications Drive Drought Resilience in Okra [*Abelmoschus esculentus* (L.) Moench] at the Seedling Stage

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ABSTRACT

Okra [Abelmoschus esculentus (L.) Moench] is an important vegetable crop for food and nutritional security in arid and semi-arid regions, but its growth is strongly affected by drought stress. Although root flexibility and physio-biochemical responses are known to support drought tolerance, their specific contributions in okra are not well understood. This study evaluated drought tolerance in 55 okra genotypes exposed to three levels of PEG 6000-induced osmotic stress (0%, 10%, and 20%) under polyhouse conditions. Drought stress delayed germination and caused significant reductions in key growth traits, including leaf area, shoot length, fresh and dry biomass, and survival percentage. Root traits such as root length, number of secondary roots, and fresh root weight also decreased; however, the root-to-shoot ratio increased under severe stress, suggesting a shift in biomass allocation as an adaptive response. Biochemical analysis showed increased chlorophyll, carotenoid, and proline contents under drought conditions, indicating the activation of stress tolerance mechanisms. Based on overall performance, genotypes G51 (Sonam), G6 (HAU-480), G10 (Bhindi Champion), and G45 (Pooja-01)

were identified as the most drought-tolerant, showing better root development and higher biomass accumulation. Principal component analysis revealed that the mean productivity index and tolerance index were major contributors to genotypic variation under stress. In addition, Field Emission Scanning Electron Microscopy (FESEM) demonstrated genotype-specific xylem modifications, where drought-tolerant genotypes exhibited reduced vessel size, likely lowering the risk of embolism. Overall, the results emphasize the role of root plasticity, xylem structure, and biochemical responses in drought tolerance of okra. Selection for traits such as increased secondary root formation and smaller xylem vessel size may support the development of drought-resilient okra cultivars for water-limited conditions.

Abstract No: B15

Physiological, Biochemical, and Molecular Dissection of Low-Light Tolerance in Rice: From Signalling Pathways to Yield Stability

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ABSTRACT

Low-light (LL) stress during the *Kharif* season, largely driven by persistent cloud cover and atmospheric dimming, reduces photosynthetically active radiation (PAR) by ~40–60%, resulting in substantial yield losses in rice. To elucidate the mechanisms conferring LL resilience, we employed an integrated systems-level framework combining physiological, biochemical, and molecular analyses in contrasting rice genotypes. Physiological assessments demonstrated that LL-tolerant genotypes effectively suppress excessive shade-avoidance responses and maintain higher photosynthetic efficiency, thereby supporting stable growth under reduced irradiance. Biochemical analyses identified Sedoheptulose-1,7-bisphosphatase (SBPase) as a key metabolic stabilizer, with sustained enzyme activity strongly correlating with biomass maintenance and final yield under LL conditions. At the molecular level, Phytochrome A (PhyA) was identified as the primary LL sensor; disruption of its signaling cascade led to down-regulation of *OsPIL1* and *Lhcb* genes, impairing light harvesting and electron transport. We further delineated a "Light-Auxin–Starch" regulatory continuum, wherein LL-mediated repression of *OsYUC11* reduced spikelet indole-3-acetic acid (IAA) levels, consequently lowering AGPase and sucrose synthase activities and constraining grain filling. LL-tolerant genotypes also displayed distinctive epigenomic signatures, including altered DNA methylation landscapes and shifts in regulatory miRNAs, collectively contributing to enhanced LL tolerance. To improve phenotypic discrimination under variable light environments, we developed a Combined Stress Tolerance and Stability Index (CSTSI), which increased selection robustness across fluctuating irradiance regimes. Additionally, bi-parental and genome-wide association mapping approaches using a panel of 192 diverse rice genotypes uncovered multiple novel QTLs and stable QTL hotspots harboring 12 key hub genes (e.g., *OsAUX1, OsSBDCP1, OsNPF5.16,* etc.) associated with photosynthesis, hormone signaling, starch biosynthesis, and stress adaptation. Superior haplotypes linked to enhanced grain number, spikelet fertility, biomass, and grain yield, along with their donor genotypes, were also identified. Collectively, these findings provide mechanistic insights and actionable physiological, biochemical and molecular targets for breeding shade-tolerant, high-yielding, and climate-resilient rice cultivars.

Abstract No: B16

Decoding stress tolerance mechanisms for climate resilience: Multi-omics approaches for future proofing crop productivity

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ABSTRACT

Plants are constantly challenged by abiotic stresses like drought, salinity and extreme temperatures, as well as, biotic factors, such as, pathogens and pests. Climate change has intensified the frequency and severity of abiotic and biotic stresses, posing a major threat to global crop productivity and food security. Developing climate-resilient crops requires a deep understanding of the complex molecular responses that enable plants to withstand such stresses. Integrated multi-omics approaches encompassing genomics, transcriptomics, proteomics and metabolomics, offer a comprehensive platform to crack stress response networks and identify key molecular mechanisms involved in resilience. In this context, the transformative role of omics integration including single-cell and spatial omics, regulatory RNA studies, stress memory and plant-microbiome interactions in deciphering plant stress tolerance mechanisms needs to be precisely explored. Combined with genome editing and big data analytics, these approaches are driving innovative strategies for precision breeding and emphasizing the importance of systems biology in promoting sustainable agriculture. Overall, integrated omics offers a promising framework to decode plant stress tolerance mechanisms and guide the development of robust cultivars capable of thriving under increasingly unpredictable climatic conditions.

Keywords: abiotic stress, biotic stress, CRISPR-Cas9, multi-omics integration, precision breeding

Abstract No: B17

Metabolomic insights into endophyte-mediated Plant defense and growth promotion in Brinjal under phytopathogen Challenge

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ABSTRACT

Plant metabolomics, a vital branch of systems biology, enables a comprehensive understanding of biochemical and metabolic changes during plant-pathogen interactions. This study investigates the metabolomic and systemic responses of brinjal plants bioprimed with fungal endophytes, particularly *Schizophyllum commune* (E1) and *Nigrospora oryzae* (E2), upon challenge by phytopathogens such as *Botrytis* sp. and *Fusarium* sp. Using advanced analytical platforms including High-Performance Liquid Chromatography (HPLC) and proton Nuclear Magnetic Resonance (1H NMR) spectroscopy, key metabolites were profiled, highlighting dynamic accumulations of phenolics, organic acids, amino acids, and vitamins associated with induced resistance. Significant upregulation of salicylic acid, cinnamic acid, and derivatives of the shikimic acid pathway was evident in endophyte-treated plants, correlating with enhanced activity of defense-related enzymes such as phenylalanine ammonia-lyase (PAL) and peroxidase (PO). These biochemical signals orchestrate the phenylpropanoid pathway, leading to biosynthesis of secondary metabolites critical for reinforcing cell walls and scavenging reactive oxygen species. Unique metabolites including quinolinic acid and glutamylphenylalanine were identified exclusively in E1-treated plants, suggesting novel defense mechanisms contributing to pathogen suppression. The integration of metabolomic data with physiological assays, seed germination, seedling vigor, and enzymatic activities underscores the pivotal role of endophyte-mediated systemic resistance in improving plant health. Formulation of E1 onto a talc-based carrier demonstrated practical potential in enhancing crop performance and disease mitigation under greenhouse conditions. This research illustrates the power of metabolomics in elucidating complex plant defense pathways activated by beneficial endophytes, providing new insights for developing sustainable bioformulations for crop protection. The metabolite signatures identified offer promising biomarkers for future studies aiming to exploit plant-microbe interactions in agricultural biotechnology and systems biology.

Keywords: Endophytes, Biocontrol, Secondary Metabolites, *Schizophyllum commune*, *Botrytis* sp., HPLC, 1H NMR

Abstract No: B18

Root anatomical plasticity and antioxidant defence govern waterlogging tolerance in finger and barnyard millet

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ABSTRACT

Waterlogging stress severely limits millet productivity in rainfed agro-ecosystems of India by disrupting root function, oxygen availability, and cellular redox balance, particularly during early growth stages. This study examined root architectural, anatomical, antioxidant, and molecular responses underlying seedling-stage waterlogging tolerance in finger millet (*Eleusine coracana* L.) and barnyard millet (*Echinochloa frumentacea*Roxb.). Waterlogging induced marked alterations in root structure and metabolism in both species, though the nature of adaptation differed distinctly. Barnyard millet exhibited pronounced root anatomical plasticity, characterized by extensive aerenchyma formation (+452.5 to +552.5%), which enhanced internal aeration and oxygen diffusion under hypoxic conditions. This structural adjustment was coupled with strong activation of anaerobic metabolism, as indicated by increased root alcohol dehydrogenase activity (+70.0%), supporting sustained root function during oxygen deprivation. In contrast, finger millet displayed comparatively limited anatomical modification and relied primarily on biochemical defence mechanisms to cope with stress. Root-induced hypoxia triggered severe oxidative stress in finger millet, evidenced by elevated hydrogen peroxide accumulation and lipid peroxidation. Tolerant finger millet genotypes responded with robust antioxidant activation, showing significant up-regulation of superoxide dismutase (+73.5%) and peroxidase (+126.5%), along with enhanced proline accumulation, thereby minimizing oxidative damage and maintaining cellular integrity, whereas susceptible genotypes exhibited weaker antioxidant capacity and greater oxidative injury. *In silico* analyses revealed conservation of key ethylene-responsive transcription factors associated with waterlogging tolerance, with RAP2-12 implicated in redox regulation in finger millet. Barnyard millet lacked SUB1A-mediated quiescence responses and likely relies on ethylene signalling mediated by ERF1A or EREB-180 to coordinate anatomical adaptation. Overall, waterlogging tolerance in millets is governed by species-specific strategies, with barnyard millet relying predominantly on root anatomical plasticity and anaerobic metabolism, while finger millet depends chiefly on strong antioxidant defence with limited structural modification. These contrasting mechanisms underscore the importance of root-centred traits for improving millet resilience in waterlogging-prone environments.

Keywords: Waterlogging stress; Root anatomy, Antioxidant defence; Anaerobic metabolism, Millet

Abstract No: B19

Biotransformation of *Ocimum sanctum* essential oil using host associated endophytic yeasts

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ABSTRACT

This investigation delved into the isolation, characterization, and biotransformation capacity of endophytic microorganisms inhabiting *Ocimum sanctum* (Holy Basil). Yeast strains residing within *O. sanctum's* leaves, stems and roots were effectively isolated utilizing Yeast Extract Peptone Dextrose Agar (YEPD) medium. Examination of their morphology unveiled distinctive colony feature. These isolated yeasts were preserved for extended periods at 80° C. The molecular identification process, involving amplification and sequencing of the ITS region that classified the yeasts as *Vichniacozymavictoria, Filobasidiummali, and Crytococcus sp.* Moreover, their potential for biotransformation was evaluated. Incubation of the yeasts with the *Ocimum sanctum* oil, followed by analysis of the resulting volatile compounds using Gas Chromatography- Mass Spectroscopy (GC-MS), indicated alterations in the oil's composition, implying the ability of endophytic yeasts to potentially modify the profile of bioactive compounds in *O. Sanctum*. This research underscores the array of endophytic yeasts linked to *O. sanctum* and their possible roles in biotransformation processes to produce specific metabolites. Further investigation is necessary to delve into the precise enzymatic pathways contributing to the observed biotransformation.

Abstract No: B20

Functional difference between betacyanins*in vitro* and *in planta*: Betanin and amaranthin enhance tyrosine-related metabolites in mustard seedlings

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ABSTRACT

Betalainic plants accumulate biosynthetically related betacyanins such as betanidin, betanin (betanidin-5-*O*-glucoside), and amaranthin [betanidin-5-*O*-(2′-*O*-glucuronyl)-glucoside]. In such plants, these pigments play a role in stress tolerance and other physiological processes. These pigments are pharmacoactive and also used as food colorants, smart indicators in packaging films, and others. Herein, we investigated the effects of incremental substitution in their structures using density functional theory (DFT), as well as *in vitro* antioxidant activity, cytotoxicity, and seedlings of *Brassica campestris L.,* a betalain-devoid crop plant. The results showed betanin's better electron-donating potential, amaranthin's better *in vitro* antioxidant activity, and the synergistic *in vitro* cytotoxic effect of all three above-mentioned betacyanins. Individual betacyanins or in combinations of two of them were not cytotoxic. Betanin (50 mmol/L) produced a comparable growth-promoting effect with 24-epibrassinolide (EBR; 10 μmol/L), a brassinosteroid. EBR and betanin did not affect total chlorophylls, but amaranthin enhanced them. Betanin enhanced tyrosine and ascorbic acid in *B. campestris* seedlings. Amaranthin neither produced a significant growth-promoting effect nor a comparable tyrosine-enhancing effect with betanin. Taken together, our findings establish that betanin is a physiologically more effective compound *in planta*, particularly in betalain-devoid *B. campestris*. Considering the importance of tyrosine and ascorbic acid in our diet and betanin's ability to enhance them in *B. campestris*, pre-harvest treatment with betanin or betanin-containing formulations may be recommended to enhance the nutritional quality.

Keywords*:* DFT,HepG2, 24-Epibrassinolide, *Brassica campestris* L., Glucosinolate

Abstract No: B21

Modulation of Curcumin and essential oil biosynthesis of *curcuma longa* under water deficit condition

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ABSTRACT

This study Examines the changes in essential oils (EOs) chemical composition and curcumin content in *Curcuma longa* under water-deficit conditions. Two varieties, Rajendra sonali (RS) and Narendra haldi(NH) were subjected to water-deficit (WD) stress by water-withholding for 30 days. Analysis of the EOs content showed that in RS, it was 0.39% in control and 3.45% in WD plant and in NH, it was 1.17% in control and 1.33% in WD. GC-MS analysis of chemical composition revealed 31 compounds in both control and water-deficit (WD) Rajendra sonali (RS) plants, comprising 19 and 16 monoterpenes, respectively.GC-MS analysis of Narendra haldi (NH) revealed 39 compounds in control plants and 38 in water-deficit (WD) plants, comprising 24 and 20 monoterpenes, respectively. α-phellandrene, p-cymene, p-cymenene, methylacetophenone, and isoascaridole were highly expressed, while sabinene, 3-carene, eucalyptol, α-terpinene, terpinolene, zingiberene, bisabolene were downexpressed under water-deficit stress conditions in RS. In NH, myroxide, isopropyl-6methyl-5-hepten-3-yn-2-ol, undecanone, 1-methoxy-6,6-dimethyl-1-cyclohexene, farnesene, curcumene, tumerone, and farnesyl acetone were highly expressed, while 2-carene, eucalyptol, Ocimene, terpinene, terpinolene, terpineol, and zingiberene were down expressed in WD conditions in both varieties. Gene expression levels of essential oil (EO) biosynthesis enzymes, including DXS, DXR, and HMGS, positively correlated with EO content. Curcumin content increased by 45% and 43% in water-deficit (WD) plants of both varieties, consistent with upregulated expression of curcumin biosynthesis enzymes DCS and CURS3. These findings implied that enhanced EOs and curcumin biosynthesis in curcuma are essential mechanisms to adapt curcuma longa against stress response.

Keywords; *Curcuma longa*, Essential oils, curcumin, gene expression, water deficit, GCMS

Abstract No: B22

Genomics-assisted phenotypic and biochemical characterization of climate-responsive aphid stress in wheat for nutritional security

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ABSTRACT

Aphid infestation is a major climate-responsive biotic stress in wheat, adversely affecting crop productivity and nutritional quality under changing environmental conditions. In this study, a diverse panel of 399 wheat genotypes was evaluated for resistance to *Sitobionavenae* and *Rhopalosiphum padi* under field and controlled growth chamber conditions. Substantial phenotypic variation across environments highlighted the influence of climate-related factors on aphid infestation and host resistance. Genome-wide association analysis using 18,239 high-quality SNP markers and the BLINK model identified 5 SNPs associated with *S. avenae* resistance and 19 SNPs associated with *R. padi* resistance across environments.The identified loci showed strong allelic effects, and candidate gene analysis highlighted genes involved in hormone metabolism, growth regulation, and stress-responsive pathways.To elucidate physiological and biochemical mechanisms underlying resistance, a subset of 38 genotypes with contrasting aphid responses was subjected to biochemical characterization. Key stress-responsive traits, including proline, total phenols, soluble proteins, and antioxidant enzymes (catalase, peroxidase, and superoxide dismutase), were quantified. Biochemical profiling revealed wide variation in stress-responsive traits, with proline content ranging from 0.08-0.23 mg g^{-1} FW, total phenols from 11.35-34.54 mg g^{-1} FW, soluble proteins from 16.22-57.77 mg g^{-1} FW, catalase activity from 398.27-4346.32 U g^{-1} FW, peroxidase activity from 0.03-2.60 U g^{-1} FW, and superoxide dismutase activity from 710.37-2814.02 U g^{-1} FW across genotypes. Molecular characterization using aphid resistance-linked SSR markers targeting known resistance genes, including *Gb*, *Dn*, *RA1* and *Sa2*, revealed allelic variation among wheat genotypes.Integration of phenotypic, genomic, biochemical, and molecular marker information demonstrates that aphid resistance in wheat is governed by coordinated genetic and stress-responsive mechanisms, providing a robust foundation for genomics-assisted breeding of climate-resilient and nutritionally stable wheat cultivars.

Keywords : Wheat; Aphid resistance; GWAS; Climate-responsive stress; Antioxidant enzymes; Nutritional security

Abstract No: B23

Developmental stage-dependent regulation of essential oil biosynthesis in*Curcuma longa*revealed by integrated transcriptomic and metabolite analysis

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ABSTRACT

Essential oil biosynthesis in *Curcuma longa* is regulated by developmental stage–specific gene expression and metabolic activity. This study examined transcriptomic changes and essential oil composition in leaves of two turmeric varieties, Rajendra Sonali and Narendra Haldi, at 4-, 6-, and 8-month growth stages. Transcriptome analysis identified genes involved in carbohydrate metabolism, signal transduction, transcriptional regulation, and secondary metabolite biosynthesis that were differentially expressed across developmental stages. Genes associated with the methylerythritol phosphate (MEP) pathway, particularly **DXS**and**DXR**, showed higher expression in mature leaves, corresponding with maximum essential oil yield at the 6-month stage. GC–MS analysis revealed monoterpenes as the dominant essential oil components, with **terpinolene** as the most abundant compound. Differential regulation of transcription factors, including zinc-finger, WRKY, MYB, and bHLH families, suggests coordinated control of essential oil biosynthesis. These findings highlight developmental regulation of essential oil production in turmeric.

Keywords: *Curcuma longa*, essential oil biosynthesis, transcriptomics, developmental stages, MEP pathway, monoterpenes

Abstract No: B24

A Comparative Analysis of Chlorophyll Estimation Methods in Diverse Crop Species

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ABSTRACT

Chlorophyll, the primary photosynthetic pigment, serves as a key indicator of plant physiological status, nitrogen availability, and overall crop productivity. Accurate estimation of chlorophyll content is therefore essential for plant physiology research, precision agriculture, and ecological monitoring. This study critically compares destructive and non-destructive methods of chlorophyll estimation to evaluate their accuracy, efficiency, and field applicability. Eight crop species *Fragaria × ananassa*, *Pisumsativum*, *Phaseolus vulgaris*, *Triticumaestivum*, *Solanumtuberosum*, *Brassica juncea*, *Ipomoea batatas*, and *Nicotianatabacum*were assessed under uniform field conditions. Two non-destructive methods (SPAD-502 Plus chlorophyll meter and GreenSeeker NDVI sensor) and two destructive solvent extraction methods (80% acetone and 100% DMSO) were employed. Spectrophotometric measurements were conducted for extracted pigments, and correlation and regression analyses were performed using R Studio.Results revealed significant inter-method variability across species. SPAD readings showed moderate positive correlation with acetone-extracted chlorophyll ($R^2 = 0.297–0.349$), indicating reasonable agreement and potential as a rapid field-based alternative. In contrast, weaker relationships were observed between SPAD and DMSO ($R^2 = 0.031–0.138$) and between GreenSeeker and acetone extraction ($R^2 = 0.037$). Correlation patterns suggest that optical sensors are influenced by canopy architecture, leaf thickness, and reflectance properties, whereas solvent extraction provides direct biochemical quantification.Overall, SPAD demonstrated comparatively better consistency with laboratory-based acetone extraction. However, species-specific calibration is essential to enhance predictive precision. The study highlights methodological strengths and limitations, providing practical guidance for selecting appropriate chlorophyll estimation techniques in research and large-scale agricultural monitoring.

Abstract No: B25

Identification of Drought-Responsive Gene Networks In Foxtail Millet Using Weighted Gene Co-expression Network Analysis

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ABSTRACT

Climate change-induced drought stress possess a serious challenge to crop productivity and nutritional security, necessitating the exploration of climate-resilient crops and their underlying molecular mechanisms. Foxtail millet (*Setariaitalica*), a nutrient-rich and drought-tolerant C4 cereal, is emerging as a promising crop for sustainable agriculture under arid condition. However, the systems-level gene regulatory networks governing drought responses during early germination remain poorly understood. The present ongoing study applies a systems biology-based in-silico approach to investigate drought-responsive gene networks in foxtail millet using WGCNA. Publicly available RNA-seq datasets generated from polyethylene glycol (PEG-6000) induced drought-stressed and control seedlings across multiple developmental stages were retrieved from NCBI Sequence Read Archive. High -quality gene expression matrices are being generated through standardized bioinformatics workflows involving quality control, read preprocessing, genome alignment, gene quantification and normalization. Normalized expression profiles are being used to construct scale-free co-expression networks for the identification of drought-associated gene modules and putative hub genes with regulatory significance. Planned functional annotation and network visualization analyses will further elucidate stress-adaptive pathways. This study is expected to provide molecular insights into drought tolerance mechanism in foxtail millet, supporting biotechnological strategies for developing climate-resilient & nutritionally secure crops.

Keywords: Foxtail millet, Drought stress, RNA-seq, WGCNA

Theme C
Biotechnological Innovations

Abstract No: C1

GM Crops Regulation

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ABSTRACT

The first transgenic plants were developed in 1983 and within a short period of time the first transgenic crop or genetically modified (GM) crop, 'Slow-ripening Tomato'(Flavr Savr) was commercialized in 1994. Subsequent development of transgenic crops expressing a variety of novel traits such as insect resistance, disease resistance, herbicide tolerance, hybrid production, improved oil quality etc., have led to the large-scale cultivation of GM crops which currently occupy 210 million hectares in 32 countries. In addition, 43 countries import foods and products derived from GM crops. The cultivated GM crops include nine non-food crops and twenty-three food crops. Substantial social, economic and environmental benefits have been realized worldwide by cultivating GM crops. India has approved commercial cultivation of Bt cotton in 2002. In the year 2025, Bt cotton was cultivated in 12.0 million hectares. The record production of 30 million bales of cotton is a testimony to the power of GM crops, especially that of cotton.

The regulation of GM crops has its historic beginning ina conference organized by Paul Berg and his colleagues in Asilomar, California, USA in 1975 to discuss the potential biohazards and regulation of biotechnology and to draw up voluntary guidelines to ensure the safety of recombinant DNA technology. Subsequently, an international agreement termed as The Cartagena Protocol on Biosafety came into effect in 2003. This Biosafety Protocol seeks to protect biological diversity from the potential risks posed by genetically modified organisms resulting from modern biotechnology. India developed a regulatory framework for approval of Genetically Modified (GM) Crops as per “Rules for the Manufacture / Use / Import / Export and Storage of Hazardous Microorganisms, Genetically Engineered Organisms or Cells, 1989” under the Environment (Protection) Act, 1986 and Rules 1989, in India.On July 24, 2024 the Supreme Courthas directed the Union Government to evolve a National Policy on GM crops in the realm of research, cultivation, trade, and commerce. The present discussion deals with the safe use, cultivation and consumption of GM crops and their products globally since 1995 in light of the Supreme Court Directive (2024) vis-à-vis GM crops regulation in India.

Abstract No: C2

Advances in Genome Editing and Prospectsin Pulses

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ABSTRACT

Genome editing technologies have emerged as transformative tool for accelerating genetic gain in crops. In last three decades, genome editing has undergone significant improvement in terms of precision, efficiency and easeand has been successfully applied in close to 120 crops and model plants.Gene editing facilitates the development of improved phenotypes for enhanced yield potential, biotic and abiotic stress resistance, nutritional enrichment, and early maturity—traits essential for strengthening resilience in the face of climate variability and growing global food demand. The technology has progressed at rapid pace with new discovery and understanding.Pulses such as chickpea, pigeonpea, lentil, grasspea, urdbean, mungbeanandfieldpeaare vital sources of plant-based protein, micronutrients, and environmental sustainability.However, their genetic enhancement has traditionally been constrained by narrow genetic bases, complex genomes, and long breeding cycles. The advent of Clustered Regularly Interspaced Short Palindromic Repeats–CRISPR-associated protein 9 (CRISPR/Cas9) and related editing platforms offers unprecedented precision and efficiency in modifying targeted genomic regions, enabling rapid incorporation of desirable traits without extensive linkage drag. A thorough understanding of biochemical pathways, gene involved and repurposing of the CRISPR/cas9 system and an efficient delivery system is required for rapid utilization in pulses.

Keywords: Gene Editing, CRISPR/Cas, Pulses

Abstract No: C3

Functional characterization of gene(s)/promoter(s) associated with the nitrogen use pathway of bread wheat (*Triticum aestivum* L.)

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ABSTRACT

Wheat is one of the most important cereal crops globally, supplying almost one-fifth of humankind's calorie and protein requirements, which necessitates continuous improvement in its productivity, given the growth rate of the global population. There is a general tendency to apply increasing amounts of nitrogenous fertilizers to maximize wheat productivity. However, the nitrogen use efficiency of bread wheat is inferior, i.e., 30-35%, implying 65-70% of available nitrogen is lost to the environment, leading to various undesirable environmental consequences, viz., emission of greenhouse gas, leaching, volatilization, etc., together with economic loss spent on lost fertilizer.My laboratory focuses on identifying key gene(s) and promoter(s) controlling nitrate uptake and translocation in bread wheat, and on improving nitrogen use efficiency through nitrate-uptake/translocation-mediated approaches, employing various genomics and proteomics approaches.Based on field-level evaluation, nitrogen-uptake-efficient wheat genotypes were identified, and further characterization revealed the contribution of the high- and low-affinity nitrate transport systems under optimal and limiting nitrate availability, employing isotope-ratio mass spectrometry with ^{15}N-labelled N-source.Based on background studies and nitrate assimilation biology, we identified a high-affinity nitrate transporter gene (*TaNRT2.1-B6*) predominantly expressed in root tissues and functionally validated it through complementation approaches, demonstrating a recovery of nitrate influx in the *atnrt2.1* mutant with 1.5-fold greater nitrate uptake. Further, we also identified its accessory proteins, which are essential for its activity by forming a two-component high-affinity nitrate transport system in wheat through various protein-protein interaction studies and validation in model systems, such as *Xenopus laevis*oocytes.Further, we identified and validated a low-affinity nitrate transporter gene orthologous to Arabidopsis NRT1.5, which is responsible for root-to-shoot nitrate transport. The upstream sequences of these genes and the corresponding GUS reporter lines revealed diverse regulatory features. Our results pave the way to strategize different approaches for improving nitrogen use efficiency of wheat utilizing these genes.

Abstract No: C4

CRISPR-Driven Innovations for Climate-Adaptive Agriculture and Nutritional Improvement."

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ABSTRACT

Climate change poses unprecedented challenges to agricultural productivity, crop quality, and nutritional security. Emerging genome-editing technologies, particularly CRISPR/Cas systems, offer powerful, precise, and rapid solutions for developing climate-adaptive and nutrient-rich crop varieties. The abstract highlights recent advancements in CRISPR-driven innovations that support climate-resilient agriculture and improved nutritional outcomes.CRISPR/Cas-mediated editing has enabled the targeted modification of genes responsible for drought tolerance, heat resilience, and salinity tolerance, allowing crops to maintain productivity under extreme environmental stresses. By knocking out negative regulators and enhancing stress-responsive genes, CRISPR facilitates the development of robust plant varieties tailored for climate variability. At the same time, CRISPR-based genetic biofortification enhances micronutrient density—including iron, zinc, provitamin A, and essential amino acids—without compromising yield, making it a highly efficient tool for combating hidden hunger.

Integrating CRISPR with multi-omics approaches, such as metabolomics, transcriptomics, and systems biology, accelerates the identification of stress-related pathways and nutrient-regulating genes. These insights enable predictive modelling of plant responses and inform strategic gene editing for improved resilience and nutrition.Furthermore, CRISPR is revolutionizing plant–soil–microbe interaction studies by enabling the engineering of beneficial microbes and modulating plant root exudates to strengthen nutrient uptake and stress mitigation. Advances in synthetic biology have expanded CRISPR applications toward designing stress-responsive regulatory circuits to optimize plant performance under fluctuating climates.Overall, CRISPR/Cas technologies represent a transformative frontier in climate-smart agriculture, offering scalable, sustainable, and precise interventions for achieving long-term nutritional security. Continued interdisciplinary research, regulatory clarity, and farmer-centered innovations will be essential to harness CRISPR's full potential in shaping a food-secure future.

Keywords: CRISPR/Cas; genome editing; climate-resilient crops; abiotic stress tolerance; genetic biofortification; multi-omics; synthetic biology; nutritional security; plant–microbe interactions; climate-smart agriculture.

Abstract No: C5

CRISPR/Cas-Based Genome Editing for Development of Low-Toxin Grass Pea (*Lathyrus sativa*)

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ABSTRACT

The UN Sustainable Development Goal 2 sets the challenge to end hunger globally by 2030.Today, some 795 million people worldwide are under nourished. Beyond supplying sufficient calories to sustain human populations, food systems are also challenged to meet their full nutritional needs. Malnutrition is still widespread in South Asia. Pulses form a crucial part of the diet in many Asian countries, due to their advantageous nutritional profiles, especially their high seed protein content and their low cost, especially when compared to animal-derived protein sources. One of these'orphan'legume crops is grass pea (*Lathyrus sativus*) also known as khesari in India. It shows remarkable tolerance to environmental stress, including both drought and waterlogging. This has made grass pea a vital source of food and feed in times of scarcity during its 8000-year history of cultivation. However, cultivation of grass pea has been limited because of its association with neurolathyrism, a devastating neurological disorder believed to be caused by β-N-oxalyl-L-2,3-diaminopropionicacid(β-ODAP),which is present in seeds and green tissues of grass pea. Environmental factors, particularly drought, have an impact on the toxin's production, which rises in response to stress. Developing varieties with low β-ODAP content has been the primary goalin grass pea breeding since the first identification of the toxin, and it is the number one trait for breeding programs in India. Recent work at the John Innes Centre, Norwich, UK based on analysis of the reference genome sequence has identified the genes encoding the final two steps on the biosynthetic pathway for β-ODAP, and the novel mechanism by which these proteins catalyse the synthesis of the toxin offering aroutetonovellowβ-ODA P traits through gene knockouts. Dual gRNA CRISPR/Cas9 editing constructs were used to create deletion mutants of genes responsible for synthesizing β-ODAP. β-ODAP levels in edited lines were analysed using LC/MS. The significant reduction in β-ODAP levels were observed in edited lines.

Keywords: CRISPR/Cas, Grass Pea (*Lathyrus sativa*), β-ODAP, Neurolathyrism

Abstract No: C6

Plant Transformation in the Era of Genome Editing: Establishing Efficient CRISPR/Cas9 Platforms in Chickpea, Rice bean, and Pearl Millet

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ABSTRACT

Plant transformation has become essential in genome editing because reliable delivery systems are crucial for precise gene modification. The success of CRISPR/Cas9 in crops relies heavily on robust regeneration and transformation protocols, especially for challenging species such as *Cicer arietinum* (chickpea), *Vigna umbellata* (rice bean), and *Pennisetum glaucum* (pearl millet). Chickpea resists in vitro regeneration and often produces chimeric plants from half-embryo explants. We developed an effective system enabling stable CRISPR/Cas9 editing. Targeting the phytoene desaturase gene (*CaPDS*) achieved 42% mutant-phenotype efficiency, confirming the platform's effectiveness. Editing *CaCKX3* and the transcription factor *CaMYB39* caused distinct changes in plants and seeds, respectively. A high-throughput pipeline is being established to characterise more than 100 chickpea genes, although detecting edited alleles in segregating seeds remains challenging. In rice bean, where genome editing had not previously been demonstrated, the phytoene desaturase gene (*VuPDS*) was targeted using a pDIRECT22A vector containing AtCas9 under a 2×CaMV35S promoter and an sgRNA driven by the AtU6 promoter. The recovery of albino mutant plantlets confirmed successful editing, marking the first report of successful editing in rice bean and offering promise for trait improvement. In pearl millet, which faces lipid degradation affecting flour shelf life, three seed-specific lipase genes (*PgLIP1*, *PgLIP2*, and *PgLIP3*) were targeted with nine sgRNAs. From 1,800 explants, 294 resistant events were regenerated; PCR confirmed Cas9 integration in 46% of plants. Sanger sequencing revealed indels in multiple T_0 events, demonstrating effective editing. Overall, these results establish optimised transformation and genome-editing methods for functional genomics and crop improvement in chickpea, rice bean, and pearl millet.

Keywords: Chickpea, Ricebean, Pearl millet, CRISPR/Cas9, Genome editing, Plant transformation, Lipase genes, PDS reporter gene, Shelf-life improvement

Abstract No: C7

Biofortified ZiP rice with elevated zinc, iron, and protein through prime editing

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ABSTRACT

Adaptive modifications in important metabolic enzymes that improve carbon fixation efficiency led to the evolution of C_4 photosynthesis; nevertheless, attempts to introduce these features into C_3 crops have met limited success. Here, we find an evolutionarily conserved residue in phosphoenolpyruvate carboxylase (PEPC), whose substitution alone gives the C_3 rice enzyme C_4-like kinetic characteristics. Using precision prime editing, we introduced a single amino acid change (Arg→Gly) at the target site and created rice lines with greater chlorophyll content, better photosynthetic rates under ambient CO_2, and improved PEPC catalytic efficiency in the presence of feedback inhibitor malate. Surprisingly, we discovered that the altered lines' seeds had noticeably greater levels of zinc, iron, and protein (ZiP), suggesting a possible biofortification strategy to fight malnutrition worldwide. We have named these nutritionally enhanced lines 'ZiP rice'. Edited plants also displayed increased seed size and weight. Overall, our findings suggest that a carefully chosen, evolution-informed change at a single amino acid position can meaningfully reshape central carbon metabolism in C_3 crops. This simple but effective strategy provides a practical way to improve photosynthetic efficiency, yield-related characteristics, and grain nutritional value without extensive genetic reconfiguration.

Abstract No: C8

Hypercompact TnpB, AI-designed nucleases, and optimized prime editing for advanced plant genome engineering

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ABSTRACT

Advancing plant genome engineering requires both diversification of nuclease platforms and improved editing precision at endogenous loci. Here, we describe the development of compact nucleases, AI-designed editors, and optimized prime-editing strategies to enhance precision genome modification in rice.The most widely used genome-editing nucleases, Cas9 and Cas12a, are large in size and come with complex IP landscape. We have developed an Indigenous plant genome editing tool using compact TnpB (~400 amino acids) nuclease. Through systematic optimization of coding sequences and guide-expression architectures, enhanced TnpB variants achieved indel frequencies of up to 33% at selected genomic loci.Artificialintelligencedriven protein design is emerging as a powerful approach for expanding the diversity of programmable nucleases. We developed plant-optimized AI-designed editors (PAiD) based on the synthetic RNA-guided nuclease OpenCRISPR-1. PAiD supports efficient gene knockout, adenine and cytosine base editing, and prime editing in rice, with locus-dependent efficiencies equal to or better than those of SpCas9.These findings establish AI-designed nucleases as functional and versatile genome-editing platforms in plants. Prime editing provides a versatile platform for introducing precise nucleotide substitutions, insertions, deletions, and combinatorial edits without inducing double-strand breaks. In rice, we optimized prime-editing configurations to enhance editing efficiency and precision across multiple endogenous targets. We improved targeted nucleotide alterations while minimizing unwanted editing consequences by optimizing editor structures and pegRNA design parameters. Using the optimized prime editor and pegRNA designs, we achieved precise nucleotide substitutions comprising single- and multi-base changes, along with targeted insertions of 2 bp and 14 bp at selected genomic loci.Across several loci, editing efficiencies were substantially increased compared to earlier configurations, demonstrating the robustness and reliability of the optimized system.Collectively, these advances expand both the diversity and precision of genome-editing platforms in rice. The development of compact nucleases, AI-designed editors, and improved prime-editing systems provides versatile tools for next-generation crop improvement.

Abstract No: C9

Management of Biological Contamination through Nanoparticles in Plant Tissue Culture

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ABSTRACT

Biological contamination is a major bottleneck in plant tissue culture, causing significant losses and reducing micropropagation efficiency and reliability. This study aimed to evaluate the efficacy and effectiveness of green-synthesised metal oxide nanoparticles for fungal contamination control in the micropropagation system. Zinc oxide (ZnO) and copper oxide (CuO) nanoparticles were synthesised using a green, plant-mediated method, with *Murrayakoenigii* and *Ocimum sanctum* leaf extracts, respectively. The nanoparticles exhibited average sizes of 46.15 nm (ZnO) and 80.79 nm (CuO), with zeta potential values of 13.6 mV and −18.8 mV, indicating moderate colloidal stability. FTIR analysis revealed key functional groups involved in nanoparticle stabilisation, with alkane and alkene groups associated with ZnO nanoparticles and alcohol groups acting as capping agents for CuO nanoparticles. The biological efficacy of the synthesized nanoparticles was evaluated during *in vitro* micropropagation of banana using meristematic explants cultured on modified Murashige and Skoog (MS) medium. Contamination frequency and *in vitro* growth parameters were recorded to assess antimicrobial efficiency and phytotoxic effects. CuO nanoparticles at a concentration of 150 mg L^{-1} showed the highest efficacy in controlling microbial contamination, whereas ZnO nanoparticles at 100 mg L^{-1} significantly enhanced in vitro growth of banana plantlets across all stages of micropropagation. Fungal contaminants isolated from infected cultures were identified as *Trichoderma* spp., *Aspergillus* spp., *Cladosporium* spp., and *Penicillium* spp. Antifungal assays demonstrated that CuO nanoparticles effectively inhibited the growth of *Trichoderma* spp. and *Cladosporium* spp., while ZnO nanoparticles showed inhibitory effects against *Penicillium* spp. Both nanoparticles were ineffective against *Aspergillus* spp., possibly due to differences in fungal morphology or nanoparticle size and interaction dynamics. Overall, the findings highlight the potential of green-synthesized nanoparticles as a sustainable approach for contamination management and growth enhancement in plant tissue culture.

Keywords: Nanoparticle, ZnO, CuO, green synthesis, micropropagation, contamination.

Abstract No: C10

A study on the identification and characterisation of circular-RNA related to drought tolerance in Tartary Buckwheat

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ABSTRACT

With the advancement of efficient bioinformatic algorithms, it has become possible to investigate complex drought stress tolerance mechanisms in underutilised pseudocereal crops with significant nutritional and functional potential. Although the role of protein-coding genes in drought tolerance is partially understood, the contribution of non-coding RNAs such as circular RNAs (circRNAs) remains largely unexplored in Tartary buckwheat (*Fagopyrum tataricum*). Hence a study has been conducted to identify drought-responsive circRNAs from Tartary buckwheat transcriptomes and to analysecircRNA–miRNA–mRNA interaction networks using in silico approaches. RNA-seq data from drought-tolerant and drought-susceptible genotypes under control and stress conditions revealed differentially expressed circRNAs. Functional annotation revealed enrichment of drought-responsive biological functions and suggested a potential miRNA sponge role of circRNAs in regulating diverse genes. These findings highlight the potential regulatory role of circRNAs in drought stress tolerance and provide a foundation for developing drought-resilient Tartary buckwheat varieties.

Abstract No: C11

Meta-QTL Analysis for dissecting the genetic architecture for waterlogging tolerance in Foxtail Millet (*Setaria italica*)

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ABSTRACT

Foxtail millet (*Setaria italica*) is a climate-resilient, short-duration C4 cereal crop valued for its nutritional quality and adaptability to marginal environments. While extensive genetic studies in foxtail millet have focused on drought and nutrient stress, waterlogging stress—an emerging threat under changing climate scenarios—remains poorly explored at the genomic level. Waterlogging induces hypoxic soil conditions that severely impair root function, nutrient uptake, and plant growth particularly in foxtail millet, which has shallow root system. The presence of genotypic variation for waterlogging tolerance has been found in foxtail millet, indicating the potential for genetic improvement. The present study aimed to identify stable genomic regions associated with waterlogging tolerance through comprehensive meta-QTL analysis. Published quantitative trait loci (QTLs) related to waterlogging and excess-moisture–associated traits were systematically collected and curated. A consensus genetic map was constructed using LPmerge in RStudio by integrating multiple linkage maps. Meta-QTL analysis was subsequently performed using BioMercator software to refine QTL positions and identify robust genomic regions governing waterlogging tolerance.Nine individual consensus genetic maps were constructed by integrating multiple linkage maps using the LPmerge package in RStudio to ensure optimal marker order and minimal map inflation.Candidate genes located within the identified meta-QTL intervals were retrieved from the foxtail millet genome database. The analysis resulted in the identification of key meta-QTL regions with reduced confidence intervals, indicating stable and reliable loci associated with waterlogging tolerance. Several candidate genes related to hypoxia response, antioxidant activity, and stress signalling pathways showed differential expression under waterlogged conditions. These findings provide the first consolidated genomic framework for waterlogging tolerance in foxtail millet. In conclusion, this study bridges a critical research gap by integrating fragmented QTL information into stable meta-QTLs and identifying potential candidate genes for waterlogging tolerance. The results offer valuable targets for marker-assisted selection and future functional genomics studies aimed at developing climate-resilient foxtail millet varieties.

Keywords: Waterlogging tolerance, Meta-QTL analysis, Consensus genetic map, Candidate genes, qRT-PCR

Abstract No: C12

Molecular Diversity Analysis of Early Maturing Elite Sugarcane Clones Using Microsatellite (SSR) Markers

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ABSTRACT

Molecular tools provide a robust and reliable means for distinguishing closely related sugarcane (Saccharum spp.) clones and for strengthening selection decisions in breeding programmes where phenotypic traits alone are often insufficient. The present investigation focused on evaluating genetic diversity among early maturing elite sugarcane clones through microsatellite or simple sequence repeat (SSR) marker analysis. Seventeen sugarcane clones were analysed using eleven polymorphic SSR markers, which successfully generated distinct molecular profiles for each genotype. A total of 123 allelic variants were detected across the analysed genotypes, with an average of 7.23 alleles per marker, reflecting substantial allelic richness. Of these, 59 alleles were common across genotypes, while 64 alleles were genotype-specific, indicating a high degree of polymorphism within the population. Among the markers employed, NKS 1, NKS 34, NKS 57 and NKS 61 produced a comparatively higher number of alleles, highlighting their greater resolving efficiency. The polymorphic information content (PIC) values varied from 0.63 (NKS 57) to 0.92 (NKS 1), with a mean value of 0.82, demonstrating the strong discriminatory capacity of the SSR markers. Genetic relationships among the clones were elucidated using UPGMA-based cluster analysis, which grouped the seventeen genotypes into five distinct clusters. Clusters I and II comprised three genotypes each, clusters III and IV included four and five genotypes, respectively, while cluster V contained two genotypes. Genotypes CoP 16437 and CoX 20458, sharing a common parental background (Co 1148), were placed within the same sub-cluster (IA), whereas genotypes CoX 20054 and CoX 20055, derived from CoPb 9181 (general cross), were grouped together in cluster II, indicating close genetic relatedness influenced by pedigree. The findings confirm that SSR marker-based analysis is an efficient approach for assessing genetic variability, establishing molecular fingerprints, and identifying genetically divergent parents, thereby contributing to more precise and effective sugarcane improvement strategies.

Keywords: Elite clones, Early Maturity, SSR markers, Genetic diversity, Dendrogram,

Abstract No: C13

From Big Genomes to Better Crops: Using Comparative Genomics, GWAS, and Genomic Selection for Trait Improvement

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ABSTRACT

Genomic information has become essential across all domains of life sciences, including health and agriculture sector, particularly with the growing use of genotyping-based diagnostics and omics-driven precision breeding. The rapid progress in next-generation sequencing (NGS) technologies over the past decade has drastically reduced sequencing costs, making whole-genome sequencing and resequencing affordable. As a result, several ambitious global initiatives, such as the 1,000-genome projects in Arabidopsis, rice, soybean, and tomato, have been completed, and similar efforts are underway across fish, birds, and other vertebrates. Access to genome sequences from large and diverse populations has transformed our understanding of genetic diversity, trait variation, and the molecular basis of complex biological processes. In plant science, coordinated international efforts have generated extensive genomic datasets for major crops, providing a valuable foundation for both basic research and applied breeding. Our research group has been using these resources to address nutritional challenges in staple crops. By examining large-scale genomic data, we have been able to trace evolutionary history, identify conserved features, and understand the functional divergence of key genes, including nutrient transporters, defence-related genes, and regulators of seed nutritional quality in rice and soybean. In soybean, we are re-sequencing important Indian genotypes and analysing with more than 1,000 whole genome resequenced genotypes to identify favourable alleles linked to nutritional traits such as reduced anti-nutritional factors, improved protein quality, desirable fatty acid composition, and enhanced seed constituents. These traits are especially important for addressing protein-energy malnutrition and the growing demand for edible oils in India. Similarly, by analysing the 3,000 Rice Genomes (3K) dataset, we have carried out genome-wide association studies (GWAS) to identify loci associated with nutritional quality traits and are now prioritizing candidate genes using information from multiple mega-genomic resources. In parallel, we have developed cost-effective analytical pipelines capable of generating high-throughput genotyping data at a fraction of the cost of whole-genome sequencing. Our genotyping-by-sequencing approach and associated analytical workflow have proven highly effective for QTL mapping, GWAS, and genomic selection in various crops. This talk will outline global mega-genomics initiatives, discuss how these large datasets can be harnessed for food, nutrition, and health, and present our efforts toward improving the nutritional quality of major crops.

Abstract No: C14

Transcriptome-based heat-responsive SSR marker development

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ABSTRACT

Abiotic stresses significantly limit plant growth and productivity, with heat stress being one of the most detrimental factors affecting crop development and yield by altering morphological, physiological, and biochemical processes. In the present study, heat stress–responsive molecular components and gene-based markers were generated and validated in Finger millet (*Eleusine coracana L.*) using transcriptomic and phenotypic evidence. RNA sequencing analysis yielded a comprehensive set of heat-responsive differentially expressed genes (DEGs), which were clearly classified into upregulated and downregulated groups, reflecting extensive transcriptional modulation under elevated temperature conditions. Functional annotation of these DEGs revealed their involvement in key heat stress–related biological processes, including stress signalling, protein protection, antioxidant activity, and metabolic regulation. From these functionally characterised DEGs, a subset of candidate heat-responsive genes was identified based on their established roles in thermotolerance and the presence of simple sequence repeat (SSR) motifs within transcribed regions. Phenotypic evaluation under optimized heat stress conditions enabled clear discrimination between heat-tolerant and heat-susceptible genotypes, supporting the molecular findings. Integration of phenotypic responses with transcriptomic evidence strengthened the relevance of the selected candidate genes. Gene-based SSR markers were successfully designed and synthesized from these candidate heat-responsive genes. In further proceedings, Genotypic profiling using the developed genic SSRs will be deployed to find amplification and detectable polymorphism among the selected genotypes, demonstrating their effectiveness in capturing genetic variation associated with heat stress response. In addition, RNA-based expression profiling of SSR-associated genes will be carried out to confirm their differential expression patterns under heat stress, providing functional validation of the developed markers. The combined genotypic and expression-based validation will highlight the close association between these genic SSR markers and heat-responsive gene regulation. The outcomes of this study will provide a functionally validated set of heat-responsive genic SSR markers and a curated list of candidate genes linked to thermotolerance in finger millet.

Keywords: Abiotic stress, RNA-seq, Genic SSR markers, phenotypic screening

Abstract No: C15

Molecular Diversity Analysis of Mid-Late Maturing Elite Sugarcane Clones Derived from Bi-parental and General Crosses Using SSR Markers

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ABSTRACT

Molecular characterization is a prerequisite for precise identification, effective utilization, and genetic improvement of elite sugarcane (*Saccharum spp.*) clones, particularly when phenotypic similarities limit accurate discrimination. The present investigation was undertaken to assess the molecular diversity among mid-late maturing elite sugarcane clones derived from bi-parental and general crosses using simple sequence repeat (SSR) markers during the 2022–23 crop season. SSR marker analysis revealed a total of 53 alleles across the studied clones, of which 37 were shared and 16 were unique, indicating considerable genetic variability within the population. The polymorphic information content (PIC) values ranged from 0.39 (SOSSR 48) to 0.78 (SOSSR 31), with an average value of 0.61, demonstrating the high discriminatory efficiency and informativeness of the SSR markers employed. Similarity coefficient analysis showed a maximum genetic similarity of 0.892 between clone pairs X 20039 and CoX 20022, while the lowest similarity value of 0.800 was observed among clone combinations such as CoX 20123 &CoX 20165, X 20039 &CoX 20130, and CoX 20022 &CoX 20130, indicating substantial genetic divergence. Cluster analysis based on the unweighted pair group method with arithmetic mean (UPGMA) grouped the clones into four major clusters. Cluster I comprised 11 clones, cluster II included 7 clones, while clusters III and IV contained one clone each. Clones sharing common parentage predominantly clustered together, reflecting the influence of pedigree on genetic relatedness. Clones CoX 20418, CoX 20412 and CoX 20118 (Co 09022 × BO 154) were grouped in cluster I, while clones X 20035, X 20039 and CoX 20022 with BO 154 (FC) parentage were grouped in cluster II. In contrast, clones CoX 20123 and CoX 20130 derived from CoN 05103 (GC) were placed in separate clusters, indicating high genetic divergence. The study confirms the utility of SSR markers as a reliable tool for molecular diversity assessment and identification of divergent genotypes, thereby facilitating informed parental selection and strengthening sugarcane breeding programmes.

Keywords: Elite clones, Midlate Maturity, SSR markers, Genetic diversity, Dendrogram, General cross, Bi-parental cross.

Abstract No: C16

DNA Profiling and Molecular Diversity Analysis of Sugarcane (*Saccharum spp.*) Seedlings Using SSR Markers

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ABSTRACT

Sugarcane (*Saccharum spp.*) is predominantly propagated through vegetative means; however, hybridization remains essential for generating novel genetic variability for crop improvement. Early-stage molecular characterization of sugarcane seedlings is critical to ensure the identification of true hybrids and to prevent the inadvertent loss of superior recombinants due to competition from selfed progenies. The present investigation aimed to assess molecular diversity among sugarcane seedlings derived from three different crosses using simple sequence repeat (SSR) markers at the seedling stage. A total of sixty seedlings were evaluated over two consecutive seasons using twenty polymorphic SSR markers. The SSR analysis revealed a total of 179 alleles across all loci, indicating a high level of genetic variability among the studied seedlings. Among the markers employed, UGSM17 and SOSSR38 exhibited the highest resolving power. The polymorphic information content (PIC) values ranged from 0.59 (SOSSR49) to 0.89 (UGSM17), confirming the high informativeness and efficiency of the SSR markers for genetic discrimination. Cluster analysis based on the unweighted pair group method with arithmetic mean (UPGMA) grouped the seedlings into three major clusters. Several seedling pairs, including BO 23–24:2.1 and CoP 22–23:3.1, BO 23–24:2.2 and CoP 22–23:3.6, BO 23–24:2.8 and CoP 22–23:3.5, CoP 23–24:3.8 and BP 22–23:1.2, and CoP 23–24:3.7 and BP 22–23:1.5, exhibited high genetic divergence. The clustering pattern clearly differentiated seedlings according to their parental origin. All seedlings derived from the biparental cross (Co 0238 × Co 775) clustered together, confirming their true hybrid nature. In contrast, seedlings from the general crosses, BO 154 and CoP 11437, were distributed across different clusters, reflecting broader genetic diversity due to diverse parental backgrounds. The study demonstrates that SSR markers are a reliable and efficient tool for DNA profiling, early identification of true hybrids, and molecular diversity assessment in sugarcane breeding programmes, thereby enhancing selection efficiency at the initial stages of crop improvement.

Keywords: Sugarcane seedlings, SSR markers, Genetic diversity, Dendrogram, General cross, Biparental cross.

Abstract No: C17

Transferability studies of SSR marker of *Physalis peruviana* for Tomato

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ABSTRACT

The molecular markers (e.g., RFLP, AFLP, SNP, etc.) allow detection of variations or polymorphisms that exist among individuals in the population for specific regions of DNA. Molecular markers have applications in gene mapping, direct identification of the gene of interest instead of the gene product, as a useful tool for screening somatic cell hybrids, used in several DNA probes etc. A marker also helps in the physical mapping of the genes using in situ hybridization. SSR markers are the most effective of all the markers for diversity studies since they are robust, co-dominant, highly reproducible and highly polymorphic. But the development of this marker is very costly. One of the methods for identification of suitable marker is transferability study in which markers validated in one plant are used to test for their ability to produce successful amplification in plant of interest. The markers developed for plants of same family are often transferable. The present study was carried out to check the transferability of SSR markers of *physalis peruviana* for successful amplification on 8 different genotypes of tomato. A total of eight markers were used to produce amplified product in 8 genotypes of tomato. Four primers were found to be transferable. These primers were used for molecular profiling of the eight genotypes. The cluster analysis based on the results divided the genotypes into three clusters.

Keywords: SSR,DNA probes,Tomato, *physalis peruviana*

Abstract No: C18

Characterisation of Toll-Like Receptor Tollo of *Macrobrachium rosenbergii* Using Computational Tools

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ABSTRACT

Crustaceans are highly valued seafood with strong socioeconomic and ecological importance. Rapid aquaculture expansion increases microbial disease outbreaks, which threaten global production. Therefore, studying immune genes particularly toll-like receptors, is crucial for improving disease resistance and management. In the present study, it was aimed to characterize the Toll-like receptor Tollo, a previously uncharacterised TLR. Sequence data for various aquatic crustacean species were retrieved from the NCBI database. BLAST analysis was performed to compare sequences between humans and crustaceans, as well as among crustacean species and the percentage identity was 81.91%. Analysis of Physico-chemical properties using ProtParam server reveals it as a hydrophilic protein with pI 5.47. InterPro conserved domain analysis of *Macrobrachium rosenbergii* toll like receptor tollo (MrTLRT)revealed the presence of conserved domains characteristic of Toll-like receptors. Domain organization consisting of leucine-rich repeat (LRR) domains, a transmembrane region, L domain like and a conserved Toll/interleukin receptor (TIR) domain. A total of 17 leucine-rich repeats (LRR), 3 L domain–like structures, and 1 interleukin-related domain were identified. AlphaFold and NCBI VAST were used to predict protein structures and compare their similarities. The crustacean TLR Tollo was found to be homologous to the complex of the TOL-1 of *Caenorhabditis elegans*. In conclusion MrTLRT is a hydrophilic, membrane-bound protein having 17 LRR with structural similarity with *C. elegans* TOL-1.

Abstract No: C19

Integrated Meta-QTL and Meta-Transcriptomic for Identification of Candidate Genes Controlling Ricinoleic Acid Content in Castor (*Ricinus communis* L)

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ABSTRACT

Castor (Ricinus communis L.) is an important industrial oilseed crop, valued for its exceptionally high ricinoleic acid content that confers unique physicochemical properties to castor oil. However, ricinoleic acid accumulation is a complex quantitative trait governed by multiple genetic loci and influenced by environmental factors, limiting the direct application of individual QTLs in breeding programs. To address this limitation, the present study employed an integrated meta-QTL (MQTL) and meta-transcriptomic approach to identify stable genomic regions and high-confidence candidate genes associated with ricinoleic acid biosynthesis in castor. A total of 197 QTLs related to oil and fatty acid traits, reported across diverse populations and environments, were integrated and projected onto a consensus genetic map. This analysis identified 11 robust MQTL regions with significantly reduced confidence intervals, thereby improving mapping precision and genetic reliability. Integration of MQTLs with transcriptomic datasets enabled the identification of differentially expressed genes co-localized within MQTL intervals. Functional annotation and pathway enrichment analyses revealed that these candidate genes are primarily involved in ricinoleic acid accumulation. Several key genes associated with ricinoleic acid synthesis were highlighted as promising targets for molecular breeding. The combined genomic and transcriptomic evidence strengthens candidate gene validation and supports the development of reliable molecular markers for marker-assisted selection. Overall, this study provides a comprehensive genetic framework linking stable MQTLs with functionally relevant candidate genes, offering valuable resources for genetic improvement and genome-editing strategies aimed at enhancing ricinoleic acid content in castor. Overall, this study provides a comprehensive genetic framework linking stable MQTLs with functionally relevant candidate genes, offering valuable resources for genetic improvement and genome-editing strategies aimed at enhancing ricinoleic acid content in castor.

Keywords:*Ricinus communis*; Ricinoleic acid; Meta-QTL analysis; Meta-transcriptomics; Candidate genes; Fatty acid biosynthesis; Molecular breeding

Abstract No: C20

Development of genomic tools for Amaranth, a C4 climate resilient model plant system

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ABSTRACT

Global food supplies have stagnated in recent decades due to heavy reliance on a limited number of C3 crops with lower resilience to the rapidly changing climatic conditions. To address these changing paradigms and to prepare for future food insecurity, there is a critical need for a C4 model plant system that can be studied using next generation breeding approaches and advanced genomic tools. Amaranth (*Amaranthus* spp.) is a nutrient rich C4 pseudocereal well suited for climate resilience due to its biochemical and anatomical adaptations. Our study aims to establish Amaranth as a model climate-resilient crop by developing genomic resources and a customisable genome editing toolkit. A collection of 93 Amaranth germplasm accessions was obtained from the Indo-Himalayan region, and a subset was phenotypically screened for betalain and lysine content under controlled salinity stress. Accessions THA113 and THA116 showed improved growth and biochemical adaptations to the induced salinity stress. Furthermore, a CRISPR/Cas9-based customisable genome editing toolkit was developed by targeting the *MgChl*I gene as a visual marker, demonstrating a robust proof-of-concept system. Guide RNAs were designed using CRISPR Local tool and the multipartite cassette was assembled using GoldenBraid (gateway cloning). The toolkit was designed for scalability and future application in functional genomics and improvement of climate-resilience traits. Overall, our work provides genomic resources and genome-editing tools to support the use of Amaranth as a C4 model plant in future research.

Keywords: Nutritional security, Genome editing toolkit, C4 model crop, Betalain, Lysine, Saline stress

Abstract No: C21

Transcriptomics Decoding of Desiccation Tolerance and Host Exploitation in *Anguina tritici*

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ABSTRACT

Transcriptome profiling of anhydrobiotic, revived, and adult stages of the wheat seed gall nematode Anguina tritici revealed key molecular mechanisms underlying desiccation tolerance and host parasitism. Using Illumina NovaSeq 6000 sequencing, high-quality read alignments were obtained from all samples, resulting in a robust draft transcriptome. The combined final assembly spanned 133.2 Mb, comprising 105,606 transcripts, representing a substantial genomic resource for understanding stress adaptation and pathogenicity in this nematode. Functional annotation and pathway enrichment highlighted the MAPK, mTOR, FoxO, and longevity-regulating pathways as central components of stress adaptation and developmental regulation. Genes linked to stress response and survival, including heat shock proteins, peroxisomal catalase, nuclear hormone receptor domains, and homologues of DAF-2 and DAF-21, indicate conserved mechanisms associated with dauer formation, oxidative stress mitigation, and metabolic regulation. Critical signaling components such as MPK-1, RSKN-1, and RAC serine/threonine kinase further emphasize coordinated cellular responses to dehydration. Effector analysis identified proteins associated with pathogenicity, including 14-3-3 proteins, SNARE-like proteins, laminin-like proteins, pectate lyase, and glycoside hydrolase family 18 enzymes, suggesting roles in host cell wall degradation, intracellular trafficking, nutrient acquisition, and host invasion. Differential expression analysis demonstrated stage-specific upregulation of stress-responsive genes during anhydrobiosis and developmental/metabolic genes in adults, with qRT-PCR validation confirming transcriptomic trends. Together, these findings provide a comprehensive molecular framework for understanding anhydrobiosis and parasitism in A. tritici, and identify potential genetic and signaling targets for nematode management and crop protection strategies.

Keywords: Wheat seed gall nematode, Anhydrobiosis, Transcriptome, Parasitism

Theme: Plant Metabolomics & Systems Biology

Objective: To understand the bionomics of the nematode, including life cycle duration and above ground parasitism in relation to wheat growth.

To investigate the biorhythm and survival strategies of Anguina tritici, the wheat seed gall nematode, particularly its exceptional ability to survive for decades in a dormant (anhydrobiotic) state.

To generate and analyze the first transcriptome assembly of A. tritici in order to identify genes and pathways associated with parasitism, stress tolerance, and longevity.

Methodology

Seed galls of wheat infected with *Anguina tritici* were collected, and second-stage juveniles (J2) were isolated for biological and molecular studies. Bionomic observations were conducted to understand the nematode's life cycle, host–parasite synchronization, and the influence of growing degree days on development. The survival strategy of the nematode in the anhydrobiotic J2 stage within seed galls during the off-season was also examined. For molecular analysis, nematode samples representing active and anhydrobiotic stages were prepared, and total RNA was extracted, followed by quality and quantity assessment. High-quality RNA was used for library preparation and transcriptome sequencing using the Illumina NovaSeq platform. Raw sequence reads underwent quality control, adapter trimming, and filtering to obtain clean reads. De novo transcriptome assembly was performed to generate the final transcript dataset, which was evaluated using BUSCO against the Nematoda database to assess completeness. Functional annotation of assembled transcripts was carried out using sequence similarity searches, Gene Ontology classification, and KEGG pathway mapping. Differential gene expression analysis was performed to identify stage-specific genes. Further analysis was focused on identifying genes and pathways associated with parasitism, survival, and stress tolerance.

Key Findings

The study revealed that the life cycle of Anguina tritici ranges from 90 to 140 days or longer, closely synchronized with wheat growth and influenced by growing degree days. The nematode survives adverse off-season conditions in the anhydrobiotic J2 stage within seed galls, enabling long-term persistence. The first transcriptome assembly of A. tritici generated 133.2 Mb of sequence data comprising 105,606 transcripts, with 80.3% completeness based on BUSCO analysis. Functional annotation and differential expression analysis identified genes encoding glycolases, lyases, hydrolases, 14-3-3 proteins, and SNARE-like effectors, which are associated with aboveground parasitism in wheat stem pith, floral primordia, and seed endosperm tissues. Homologues of **CBR-DAF-2 and CBR-DAF-21** suggest the involvement of dauer formation and longevity pathways in survival. Additionally, key stress-related signaling pathways, including MAPK, ErbB, FoxO, and mTOR, were identified, with heat shock proteins and protein kinases playing central roles in stress tolerance. Overall, the study provides foundational molecular insights into the parasitic adaptation and long-term desiccation survival mechanisms of A. Tritici

Abstract No: C22

Genomic Identification of Blast Resistance Genes in Finger Millet for Sustainable Nutrition under Climate Change

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ABSTRACT

Finger millet (*Eleusine coracana* L.) is a nutrient-rich and climate-resilient minor cereal; however, its productivity is severely constrained by blast disease caused by *Pyricularia grisea*, with yield losses reaching up to 82% under severe infection. Despite its inherent stress tolerance, molecular improvement for blast resistance in finger millet remains limited due to insufficient genomic resources. To address this gap, the present study employed an integrative meta-analysis combined with comparative genomics to identify candidate genes associated with blast disease tolerance. Marker–trait associations (MTAs) were compiled from five published studies on blast resistance, resulting in 182 MTAs, of which 41 showed significant association with blast tolerance. Candidate genes were retrieved based on the physical positions of MTA-linked markers using the Phytozome and NCBI databases. Additionally, blast resistance–related genes reported in rice were collected from nine independent studies and used as reference sequences for cross-species analysis. A total of 60 rice genes associated with blast tolerance were BLASTed against the finger millet genome, and the most significant homologs were selected. After redundancy removal, conserved genes containing leucine-rich repeat (LRR) domains were identified through sequence alignment using Clustal Omega. Furthermore, rice pathogenesis-related (PR) genes were analyzed to detect homologous counterparts in finger millet. This integrated approach led to the identification of 49 putative candidate genes distributed across all finger millet chromosomes, including 33 PR genes and 29 blast-related genes derived from rice reference sequences. Functional annotation revealed that these genes encode key defense-related components, such as NB-LRR proteins, protein kinases, F-box family proteins, and the disease resistance protein RPS2, which play critical roles in pathogen recognition, signal transduction, and stress response pathways. These candidate genes constitute a valuable genomic resource for understanding blast resistance mechanisms and facilitate the development of climate resilient blast-tolerant finger millet cultivars through marker-assisted and genomics-assisted breeding strategies.

Keywords: Finger millet, Blast disease, Meta-analysis, Marker–trait association, Comparative genomics, NB-LRR, Stress tolerance

Abstract No: C23

Development of Plant Expression Construct for Crispr*/Cas9* based Genome Editing of *Stay Green 1* Gene in Tomato

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ABSTRACT

Tomato (*Solanum lycopersicum* L.) is an economically important horticultural crop and a major dietary source of health-promoting carotenoids, particularly lycopene. Lycopene accumulation during fruit ripening determines both nutritional quality and consumer appeal. Regulation of pigment biosynthesis and chlorophyll degradation plays a crucial role in fruit colour development. The *STAY GREEN 1* (*SGR1*) gene is a key regulator of chlorophyll breakdown and has been shown to influence carotenoid accumulation during tomato fruit ripening. Targeted modification of this gene offers a promising approach for improving fruit quality through genome editing. The present study focuses on the development of a plant expression construct for *CRISPR/Cas9*-mediated genome editing of the *SGR1* gene in tomato. The commercial cultivar Pusa Ruby has been selected as the experimental material. Initially, the coding sequence of the *SGR1* gene will be amplified, cloned, and sequenced to identify varietal-specific sequence features. Based on the genomic information obtained, specific target sites within exon regions of *SGR1* will be identified for guide RNA (gRNA) design. Bioinformatic tools will be used to ensure high target specificity and to minimize potential off-target effects. Selected gRNA sequences will be assembled under a plant-compatible RNA polymerase III promoter, while the *Cas9* endonuclease will be expressed using an appropriate plant promoter. Both components will be combined into a single binary plant expression vector using a modular cloning strategy. The resulting *CRISPR*/*Cas9* construct will be suitable for Agrobacterium-mediated delivery into tomato plants for targeted disruption of *SGR1*. This study aims to establish a reliable genome editing construct for functional analysis of *SGR1* and for future improvement of tomato fruit pigmentation and quality. The developed construct may serve as a valuable tool for precise genetic manipulation and contribute to the advancement of genome editing-based crop improvement strategies in tomato.

Keywords: Tomato, *CRISPR*/*Cas9*, *STAYGREEN* 1 (*SGR1*), Genome editing, Lycopene, Plant expression construct

Abstract No: C24

Molecular Detection and Screening of Viral Pathogens Infecting Pigeonpea (*Cajanus cajan*) in Bihar

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ABSTRACT

Pigeonpea (*Cajanus cajan*) is a vital legume crop in India, acting as a primary protein source and a key component of sustainable agriculture. However, yield is significantly affected by biotic stresses, with viral diseases causing an estimated annual loss of over USD 300 million in India. Among these, Sterility Mosaic Disease (SMD), caused by *Pigeonpea sterility mosaic virus* (PPSMV), and Yellow Mosaic Disease (YMD), caused by *Mungbean yellow mosaic India virus* (MYMIV), are the most destructive.

This study was aimed to survey and identify viral pathogens associated with symptomatic pigeonpea across various regionsof Bihar. Leaf samples exhibiting characteristic symptoms including mosaic, leaf curling, chlorotic rings, stunted growth and partial or complete cessation of flower production (i.e. sterility) were collected. Total nucleic acid was isolated from symptomatic tissues for RNA viral detection. First-strand cDNA synthesis was performed *via* Reverse Transcription, followed by Polymerase Chain Reaction (PCR) using specific primers targeting the coding regions of proteins of PPSMV. Additionally, genomic DNA was isolated to screen for DNA viruses (MYMIV) using specific PCR assays.

Preliminary molecular analysis confirmed the presence of PPSMV, yielding amplicons of the expected molecular weights for the targeted gene segments. However, MYMIV was not detected in the analyzed samples. While six distinct viruses are known to infect pigeonpea across India, this study provides critical molecular evidence specifically for PPSMV incidence in Bihar. Further cloning and sequencing of these amplicons are underway to decipher the strain diversity. These findings are crucial for understanding regional epidemiological data and formulating effective management strategies.

Keywords : Pigeonpea, PPSMV, SMD, Molecular Screening, Bihar

Abstract No: C25

Meta-QTL Analysis Identifies Phosphorus and SiliconAssociated Genetic Loci Governing Arsenic Uptake and Transport in Rice

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ABSTRACT

Rice (*Oryza sativa* L.) farming in the Gangetic floodplains of India haslong provided nutritional and socioeconomic sustenance to the inhabitants of this region, whichis being compromised by rising arsenic pollution in the river-basin. As arsenic (As)utilises both the phosphorus (P) and silicon (Si) transporters for its uptake and translocation in rice, it not only leads to toxic accumulation in plant tissues but also suppresses plant growth by interferingwith the uptake of the essential nutrients in the plant. To enable genetic improvement of arsenic tolerance in rice, stable quantitative trait loci(QTLs) related to As, Si and P uptake and accumulation were identified and subjected to meta-analysis to identify high-confidence interval genomic regions governing arsenic metabolism in rice. From a total of 354 reported QTLs,numerous effectivemeta-QTL (MQTL) hotspots have been determined with a significantly narrowed down confidence interval, and 85% of these MQTLs have been validated by colocalised marker-trait associations from published association mapping studies. Candidate genes involved in silicon and phosphate transport, glutathione metabolism, transcriptional regulation, auxin efflux, and metal ion binding were found in the core MQTL regions. In silico expression analysis and functional validation of these genes will be conducted in future research, and collectively, these findings will provide further insights into genomic regions that can be utilised in marker-assisted breeding programs to develop arsenic-tolerant rice varieties.

Keywords : Arsenic, Quantitative trait loci, Meta-analysis, Marker-trait associations

Abstract No: C26

RbohB-Type Respiratory Burst Oxidase Homolog Genes: Potential Targets for Genome-Editing-Based Improvement of Heat Stress Tolerance in Crops

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ABSTRACT

Heat stress is one of the major abiotic stresses limiting crop yields worldwide. It affects crop plants primarily by inducing excessive production of reactive oxygen species (ROS), which leads to oxidative damage of cells and tissues. This, in turn, adversely impacts plant growth and development and ultimately results in a significant yield penalty. Respiratory Burst Oxidase Homologs (*Rboh*s) constitute a multi-gene family comprising numerous members with diverse functions in plants. The *RbohB*class of this gene family encodes a plasma membrane–localized NADPH oxidase, which represents one of the major ROS-producing enzyme systems in plants. These enzymes primarily catalyze the production of superoxide radicals, which are rapidly converted into hydrogen peroxide, particularly under heat stress conditions. Elevated activity of *RbohB*-type proteins under heat stress can exacerbate oxidative damage, thereby acting as negative regulators of heat stress tolerance. Increased expression or activity of this gene enhances the susceptibility of crop plants to heat stress, making it a potential target for improving heat stress tolerance through loss-of-function mutations using genome-editing tools. Homologs of this gene have been identified in major crops such as rice, where CRISPR/Cas9-mediated knockout of *OsRbohB* has resulted in alleviation of heat-induced damage and improvement in grain yield and quality under prolonged heat stress conditions. This serves as a compelling proof of concept and highlights *RbohB*-type genes as promising targets for enhancing heat stress tolerance in other economically important crops, including pulses, oilseeds, and vegetables, where their identification and functional validation remain limited.

Keywords: Respiratory Burst Oxidase Homolog (*Rboh*), Heat Stress Tolerance, Reactive Oxygen Species (ROS), Genome Editing, CRISPR/Cas9

Theme D
Plant-Soil-Microbe Interactions

Abstract No: D1

Harnessing plant-associated bacterium for sustainable agriculture

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ABSTRACT

Controlling plant diseases in an eco-friendly and sustainable manner remains a challenge for sustainable agriculture. We have isolated a novel bacterium *Burkholderiagladioli* strain NGJ1 from rice that demonstrates fungal eating properties. We demonstrated that the bacterium delivers a prophage tail-like protein (Bg_9562) using a specialized secretion system (Type III secretion system)into the fungal hyphal to forage over them. The purified Bg_9562 protein demonstrates broad-spectrum antifungal activity. Notably, the heterologous overexpression of Bg_9562 or exogenous treatment with purified protein not only imparts fungal disease tolerance but also bacterial disease tolerance in tomato. Thedefense-inducing ability of the proteinlies within 18-51 aa region and is due to sequence homology with the bacterial flagellin epitope.Ourdataemphasize that on one hand, Bg_9562 is important for the endophytic growth of *B. gladioli*, while on the other hand, plant perceivesitas a MAMP (microbes-associated molecular pattern) usinga specialized receptor andelicits immune response.We are currently exploring means to deploy the Bg_9562 protein/peptide for controlling fungal and bacterial diseases in crop and horticultural plants.

Abstract No: D2

Microbes for water stress management: Resources, applications and mechanisms

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ABSTRACT

Water stress poses a major challenge to global agricultural productivity, necessitating sustainable and biologically driven strategies to enhance crop resilience. Microorganisms inhabiting extreme and marginal ecosystems represent a valuable but underutilized resource for stress management. In recent past we have studied, plant growth–promoting bacteria and archaea obtained from extremophytes or extreme environmental conditions for their application and mechanistic roles in mitigating water stress in chickpea and wheat.

Bacterial isolates obtained from chasmophytic wild *Chenopodium* were evaluated for their ability to alleviate drought stress in chickpea. Ten selected bacteria with multiple plant growth–promoting traits and tolerance to pH, salinity and osmotic stress were evaluated on Chickpea grown with water stress under Greenhouse conditions. The results revealed that *Pseudomonas* sp. LN75, *Bacillus paralicheniformis* L38, *Enterobacter hormachei* subsp. *xiangfengensis* LJ89, *B. paramycoides* L17 and *Micrococcus luteus* LA9 significantly enhanced plant growth and nutrient acquisition under water stress. Field validation confirmed consistent yield improvement under drought, with *Pseudomonas* sp. LN75 producing the highest chickpea yield (1363 kg ha^{-1}). This represents the first report demonstrating the drought-alleviating potential of chasmophyte-associated bacteria in a crop plant. In another study*Bacillus* sp. BT3 and *Klebsiella* sp. HA9 (isolated from the coastal sands of A&N island) further demonstrated the efficacy of bacterial inoculants in wheat under drought conditions. These strains improved morphological, physiological and biochemical traits, strengthened antioxidant defenses and modulated osmotic balance, while significantly enhancing the expression of drought-responsive genes.

To broaden the microbial spectrum, the role of archaea in drought tolerance was investigated using the haloarchaeon *Halolaminapelagica* CDK2 (isolated from Runn of Kutch) in wheat. Inoculated plants exhibited significant improvements in chlorophyll content, relative water status and root system architecture under water stress. Enhanced antioxidant enzyme activity and accumulation of sugars and proteins were accompanied by reduced osmolyte buildup, lipid peroxidation and reactive oxygen species. Notably, haloarchaeal inoculation up-regulated key stress-responsive genes (*DHN, DREB, L15* and *TaABA-8OH*), indicating transcriptional regulation as a central mechanism of stress mitigation.

Overall, these findings highlight the potential of microbial resources from extreme environments to mitigate water stress through integrated mechanisms involving nutrient mobilization, root system enhancement, oxidative stress regulation and molecular signaling. Harnessing such microbes as bioinoculants offers a promising, eco-friendly strategy for improving crop productivity in water-limited environments.

Abstract No: D3

An insight into Groundnut Bud Necrosis Virus Encoded Non-structural Proteins

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ABSTRACT

Groundnut Bud Necrosis Virus (GBNV) is a tospovirusthat infects several commercially important crops in India. They arespherical enveloped particles (80-110 nm) that encapsidate three negative single-stranded RNA genomes (S, M, and L). M and S RNA encode for two non-structural proteins, NSm and NSs, respectively. These non-structural proteins are not components of virions but are involved in evading the host's immune response and in cell-to-cell movement of virions. NSm is a movement protein involved in cell-to-cell movement of Viruses through Plasmodesmata. NSs binds to siRNA and suppresses Post-transcriptional Gene Silencing. In earlier studies, it was shown that GBNV NSm associates with the membrane and remodels the ER network to form vesicles through its C-terminal coiled-coil domain.

GBNV NSmbindsto GTP and ATP *in vitro*. The binding assay was performedusing ATP- and GTP-Agarose beads, UV-Cross-linking, and the Intrinsic fluorescence quenching method.However, the ATPase and GTPase activity of NSm still needs validation. The cell-to-cell movement of the Virus, facilitated by the Movement protein, is an energy-dependent process. Therefore, it may be that NSm requires these NTPs to modify plasmodesmata and thereby is involved in the cell-to-cell movement of GBNV. It also undergoes phosphorylation bya kinase present in the *crude extract of N. benthamianaleaves*,and two sites were identified. One site was identified as conserved and found to be essential for NSmlocalisation to plasmodesmata. Another non-structural Protein, NSs, was also shown to associate with NSm*in vitro*. NSs localise to the cytosol, but when NSm and NSs are coexpressed in *N. benthamiana*, NSs relocalise to the membrane and the plasmodesmata, suggesting that NSm-NSs interaction might have an essential role in cell-to-cell movement.However, further functional implications of NSm: NSs interaction are under study.

Abstract No: D4

Isolation and screening of Zinc Solubilizing Bacteriafrom Pulses Rhizosphereand their Effect on In vitro Solubilization of Zinc Oxide Compound

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ABSTRACT

Zinc is an essential micronutrient required for various physiological and biochemical functions in plants, yet its availability in soils is often limited due to its presence in insoluble forms. Zinc deficiency in agricultural soils especially in pulse-growing regions of India, poses a significant constraint to crop productivity and nutritional quality. This study aimed to isolate and characterize zinc solubilizing bacteria (ZSB) from the rhizosphere of major pulse crops-Mung bean (*Vigna radiata*), Urd bean (*Vigna mungo*), pigeon pea (*Cajanuscajan*), lentil (*Lens culinaris*) and chickpea (*Cicer arietinum*)-to evaluate their potential for zinc oxide (ZnO) solubilization under in vitro conditions. Ten bacterial isolates were obtained through serial dilution and plating methods from rhizospheric soils of pulse crops collected from different agricultural locations in Bihar. The isolates were subjected to morphological and biochemical characterization, including catalase and oxidase activity tests. Their zinc solubilization ability was first screened qualitatively using Tris minimal agar medium amended with 0.1% ZnO and solubilization was assessed based on halo zone formation, solubilization index (SI), solubilization efficiency (SE) and Khandeparkar's selection ratio. Quantitative assessment was carried out in broth

culture, where pH changes and zinc concentrations were measured at 5, 10 and 15 days after incubation. Zinc concentration in the broth was estimated using Atomic Absorption Spectrophotometry (AAS). Among the ten isolates, AJP-6 and AJL-8 demonstrated superior zinc solubilization performance. AJP-6 exhibited the highest halo zone diameter (27 mm), SE (337.55%) and significant ZnO solubilization in broth (249.75 mg/L at 15 days), accompanied by a substantial reduction in medium pH (5.53). AJL-8 closely followed with 234.23 mg/L ZnO solubilized and a pH of 5.59 at the same interval. These results indicate active organic acid production and high metabolic efficiency in mobilizing insoluble Zn. The findings suggest that native ZSB strains such as AJP-6 and AJL-8 have significant potential as bioinoculants for zincdeficient soils, especially in pulsebased cropping systems. Their application may reduce dependence on chemical fertilizers, enhance micronutrient availability and support sustainable agricultural practices. Further in vivo trials are warranted to validate their efficacy under field conditions.

Key Words : Zinc solubilizing bacteria, Zinc oxide, Rhizosphere, Pulse crops, Bioinoculants, Solubilization index (SI), Solubilization efficiency (SE), Micronutrient management.

Abstract No: D5

Harnessing the potential of *Trichodermaasperellum*for the control of different diseases in medicinal plants

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ABSTRACT

Medicinal plants are cultivated and also occur naturally in the wild across the country. They are widely used in traditional herbal remedies and for the extraction of phytochemicals employed in homoeopathic and Ayurvedic medicines, cosmetics, nutraceuticals, dietary supplements, functional foods, and aromatherapy oils. However, these plants are susceptible to several diseases such as leaf spots, rots, and blights, which adversely affect their quality, yield, and market value. The use of chemical fungicides for disease management in medicinal plants is not preferred, as chemically treated extracts have limited market acceptance and economic viability.*Trichoderma*spp. have been widely studied, and are presently marketed as biopesticides, biofertilizers and soil amendments, due to their ability to protect plants, enhance vegetative growth and reduce pathogen populations under numerous agricultural conditions. The present study was performed to assess the efficacy of *Trichodermaasperellum* strain against pathogens of medicinal plants *in vitro* and in field conditions. *In vitro* study, *Trichodermaasperellum* was evaluated against 10 different plant pathogens of medicinal plants namely Ashwagandha (*Alternariaalternata* and*Fusariumsolani*), Sarpgandha (*Colletotrichum* sp. And*Alternariaalternata*.), Tulsi (*Colletotrichumgloeosporioides* and *Alternariaalternata*), Mint (*Curvularia* sp. And*Alternariaalternata*), Kalmegh (*Corynesporacassiicola*) Mandukparni (*Cochliobolus* sp. and *Alternaria* sp.) by Dual culture plate method. Maximum inhibition 56.36 per cent was recorded against *Fusariumsolani.* This was followed by inhibition of *Cochliobolus* sp. where the reduction in percent growth was 55.38 per cent. *T. asperellum* was also found effective against *Alternaria* sp. isolated from Ashwagandha (53.06%), *Alternaria* sp. from Sarpagandha (53.51%), and *Curvularia* sp. (52.12%). In field study, the FYM enriched with *Trichoderma*, *Pseudomonas*followed by foliar spray of neemoil and copper oxychloride were tested in field against Leaf spot of Kalmegh. The pooled data of three years (2021-22 to 2023-24) reviled that significantly minimum per cent disease index (9.13%) was recorded in treatment spraying of Tebuconazole + Trifloxystrobin @ 0.1% at the onset of disease followed by treatment (T3)Soil treatment *P. fluorescence* @30kg/ha + *T. asperellum*@30kg enriched with 15 t FYM/ha + Neem Cake @ 2t/ha found most effective and PDI was recorded (16.66%). Maximum fresh biomass was also recorded in T3 (54.45 q/ha) followed by T9 (51.39q/ha) and both were at par with each other. Maximum PDI (44.09%) was recorded in control. However, Soil treatment *P. fluorescence* @30kg/ha + *T. asperellum*@30kg enriched with 15 t FYM/ha + Neem Cake @ 2t/ha is eco-friendly and may be recommended for the management of leaf spot disease of Kalmegh.

Abstract No: D6

Isolation and characterization of native bacteria and its*in vitro* antagonistic activity against *Rhizoctonia solani* causing sheath blight of rice

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ABSTRACT

Sheath blight of rice, caused by *Rhizoctonia solani* Kuhn, remains one of the most destructive diseases of rice, significantly impacting yield and crop quality. Conventional chemical-based management practices, though effective, pose risks of environmental pollution, pathogen resistance, and disruption of beneficial microbial communities. Consequently, there is an urgent need to develop eco-friendly, sustainable alternatives for disease management. In this context, the present investigation was undertaken to explore the antagonistic potential of native bacterial isolates against *R. solani* under *in vitro* conditions. Total 28 native bacterial isolates were isolated through standard dilution techniques samples collected from the upland, medium land and low land agro ecosystems of rice. These isolates were systematically screened for their antagonistic activity against *R. solani* through dual culture in vitro assays. The antagonistic evaluation revealed significant variability among the isolates, with several strains demonstrating remarkable mycelial growth inhibition of the pathogen. Among all28 isolates, JBR M5, isolated from the medium land rhizosphere, exhibited the highest antagonistic efficacy, achieving 83.67% mycelial inhibition by the 10th day of incubation. Similarly, upland isolate SBR-U5 (78.00%) and lowland isolates DBR-L12 (79.11%) and SBR-L7 (77.89%) also demonstrated strong antagonistic activities.Potential selected isolates were also evaluated for their ability to enhance seed germination and seedling vigour under controlled conditions. The results indicated that JBR-M5 not only exhibited the highest antagonistic potential but also significantly improved seedling growth parameters, recording highest seed germination 96.53% and vigour index of 2583. Followed by other isolatesSBR-U5 (95.70% & 2121), and SBR-L6 (92.54% & 2268) seed germination and seedling vigour respectively as compare to control 80% seed germination &1014 vigour index.The most promising isolate, JBR-M5, underwent molecular identification through 16S rRNA gene sequencing. The sequence analysis revealed a 99.73% similarity with *Alcaligenes faecalis* strain IMH 12118, confirming its identity. This molecular characterization not only substantiated the observed biocontrol efficacy but also aligned with previous research reporting *A. faecalis* as a potent antagonist of *R. solani* in rice ecosystems.

Keywords: Native bacteria, Sheath blight of rice, *Rhizoctonia solani*,*Alcaligenes faecalis*

Abstract No: D7

Trichoderma asperellum and *Bacillus subtilis* : Efficient bioagents for management of *Meloidogyne incognita* race II infesting black gram (*Vigna mungo* L.)

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ABSTRACT

Meloidogyne incognita, a major disease causing nematode in black gram (*Vigna mungo* L.), leading to severe losses in yield and quality of protein. An experiment was conducted at RPCAU, Pusa, in 2024, to see the effect of fungal and bacterial bioagents, *Trichoderma asperellum* and *Bacillus subtilis* along with FYM on the yield and growth of the crop and also on the nematode. There were seven treatments in three replications: *Trichoderma asperellum* and *Bacillus subtilis* @ 2.5 kg and 5 kg along with FYM @ 2.5 t/ha (T_1 to T_4), FYM as an individual treatment @ 2.5 t/ha (T_5), carbofuran 3G as treated check @ 2 kg a.i./ha (T_6) and one untreated check (T_7) for comparison. The bioagents were applied as soil treatment, 15 days before sowing. The variety used, was, Pant Urd 31. The experimental design was Randomized Block Design. After 60 days of inoculation, the data were observed and analysed statistically. It was found that the bioagents, *Trichoderma asperellum* and *Bacillus subtilis* @ 2.5 kg and 5 kg along with FYM @ 2.5 t/haas soil application have significant effect on the yield increase and nematode population decrease. The treatment of bioagent, *Bacillus subtilis* @ 5 kg along with FYM @ 2.5 t/ha,was found highly significant compared to other treatments in increasing the pod yield by 344 % and in decreasing the final nematode population by 55.40 % in soil and 71.36 % in root with a root knot index of 2.67 only, followed by *Bacillus subtilis* @ 2.5 kg along with FYM @ 2.5 t/ha, *Trichoderma asperellum* @ 5 kg along with FYM @ 2.5 t/ha, *Trichoderma asperellum* @ 2.5 kg along with FYM @ 2.5 t/ha and FYM @ 2.5 t/ha. Considering the residual toxicity and cost, the bioagents were found beneficial than the chemical treatment.

Keywords: *Trichoderma asperellum*, *Bacillus subtilis*, biomanagement, *Meloidogyne incognita*, black gram

Abstract No: D8

Screening of Endophyte-Based Biocontrol Strategy for Red Rot of Sugarcane with Plant Growth-Promoting Benefits

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ABSTRACT

A total of 71 endophytic bacteria were isolated collectively from the root, stem and leaf of two sugarcane varieties BO 91 and CoP 16437 in this study. Further, these endophytes were tested for in vitro inhibition against the red rot pathogen (*Colletotrichum falcatum*). Out of 71, only 37 bacteria were able to show in vitro inhibitory action against the pathogen. Besides inhibiting their mycelial growth, some of these endophytes were able to synthesize various PGP traits such as IAA, phosphate solubilization, Potassium, Zinc solubilization, siderophore and ammonia production. These endophytes were found helpful in promoting the growth of the plant in a direct and indirect way. Six bacterial isolates with more than 65% inhibitory activity against the pathogen and PGP attributes were further characterized through 16S rRNA gene sequencing. On the basis of the phylogenetic analysis, the six endophytic antagonists were identified as *Microbacteriumarborescens* (BR2), *Bacillus safensis* (BR6), *Microbacteriumginsengiterrae* (BR21), *Glutamicibacterhalophytocola* (CR7), *Bacillus tequilensis* (CS1), *Bacillus safensis*(CS2). This study demonstrated that endophytic bacteria are an untapped source of natural products and can be exploited for yield attributes and red rot control in sugarcane.

Keywords: Endophytes, Sugarcane, Red rot, Biocontrol, Plant growth promotion, 16S rRNA

Abstract No: D9

Exploration of Phosphate-Solubilizing Bacteria from Natural Farming Bioinputs and the Impact of their Consortium with *Jeevamrit* on Wheat Growth

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ABSTRACT

Phosphorus (P) is a key macronutrient that limits crop productivity due to its low accessibility and fixation in calcareous soil. The low phosphorus use efficiency of conventional P fertilizers presents both economic and environmental challenges. The present study was attempted to explore phosphate-solubilizing bacteria (PSB) from natural farming bioinputs and to evaluate the effect of a consortium of promising isolates in combination with *Jeevamrit* on the growth performance of wheat (*Triticum aestivum*). A total of 30 bacteria were isolated from *Jeevamrit*and *Ghanajeevamrit*. Among these, 12 isolates showed phosphate-solubilizing activity, with isolate ISJM-12 exhibiting the highest solubilization index (3.44). All phosphate-solubilizing bacterial isolates were further evaluated for plant probiotic traits, including zinc solubilization, indole-3-acetic acid (IAA) production, and exopolysaccharide (EPS) production. All isolates showed zinc-solubilizing activity, while 11 isolates exhibited a positive outcome for EPS production. However, two isolates, ISJM-12 and ISJM-8, exhibited the highest values for IAA production, and the consortium of these two potential strains was further selected for field evaluation. Field experiments were conducted at the Natural Farming Unit, RPCAU, Pusa, using the wheat variety *HD-2967*. Growth attributes, including plant height, number of tillers, and chlorophyll content, were recorded at different growth stages and demonstrated a significant positive response to consortium-based treatments combined with *Jeevamrit*. Hence, the present study provides an overview of the potential of the consortium of PSB in combination with *Jeevamrit*as an effective strategy and a sustainable alternative to chemical fertilizers for improving crop performance.

Keywords : *Jeevamrit*, *Ghanajeevamrit*, Phosphate-solubilizing bacteria, Wheat, Plant probiotic traits

Abstract No: D10

Study on Biodegradation of Litchi Leaf Litter Using Lignocellulolytic Microbes

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ABSTRACT

Litchi *(Litchi chinensis*) is a subtropical fruit cultivated largely in Southeast Asia. India is the second largest producer in the world for Litchi fruits, and generates a substantial amount of leaf litter every year. The decomposition rate of litchi leaf litter is very low due to its high lignocellulosic content, and a high carbon-to-nitrogen ratio. This study aims at assessing the significance of lignocellulolytic microbes in the decomposition of litchi leaf litter and their contribution to nutrient cycling in soil. A total of 45 microbial isolates, consisting of 26 fungal and 19 bacterial isolates, were evaluated for their potential role in assisting the decomposition process. The bacterial isolates were mainly tested for their cellulose-degrading activity and the fungal isolates for their lignin-degrading activity. During the screening, around 10 of the 19 bacterial isolates showed cellulase production while 18 of the tested 26 fungal isolates were able to degrade lignin. Further tests involving the use of Litchi leaf powder as a substrate enhanced the growth of fungal isolates. Physical and chemical treatments of litchi leaf litter were also performed to improve microbial accessibility. Based on their degradation ability, five fungal and four bacterial isolates were chosen for further analysis. Results from this study identified fungi as a major contributor to lignin degradation and bacteria as a contributor for cellulose degradation.

Keywords: Litchi, Decomposition, Litchi leaf litter, Lignocellulolytic microbes.

Abstract No: D11

STUDY ON EFFECT OF DIFFERENT SOURCES AND MODES OF NITROGEN APPLICATION ON YIELD AND BIOCHEMICAL PARAMETERS OF RICE (Oryza sativa L.)

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ABSTRACT

A field experiment was conducted in two varieties of rice viz. GR-23 and GNR3 grown and were analyzed for biochemical responses and yield under different sources and modes of nitrogen application. The two rice varieties, GR-23 (high protein) and GNR-3 (low protein) exhibited different nitrogen uptake patterns showing higher nitrogen uptake in tillering and panicle initiation in GNR-3 and GR-23 respectively. The Recovery efficiency of nitrogen (NUE) was higher in GR-23 compared to GNR-3 where the nitrogen treatment N1 (100 % RDN as urea in soil) showed the highest followed by N3 (75 % RDN as urea in soil with two foliar sprays of nano urea). Among the different nitrogen treatments, N1 showed maximum grain and biomass yield followed by N3 (75 % RDN + 0.4 % IFFCO nano urea). Foliar spray of nitrogen in two different forms enhanced the assimilatory enzyme activities within 24-48 h post spray application where foliar application of urea (2 %) showed much higher activity compared to foliar application of nano urea (0.4 %) and the treatment N2 (75 % RDN as urea in soil with two foliar sprays of urea) showed the maximum assimilatory enzyme activities viz. Nitrate Reductase(NR), urease, Glutamine Synthetase(GS), Glutamine 2-Oxoglutarate Aminotransferase(GOGAT), Glutamate Dehydrogenase(GDH) and Asparagine Synthetase (AS) within 24- 48 h post spray application, whereas the amino acid glutamate, glutamine, aspartate and asparagine concentrations were higher in the treatment done with foliar nano urea spray compared to urea spray application and the nitrogen treatment N3 showed maximum concentration. Much variations were not seen in the enzymatic activity of the soil due to foliar application of urea or nano urea sprays.

Key words : Nano urea, Foliar sprat, NR, GS, GOGAT

Abstract No: D12

Screening of Cellulo-Ligninolytic bacteria and fungi for Enhance Saccharification of Sugarcane Bagasse for Bioethanol Production

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ABSTRACT

Increasing demand for sustainable and renewable energy sources has intensified research on bioethanol production from lignocellulosic biomass. Sugarcane bagasse, an abundant agro-industrial residue represents a promising and cost-effective substrate for bioethanol production due to its high cellulose (40–50%) and hemicellulose (25–30%) content. The present study aimed to evaluate the production of bioethanol from sugarcane bagasse as it is able to produce 0.35–0.37 L ethanol per kg of dry mass.The main hinderance of using such feedstock into bioenergy form is its lignocellulosic composition which is very difficult to break into simple sugars.In the present study, a total of **30** mushroom samples were collected from different locations of RPCAU and were screened for lignocellulose-degrading potential using selective media containing carboxymethyl cellulose (CMC), Xylan and ABTS for cellulase, hemicellulose , and lignin-degrading activities, respectively.Out of which **16** isolates showed maximum growth on CMC plates,**19** isolates showed maximum growth on Xylan and **26** showed maximum growth on ABTS plates.Based on their overall ligno-cellulolytic ability and prominent halozone formation a total of **27** isolates were selected for further studies. Bushnell Hass (BH) media was prepared using **20%** physically pretreated sugarcane bagasse powder used as the carbon source and the selected mushroom isolates were inoculated and incubated, The plates showing maximum growth were assayed using the DNSA at incubation intervals of 3, 6, 9, and 12 days.The results revealed a significant release of reducing sugars, with values ranging from **35.43** to **38.07** mg/g of dry substrate, indicating efficient degradation of sugarcane bagasse by the selected isolates. Mushroom isolates exhibiting higher reducing sugar production will be further utilized for bioethanol production using a suitable promising Yeast culture. Bioethanol yield will be estimated by the potassium dichromate method and HPLC.

Keywords: Sugarcane bagasse; Lignocellulosic biomass; Physicochemical pretreatment; Enzymatic hydrolysis; Saccharomyces cerevisiae; Fermentation; Reducing sugars

Abstract No: D13

Targeted alterations in conserved structural motif in central repeat domain of a Xanthomonas oryzae pv. oryzae TALeffector to study effect on virulence in rice

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ABSTRACT

Transcription activation like effector, a critical determinant of rice-Xoo interaction which is deployed by Xanthomonas oryzae pv. oryzae via T3SS to hijack the host machinery is the DNA binding protein distinguished by highly conserved central repeat domain made up of tandem repeats, each of typically 34 amino acids long. The repeat sequences are highly conserved except the 12th and 13th residues of each repeat, known as Repeat Variable Diresidue (RVD). The sequence and number of RVDs of a TALeffector decides its specificity for host target. SWEET13, is one of the major bacterial blight associated susceptibility genes in rice and is targeted by its cognate TALeffector PthXo2 to facilitate growth and proliferation of Xoo strains harbouring PthXo2 to cause disease on indica rice. Allelic polymorphisms in japonica allele of SWEET13 gene evades binding of PthXo2 and hence is resistant. However, PthXo2B, an ortholog of PthXo2 harbors aberrant repeats of 36 amino acids in two of its repeats causing frameshift in binding, and thus targets japonica allele. Previous studies carried out in our lab on functional characterization of PthXo2B from an Indian Xoo strain IX-221 (named as Tal7) revealed it to cause disease in both indica and japonica rice. However, its RVD and aberrant repeat identical designer TALeffector with custom repeat backbone did not mimic Tal7. Sequence comparison identified motifs MAIAN and LTPT specifically found in repeats harbouring 'NN' only in PthXo2 orthologs, vis-à-vis VAIAS and LTPD being custom motifs in dTALes and other natural TALes. So, we hypothesized that besides the RVD and aberrant repeats, repeat backbone also may have a role in impacting targeting profile of a TALeffector. This work was designed to test this by generating dTALes with the motifs as in the native Tal7 and also to generate variants of Tal7 to test whether either or both motifs and if its location in 4th or 6th repeat matters. PCR directed site directed mutagenesis was carried out through primers harbouring the modified bases coding for desired amino acids for incorporation in 4th and 6th repeat sequence carrying plasmids. All 21.5 repeats constituting the Tal7 including the 4th and 6th repeats as modified in this work were sequentially assembled using Golden gate cloning and cloned into expression vector through Gateway cloning followed by transformation of Xoo strain PXO99A-ME2 with the expression constructs. Thus, five different variants of Tal7 were custom designed and generated for complementation into a non-virulent Xoo strain for studying the significance of repeat backbone variations in virulence of TALeffector. The custom designed constructs ready for artificial infections on indica rice, to test if, with the unique motifs the dTALes have gained virulence on indica rice. If the hypothesis holds true, the TALeffector-host DNA binding will have to be relooked from new/novel perspective going beyond the RVD-EBE, that prevails today.

Keywords: dTALEs, TALeffector, Golden gate cloning, Gateway cloning

Abstract No: D14

Evaluation of Bacterial and Cyanobacterial Isolates for Arsenic Detoxification

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ABSTRACT

Arsenic contamination of groundwater and agricultural soils is a serious environmental and agronomic challenge, particularly in the Gangetic plains of India, including Bihar. Prolonged use of arsenic-contaminated irrigation water leads to arsenic accumulation in soil and its subsequent uptake by crops such as wheat, thereby posing significant risks to food safety and human health. The present investigation was undertaken to evaluate the arsenic tolerance, detoxification potential, and exopolysaccharide (EPS) production ability of selected bacterial and cyanobacterial isolates, with an objective to identify potential bioinoculants for arsenic stress mitigation. A total of thirty bacterial and cyanobacterial isolates were obtained from the culture repository of the Department of Microbiology, RPCAU, Pusa. The isolates were purified, maintained, and screened for arsenic tolerance using plate assay and liquid broth assay under varying arsenic concentrations (20–100 ppm). Microbial growth was assessed qualitatively on arsenic-amended agar plates and quantitatively by measuring optical density (OD_{600}) at 24, 48, and 72 hours in liquid medium. Arsenic-tolerant isolates were further evaluated for EPS production using sucrose-supplemented growth media. EPS was extracted by ethanol precipitation and quantified using gravimetric analysis. The results demonstrated a concentration-dependent decline in microbial growth; however, several isolates exhibited substantial tolerance to elevated arsenic levels. Eighteen isolates showed higher survival on arsenic-supplemented media, while thirteen isolates maintained stable growth in liquid medium under arsenic stress. Among these, ten isolates were identified as efficient EPS producers, with five isolates exhibiting superior EPS yield. The combined arsenic tolerance and EPS-producing capability of these isolates suggests their potential role in arsenic immobilization and detoxification. The study highlights the potential application of selected bacterial and cyanobacterial isolates for arsenic detoxification and proposes their further evaluation under pot conditions using wheat crop for sustainable management of arsenic-contaminated soils.

Abstract No: D15

Effect of methanol extract of *Schizophyllum commune* against different phytopathogens

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ABSTRACT

This study investigates the antimicrobial potential of *Schizophyllum commune* methanolic extracts against several plant pathogenic fungi and bacteria. The extracts exhibited significant dose-dependent antifungal and antibacterial activity across concentrations ranging from 2000 to 5000 ppm. In antifungal assays, *Cercospora sp*. and *Fusarium sp*. were the most responsive, showing inhibition zones of 27.0 mm at 5000 ppm. Moderate responses were observed for *Colletotrichum sp*. and *Curvularia sp.,* with inhibition zones ranging from 6.7 mm to 21.0 mm and 9.0 mm to 19.0 mm, respectively. The least responsive fungi were *Alternaria sp*. and *Bipolaris sp*., with maximum inhibition zones of 16.3 mm and 17.3 mm, respectively. For antibacterial activity, the methanolic extracts showed strong effects against *Pseudomonas sp*. and *Bacillus sp*., with inhibition zones reaching 25.0 mm and 23.0 mm, respectively, at 5000 ppm. *Xanthomonas sp*. and *Rhizobium sp*. also demonstrated significant inhibition, albeit at lower levels (21.0 mm and 18.67 mm, respectively). These results confirm the broad-spectrum antimicrobial potential of *S. commune* extracts, highlighting their possible use as natural agents for plant disease management, particularly for combating *Fusarium* and *Pseudomonas* infections. Future research should focus on identifying the specific bioactive compounds responsible for these effects and assessing their efficacy under field conditions.

Keywords : Schizophyllum commune, methanolic extract, antimicrobial activity, plant pathogens, biocontrol, zone of inhibition.

Abstract No: D16

Plant Soil Microbe Interactions for Prebiotic Development: Xylanase-Based Production of XOS from Agricultural Biomass

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ABSTRACT

Agricultural crop residues are abundant, renewable, and inexpensive resources with strong potential to produce value-added nutraceuticals. Xylo-oligosaccharides (XOS) are emerging prebiotic molecules but their commercial production is largely dependent on food crops such as jerusalem artichoke, chicory root, and asparagus which is expensive and competes with human consumption. In this study, soil samples were screened for xylanase producing bacteria and the most potent strain (W2) was subjected to morphological, biochemical, and molecular characterization. Phylogenetic analysis identified the strain as *Bacillus pumilus*. Xylanase produced by this isolate was characterized under different physical conditions and was found to be an alkaliphilic enzyme with optimum activity at pH 8.0 and 40 °C. The enzyme also exhibited considerable thermal stability at higher temperatures, making it suitable for industrial bioprocessing. The crude xylanase was used to saccharify agro-waste substrates, including wheat bran and sugarcane bagasse, for the generation of XOS. The produced oligosaccharides were identified and confirmed using paper chromatography. Thus, enzymatic hydrolysis produced XOS without generating unwanted by-products, a significant advantage over chemical hydrolysis. The prebiotic functionality of the hydrolysate was evaluated using three probiotic strains—*Lactobacillus lactis*, *Lactobacillus casei*, and *Bacillus clausii*. Enhanced growth of all three probiotics indicated the strong prebiotic nature of the XOS generated through this process. Overall, the study presents a sustainable and economically viable strategy to convert agricultural residues into valuable prebiotics. The alkaliphilic xylanase from *Bacillus pumilus* W2 shows strong potential for application in prebiotic and probiotic formulations. This approach can minimize agricultural waste disposal issues and support the development of gut health promoting functional foods.

Keywords: Xylooligosaccharides; Xylanase; Enzymatic hydrolysis; Prebiotics; Agro-waste valorization; Paper chromatography

Abstract No: D17

Bioconversion of Sugarcane Bagasse into Bioethanol Using Lignocellulose-Degrading Microorganisms

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ABSTRACT

Rising demand for sustainable and renewable energy sources has core research on bioethanol production from lignocellulosic biomass. As, an abundant agro-industrial residue, Sugarcane Bagasse is a promising and cost-effective substrate for bioethanol production due to its high cellulose (40–50%), hemicellulose (25–30%) and lignin (20-25%) content. The current study focused to evaluate the production of bioethanol from sugarcane bagasse as it is able to produce 0.35–0.37 L ethanol per kg of dry mass**.** The main hinderance of using such feedstock into bioenergy form is its lignocellulosic composition which is tough to break into monomeric sugars. In the present study, a total of **11** fungus samples and **21** bacterial samples were collected from Department of Microbiology and were screened for lignocellulose-degrading potential using selective media containing carboxymethyl cellulose (CMC), Xylan and ABTS for cellulase, hemicellulose, and Lacasse activities, respectively. Out of which **6** bacterial isolates showed maximum growth on CMC, Cellulose and Xylan plates and **9** fungal samples showed maximum growth on ABTS plates. Based on their overall ligno-cellulolytic ability and prominent halozone formation a total of **15** isolates were selected for further studies. Bushnell Hass (BH) media was prepared using **20%** physically pretreated sugarcane bagasse powder was utilized as a carbon source and only 10 isolates showed maximum growth were further screened for release of reducing sugars using DNSA assay at incubation intervals of 3, 6, 9, and 12 days. The selected isolates were demonstrated efficient degradation of sugarcane bagasse, releasing significant amounts of reducing sugars ranging from **35.43** to **38.07** mg/g of dry substrate. Both fungal and bacterial isolates exhibiting higher reducing sugar production will be further utilized for bioethanol production using a suitable promising Yeast culture. Bioethanol yield will be estimated by the potassium dichromate method and HPLC.

Keywords: Sugarcane bagasse; Fungal and Bacterial isolates; Physicochemical pretreatment; Saccharification; *Saccharomyces cerevisiae*; Fermentation; Reducing sugars

Abstract No: D18

Role of Soil Health and Soil–Plant Interactions in Ensuring Nutritional Security under Climate Change

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ABSTRACT

Soil health plays a pivotal role in sustaining agricultural productivity and ensuring nutritional security under changing climatic conditions. Climate change–induced stresses such as drought, erratic rainfall, rising temperatures, and soil degradation have adversely affected soil physical, chemical, and biological properties, ultimately impacting crop growth and nutrient availability. Therefore, maintaining soil health is essential for developing resilient and sustainable food production systems. Healthy soils support efficient nutrient cycling, improved soil structure, enhanced water-holding capacity, and active soil microbial communities, which together contribute to better crop performance and nutritional quality. Soil organic matter, soil microorganisms, and beneficial plant–microbe interactions are key components influencing nutrient uptake, stress tolerance, and crop productivity. Improved soil management practices such as organic amendments, balanced fertilization, and conservation agriculture have shown significant potential in enhancing soil resilience and crop nutrient content under climate stress conditions. The present review highlights the importance of soil health and soil–plant interactions in achieving nutritional security in the era of climate change. Emphasis is placed on the role of soil properties and soil biological processes in sustaining crop nutrition and productivity. The review also discusses the need for integrated soil management strategies to improve soil resilience, enhance nutrient use efficiency, and support climate-resilient agriculture. Strengthening soil health–based approaches can play a crucial role in ensuring sustainable food and nutritional security for the future.

Keywords: Soil health, climate change, nutritional security, soil–plant interactions, sustainable agriculture

Abstract No: D19

Interactions effects of pseudomonas trichoderma bacillus combination Interaction effects of Pseudomonas, Trichoderma and Bacillus combination Against sheath blight and bacterial leaf blight Pathogen of rice

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ABSTRACT

Rice (*Oryza sativa L.)* is an important cereal crop contributing substantially to food security in India. Its production is adversely affected by sheath blight caused by *Rhizoctonia solani* and bacterial leaf blight caused by *Xanthomonas oryzae pv. oryzae*. These diseases commonly develop under intensive cultivation practices and favourable climatic conditions, resulting in reduced yield and crop quality. Conventional chemical control measures provide temporary relief but raise concerns related to environmental safety, cost of cultivation, and long-term sustainability. Hence, biological disease management using beneficial microorganisms has gained importance. The present study was undertaken to evaluate the antagonistic potential and interaction effects of *Pseudomonas, Trichoderma, and Bacillus*, applied individually and in combination, against sheath blight and bacterial leaf blight of rice. Under in vitro conditions, twenty-two microbial isolates were screened for antagonistic activity using the dual culture technique. Six *Pseudomonas* isolates recorded inhibition of R. solani ranging from 68–75%, *Bacillus* isolates showed moderate inhibition between 56–71%, while *Trichoderma* isolates exhibited the highest inhibition levels (79–84%). Against *X. oryzae pv. oryzae*, effective isolates showed moderate suppression (52–68%) in dual culture and agar diffusion assays. The isolates also produced ammonia and hydrogen cyanide and exhibited extracellular enzyme activities such as chitinase, cellulase, and amylase. Compatibility studies confirmed mutual compatibility among selected Pseudomonas, Trichoderma, and Bacillus isolates, enabling consortium development. Based on in vitro performance, effective individual agents and compatible combinations were evaluated under pot culture conditions using rice variety Mansuri during the Kharif season. Separate experiments were conducted for sheath blight and bacterial leaf blight. Disease incidence and severity were recorded using the IRRI Standard Evaluation System. The combined application of *Pseudomonas + Trichoderma + Bacillus* reduced sheath blight severity to 18–22% compared to 55–60% in pathogen-inoculated control, while bacterial leaf blight severity was reduced to 20–25% compared to 50–58% in control. The combined treatment also improved plant growth parameters. The study demonstrates that compatible microbial consortia offer an eco-friendly and sustainable approach for integrated management of sheath blight and bacterial leaf blight in rice.

Keywords: Rice, sheath blight, bacterial leaf blight, *Pseudomonas, Trichoderma, Bacillus*, dual culture assay, IRRI Standard Evaluation System, biocontrol consortia

Abstract No: D20

Role of Mycorrhiza in Stress Management of Plants with Reference to Nematodes

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ABSTRACT

Soil microbial communities - comprising mycorrhiza ,bacteria, fungi, including nematophagous fungi, actinomycetes and protozoa - constitute dynamic networks that may suppress populations and damage by plant-parasitic nematodes through direct antagonism (parasitism, predation, antibiosis), indirect modes of action such as competition, nutrient modification and induction of plant systemic resistance. Plant-parasitic nematodes (PPNs) are responsible for heavy crop losses worldwide that range from 12% to 20%, an enormous amount of USD 100 to 150 billion every year. *Meloidogyne* spp., root-knot nematodes, are the most notorious ones as they harass more than two thousand plant varieties across the globe. Beneficial microbes in suppressive soils are present in numbers of 106–108 CFU/g and they provide a natural limit to the nematode population. Microbes of the genera *Bacillus, Pseudomonas, Streptomyces, Trichoderma* and *Glomus intradices*have been reported to cause a decrease of up to 80% in egg hatch and 40% in some studies. The application of metagenomic techniques has revealed that soils that suppress have a microbial diversity of 20–40% more thanconducive soils. There is symbiotic associations between plant roots and beneficial fungi that play a vital role in plant stress management. These fungi colonize the root system and extend their hyphae into the surrounding soil, significantly improving the plant's ability to absorb water and nutrients, especially phosphorus, nitrogen, and micronutrients. Through this association, plants gain enhanced tolerance to both abiotic and biotic stresses. One important biotic stress affecting plants is infestation by plant-parasitic nematodes, such as root-knot and cyst nematodes. These nematodes damage roots, disrupt water and nutrient uptake, and ultimately reduce plant growth and yield. Mycorrhizal fungi help plants manage nematode stress through several direct and indirect mechanisms. Firstly, mycorrhizal colonization improves overall plant vigor and root health. Secondly, mycorrhizae can alter root morphology and physiology, making roots less attractive or less suitable for nematode penetration and reproduction. In some cases, mycorrhizal infection reduces nematode population density in the rhizosphere. Another important role of mycorrhizae is the activation of plant defense mechanisms. Mycorrhizal fungi can induce systemic resistance in host plants by stimulating the production of defense-related enzymes, phenolic compounds, and phytohormones. This enhanced defense response limits nematode infection and suppresses their development within roots. Additionally, mycorrhizae influence the soil microbial community by promoting beneficial microorganisms that act antagonistically toward nematodes. This creates a more balanced soil ecosystem that naturally suppresses nematode populations. In conclusion, mycorrhizae play a crucial role in managing plant stress caused by nematodes by improving nutrition, enhancing plant defense, modifying root structure, and regulating soil biology. Their use in sustainable agriculture offers an eco-friendly approach to reducing nematode damage and improving plant health and productivity. Application of 25g AMF per plant in soil around root zone increase plant vigor in banana crop.

Keywords: Mycorrhiza, Nematode ,stress, Microbes

Abstract No: D21

Role of Rhizospheric Microbial Growth Regulators in Sustainable Production of Chrysanthemum and Marigold

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ABSTRACT

Chrysanthemum and marigold are commercially important flowering crops widely cultivated for their aesthetic, cultural, and medicinal value. Conventional floricultural production relies heavily on chemical fertilizers, which can adversely affect soil health and environmental sustainability. Multitasking plant growth–promoting rhizobacteria (PGPR) enhance nutrient availability, stimulate phytohormone production, improve soil microbial activity, and promote overall plant growth and flowering. Therefore, the present study explores the role of multitasking bioinoculants in improving growth, development, and sustainable floricultural production of chrysanthemum and marigold. Rhizosphere soil was collected from healthy chrysanthemum and marigold plants (different cultivars, locations). Samples were collected from a depth of 5–15 cm to ensure active microbial presence. Samples were stored chilled and processed within 24–48 h. Isolation of bacteria was done by the serial dilution followed by the spreading and streaking method. The combined use of the spread plate and quadrant streak methods resulted in the successful isolation of 62 pure bacterial isolates. All isolates were maintained as pure cultures and were considered suitable for further functional screening, including nutrient solubilization and hormonal assays. A total of 62 bacterial isolates were screened for their potassium (K), zinc and phosphate (P) solubilization ability and IAA production activity. Out of 62 isolates, 15 isolates were selected for the treatment in chrysanthemum and marigold. Four best isolates were selected out of 15 to construct consortia. It was developed by pairwise compatibility tests among potential isolates. A pot (completely randomized design) and field (randomized block design) study was conducted without any grouping with the treatments of control (uninoculation), single strains, consortium, and standard fertiliser dose (full nitrogen rest at 50% reduced fertilizer with inoculant). Different bacterial isolates randomly applied to pots. Field biometric parameters will be recorded at different plant stage.

Keywords: Chrysanthemum, Marigold, Multitasking bioinoculants, Plant growth–promoting rhizobacteria (PGPR) Sustainable floriculture.

Abstract No: D22

A study on microbial mediated Bioethanol Production from Maize cob and seed

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ABSTRACT

Maize (*Zea mays L.)* is one of the most widely cultivated crops globally, contributing about 39% to total grain production. In India, it ranks as the third most important cereal grown throughout the year.India generates significant maize cob waste, with estimates suggesting millions of tonnes annually from its large maize production (around 38 million tonnes/year), making it a promising bioenergy feedstock. The main hinderance of using such feedstock into bioenergy form is its lignocellulosic composition which is very difficult to break into simple sugars. In the present study, a total of 30 mushroom samples were collected from different locations of RPCAU and were screened for lignocellulose-degrading potential using selective media containing carboxymethyl cellulose (CMC), Xylan and ABTS for cellulase, hemicellulose, and lignin-degrading activities, respectively. Out of which 16 isolates showed maximum growth on CMC plates,19 isolates showed maximum growth on Xylan and 26 showed maximum growth on ABTS plates. Based on their overall ligno-cellulolytic ability and prominent halo zone formation a total of 27 isolates were selected for further studies. Bushnell Hass medium was prepared using 20% physically pretreated maize cob powder as the sole carbon source, and the selected mushroom isolates were inoculated. The plates showing maximum growth were assayed using the DNSA at incubation intervals of 3, 6, 9, and 12 days. The results revealed a significant release of reducing sugars, with maximum values ranging from 35.43 to 40.07 mg/g dry substrate, indicating effective degradation of maize cob by the selected isolates. Promising mushroom isolates showing higher sugar release will be further utilized for bioethanol production using a suitable yeast culture. The study highlights the potential of lignocellulolytic mushrooms in the sustainable utilization of maize cob for bioethanol production and contributes to the development of eco-friendly biofuel technologies.

Keywords: Bioethanol, Maize cob, Lignocellulosic biomass, Mushroom isolates, ABTS assay, DNSA method

Abstract No: D23

Development and Evaluation of PGP Based Consortia for Growth, Yield and Quality of Finger Millet Crop

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ABSTRACT

Isolation and characterization of rhizospheric and endophytic bacteria from *Eleusine coracana* (finger millet) as biofertilizers which aims to reduce chemical fertilizer dependence and enhance crop productivity through natural and eco-friendly alternatives. In the current study, a total of 26 bacterial isolates were obtained—12 from endophytic tissues (stems and roots) and 14 from rhizospheric soils of finger millet grown in different fields of Pusa campus, TCA Dholi, BISA farm, Pusa, Samastipur, Bihar. Standard microbiological techniques, including serial dilution, spread plating, quadrant streaking, and slant preservation, were employed to ensure pure culture isolation. The core PGP traits examined included solubilization of phosphorus, zinc, and potassium; production of indole-3-acetic acid (IAA), Gibberellic Acid (GA). These traits are pivotal for nutrient mobilization and plant health. Phosphate solubilization was confirmed through Pikovskaya's agar medium. Zinc solubilization was assessed using nutrient agar supplemented with zinc oxide. This micronutrient is essential for enzyme activation and hormonal regulation in plants. Potassium solubilization, critical for water balance and stomatal functioning in plants, was analyzed using Aleksandrow medium. IAA production, critical for root architecture and nutrient acquisition, was confirmed in six isolates, with colorimetric quantification via Salkowski's reagent showing optical density (OD) values up to 1.414 at 540 nm. Furthermore, five isolates demonstrated GA production—a key factor for shoot elongation and chlorophyll enhancement with OD values reaching 0.992 using the 2,4-Dinitrophenylhydrazine (DNPH) method. Both were validated via a specialized HPLC approach.The effectiveness of these bacterial strains was further validated through germination assays and pot experiments using finger millet as a model crop. This multifactorial synergy is vital for the development of robust microbial consortia-based biofertilizers.

Keywords: Finger Millet, PGP, Endophytes and Rhizospheric bacteria, IAA, Gibberellic Acid

Abstract No: D24

Synergism of Microbial Consortia on Nutrient Dynamics, Stress Resilience and Fruit Quality in Horticultural Crops

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ABSTRACT

Modern fruit production faces significant productivity gaps due to deteriorating soil health, chemical over-dependence and increasing abiotic stressors. To address these challenges, the transition from conventional inputs to microbial consortia—comprising Plant Growth-Promoting Rhizobacteria (PGPR), Arbuscular Mycorrhizal Fungi (AMF) and endophytes is essential. Unlike single-strain applications, these consortia provide synergistic effects that optimize the soil-plant interface and the internal endosphere. The mechanism involves a dual-action approach: facilitating nutrient acquisition and activating systemic defense. Microbial organic acid secretion drives phosphorus solubilization, converting fixed soil minerals into accessible forms to ensure steady macro-nutrient availability. Simultaneously, the consortia bolster stress and disease resistance by inducing systemic resistance (ISR) and modulating phytohormones. A key advantage is the microbial production of ACC (1-Aminocyclopropane-1-carboxylic acid) deaminase, which lowers "stress ethylene" levels, acting as a biological buffer that maintains physiological stability and cellular turgor during drought, salinity and pathogen pressure. The integration of these microorganisms ensures robust growth and development by mitigating the metabolic costs of environmental stress. This physiological optimization manifests in a marked improvement in overall fruit quality, characterized by superior physical attributes like fruit weight and firmness, alongside enhanced biochemical profiles, including improved sugar-acid ratios and extended post-harvest shelf-life. Harnessing these integrated microbial networks is an emerging strategy for achieving sustainable horticultural productivity, climate resilience, and premium fruit quality across diverse agroclimatic zones.

Keywords: Microbial Consortia, Endophytes, Phosphorus Solubilization, Stress Resilience, Fruit Quality

Abstract No: D25

Bacterial Assisted Zinc Biofortification Across Diverse Agro-Ecosystems and their Impact on Crop Productivity and Soil Health

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ABSTRACT

Micronutrient deficiency and climate-induced stresses are major constraints limiting crop productivity and nutritional security in diverse agro-ecosystems of India (hill agriculture, saline conditions, different locations of north India i.e., *Terai* and *Katchar* region). To address these challenges, the present study explores the potential use of plant growth–promoting rhizobacteria (PGPR) and zinc-solubilizing bacteria as eco-friendly bioinoculants for improving crop productivity, nutrient biofortification, and soil health. Effective bacterial strains were isolated from different rhizosphere (millet, wheat, and legume) and characterized for zinc solubilization, stress tolerance, and plant probiotic traits. Selected strains showed a high solubility potential for zinc, analysed by atomic absorption spectroscopy and Field Emission-Scanning Electron Microscopy/Energy Dispersive X-ray (FE-SEM/EDX), and the organic acids produced by the strains were determined by UPLC-MS. When inoculated with potential bacteria/consortium, significant improvements in growth, yield characteristics, and zinc content were recorded under pot and field trials in rice (different sites), wheat (saline conditions), and kidney bean (hill areas). Bacterial treatments with zinc source (ZnO) enhanced zinc content in the rice grains; however, in wheat, salinity-tolerant bacteria improved grain zinc content under salinity stress condition. In kidney bean, grown across varied altitudinal zones of hill region of Uttarakhand, cold-adaptive bioinoculants not only increased yield and grain zinc content but also reshaped the rhizospheric microbial community, as evidenced by metagenomic analyses. Overall, studies show that bacterial inoculants and consortia can improve the zinc content of edible parts of crops, crop growth and resilience, enzymatic activity and physiochemical properties of soil in different agroclimatic regions, making them a viable alternative to chemical fertilizers and an environmentally safe strategy for biofortification and long-term agricultural sustainability.

Keywords: Biofortification, Cold-adaptive bioinoculants, Hill agriculture, Salinity stress, Zinc solubilizing bacteria, *Terai* and *Katchar* region

Abstract No: D26

Harnessing Native Diazotrophic Bacterial and Cyanobacterial Consortia to Enhance Rice Growth and Nitrogen Assimilation under Acidic Soil Conditions

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ABSTRACT

Jharkhand, known as the “Land of Forests,” is predominantly rainfed, with rice cultivated on nearly 67.3% of the agricultural area but producing low yields (10–14 q ha^{-1}). Rice productivity in this region is constrained by sloping and rocky terrain, soil erosion, limited water availability, acidic soils, poor soil fertilityparticularly nitrogen deficiencyand inefficient input use. Nitrogen is a critical macronutrient for rice growth, yet excessive dependence on synthetic nitrogen fertilizers has led to environmental concerns. Biological nitrogen fixation through diazotrophic microorganisms offers a sustainable and eco-friendly alternative.The present study aimed to evaluate the effectiveness of native diazotrophic bacterial and cyanobacterial consortia in enhancing rice growth, nitrogen assimilation, and yield under acidic soil conditions of Jharkhand. Native diazotrophic bacterial strains isolated from Jharkhand soils, namely *Brucella oryzae* (B1), *Brucella ciceri* (B2), and *Pseudomonas nitroreducens* (B3), were used to develop a bacterial consortium. A cyanobacterial diazotrophic consortium (F1–4; F2) comprising *Anabaena torulosa* (BF1), *Nostoc carneum* (BF2), *Nostoc piscinale* (BF3), and *Anabaena doliolum* (BF4) was also evaluated.Field experiments were conducted at ICAR–IARI, Jharkhand, using two rice varieties, Abhishek and IR 64 DRT 1, under transplanted conditions. Carrier-based inoculants prepared using vermiculite and paddy straw compost (1:1) were applied across four treatments per variety. Soil and plant samples were collected at tillering, panicle initiation, maturity, and harvesting stages.Results revealed that treatment T5 (75% N + 100% PK + bacterial diazotrophic consortium) significantly enhanced indole-3-acetic acid production, nitrate reductase and glutamine synthetase activities, and improved soil enzyme activities such as dehydrogenase and urease at critical growth stages in both varieties. Yield and yield-attributing traits were also significantly improved with microbial inoculation, highlighting the potential of native diazotrophic consortia as a sustainable strategy for reducing chemical nitrogen inputs in acidic rice-growing soils.

Keywords: Diazotrophs, Bacteria, Cyanobacteria, Rice, *Pseudomonas*

Abstract No: D27

Screening of Endophyte-Based Biocontrol Strategy for Red Rot of Sugarcane with Plant Growth-Promoting Benefits

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ABSTRACT

A total of 71 endophytic bacteria were isolated collectively from the root, stem and leaf of two sugarcane varieties BO 91 and CoP 16437 in this study. Further, these endophytes were tested for in vitro inhibition against the red rot pathogen (*Colletotrichum falcatum*). Out of 71, only 37 bacteria were able to show in vitro inhibitory action against the pathogen. Besides inhibiting their mycelial growth, some of these endophytes were able to synthesize various PGP traits such as IAA, phosphate solubilization, Potassium, Zinc solubilization, siderophore and ammonia production. These endophytes were found helpful in promoting the growth of the plant in a direct and indirect way. Six bacterial isolates with more than 65% inhibitory activity against the pathogen and PGP attributes were further characterized through 16S rRNA gene sequencing. On the basis of the phylogenetic analysis, the six endophytic antagonists were identified as *Microbacterium arborescens* (BR2), *Bacillus safensis* (BR6), *Microbacteriumginsengiterrae* (BR21), *Glutamicibacterhalophytocola* (CR7), *Bacillus tequilensis* (CS1), *Bacillus safensis*(CS2). This study demonstrated that endophytic bacteria are an untapped source of natural products and can be exploited for yield attributes and red rot control in sugarcane.

Keywords : Endophytes, Sugarcane, Red rot, Biocontrol, Plant growth promotion, 16S rRNA

Abstract No: D28

Isolation and characterization of Mycorrhiza, Trichoderma and PSB associated with lentil crop

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ABSTRACT

Pulse production is very crucial for global food security, but it is difficult to grow due to poor soil, pathogenicity, and over-reliance on chemical fertilizers. This study focuses mainly on the isolation and screening of the mycorrhizal, PSB, and Trichoderma associated with the lentil plant. The selected microbes not only avail the nutrients required for the crop but also protect it from pathogens, enhance nutrient uptake, and uplift it from the various abiotic stresses. Mycorrhiza enhances nutrient and water uptake, PSB solubilizes fixed soil phosphorus, and Trichoderma provides biocontrol against soil-borne diseases. In this study, it was targeted to make a mycorrhizal cocktail of various strains isolated from the grassland, forestry field, and lentil field. The selected cocktails from various ecosystems were then applied to the plant to observe the infection percentage or colonization behavior of each. Isolation of the Trichoderma was done from the infected plant and lentil field soil with the help of the targeted media. Three morphologically different Trichoderma isolates were finalized based on the growth characteristics and microscopic observation. The selection of the potential strain will be based on the efficacy of antagonistic activity as well as the positive effect on the growth and development of the plant. The isolation of PSB was done from the lentil field soil on pikovaskya media (as enrichment media), followed by spread plating to the purification step based on the solubilization of the fixed salt over the plate. Around 39 isolates were collected from four different sites of the lentil field. In the path ahead, the effect of each isolate will be observed for the combined growth, and their formulations will be developed for the inhibition of the lentil wilt.

Keywords : Biofertilizers, sustainable pulse production, biocontrol agent, microbial amendment

Abstract No: D29

Characterization of Compost-Derived Bacteria Involved in Button Mushroom Cultivation

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ABSTRACT

Mushroom composting is a thermogenic solid-state fermentation process driven by the succession of diverse microbial communities that transform raw organic materials into a selective substrate suitable for mushroom cultivation. This compost serves as a rich niche for both mesophilic and thermophilic bacteria that actively degrade complex organic residues, leading to compost stabilization. In the present study, bacterial populations were isolated from compost previously used for button mushroom production at the Department of Microbiology, Dr. Rajendra Prasad Central Agricultural University, Pusa. Serial dilutions (10^{-5} and 10^{-6}) of compost samples were prepared and plated using standard plating and streaking techniques, followed by incubation at 45 °C and 65 °C. A total of twelve bacterial isolates (designated I1–I12) were obtained and characterized based on morphological features using Gram staining and endospore staining. Among these isolates, ten were identified as rod-shaped, Gram-positive, endospore-forming bacteria, while two isolates (I4 and I7) were rod-shaped, Gram-negative, and non-spore-forming.All isolates were further screened for cellulolytic and xylanolytic activities using carboxymethyl cellulose (CMC) and xylan agar plate assays, respectively. Enzyme production was confirmed by the formation of distinct clearance zones around bacterial colonies. Quantitative estimation of CMCase and xylanase activities was performed using standard calibration curves of D-glucose and xylose, with one unit of enzyme activity defined as the release of 1 μmol of reducing sugar per minute. Most isolates exhibited significant CMCase activity, reaching peak values ranging from 0.5 to 0.9 U mL^{-1} after 72 hours of incubation, except for isolates I4 and I9, which showed comparatively lower activity. In contrast, notable xylanase activity was observed in six isolates (I1, I2, I4, I8, I9, and I10), with maximum activities between 9.0 and 12.0 U mL^{-1} at 72 hours, whereas the remaining isolates displayed consistently lower enzyme production. The results indicate that compost-derived bacterial isolates possessing cellulolytic and xylanolytic capabilities can be effectively utilized as microbial inoculants to enhance button mushroom compost preparation.

Keywords: Compost, Cellulose, Xylanase, CMCase, Thermogenic

Abstract No: D30

Assessment of Resistance Inducing Agents against Red Rot of Sugarcane

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ABSTRACT

Sugarcane (*Saccharum officinarum* L.) is a crop of immense economic and industrial significance, widely cultivated in tropical and subtropical regions in the world. It is cultivated across 123 countries, supplying three fourth of global sugar demands. Despite its economic importance, sugarcane production faces severe threats from red rot disease caused by *Colletotrichum falcatum* that may spread via the soil and setts and cause significant crop losses, aptly termed the "cancer of sugarcane". In this study five resistance inducing agents viz., Iso-Nicotinic Acid (INA), β- Amino Butyric Acid (BABA), Salicylic Acid (SA), Potassium Silicate (PSi), Benzothiadiazole (BTH) @ 0.01% concentration each except potassium silicate @0.2% and one chemical fungicide in combination Azoxystrobin 18.2% + Difenoconazole 11.4% (Amistar Top) @ 0.1% as standard check were evaluated by treating the setts before planting and two foliar sprays with same molecule at 90 and 120 days of planting for their efficacy on a red rot susceptible sugarcane cultivar CoSe 95422 in the year 2024-25. Field trials indicated that fungicide (Azoxystrobin 18.2% + Difenoconazole 11.4%) @ 0.1% showed superior germination (39.7%) with lowest settling mortality (3.6%), achieving highest yield (90.2 t/ha) and maximum juice quality metrics (Brix: 21.27%), Pol: 18.68%, Purity: 87.82%). Among resistance inducers, potassium silicate emerged most effective with 37.4% germination, 4.8% settling mortality, 85.5 t/ha yield and excellent juice quality parameters (Brix: 20.22%), Pol: 17.44%, Purity: 86.25%). Disease assessment at 270 days of planting clearly revealed that fungicide Azoxystrobin 18.2% + Difenoconazole 11.4%) @ 0.1% had exceptional efficacy (6.20 PDI, 78.40% disease reduction over control 28.70 PDI), while potassium silicate achieved remarkable disease suppression (7.70 PDI, 73.17% disease reduction over control), establishing it was the most effective resistance inducer and at par to fungicide. Benzothiadiazole and salicylic acid also demonstrated significant disease control with 62.21% and 52.96% disease reduction over control, respectively.

Keywords: Sugarcane, red rot, *Colletotrichum falcatum,* resistance inducers

Abstract No: D31

Role of Tomato Rhizospheric Bacteria in Enhancing Plant Growth and Sustainable Agricultural Practices

Amarendra Kumar

ABSTRACT

Tomato (*Solanum lycopersicum* L.) is among the most economically significant horticultural crops worldwide; however, its productivity is frequently constrained by declining soil fertility, nutrient deficiencies, and diverse biotic and abiotic stresses. Rhizospheric bacteria inhabiting the tomato root zone play a crucial role in promoting plant growth, health, and stress resilience, offering sustainable and environmentally friendly alternatives to conventional agrochemicals. These plant growth–promoting rhizobacteria (PGPR) enhance tomato development through multiple direct and indirect mechanisms, including biological nitrogen fixation, phosphate solubilization, phytohormone synthesis, siderophore production, and suppression of soil-borne phytopathogens. Additionally, rhizospheric bacteria improve nutrient acquisition and stress tolerance by modulating root architecture and inducing systemic resistance in plants. The application of PGPR in tomato cultivation has been shown to significantly enhance seed germination, vegetative growth, fruit yield, and quality while reducing dependence on chemical fertilizers and pesticides. Integrating tomato-associated rhizospheric bacteria into sustainable agricultural systems not only improves crop productivity but also supports soil health, enhances microbial diversity, and mitigates the environmental impacts associated with intensive farming practices. Overall, this study highlights the functional importance of tomato rhizospheric bacteria as key biological inputs for achieving sustainable and resilient tomato production.

Keywords : Tomato; Rhizospheric bacteria; Plant growth-promoting rhizobacteria; Sustainable agriculture; Soil health

Abstract No: D32

In vitro solubilization of Potash feldspar by the potassium solubilizing bacteria isolated from calcareous soils of north-west plain of Bihar

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ABSTRACT

Potassium is an essential macronutrient required for plant growth. However, in calcareous soils a major proportion of potassium remains fixed in insoluble mineral forms, limiting its bioavailability. Potassium solubilizing bacteria (KSB) are capable of mobilizing mineral bound potassium through various biochemical mechanisms. An experiment was conducted to study "In vitro solubilization of Potash feldspar by the potassium solubilizing bacteria isolated from calcareous soils of north-west plain of Bihar" at Department of Microbiology, CBS&H, RPCAU, PUSA. This study aimed to isolate, screen and characterize efficient KSB and to evaluate their potassium solubilization potential under laboratory conditions.Rhizospheric soil samples collected from rhizospheric soils of different crops were processed using the serial dilution and plating technique on Aleksandrov medium, resulting in the isolation of 42 bacterial isolates. Preliminary qualitative screening showed that only 8 isolates produced distinct halo zones, indicating their potassium solubilizing ability. The halo zone diameter among the isolates ranged from 0.9 to 1.45 cm, while the solubilization index (SI) and solubilization efficiency (SE) varied from 1.86 to 5.38 and 128.6% to 362.5% respectively.Among them, isolates KSB-6 and KSB-12 exhibited comparatively higher solubilization zones measuring approximately 1.35 and 1.40 cm respectively, after 5 days of incoculation. Morphological characterization revealed that out of the eight potassium solubilizing isolates, seven were Gram-negative and biochemical characterization showed that all isolates were positive for catalase activity, while six isolates exhibited positive reactions for the Methyl red, Voges-Proskauer and Urease tests. Quantitative estimation of potassium solubilization was carried out in Aleksandrov broth containing potash feldspar at different incubation intervals and potassium concentration in the broth was measured using Flame photometer. Potassium solubilization by different isolates ranged from 28.30 to 44.62 µg/L at 15 days after inoculation. Among these, isolates KSB-6 and KSB-12 exhibited the highest potassium solubilization, recording values of 44.32µg/L and 44.62 µg/L, respectively. The finding indicate that native efficient potassium solubilizing bacterial isolates, particularly KSB-6 and KSB-12, have promising potential for use as bioinoculants in calcareous soils. Their utilization could minimize the reliance on chemical potassium fertilizers, enhance potassium availability and contribute to sustainable agricultural practices.

Key Words : Potassium solubilizing bacteria, Potash feldspar, Calcareous soil, Aleksandrov medium, Halo zone, Solubilization index (SI), Solubilization efficiency (SE), In vitro solubilization, sustainable agriculture.

Abstract No: D33

Genetic Divergence and Host-Specific Virulence Determinants of the Pearl Millet Blast Pathogen in India

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ABSTRACT

Blast disease, caused by the fungus *Magnaporthe grisea*, has emerged as a destructive pathogen of pearl millet in arid regions of Asia and Africa. This study investigated the pathogenicity, population structure, and genetic diversity of the pathogen using 17 pearl millet isolates and three non-pearl millet isolates (from rice, finger millet, and *Eleusine indica*) collected in India. Pathogenicity tests revealed high virulence in Delhi region isolates, particularly PMg_LB2, which caused 77.8% disease severity. Host range experiments demonstrated that while pearl millet and finger millet isolates display cross-infectivity, they fail to infect rice. Conversely, rice isolates are host-specific. Notably, the grass isolate (*Eleusine indica*) infected all three hosts, suggesting a potential role in disease epidemiology. Phylogenetic analysis using housekeeping and virulence genes showed that pearl millet isolates form a genetically distinct clade with low nucleotide polymorphism, diverging significantly from rice and finger millet isolates. Mating type analysis indicated a predominance of MAT 1-1, although three specific virulent isolates belonged to MAT 1-2. Comparative whole-genome annotation identified four hypothetical virulence loci specific to pearl millet *Magnaporthe*. These loci were also present in Napier grass (*Pennisetum purpureum*) isolates, indicating shared virulence traits within the *Pennisetum* genus. qPCR analysis confirmed that the expression of these loci increases progressively in susceptible pearl millet genotypes compared to resistant lines. This study conclusively demonstrates that the *Magnaporthe* population infecting pearl millet is genetically distinct from those infecting other cereals and identifies key virulence loci involved in disease establishment.

Keywords : Pearl Millet, *Magnaporthe grisea*, Genetic diversity, Host Specificity, Virulence Loci, qPCR Expression

Abstract No: D34

Assessment of Lactic Acid Bacteria for Bioconversion of Mustard Crop Residues”

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ABSTRACT

Mustard (*Brassica spp*.) is an important oilseed crop widely cultivated for its seeds, leaves, and other plant products. After harvest, a substantial amount of crop residue such as stalks, leaves, and pods is left in the field. These residues are rich in nutrients, including proteins, dietary fiber, polyphenols, calcium, and potassium. However, despite their nutritional value, mustard residues are unsuitable for direct use as animal feed due to the presence of anti-nutritional factors, particularly glucosinolates, which can cause adverse effects such as iodine deficiency, hypertrophy of the liver, kidney, and thyroid gland.

The present study focuses on screening lactic acid bacteria (LAB) for their potential to reduce glucosinolate concentration in mustard crop residue through microbial fermentation. LAB are considered promising probiotics due to their strong fermentative ability, safety status, and capacity to enhance nutrient availability and shelf life. During fermentation, LAB produce lactic acid, bacteriocins, and hydrogen peroxide, which inhibit foodborne and intestinal pathogens.

In this study, 16 LAB isolates were selected based on exopolysaccharide production and pH reduction ability. Further evaluation will involve assessing glucosinolate reduction in MRS broth inoculated with LAB at different glucosinolate concentrations (20–100 ppm). Additionally, the growth performance of bacterial isolates in nutrient broth supplemented with glucosinolates will be monitored by measuring optical density (OD_{600}) at 24, 48, and 72 hours.

Keywords: Glucosinolate, Silage production, Fermentation, Lactic acid bacteria.

Abstract No: D35

Surfactin-Like Lipopeptides from *Bacillus subtilis* BCL2 Mediate Broad-Spectrum Antifungal Activity Against Soil-Borne Phytopathogens

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ABSTRACT

The increasing resistance among phytopathogens has intensified the need for sustainable and effective alternatives to traditional chemical control in agriculture. In this study, bacterial isolates were tested for their antagonistic potential against key soil-borne fungal pathogens, including *Fusarium udum, Rhizoctonia solani, Sclerotium rolfsii, and Macrophominaphaseolina.* Antagonism, measured by dual-spot assays, showed inhibition levels ranging from 15.29% to 66.15%, indicating significant variability among isolates. Among these, *Bacillus subtilis* BCL2 exhibited the highest and most consistent antifungal activity and was therefore chosen for detailed analysis. PCR-based molecular screening using primers specific for antimicrobial peptide encoding genes confirmed the presence of biosynthetic gene clusters associated with the production of bioactive metabolites. To assess metabolite diversity, the strain was cultured in multiple growth media and then extracted with solvents of varying polarity. The resulting crude extracts displayed strong inhibitory activity against *Macrophominaphaseolina* in well-diffusion assays. Comprehensive metabolite profiling using liquid chromatography-mass spectrometry (LC-MS) uncovered a complex spectrum of secondary metabolites produced by *B. subtilis* BCL2. Subsequent purification of the crude extract was carried out via Sephadex A-25 column chromatography employing stepwise NaCl gradients. Protein-enriched fractions were identified using the Bradford assay, concentrated through dialysis and sucrose treatment, and evaluated for antifungal activity. The purified fractions exhibited pronounced inhibition of *M. phaseolina*. Further TLC characterization suggested that the active components possess properties consistent with surfactin-like lipopeptides, highlighting *B. subtilis* BCL2 as a valuable source of potent antimicrobial compounds with significant potential for biological control of plant diseases.

Keywords: Biocontrol agents; *Bacillus subtilis*; Antimicrobial lipopeptides; Phytopathogens; LC–MS analysis

Abstract No: D36

Nanocomposite-Based Management of Root Knot Nematode (*Meloidogyne incognita*) and Enhancement of Plant Growth in Okra

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ABSTRACT

The present study evaluated the effect of nanocomposite treatments on plant growth parameters and the multiplication of *Meloidogyne incognita* in okra (*Abelmoschus esculentus* L.). The results revealed that all treatments significantly improved plant growth and suppressed nematode infestation compared to the inoculated control (nematode alone). Treated plants exhibited a notable reduction in the number of root galls, egg masses per root system, number of eggs per egg mass, and final nematode population in the soil. Among the treatments, the combined application of AgNP @ 50 ppm and ZnONP @ 50 ppm proved most effective in enhancing plant growth parameters. However, maximum suppression of nematode multiplication and final nematode population in soil was observed with carbofuran @ 1.5 g /pot and seed treatment with AgNP @ 50 ppm + ZnONP @ 50 ppm. Biochemical analysis further indicated that seed treatment with AgNP @ 50 ppm + ZnONP @ 50 ppm significantly increased nitrogen, phosphorus, potassium, total soluble sugars, and total free amino acid contents compared to other treatments. These findings highlight the potential of nanoparticle-based treatments as an effective strategy for improving plant growth and managing root-knot nematode infestation in okra.

Keywords: Nanocomposite; Silver nanoparticles; Zinc oxide nanoparticles; *Meloidogyne incognita*; Okra; Plant growth; Biochemical changes

Abstract No: D37

GC-MSBased Metabolomic Analysis of *Trichoderma asperellum* and *Bacillus velezensis*against *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (Foc TR4)

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ABSTRACT

Fusarium wilt caused by *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (Foc TR4) is one of the most destructive diseases threatening global banana production. The persistence of the pathogen in soil and the limited effectiveness of chemical control measures have intensified the need for environmentally safe and sustainable disease management strategies.Biological control using antagonistic microorganisms has emerged as a sustainable alternative to chemical management, yet the underlying metabolic interactions remain insufficiently understood. The metabolomic interactions of *Trichoderma asperellum* and *Bacillus velezensis*in suppressing FocTR4, with an emphasis on identifying key bioactive compounds involved in pathogen inhibition. By using untargeted metabolomics approaches based on gas chromatography-mass spectrometry (GC-MS), metabolic profiles were generated from mono and co-cultures of *T. asperellum* and *B. velezensis*in the presence and absence of the pathogen.The GC-MS peak profiles revealed a diverse array of metabolites associated with antagonistic activityduring microbial interactions. Co-cultivation of these antagonistic microorganisms and Foc TR4 resulted in the production of antifungal compounds like ester, dipeptides and ether which inhibits the growth of the pathogen. Key metabolites putatively identified included Pyrrolo[1,2-a]pyrazine-1,4-dione, hexahydro- from *B. velezensis*, along with 5-Hydroxymethylfurfural associated with *T. asperellum*.In addition to direct pathogen suppression, these microorganisms enhance plant growth promotion and reducing yield losses caused by Fusarium wilt. The above findings suggest that the application of these biocontrol agents exhibits direct antifungal effect on pathogen's metabolism.Overall, this study provides insights into the metabolomic basis of microbial relationship. Understanding the complex metabolic interactions among *T. asperellum*, *B. velezensis*and Foc TR4 offer a scientific foundation for developing effective metabolite-based biocontrol formulations.

Key words : Banana, Foc TR4, GC-MS, Metabolomics, Biological control

Abstract No: D38

Selection of competitive and efficient *Mesorhizobium* strains to optimize chickpea growth and soil health

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ABSTRACT

Legumes play a key role in sustainable agriculture through their ability to form symbiotic relationships with nitrogen-fixing rhizobia.*Mesorhizobium*, a major root symbiont, is known to influence nodulation, nitrogen fixation and yield in chickpea. In comparison to other non-specific N-fixing *Rhizobial*strains, *Mesorhizobium*is known for its superior symbiotic efficiency, host specificity and environmental adaptability. However, there is a significant lack of research on its competitiveness and nodule occupancy. In the present study, experiments were conducted to assess the growth kinetics of 12 *Mesorhizobium* strains and to evaluate their plant growth-promoting activities towards enhancing competitiveness for nodulation. All strains showed different growth rates, ranging from 0.10 to 0.26 per hour, and generation times ranging from 2.64 to 6.66 hours. All 12 strains generated diverse intrinsic antibiotic profiles. Strains C101 and C95 showed maximum bacteriocin production potential against the other *Mesorhizobium*strains. Strain C101 showed considerable P, K, Zn solubilization potential and nitrate reductase activity. Furthermore, a field study was conducted by seed priming to evaluate the persistence and effectiveness of these treatments under environmental conditions. Strain C101 significantly enhanced the plant growth parameters, such as shoot length, fresh weight, leaf IAA, total pigments and nitrate reductase activity by 52, 80, 54, 37, 72% respectively, in contrast to 100% PK application in uninoculated plants. Strain C101 increases root fresh weight, IAA, nodule number, nodule weight and leghaemoglobin content by 80, 55, 46, 79%, respectively. In C101 inoculated soil, an increase of 2.5-fold in dehydrogenase activity, a 2.17-fold increase in available N, and a 63% increase in soil glomalin were observed. Principal component and multivariate analyses illustrated the significant interactions among the plant and soil attributes, highlighting that C101 inoculation can be a promising intervention for enhancing soil nutrient availability, growth and productivity in chickpea.

Keywords: Chickpea, *Mesorhizobium*, Bacteriocin, Nodule occupancy

Abstract No: D39

Nutrient heterogeneity shapes bacterial diversity and functions in wheat fields of the lower Indo Gangetic Plain

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ABSTRACT

Understanding how plant roots interact with soil microbes under variable environmental conditions is fundamental for improving nutrient use efficiency and resilience in agroecosystems. While the rhizosphere is known to drive microbial selection and nutrient cycling, its functioning remains poorly characterized in tropical alluvial soils, where strong edaphic gradients and intensive cultivation alter microbial assembly processes. The lower Indo-Gangetic Plain (IGP), a major wheat-producing region of India facing nutrient depletion, salinity stress, and soil degradation, represents one such understudied environment. To address this gap, a comparative, multisite field investigation was conducted across seven wheat-growing locations, integrating full-length 16S rRNA gene sequencing with detailed soil physicochemical profiling. Rhizosphere-bulk differentiation was context dependent, driven by soil electrical conductivity, phosphorus, and potassium. Two core microbiomes emerged: a rhizosphere core enriched in nutrient-responsive taxa shaped by root effects, and a bulk soil core dominated by locally adapted decomposer taxa structured by site-specific soil conditions. Functional prediction analyses indicated enhanced denitrification, sulphur oxidation, and hydrocarbon degradation in rhizospheres, reflecting adaptive metabolic reconfiguration to fluctuating nutrient and redox regimes. Phylum-level co-occurrence networks exhibited greater modularity and connectivity in rhizospheres, suggesting stronger cooperative organization under root influence. This first comprehensive multi-site study in the lower IGP showed how microbial assembly, functional enrichment, and network complexity in wheat-based systems throughout the lower Indo-Gangetic Plains are influenced by soil electrical conductivity and nutrient heterogeneity.By linking soil chemistry to microbial functioning, this study advances rhizosphere ecology and supports regionally adaptive microbiome management for sustainable wheat production in nutrient-stressed tropical soils.

Key Words: Wheat; Lower IGP; Microbiome; Indicator Genera; Core Genera; Co-occurrence Network; Functional Profile

Abstract No: D40

Chitosan-Induced Suppression of *Fusarium* Wilt and Genome-Wide Identification of Pathogenesis-Related Protein-1 (PR-1) Genes Reveals a Candidate Defence Marker in *Cicer arietinum* L.

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ABSTRACT

Chickpea (*Cicer arietinum* L.) production is severely affected by *Fusarium* wilt caused by *Fusarium oxysporum* f. sp. *ciceris* (Foc), a destructive soil-borne pathogen that compromises yield stability. Reliance on chemical fungicides for disease management raises environmental and sustainability concerns, necessitating alternative strategies. Chitosan, a natural biopolymer, has emerged as a promising agent due to its combined antifungal activity and capacity to elicit plant defence responses. The present study integrates experimental disease management with a comprehensive genome-wide bioinformatic analysis to elucidate Chitosan-mediated resistance mechanisms in chickpea.In the experimental phase, Chitosan concentrations ranging from 0.05 to 2.0% were evaluated against Foc. Complete inhibition of fungal growth was observed at 2.0% under in vitro conditions; however, this concentration adversely affected seed viability. A concentration of 0.5% was identified as optimal, effectively suppressing pathogen growth while maintaining seed germination. Pot culture bioassays further demonstrated that seed priming with 0.5% Chitosan in combination with a plant growth-promoting rhizobacteria (PGPR) isolate resulted in a pronounced synergistic effect, reducing wilt incidence to 8.55% compared with 77.61% in untreated control plants.To investigate the molecular basis of induced resistance, a comprehensive genome-wide bioinformatic analysis was performed to identify Pathogenesis-Related Protein-1 (PR-1) genes in chickpea. Reference PR-1 protein sequences from *Arabidopsis thaliana* and *Oryza sativa*were used for homology-based identification. Candidate chickpea PR-1 proteins were identified through BLASTp analysis, followed by removal of redundant sequences. Multiple sequence alignment was conducted to assess sequence conservation, and phylogenetic reconstruction was performed using the major *Arabidopsis* PR-1 protein as a reference to determine evolutionary relationships. Building on these findings, further validation is underway through isolation of RNA and quantitative real-time PCR (qRT-PCR)-based expression profiling to confirm the responsiveness of the identified PR-1 gene under Chitosan treatment and pathogen challenge.

Keywords: Chitosan,*Fusarium* wilt,Pathogenesis-Related Protein-1, Induced systemic resistance (ISR)

Abstract No: D41

Starch bioengineering through Microwave treatment in Proso Millet Seed germination

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ABSTRACT

Inspired by the exploration of underutilized Millet to address seed germinationand seedling establishment concerns.BR-7 a popular Proso-millet variety was subjected to microwave treatment to modify the starchto enhance seed germination rate and its vigour. The study examined the effects of varying power levels (270, 450, and 630 W) and a processing time of 20 and 30 seconds on the starch properties. The findings revealed that microwave treatment led to modifications in the spatial structure of starch, affecting its functional characteristics like water holding capacity. FTIR analysis indicated that the microwave treatment highly altered the short-range order of starch molecules more than the double helix structureand the DSC thermogram depicts the significant change in the hydrogen bonding of starch granules, which is directly correlated with the increase in the water absorption capacity of the Proso millet seeds and significantly enhance the seed germination.Notably, the seed germination percentage from 60 percent 90 percentat a power of 450 W for the 20 second duration. The physiological properties improved significantly, with a change inroot lengthfrom 37 percent and shoot length changes 70 percent compared to non-treated. Starch degradation relies on coordinated hydrolase activities, including α-amylase and β-amylase, which break down amylopectin and amylose into maltose and glucose; bioengineering restores suppressed enzyme levels in stress-affected grains. These results provide a theoretical foundation for the utilization of microwave and illustrate the effectiveness onstarchmodificationfor better seed germination.

Keywords : Seed Germination, Starch bioengineering, Microwave priming

Theme E
Advances in Nutritional Biochemistry & Post-Harvest Management

Abstract No: E1

Genomic Dissection and Biotechnological Manipulation of Grain Quality–Associated Pathways in Pearl Millet

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Introduction

Ensuring nutritional security through sustainable enhancement of crop productivity and grain quality is a major priority in contemporary agricultural research. Pearl millet (*Pennisetum glaucum*), a staple cereal for millions in arid and semi-arid regions, plays a crucial role in food and nutritional security owing to its superior mineral content, dietary fiber, and energy density compared to major cereals. Strengthening grain quality while maintaining yield stability in pearl millet directly addresses protein–energy malnutrition and micronutrient deficiencies in vulnerable populations.

Grain nutritional attributes are determined by tightly regulated biochemical and molecular mechanisms that govern lipid metabolism, carbon allocation, and cellular signaling during grain development. Gene families involved in membrane lipid remodeling and signal transduction are increasingly recognized as key modulators of these processes. Systematic identification and functional exploration of such gene families provide a strong foundation for genomics-assisted improvement of grain quality traits.

Although climate variability can influence nutrient stability and productivity, the primary focus of crop improvement remains the enhancement of intrinsic nutritional quality and yield potential. Integrating biochemical insights with modern biotechnology offers effective strategies to translate genomic knowledge into tangible improvements in pearl millet.

Genome-Wide Identification of Biochemically Relevant Gene Families

Genome-wide analysis of gene families associated with lipid metabolism and cellular signaling represents an essential step toward improving grain nutritional traits. Comprehensive characterization of the phospholipase gene family in pearl millet revealed extensive structural conservation, chromosomal distribution, and evolutionary relationships with other cereals. These genes are implicated in membrane dynamics, lipid turnover, and intracellular signaling pathways that influence grain development and quality.

Synteny analysis and motif conservation highlighted candidate phospholipase genes with potential roles in regulating grain lipid composition and metabolic stability. Such traits are directly linked to energy density and grain storability, both of which are critical components of nutritional security. This genomic resource provides a targeted framework for selecting candidate genes for functional validation and trait improvement in pearl millet.

Biochemical Significance of Lipid Metabolism in Grain Quality

Lipids play a central role in determining grain quality by influencing caloric value, membrane integrity, and metabolic signaling during seed maturation. Phospholipases regulate the hydrolysis and remodeling of membrane phospholipids, generating lipid-derived signaling molecules that modulate downstream metabolic pathways. Perturbations in these pathways can affect grain filling efficiency, nutrient partitioning, and seed viability.Understanding the biochemical roles of lipid-modifying enzymes enables a more precise linkage between gene function and nutritional outcomes. Targeting such pathways offers opportunities to optimize grain composition without compromising yield, aligning productivity with nutritional enhancement.

Efficient Transformation Platforms for Functional Validation

Despite the availability of genomic resources, functional characterization of candidate genes in pearl millet has been limited by technical constraints in genetic transformation. The development of a simple, seed-piercing *Agrobacterium*-mediated transformation protocol represents a significant methodological advance for pearl millet and finger millet. This approach bypasses complex tissue culture steps, reduces genotype dependency, and enables reproducible recovery of stable transformants.Successful application of this method for CRISPR/Cas-mediated genome editing demonstrates its utility for precise manipulation of genes involved in grain quality and metabolic regulation. Such transformation platforms are critical for validating genomic targets and accelerating trait deployment in nutritionally important but traditionally under-served crops.

Linking Genomics, Biotechnology, and Nutritional Security

The integration of genome-wide gene family analysis with efficient transformation technologies creates a robust pipeline for improving grain nutritional quality and productivity in pearl millet. By enabling targeted modification of biochemically relevant pathways, these approaches support the development of varieties with enhanced energy density, improved metabolic stability, and consistent grain quality.While environmental stresses, including those associated with climate variability, can modulate crop performance, strengthening the intrinsic biochemical and genetic architecture of pearl millet remains central to achieving nutritional security. Advances in biotechnology facilitate this goal by translating molecular knowledge into practical crop improvement strategies.

Conclusions and Future Perspectives

The studies synthesized here highlight the importance of integrating biochemical pathway analysis, genomics-assisted target discovery, and streamlined transformation systems to enhance nutritional security and quality-related traits in pearl millet. Future efforts should focus on functional validation of candidate genes under field conditions, integration with breeding programs, and expansion toward multi-omics approaches to refine trait selection.Such integrative strategies position pearl millet as a key contributor to sustainable food and nutritional security, combining productivity with enhanced grain quality to meet the demands of growing populations.

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Abstract No: E2

Biochemical characterization and nutrient quality profiling of microgreens for innovative functional food development

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ABSTRACT

This study aimed to evaluate the nutritional quality and antioxidant potentialof selected vegetable microgreens to assess their suitability as functional foods for improving dietary quality. Microgreens—young vegetable seedlings harvested at 7-21 daysrepresent an emerging class of functional food ingredients combining exceptional nutritional density and unique sensory attributes. Sixteen commonly consumed vegetable species from Brassicaceae, Amaranthaceae, Apiaceae, and Fabaceae families, cultivated under controlled polyhouse conditions and harvested at microgreen stage. The microgreens were analyzed for macronutrients (vitamin C, protein, crude fiber), essential minerals (iron, zinc, potassium, calcium), antioxidant capacity, and anti-nutritional oxalate content. A novel Nutrient Quality Score (NQS) integrating seven encouraged nutrients minus limiting factors, and an Antioxidant Index (AI) consolidating phenolic content, DPPH scavenging, and FRAP assays were developed for evidence-based ingredient selection. Results demonstrated significant inter-species variation with distinct functional food applications. Vitamin C-rich microgreens—radish (97.88 mg/100g FW), kale (90.87), and broccoli (89.47) found suitable for including them as immune-supporting ingredients for functional beverages. Protein-rich fenugreek (4.42 g/100g FW) and beetroot (4.30) offer plant-based fortification for nutrition bars. High-fiber species broccoli (11.95 g/100g DW) and cabbage (11.48) can be exploited for digestive health products. Mineral profiling revealed fenugreek and palak as iron and zinc sources for biofortification applications, while celery and parsley provided exceptional calcium. NQS rankings designated palak, broccoli, fenugreek, kale and radish as elite functional ingredients. The integration of Nutrient Quality Score provides a standardized tool for evidence-based ingredient selection, enabling functional food developers to make informed decisions aligned with specific health claims and regulatory requirements.

Keywords : Microgreens, Functional foods, Nutrient Quality Score, Antioxidant Index, Biofortification

Abstract No: E3

Glycemic Index and Biochemical Complexity: Sensor-Driven Insights for Nutritional Precision

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ABSTRACT

The Glycemic Index (GI) has long been a central metric for understanding post-prandial glucose responses, yet its interpretation often overlooks the underlying biochemical complexity of foods and individual metabolic variability. In this talk, I will present an integrative framework that combines advanced sensor technologies, biochemical profiling, and data-driven analytics to reinterpret GI in the context of nutritional precision.By coupling these sensor data with deep biochemical characterization of food matrices — including macronutrient interactions, bioactive constituents, and structural complexity — we demonstrate a multi-layered understanding of how foods impact glycemic responses across diverse individuals.

A key innovation discussed will be the RAAGIS (Rapid Assessment and Adaptive Glycemic Interpretation System) platform, which integrates high-resolution sensor outputs with individualized metabolic fingerprints to predict glycemic outcomes with improved accuracy and responsiveness. RAAGIS leverages machine learning models trained on both in vitro digestion kinetics and in vivo sensor data to generate adaptive GI estimates that reflect individual physiological and biochemical contexts. We did a comparative evaluation of six established methods enabled identification and optimization of the most effective approach, achieving strong predictive accuracy (MAE 0.81, RMSE 0.89) while lowering per-sample costs by 37-fold. Validation with 53 rice accessions revealed predictive GI (pGI) values ranging from 46.98 to 87.26 and Inherent Glycemic Potential (IGP) values between 23.27 and 44.01. To enhance glucose detection in complex digesta, we further developed a non-enzymatic electrochemical nanosensor based on V_2O_5–Ti_3AlC_2MXene nanohybrids. The sensor exhibited high selectivity, with performance confirmed through SEM, HRTEM, SAED, EIS, and EDS analyses, and showed strong correlation with conventional colorimetric assays ($R^2 = 0.857$). Integration of machine learning models, including decision trees ($R^2 = 0.991$) and random forests ($R^2 = 0.984$), further improved predictive robustness. Importantly, this study established the first significant correlation between pGI and IGP, providing a new framework for nutritional evaluation. Overall, the integration of optimized *in vitro* digestion, nanosensor technology, and AI offers a rapid, cost-effective strategy for advancing low GI food design and supporting dietary management of metabolic health.

Keywords: Glycemic Index, Electrochemical Sensor, Machine Learning

Abstract No: E4

Vertical farming of strawberry as a climate-resilient approach to sustainable food systems and nutritional security

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ABSTRACT

Strawberry (*Fragaria* × *ananassa* Duch.) is a valuable, phytochemical-rich fruit crop increasingly affected by climate variability, shrinking cultivable land, and resource inefficiencies in open-field environments. Combining vertical farming, hydroponics, and artificial full-spectrum light (AFSL) provides a climate-resilient approach for sustainable food production and nutritional security. This study examined various strawberry genotypes using hydroponic and vertical farming systems to optimize yield, light efficiency, and fruit quality across different levels indoors and outdoors. Significant genetic diversity was found for yield and morphological traits, with genotypic and phenotypic coefficients of variation reaching up to 94.14% and 121.43% for fruit-related traits. Path analysis indicated that the average yield per plant ($p=0.953$) and the number of fruits per plant ($p=0.821$) were the main contributors to overall yield. Outdoors, 2 hours of AFSL at the third level yielded the highest at 363.63 g per plant, similar to the natural light top level at 362.54 g, suggesting that supplemental lighting effectively compensates for lower light levels. Indoors, 6 hours of AFSL at mid-levels produced the best yields (240.16 g/plant), followed by 8 hours (221.28 g per plant), with increased chlorophyll, carotenoids, and phytochemicals in the fruit. Principal component analysis showed that light intensity was the main factor affecting outdoor yield, while photoperiod was more influential indoors. Genotypes 'Rania', 'Nabila', 'Winter Dawn', 'Sweet Charlie', and 'Winter Star' consistently displayed superior morphological traits and yields comparable to 'Camarosa', indicating their suitability for soilless vertical cultivation. Overall, vertical strawberry farming offers a climate-resilient, resource-efficient system capable of maintaining productivity and nutritional quality amid changing climatic and urban environments.

Keywords: Vertical farming, Climate-resilient agriculture, Artificial full-spectrum light, Sustainable productivity, Nutritional security

Abstract No: E5

Enhancement of Antioxidant Quality of Sesame Seed Oil through Biofertilizer Application

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ABSTRACT

Sesame (*Sesamumindicum* L.) seed oil is valued for its high antioxidant potential, primarily attributed to lignans such as sesamin and sesamolin. Enhancing these bioactive compounds through eco-friendly agronomic interventions is of considerable importance. The present study evaluated the effect of biofertilizer application on the expression of lignan biosynthetic pathway genes and antioxidant activity of sesame seed oil. Three sesame genotypes (Krishna, Tilottama and Rama) were subjected to different biofertilizer treatments involving *Bacillussubtilis*, *Pseudomonas fluorescens*,*Azotobacter*, Azospirillum and their combinations, and multi-biofertilizer consortia applied as seed treatment, foliar application, and their combinations.Gene expression analysis of key cytochrome P450 genes, SiCYP81Q1 and SiCYP92B14, associated with sesamin and sesamolin biosynthesis, was carried out using Real Time PCR and Tubulin gene as internal control. Antioxidant activity of extracted sesame seed oil was assessed through DPPH radical scavenging assay and IC_{50} determination. Results revealed significant upregulation of both genes under biofertilizer treatments compared to control. Genotypes Tilottama and Rama exhibited higher fold change in gene expression, with Rama showing maximum induction of SiCYP92B14. Among treatment schedules, foliar application at flowering stage was most effective. The combined application of *Bacillus subtilis* and *Pseudomonas fluorescens* resulted in superior gene expression and enhanced antioxidant activity, reflected by lower IC_{50} values.

The study demonstrates that targeted biofertilizer application can effectively modulate lignan biosynthetic gene expression and improve antioxidant properties of sesame seed oil. Foliar application of Bacillus and Pseudomonas at flowering emerges as a promising, sustainable strategy for improving the nutraceutical quality of sesame.

Keywords: Biofertilizers, Sesame, Antioxidant activity, Lignan, SiCYP81Q1 and SiCYP92B14

Abstract No: E6

Evaluation of Antioxidant Potential of Fruit Extracts

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ABSTRACT

Fruits are recognized as rich sources of bioactive phytochemicals that play a vital role in antioxidant defence and nutritional health. The present investigation aimed to estimate phenolic compounds, flavonoids, flavonols, anthocyanins, antioxidant activities, carotenoids, and vitamins (A, E, and C) in nine selected fruits. The fruits were pomegranate, apple, bitter orange, amla, pineapple, Indian pummelo, guava, pear, and cucumber expressed on a fresh weight (Fwt.) basis. Total phenolic content ranged from 68.7 to 905.4 mg GAE/100 g Fwt, with bitter orange and pear exhibiting the highest values. Anthocyanin content varied between 43.9 and 363.3 mg CAE/100 g Fwt, and pomegranate showed a significantly higher concentration. Flavonoid content ranged from 61.9 to 805.0 mg catechin/100 g Fwt, while flavonols varied from 22.3 to 364.7 mg quercetin/100 g Fwt, with pomegranate, amla, and pear showing elevated levels. Antioxidant potential evaluated using DPPH, FRAP, H_2O_2 radical scavenging, and total antioxidant capacity assays revealed strong activity, particularly in pomegranate, apple, and amla. DPPH scavenging activity ranged from 144.0 to 564.0 mg AA/g Fwt, FRAP values were highest in amla (215.7 mg BHT/g Fwt), and total antioxidant capacity ranged from 84.7 to 310.0 mg AA/g Fwt. Carotenoid content ranged from 6.15 to 97.0 mg/g Fwt, while vitamins A, E, and C were present in appreciable quantities, with amla and guava showing significantly higher vitamin C content (up to 176.0 mg AA/g Fwt). All data are presented as mean ± SD (n = 9), based on three independent parallel experiments. Statistical significance was set at $p < 0.05$. The findings highlight considerable variation in phytochemical composition and antioxidant capacity among fruits, supporting their potential application as functional foods and natural antioxidant sources.

Keywords: Antioxidants, Indigenous Fruits, Phytochemical of fruits, Fruit-based nutraceuticals and Oxidative stress mitigation

Abstract No: E7

A Study on the Psychological and Environmental Triggers of Dietary Choices among Men

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ABSTRACT

Poor nutritional diet among young adult men is driven by a synergistic collapse of cognitive and psychological resources. Chronic academic stress and decision fatigue lead to psychological depletion, which diminishes willpower and causes individuals to prioritize immediate convenience over long-term health goals. This study utilized a mixed-methods approach to analyse the behaviours of candidates and early-career researchers. Key variables assessed included perceived academic stress, cooking self-efficacy, and the frequency of convenience food intake, habits between low-stress and peak-stress intervals. By identifying scholars as an underrepresented and vulnerable population in behavioural health, this research focus on individual responsibility to institutional responsibility. It highlights how high-level cognitive labour creates unique dietary vulnerabilities that traditional nutritional education fails to address. The research study the differential impact of psychological distress versus immediate environmental triggers. The primary goal was to pinpoint the specific drivers that override conscious nutritional intent in time-constrained, high-pressure academic settings. Analysis revealed that environmental and academic stress are the most powerful predictors of poor dietary choices. While psychological distress provides the underlying drive, the immediate availability of fast-food acts as the decisive trigger. convenience food consumption surges during peak stress periods, Effective health promotion must move beyond individual education toward structural interventions. Enhancing the accessibility of healthy options within the academic ecosystem is essential to buffer scholars against the environment.

Keywords : Convenience Food, Psychological Triggers, Academic Stress, Environmental Triggers, Dietary Quality, Health Promotion.

Abstract No: E8

Effect of Vitamin D on Functionality of Endothelial Colony-Forming Cells Cultured from Coronary Artery Disease Patients

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ABSTRACT

Coronary artery disease (CAD) is characterized by endothelial dysfunction and impaired vascular repair. Endothelial colony-forming cells (ECFCs), a highly proliferative endothelial progenitor population, play a key role in endothelial regeneration; however, their number and function are compromised in CAD. Vitamin D has emerged as a cardiovascular modulator influencing endothelial function through vitamin D receptor (VDR)–mediated pathways. This study evaluated whether in vitro vitamin D supplementation could restore the functional capacity of ECFCs derived from CAD patients. Peripheral blood samples were obtained from 20 clinically diagnosed CAD patients. ECFCs were successfully expanded from 30% of samples. Cells were characterized morphologically and immunophenotypically using flow cytometry and immunofluorescence for endothelial markers (CD31, VEGFR2, CD146), progenitor markers (CD34, CD117), and exclusion of hematopoietic lineage markers (CD45, CD14). Functional endothelial properties were confirmed by lectin binding and acetylated LDL uptake. ECFCs were treated with 20 nM vitamin D for 24 hours. Functional assessment included population doubling time (PDT), Ki67 expression, wound migration, cell adhesion, and Matrigel tube formation assays. VDR expression was analyzed by western blotting, and angiogenic protein modulation was assessed using a human angiogenesis array profiling 50 mediators.Vitamin D significantly enhanced ECFC proliferation, evidenced by reduced PDT and increased Ki67 expression. Treated ECFCs demonstrated improved migration, adhesion, and angiogenic capacity, with increased tube length and branching. Angiogenesis profiling revealed upregulation of pro-angiogenic factors (VEGF, VEGFR2, PDGF) along with angiostatin, indicating restoration of angiogenic balance. VDR expression was markedly increased following vitamin D treatment. In vitro vitamin D supplementation restores and enhances ECFC functionality in CAD patients through VDR-mediated mechanisms, supporting its potential role as an adjunct strategy to improve endothelial repair and vascular regeneration in CAD.

Keywords : Vitamin D, ECFCs, Coronary artery disease, VDR, Endothelial repair

Abstract No: E9

Effect of Non-Thermal Pretreatment and Convective Drying on Bioactive Compounds, Antioxidant Capacity, Microstructure, FTIR, and Sensory Quality Attributes of Litchi

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ABSTRACT

This study optimized ultrasound-assisted osmotic dehydration (USOD) of litchi quarters using response surface methodology with a Box-Behnken design to maximize water loss and minimize solid gain. Independent variables were ultrasound amplitude (20-40%), sonication time (10-30 min), and sucrose concentration (20-60% w/w), using a 4:1 solution-to-fruit ratio. Water loss and solid gain ranged from 8.45-28.87% and 2.17-6.73%, respectively. Optimal conditions (34.79% amplitude, 30 min, 40% sucrose) predicted 23.76% water loss and 3.89% solid gain, with second-order regression models showing good fit. The effect of USOD pretreatment followed by convective drying at 60°C was evaluated in comparison with untreated samples. USOD-pretreated samples showed significantly ($P < 0.05$) higher lightness (L* 46.69), lower moisture content (11% dry basis) and water activity (0.40), greater phenolic retention (10.72 mg GAE/g DW), higher flavonoid content (3.17 mg QE/g DW), and enhanced DPPH scavenging activity (65.47%). In addition, these samples exhibited significantly ($P < 0.05$) lower hardness (4.7 N), higher rehydration ratio (2.89), lower shrinkage (72.13%), and superior sensory acceptability (7.4). Scanning electron microscopy revealed noticeable microstructural alterations in USOD-pretreated samples compared with fresh and control samples, while FTIR analysis confirmed greater antioxidant retention in USOD-pretreated dried litchi quarters.

Keywords: Litchi, Ultrasound assisted osmotic dehydration, Total Phenolic Content, Total Flavonoid Content, DPPH scavenging activity, SEM, FTIR.

Abstract No: E10

A Study on the Psychological and Environmental Triggers of Dietary Choices of Research Scholar

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ABSTRACT

Academic research environments are characterized by intense productivity demands, often leading to chronic time scarcity and elevated psychological stress. This high-pressure setting has been widely linked to the prioritization of convenience in daily life, potentially resulting in adverse health behaviours, particularly poor dietary choices. This study targets research scholars a population underrepresented in nutrition studies despite facing professional pressures. This research aimed to systematically study the differential impact of psychological factors and immediate environmental triggers on the reliance on nutritionally poor convenience foods among time-constrained research scholars. A mixed-methods approach was employed. Quantitative data was collected via a cross-sectional survey (N=37) administered specifically to research scholars (primarily doctoral candidates), assessing perceived time scarcity, psychological distress, cooking self-efficacy, and frequency of convenience food consumption. Quantitative analysis revealed that environmental proximity (beta = 0.45, $p < 0.01$) and perceived academic stress (beta = 0.26, $p = 0.16$) were the most notable predictors of increased convenience food consumption. While perceived stress was a consistent psychological driver, the immediate proximity of fast-food options emerged as the most statistically significant environmental trigger, often overriding conscious nutritional intent. Scholars in the high-stress category reported consuming convenience meals 22.3% more frequently compared to those in low-stress periods. Poor dietary choices among research scholars are not solely a result of time scarcity but are driven by a synergistic combination of psychological depletion (stress, decision fatigue) and a proximal, obesogenic food environment. Institutional health promotion efforts must therefore move beyond simple nutritional education to implement structural changes that buffer scholars against environmental defaults, focusing on increasing the convenience and accessibility of healthy food options within the academic ecosystem.

Keywords: Convenience Food, Psychological Triggers, Academic Stress, Environmental Triggers, Dietary Quality, Health Promotion.

Abstract No: E11

Recent Advances in heat sensitive nutrient preservation through Innovative technologies

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ABSTRACT

The objective of food preservation technologies is based on the prevention of microbial growth or microbial inactivation. Food preservation methods include thermal, electrical, chemical and radiation techniques. Although the application of thermal-based technology is cost effective but as in the case of products leads to the various transformation of food products triggering side reaction that causes undesired changes in nutritional, physicochemical, and sensory attributes. The cleaning and disinfection process involves excess use of water and wastewater discharge which becomes a challenge during the era of climate change. Therefore, engineering solutions emerged to produce safe and contamination free products with better shelf life and quality. Fruits and vegetables are perishable items with essential water-soluble nutrients such as vitamin B, C and other important constituents which generally destroyed during the conventional food processing methods. Main purpose of this review is to provide lime light the advanced food preservation techniques, with focus on fruits, vegetables. As these advanced technologies are engineering based green technology along with its promising and multidimensional applicability in the food industries. High hydrostatic pressure, ozonation, pulsed electric field, ultra sonification, cold plasma and ultraviolet irradiation. Pulsed electric field processing is a new food pasteurization method uses short bursts of high voltage electric fields on foods, applies high voltage pulses (20–80 kV/cm) with a duration of milliseconds to microseconds to treat liquid foods placed between two electrodes. Ozonation is a method using ozone gas (O_3) to kill microbes, remove ethylene, acting as a powerful sanitizer without chemical residues, applied in gas or dissolved-in-water forms, with effectiveness depending on concentration, contact time, and temperature. Cold plasma technique uses ionized gas at room temperature to inactivate microorganisms on food surface. Plasma is generated by applying energy to a gas, carrying the gas molecules to ionize and form reactive species, including ions, electron radicals and UV photons and these reactive species interact with microbial cell membranes, DNA and proteins leading to cellular damage of the microbes.

Abstract No: E12

Enhancing Nutrient Bioavailability in Pearl Millet through Ultrasound-Assisted Processing and Functional Food Development

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ABSTRACT

Pearl millet (*Pennisetum glaucum*) is a climate-resilient, nutrient-dense cereal with significant potential to contribute to nutritional security and sustainable food systems. However, its wider utilization is constrained by the presence of antinutritional factors and limited availability of diversified, consumer-acceptable food products. The present study addresses these challenges by integrating nutritional biochemistrydriven process optimization with postharvest engineeringbased functional food development. Ultrasound-assisted hydration was investigated as a non-thermal pre-treatment strategy to reduce antinutritional factors and enhance nutrient bioavailability. Response Surface Methodology (RSM) was employed to optimize ultrasound amplitude, treatment time, and grain-to-water ratio, with phytates, tannins, raffinose family oligosaccharides, degree of starch gelatinization, amylose content, resistant starch, vitamins, and mineral retention as key responses. Optimized ultrasound treatment significantly reduced antinutrients while preserving micronutrients and improving functional starch characteristics.Subsequently, the nutritionally optimized pearl millet was utilized to develop a range of value-added functional foods, including complementary food blend, extruded snack, puffed flake, and roasted grain mixture, using resource-efficient postharvest processing techniques such as grinding, blending, extrusion, puffing, flaking, and roasting. Extrusion parameters were optimized to achieve desirable expansion, texture, and sensory quality, while complementary foods were formulated to meet age-specific nutritional requirements. The developed products demonstrated improved palatability, functional properties, and storage stability, offering healthier alternatives to conventional cereal-based foods.Overall, this integrated approach demonstrates how engineering solutions in postharvest management, coupled with advances in nutritional biochemistry, can effectively preserve nutrients, improve bioavailability, and enable the development of innovative, millet-based functional foods. The findings support the strategic promotion of pearl millet as a sustainable, climate-resilient crop for enhancing dietary diversification and nutritional security.

Keywords: Pearl millet, Nutritional biochemistry, Postharvest engineering, Ultrasound processing, Functional foods, Nutritional security.

Abstract No: E13

Enhancing post-harvest quality and storage longevity of *Capsicum annuum* L. using nano-selenium

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ABSTRACT

Post-harvest losses of horticultural produce remain a critical worldwide concern, largely attributable to suboptimal storage and accelerated ripening processes. In India alone, post-harvest losses are estimated to exceed ₹152,790 crore annually, posing a serious threat to food and nutritional security. Rapid ripening driven by elevated metabolic and respiratory activities leads to premature senescence, tissue softening, and microbial decay. In this context, nanotechnology-based interventions offer distinct advantages over conventional post-harvest treatments due to their higher bio efficacy at lower dosages. The present study investigated the efficacy of nano-selenium (Se-NPs), exploiting selenium's redox-modulatory and antioxidative properties, in regulating ripening and preserving post-harvest quality of *Capsicum annuum* L. fruits. Exogenous application of Se-NPs at 8 mg L^{-1} during 7 days of storage significantly reduced decay incidence, physiological weight loss, and fruit softening, while maintaining total soluble solids. Cytotoxicity evaluation using HEK-293 cell and haemolysis assays confirmed the biocompatibility of Se-NPs at the applied concentration. Mechanistically, Se-NP treatment alleviated fruit coat deterioration by suppressing ion leakage, lipid peroxidation, and cell wall disassembly, accompanied by enhanced polyamine accumulation. Transcript analysis revealed downregulation of lipoxygenase, indicative of delayed ripening and membrane stabilization. Additionally, Se-NPs improved photochemical quenching, chlorophyll fluorescence parameters, and malate metabolism, supporting sustained fruit coat photosynthetic competence. A noticeable reduction in respiratory rate was associated with lower reactive oxygen species accumulation, decreased DNA damage, and delayed programmed cell death. Enhanced activities of antioxidant enzymes, including peroxidase and glutathione reductase, together with elevated ascorbate and glutathione pools, further strengthened redox homeostasis. Conclusively, these findings demonstrate that nano-selenium represents a promising, safe, and sustainable post-harvest strategy for extending shelf life, minimizing fruit losses, and continuing the commercial value of *Capsicum* fruits.

Keywords: Post-harvest, Horticulture, Nanotechnology, Reactive oxygen species, Antioxidant, shelf life.

Abstract No: E14

Assessment of heavy metal bioaccumulation in edible crops and associated human health risks

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ABSTRACT

The primary aim of this review is to assess the extent of heavy metal accumulation in edible crops grown in contaminated soils at opencast mining and rampant industrialization areas. The study aims to correlate soil metal concentrations with plant uptake, report the toxicity of different heavy metals, their major exposure pathways and assess the associated health risks to consumers through dietary intake. Data on different phytoremediation indices such as Bioconcentration factor (BCF), Translocation Factor and (TF), Health Risk Indices (HRI) such as Hazard Quotient (HQ), Hazard Index (HI) of edible crops (Cereals, vegetables, fruits) were reviewed and compared across various geographical locations. The outcomes noted that edible crops especially leafy vegetables show higher metal bioaccumulation. Opencast mining activities were the major threat of soil contamination. Reported data from researches reveals that HRI exceeds safety threshold, indicating a significant risk to several detrimental health hazards such as kidney damage, liver dysfunction, neurological disorders, reproductive issues, and even cancer. The review concludes that nutritional benefits of edible crops do not outweigh the heavy metal induced health risk. This review laid the basis of further in-depth and rigorous investigation on health risk assessment in multi-metal contaminated areas and formulate regulations for their consumption in order to safeguard public health.

Keywords: Edible crops, Heavy metals, Health risk assessment, Phytoremediation indices

Abstract No: E15

Study of Nutrient Distribution According to the Growth Pattern of DendrocalamusHamiltonii

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ABSTRACT

The distribution of nutritional components in Dendrocalamushamiltonii was studied during the research to evaluate their importance for health. The presence of nutrients in different parts of the bamboo was examined throughout its growth cycle. Observations showed that the number of culms or clumps ranged from 50 to 57, with total biomass between 29.1 and 34.2 kg per 100 g of culm. The biomass distribution was 70% in the culm, 22% in the branches, 3% in the leaves, and 5% in the rhizomatous parts. A major nutrient in bamboo biomass is potassium, along with nitrogen, magnesium, calcium, and phosphorus. Their relative amounts were K>N>Mg>Ca>P in branches and N>K>Mg>Ca>P in leaves. The main aim was to demonstrate the presence of nutrients in different bamboo portions, which can mitigate malnutrition, improve food security, and boost the immune system. The study site is located at Nirmali College, Nirmali. It is situated at 26.32°N 86.58°E. Nirmali is a small town in the northernmost part of Bihar State, in the district of Supaul. During work, nursery management practices were done. After the hardening of *Dendrocalamushamiltonii,* seedlings were used for raising a bamboo plantation. A nursery was prepared, 15X10m, filled with a mixture of soil, sand, and vermicompost 3:1:2. Seedlings of 6-8cm height were used during plantation. About 20-25seedlings were planted in1.5m^2 of nursery bed. Watering of plants was done from time to time for proper growth and moisture maintenance. From the study area selection, any five clumps were randomly selected, and after that number of culms was counted in the selected 5-clumps. Now, observation of DBH, height, basal area growth and number of nodes in all culms was completed. For the estimation of total biomass in relation to organic productivity for 3-CPTs from each clump group. After felling, subdivided into leaves, branches, rhizome, and culms. Fresh weight of each component was estimated in the field. Now each components were brought to dry in the oven at 103 °C in the laboratory. Oven-dry weight of components was estimated. Total standing biomass of each clump group was calculated by dividing the total number of each clump by the average dry weight of the samples.According to observations, the number ofculms produced from 3 years old culm X-1, X-2, X-3, X-4, X-5 was counted, and these were 10-15,and the nodes were5-7 respectively. The maximum height at DBH, basal area girth was 4.7m, 1.2cm, 2.6cmrespectively. Per cent contribution of biomass components with respect to the contribution of different bamboo portion total above-ground biomass. Observations showed that the number of culms or clumps ranged from 50 to 57, with total biomass between 29.1 and 34.2 kg per 100 g of culm. The biomass distribution was 70% in the culm, 22% in the branches, 3% in the leaves, and 5% in the rhizomatous parts. A major nutrient in bamboo biomass is potassium, along with nitrogen, magnesium, calcium, and phosphorus. Their relative amounts were K>N>Mg>Ca>P in branches and N>K>Mg>Ca>P in leaves.

Keywords: *Dendrocalamushamiltonii*, nutrients, biomass, culm, food security, immune system

Abstract No: E16

Effect of Hydrocolloids dip on shelf life of litchi

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ABSTRACT

Postharvest losses of fresh litchi are a major constraint affecting marketability and shelf life, necessitating the development of safe and sustainable preservation strategies. The present study was undertaken to evaluate the effectiveness of different edible coating formulations based on natural biopolymers for enhancing postharvest quality and storage stability of fresh litchi. Seven treatments were investigated, including a control (water dip for 30 min) and coatings formulated using carboxymethyl cellulose (CMC), gum Arabic, sodium alginate, and glycerol as a plasticizer. Coated samples were evaluated during 5 days storage for key physicochemical and quality parameters to assess their ability to reduce moisture loss, maintain firmness, and delay senescence compared to the untreated control. The result showed that the least weight loss (7.15%) observed in dipping treatment with a combination of CMC (1%) and gum Arabic (1%) compared to the 13% in control. Colour change in terms of browning index was also least in the above combination (1.53) compared to control (2.71). The other parameters like TSS, acidity and vitamin C as well as bioactive compounds in terms of phenolic compounds showed least changes in CMC and gum Arabic dip, which shows that edible coatings is a promising approach for extending shelf life and improving the marketability of fresh litchi under ambient storage conditions

Keywords : Hydrocolloids; Dipping treatment; Plasticizer; Shelf-life; Senescence

Abstract No: E17

Drying optimization of fenugreek microgreens using the RSM

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ABSTRACT

Fenugreek (*Trigonella foenum-graecum*) microgreens are known for their rich content in various nutrient and vitamins, with its increasing medicinal use. However their high moisture content limits their shelf-life stability. Drying being one of traditional method of preservation, thus increase it usability but inappropriate drying condition may lead to excessive nutrition loss and higher energy uptake. Thus, this study aims at optimizing the drying condition for fenugreek microgreens by taking the drying temperature and time as its independent variable and moisture removed and vitamin C as the dependent variable.

The Response Surface Methodology (RSM) was used to study the combined effect of drying temperature(40–60 °C) and drying time (60-180 min). The 13 runs provided by RSM was analyzed under the quadratic model. The vitamin c response were taken in mg/100g of fresh weight and moisture removed was taken in percentage (%).

The analysis shows the model was significant and lack of fit was not significant for both the responses, with the p-value(<0.0001) in range. The Predicted R^2 being less than 1 is in reasonable agreement with the Adjusted R^2 i.e. the difference is less than 0.2, for both the responses. The numerical optimization provide the selected condition with temperature at 49.879°C and time at 180 min, for maximum moisture removed and maximum Vitamin C content. The error between the predicted response and observed is less than 10%, thus this model is accepted for the optimized drying condition for fenugreek microgreens. Hence this result are useful for functional food applications and value-added powder production.

Keywords-: Fenugreek, Drying, Moisture Removed (%), Response Surface Methodology (RSM),

Abstract No: E18

Integrating Biochemistry and Biotechnology to Enhance Fruit Crop Resilience and Nutritional Security under Climate Change

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ABSTRACT

Climate change is increasingly influencing fruit production by altering yield, quality, and nutritional composition, which directly affects global nutritional security. Fruits play a crucial role in human diets as rich sources of vitamins, antioxidants, minerals, and health-promoting bioactive compounds. Advances in biochemistry have improved our understanding of how fruit crops respond to environmental stresses through changes in metabolism, antioxidant activity, and secondary metabolite production. These insights help identify fruit varieties better adapted to heat, drought, salinity, and oxidative stress. At the same time, modern biotechnological tools such as tissue culture, molecular breeding, genetic engineering, and omics approaches are supporting the development of climate-resilient fruit crops with improved nutritional quality and productivity. In addition, biotechnology-based post-harvest innovations, including edible coatings, bio-preservatives, and nano-formulations, are proving effective in reducing post-harvest losses while maintaining fruit freshness and nutrient retention. Overall, the integration of biochemical knowledge with biotechnological advances in fruit science offers practical and sustainable solutions for improving fruit production and ensuring nutritional security under changing climatic conditions.

Keywords:- Climate change, Fruit crops, Nutritional quality, Biochemistry, Biotechnology, Abiotic stress, Post-harvest management.

Abstract No: E19

Isolation of Benzimidazoles and it's Derivatives from the plant *Acacia concinna*"

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ABSTRACT

Acacia concinna pods provide a natural, surfactant-type catalyst for the synthesis of greener Benzimidazole and its derivatives that provides an environmental and practical benefits over traditional methods. Benzimidazole and its derivatives have emerged as an essential compound in the evolution of herbal chemistry due to their multifunctional chemical structure and environmental compatibility. Structurally, benzimidazole consists of a fusion between benzene and imidazole rings, forming a stable heterocyclic framework capable of sustainable molecular modifications. In recent years, we are emphasized with eco-compatible and energy-efficient synthetic strategies, including solvent-free reactions, plant-based catalysts such as *Acacia concinna* extracts, and Nano catalysts derived from metals like iron and copper. ***Acacia concinna* pod extracts enable greener, additive-free synthesis of 1,2-disubstituted benzimidazole derivatives.** The method uses a 20% w/v aqueous extract as a surfactant-type catalyst for one-pot condensation of o-phenylenediamine with aldehydes at room temperature. These innovations embody the principles of herbal chemistry by minimizing hazardous waste, reducing dependence on toxic solvents, and enhancing overall reaction efficiency. In the context of herbal chemistry, benzimidazole derivatives exhibit a strong synergy with phytochemicals and natural extracts, enhancing their pharmacological attributes—particularly antioxidant, antimicrobial, anti-inflammatory, and anticancer properties. Biogenic synthetic approaches inspired by natural enzyme pathways highlight the potential for integrating biological catalysis with green synthesis. Furthermore, the eco-designed modifications of Benzimidazole compounds represent an important step toward developing non-toxic, sustainable pharmaceuticals with minimal ecological impact.Their adaptability across diverse biological systems and low environmental footprint makes these molecules vital in bridging sustainable organic synthesis and modern medicinal chemistry. Overall, Benzimidazole and its derivatives stand as a promising example of how chemical innovation can align with the goals of environmental preservation and green technological advancement.

Keywords: Antioxidant, Benzimidazole, Biogenic, Catalyst & Extract

Abstract No: E20

Agro-morphological characterization in relation to drought tolerance in vegetable pea (*Pisum sativum* L.)

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ABSTRACT

Twenty-eight genotypes of vegetable pea (*Pisum sativum* L.) were evaluated during the Rabi season (2023–24) under normal and drought conditions using a rainout shelter in a randomized block design with three replications. Significant differences among genotypes were observed for all morphological and biochemical traits, while genotype × environment interaction was non-significant. Seed yield under both environments served as the primary criterion for screening drought tolerance using drought tolerance index (DTI), drought susceptibility index (DSI), and tolerance index (TI).

Genotypes such as Arka Ajit, KSP-110, RPCAU-23-9, and Kashi Ageti showed superior mean performance for biological yield, shelling percentage, and harvest index under both conditions. Kashi Samridhi, Kashi Mukti, Pusa Pragati, and Kashi Ageti exhibited better performance for root length, pod yield, seed yield, plant height, nodulation, and number of pods per plant. Enzyme activities (peroxidase, catalase) and proline content increased under drought stress, indicating adaptive physiological responses.

Cluster analysis revealed substantial genetic diversity. Under normal conditions, maximum inter-cluster distance was observed between clusters IV and VI, while under drought it was between clusters IV and VIII, suggesting scope for hybridization. In drought conditions, cluster VII recorded the highest biological yield, while cluster II showed superior root traits and shelling percentage. Cluster VIII exhibited maximum catalase and peroxidase activity.

DTI ranged from 0.347–1.221 (mean 0.9152), DSI from 0.425–1.619 (mean 1.0085), and TI from 1.328–4.980 (mean 2.8635). Genotypes such as Kashi Samridhi, RPCAU-23-17, AP-3, Kashi Uday, Arka Priya, Arka Uttam, Pusa Pragati, and Arka Ajit were identified as drought tolerant (high DTI, low DSI).

Overall, traits like proline content, root length, seed yield, and number of pods per plant were identified as reliable selection criteria. These genotypes can serve as potential donors for breeding drought-resilient vegetable pea varieties suited to water-limited regions.

Abstract No: E21

AI-Integrated Electronic Nose for Preserving the Post-Harvest Seed Quality, Ensuring Food and Nutritional Security under Climate Change

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ABSTRACT

Post-harvest losses, nutrient degradation, and seed quality deterioration during storage have increased significantly due to extreme environmental variability caused by climate change, posing a significant threat to global nutritional security through reduced crop productivity. Advanced sensing technology integrated with nanotechnology and artificial intelligence may offer transformative solutions for real-time and accurate post-harvest management as well as monitoring of seeds during processing, storage, and seed quality testing. These systems utilize machine learning algorithms to analyzebiochemical traits andseed quality traits in relation to moisture variations under variable environmental conditions. The optimization of seed characteristics for improved protein content, micronutrient density, and stress tolerance can be achieved by using these systems,contributing to long-term food and nutritional security. The AI-integrated Electronic Nose technology employs gas sensor arrays to detect volatile organic compounds released during seed deterioration, fungal contamination, and storage-induced biochemical changes. By applying pattern recognition algorithms, the system enables rapid, non-destructive, and cost-effective monitoring of seed quality, reducing post-harvest losses and ensuring nutrient retention.These technologies create a smart, end-to-end agricultural modelfrom climate-resilient seed development to intelligent post-harvest quality management, supporting sustainable agriculture, minimizing storage losses, and strengthening nutritional security in the era of climate change.

Keywords: Artificial Intelligence, Electronic Nose, Seed Quality Monitoring, Nutritional Biochemistry, Post-Harvest Management

Abstract No: E22

Probiotic-driven Biofortification: Harnessing folate producing probiotics for functional soymilk development

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ABSTRACT

Folate (vitamin B_9) is an indispensable water-soluble micronutrient that participate in “One carbon metabolism”- an intricate circuitry of cellular growth and genomic stability. This metabolic system integrates a series of interdependent reactions essential for nucleotide biosynthesis, methylation processes and amino acid interconversion. Folate, a generic term for pteroylglutamic acid and its derivatives, is derived mainly from leafy vegetables, legumes, and citrus fruits. Megaloblastic anaemia, cancer, and neural tube defects are just a few of the many issues that can arise from a folate deficiency, which is due to either by an inadequate intake of folate or an inability to absorb folate from food sources like meat, liver, and legumes. Given its essential function in cell metabolism, folate demand increases 5 to 10 times for pregnant women due to rapid cell growth of developing foetus. To protect against health complications related to Folate deficiency around 69 countries have implemented mandatory Folate fortification and 47 countries have voluntary Folate fortification.

Dietary supplements and food fortification programs around the world use folic acid (FA), a synthetic form of folate. When dietary FA consumption is excessive, it can lead to DHFR enzyme saturation or inhibition, which in turn causes the build-up of un-metabolized folic acid (UMFA)leading to the development of the syndrome likemasking vitamin B12 shortage symptoms, elevated incidence of gestational diabetes mellitus (GDM) in women, and negatively influence NK cell cytotoxicity, inflammation, asthma, and allergic reactions in both children and women. A better alternative to synthetic folate is to supplement with a bioactive reduced version such 5-MTHF, which is readily accessible in human plasma. One potential approach that has received increased attention of researchers is the deployment of folate-producing bacteria for development offolate-enriched fermented products. However, folate production ability and capacity arestrain-specific and are greatly influenced by growing conditions. The extracellular folate produced by probiotic starter cultures can increase folate levels in fermented foods, offering a natural supply without health risks. Lactic acid bacteria (LAB) are the most common type of probiotic microorganisms and are categorised as "Generally Recognized as Safe (GRAS)". A good way to choose probiotics is important to make sure they are good for your health. Additionally, for probiotics to be effective, the microorganisms used to make them must meet certain criteria, such as being safe for humans to consume, having the capacity to survive in the digestive tract,

adhering to the intestinal epithelium, colonizing the gastrointestinal tract, producing antimicrobial substances, and remaining viable and stable throughout processing and storage.

Our study utilized a total of 20 strains from the Lactic Acid Bacteria category. All 20 strains showed some varied result in growth at Folic Acid Casei Medium (FACM.) Isolates were tested for their ability to produce extracellular folate using Ultra-performance liquid chromatography (UPLC). *Lactiplantibacillus plantarum* strain JCM 1149 gave highest extracellular folate production (195.96 ppm). Out of 20 strains,we selected eight (8) probiotics from our study whose extracellular folate production meets or exceeds the daily requirement for pregnant women by 30%. The survival rates of *Lactiplantibacillus plantarum* strain JCM 1149, *Lactiplantibacillus plantarum* strain JCM 5805, and *Lactiplantibacillus plantarum* strain JCM 1136 governed survivability of 51%, 63%, and 78% after exposure to pH levels of 1.5, 2.0, and 2.5 respectively. The survival rates of *Lactiplantibacillus plantarum* strain JCM 1149 were 73.99%, 64.18%, and 58.25% at bile concentrations of 0.3%, 0.6%, and 0.9%, respectively, while *Lactiplantibacillus plantarum* strain JCM 5805 retained 50.39% at 1.2%. The resilience of LAB to gastric juice was assessed by the survival rate of LAB following incubation in simulated gastric juice. *Lactiplantibacillus plantarum* strain JCM 5805 had the highest survival rate (66.92%) after 4 hr enduring on gastric juice. Besides this, we tested selected lactic acid bacteria against a panel of 5 different antibiotics. *Lactiplantibacillus plantarum* strain JCM 1149 exhibited resistance to erythromycin, penicillin, kanamycin, and rifampicin, while being susceptible to chloramphenicol. The cell surface hydrophobicity of examined strains varied from 39.91% to 71.24% under toluene, 28.53% to 61.63% under xylene, 36.94% to 57.54% under chloroform, 43.33% to 62.29% under hexane and 32.70% to 58.93% under octane. The autoaggregation percentages for the *Lactiplantibacillus plantarum* strain JCM 1149, *Lactiplantibacillus plantarum* strain JCM 5805 and the *Lactiplantibacillus plantarum* strain JCM 1136 isolates were 78.10%, 69.30%, and 63.51%, respectively, after 5 hours, showing highest aggregation in comparison to other probiotic strains used in our study. The antagonism property of LABs for *Penicillium chrysogenum*and for *Aspergillus niger*was in 39.79% - 54.76% and 42.19% - 56.01% range respectively. The ability of LABs to scavenge free radical was determined using DPPH, FRAP and ABTS radical scavenging assay method and it varied between 31.84% to 49.75%, 31.52% to 46.43% and 35.64% to 51.08% respectively. This can play a key role in sustaining the viability and quality of a product. The range of results for α-glucosidase inhibition by the eight isolates that were tested was 39.86% to 66.80%, while the range for α-amylase inhibition was 42.37% to 70.78% and that can be beneficial for diabetes prevention by lowering the free glucose levels. In terms of antioxidative and anti-diabetic *Lactiplantibacillus plantarum* strain JCM 1149 and *Lactiplantibacillus plantarum* strain JCM 5805 showed significant result in compared to others. The correlation heatmap revealed clear interrelationships among probiotic attributes, indicating a tendency for functional traits to co-occur. The NaCl tolerance exhibited strong positive associations with carbohydrate utilisation ($r = 0.93$, $p < 0.01$) and prebiotic utilisation ($r = 0.88$, $p < 0.01$), suggesting that osmotolerance is often linked to greater metabolic adaptability. Similarly, pH tolerance correlated highly with cell surface hydrophobicity ($r = 0.88$, $p < 0.01$) and gastric juice survivability ($r = 0.92$, $p < 0.01$), implying that acid-resistant strains may possess enhanced adhesion and gastrointestinal persistence. The PCA biplot further provides a clear overview of the multivariate relationships between the eight probiotic strains and their measured functional attributes. Strains located on the left-hand side of PC1—particularly *Lactiplantibacillus plantarum* strains (JCM 1149, JCM 5805, JCM 1136, JCM1132)—showed strong positive associations with multiple probiotic traits, including NaCl tolerance, pH tolerance, autoaggregation, gastric juice survivability, carbohydrate utilization, prebiotic utilization and antidiabetic activity. These traits tended to co-occur, suggesting a robust functional profile beneficial for probiotic applications.

Lactic acid bacteria (LAB) are a diverse group of bacteria that make fermented foods. LAB species include *Pedicoccus, Lactobacillus, Streptococcus, Lactococcus, Leuconostoc, Enterococcus*. Milk is the healthiest food and contains folate-binding protein, making it the best fermentation medium for folate storage. The fermentation of milk with folate-producing lactic acid bacteria can provide natural folate-rich fermented foods to avoid folate deficiency without adverse effects. Despite the popularity of dairy-based functional meals, plant-based milk alternatives like soymilk are gaining ground due to their similar composition. Health concerns such as lactose, starch, cholesterol, and allergies, as well as rituals, are driving demand for non-dairy foods. Consequently, fermentation has proven highly effective in enhancing nutritional content, organoleptic quality, reducing ANFs, modifying textural and structural properties, and producing a wide range of plant-based proteins alternative.

Fermented soymilk was prepared by inoculating the sterilized soymilk with overnight grown log culture of high folate producing strains (10%). Then fermented samples were taken for extracellular folate determination, microbiological analysis, physiochemical, antinutritional and antioxidant. All tested strains recorded growth rate between 7.52 to 7.92 log CFU/ml at 10^{-4} dilution. Soymilk fermented by the 8 strains had extracellular folate values ranging from 79.32 ppm (mg/l) to 158.16 ppm (mg/l). *Lactiplantibacillus plantarum* strain JCM 5805 fermented soymilk showed highest percentage of increament in folate (61.79%) over nonfermented soymilk. LABs fermentation demonstrated differing levels of acidification, with *Lactiplantibacillus plantarum* strain JCM 5805 displaying the most significant pH decrease (4.21), the highest total acidity (0.70%), and the most total soluble solids (6.9 °Brix) among the evaluated strains. The total soluble protein content in fermented soymilk ranged from 142.70 µg/ml to 202.09 µg/ml. The carbohydrate levels significantly diminished post-fermentation in Fermented soymilk (FSM) with strain 5805 (161.91 µg/ml) and FSM with strain 1149 (168.36 µg/ml) compared to NFSM (282.25 µg/ml). Extracellular folate release and lactic acid bacteria assisted breakdown of high-protein fermented soymilk can enhanced GABA level. The GABA content in fermented soymilk ranged from 4.13 mg/ml to 6.26 mg/ml, with the *Lactiplantibacillus plantarum* strain JCM 5805 exhibiting the greatest level (6.26 mg/ml) of GABA. Besides this, various LABs showed strong glucosidase activity with a range of 1.49 U/ml/min to 4.69 U/ml/min in compared to nonfermented soymilk (0.89 U/ml/min) and *Lactiplantibacillus plantarum* strain JCM 1149 showed highest activity of 4.69 U/ml/min. Each fermented sample were analyzed to check the presence of various main flavor volatile compounds like 2-pentylfuran, Hexanol, Hexanal, and pentanol etc along with others. *Lactiplantibacillus plantarum* strain JCM 1136 showed significant result in reduction (93.95%) of hexanal followed by *Lactiplantibacillus plantarum* strain JCM 1149 (92.05%). Also various LABs showed good amount of total phenolic content (TPC) and total flavonoid content (TFC) with a range of 18.45 mg GA/ml to 28.45 mg GA/ml and 19.76 mg quercetin/ml to 45.60 mg quercetin/ml respectively.

A healthy gut microbiome, which can be facilitated by nutritional and lifestyle changes, such as the intake and use of a wide range of probiotics, can help the gut to avoid living with neurological illnesses, digestive illnesses, gastric ulcers, atopic diseases. Probiotic strains that make folate can raise the levels of folate in fermented foods. Probiotic bacteria based folate biofortification can also act as medicines for intestinal disorders, enhance anti-inflammatory and prevent various food borne infections. Furthermore, differences in gut microbiota makeup and metabolism among individuals may affect the efficacy of probiotic therapies for folate synthesis. However, the folate content of fermented foods enhanced by LAB is typically still have too little folate to make a substantial contribution to meeting folate needs.

Theme F
Innovative Processing and Genomic Strategies for High-quality animal and Fish-Based Foods

Abstract No: F1

Harnessing multi-omics and nanobiotechnological interventions for mitigating climate change-induced abiotic and biotic stresses

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ABSTRACT

Climate change has become a new reality of the 21st century and is one of the most important global environmental challenges with implications on agriculturewhichconstantly encountersaggravated abiotic and biotic stresses.There is need to adopt climate smart approach combining adaptation and mitigation aspects in a way that enhance sustainable crop and fish productionfor livelihood improvement and food security.Microbiomesand metabolome are crucial for climate-resilient agriculture, enhancing crop and fish survival.Plants and fish establish specific interactions with microorganisms, which are vital for promoting growth and resilience. Multi-omics approaches based on metagenomics, epigenomics, transcriptomics, proteomics, and metabolomics move beyond traditional culturing methods to reveal the full functional potential of microbial communities. Multi-omics data help elucidate the intricate molecular mechanisms and metabolic pathways. These approaches allow for the real-time monitoring of microbial community dynamics and functions, leading to the discovery of previously unknown genes and microbial species with significant functional traits, which are often difficult to culture in a laboratory setting. Additionally, nanobiotechnological interventions for climate-resilient agriculture involve manipulating materials at the nanoscale to enhance crop production, improve resource efficiency, and mitigate abiotic/biotic stresses. This paper aims to harness multi-omics and nanobiotechnological interventions for mitigation of abiotic and biotic stresses with the major emphasis on contaminants of environmental and emerging concern in crops and fish.

Keywords : Climate change; Abiotic and biotic stresses; Emerging Contaminants; Plants and Fish associated biofilm and Biofloc;Hydrogel; Multi-omics and nanotechnological interventions.

Abstract No: F2

Characterization and Emerging Application of Marine Lipopolysaccharides in Health and Nutrition

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ABSTRACT

Lipopolysaccharides (LPSs) are the major components of the outer membrane of Gram-negative bacteria. The lipopolysaccharide (LPS) isolated from *Marinobacterlitoralis* BK09 identified using 16S rRNA gene sequence similarity analysis was characterized. The GCMS analysis showed that the LPS contained 3-hydroxy-dodecanoic acid (C12:0 3OH) (49%), dodecanoic acid (C12:0) (24%), and decanoic acid (C10:0) (19%) as major fatty acids, and the polysaccharide constituents were fucose (53.79%), xylose (28.04%), and mannose (18.15%). The swarming motility of *Pseudomonas aeruginosa* PA01 was almost reduced by the LPS. Additionally, it had no negative impact on cell proliferation while reducing biofilm development by 50%. The LPS decreased the synthesis of virulence factors including pyocyanin pigment up to 40%. There was no gelation activity of limulus amoebocyte lysate (LAL) in the LPS. The LPS's ability to suppress swarming motility, pyocyanin synthesis, and biofilm formation indicates that it may be used to treat *P. aeruginosa* infections. The use of LPSs in food, health, and nutraceuticals is emerging nowadays, and it is not challenged.

Abstract No: F3

Standardize the IVF proceduresfor quality Embryo production using OPU- IVF techniques in Indigenous cattle (*Bosindicus*)

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ABSTRACT

The objectives of the study were to standardization of the OPU process and IVF techniquesto determine oocyte recovery rate and quality embryo production in the indigenous breedsviz. Sahiwal, Gir, Gangateri, and Bachaurreared in the Centre of Excellence on Indigenous Breed (CoEIB), RPCAU, Pusa cattle farm and were chosen for the study.OPU was done to aspirate the oocytes followed by IVM and the matured oocytes were processed for IVF, which then kept for In vitro culture (IVC). A total of 19 OPU sessions were carried out and 269 oocytes retrieved and processed for In vitro culture and 109 embryos were produced. The best average oocyte recovery resulted in Sahiwal (14.03±0.12) followed by Gir (11.83 ± 0.11). In the remaining two breeds,Gangateri and Bachaurthe average oocyte recoveries were 8.12 ± 0.44 and 5.13 ± 0.21 per OPU session respectively. In Sahiwal and Gir breed a significantly ($p<0.05$) high Grade-A oocytes were recovered (52.11±0.21% and 41.02±0.40%) as compared to the Gangateri, and Bachaur breed. Results of oocyte recovery and IVP are significantly influenced by the breed ($P< 0.01$). Also maturation rate (74.21%) and fertilization rate (68.02%) were recorded.In conclusion, the process is standardized for Ovum Pick Up, In vitro Maturation, In vitro Fertilization, and In vitro Culture. Also it was found in our study that Sahiwal and Gir presented higher oocyte recovery and embryo production followed by Gangateri and Bachaur breed.

Key words: In vitro culture, In vitro fertilization, In vitro maturation, Ovum pick up.

***Focus Area**-"Innovative processing and Genomic Strategies for High-Quality Animal and Fish-Based Foods".*

Abstract No: F4

Diversityand Feeding behavior of *Cypriniform Locahes* in North Bihar River systems, India

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ABSTRACT

This study presents the first systematic assessment of loach fish diversity and feeding habits of selected loach species of North Bihar, conducted from September 2024 to August 2025. North Bihar is characterized by extensive floodplain wetlands locally known as *mauns* and *chaurs*, along with a dense network of rivers. These diverse aquatic habitats support rich ornamental fish resources, including loaches. A total of seven loach species belonging to four genera and three families were recorded from four (Bagmati, Gandak, BurhiGandak, and Koshi) major rivers of North Bihar. The documented species included *Botialohachata* (Yoyo loach), *Botiadario* (Tiger loach), *Lepidocephalichthysguntea* (Indian spiny loach), *Lepidocephalichthysthermalis* (Spotted loach), *Paracanthocobitisbotia* (Sand loach),*Paracanthocobitismackenziei(*Robust zipper loach*),* and *Canthophrysgongota* (Moose-faced loach). Family-wise distribution revealed two species under Botiidae, three under Cobitidae, and two under Nemacheilidae, with the highest species richness observed in the family Cobitidae.Based on relative abundance, *B. lohachata* and *B. dario* were selected for detailed feeding habit analysis. Gut content examination indicated that *B. lohachata* exhibited a predominantly piscivorous feeding strategy, dominated by insects (34%), followed by crustaceans (21%) and worms (13%). In contrast, *B. dario* showed a worm-dominated diet (66%), followed by unidentified matter (20%) and fish (9%).The results highlight that North Bihar rivers support **moderate but ecologically significant loach diversity**, with species showing **distinct dietary niche partitioning**.

Key words: Loach species, Rivers, Floodplain wetlands, Gut content, Feeding habits

Abstract No: F5

Protective Role of Graded Dietary Vitamin E against Bisphenol A-Induced Physiological and Reproductive Alterations in Male Oreochromis niloticus

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ABSTRACT

The present study evaluated the ameliorative role of graded dietary vitamin E against Bisphenol A (BPA)-induced stress in male Oreochromis niloticus (100 ± 5 g) during a 45-day exposure period. Fish were distributed into two control groups—one without BPA and one exposed to BPA—and five treatment groups exposed to BPA and fed diets supplemented with 0.02%, 0.04%, 0.06%, 0.08%, and 0.1% vitamin E (basal level 0.01%). Hematological indices, antioxidant enzymes (SOD and CAT), hepatic markers (GOT and GPT), serum testosterone levels, and testicular histology were assessed.BPA exposure altered hematological parameters, antioxidant enzyme activities, hepatic enzyme markers, and serum testosterone levels, along with structural alterations in seminiferous tubules and spermatogenic cells.Dietary vitamin E supplementation gradually exhibited dose-dependent ameliorative activity, with progressive normalization of physiological and biochemical parameters and improved testicular histoarchitecture across treatment groups.The findings indicate that dietary vitamin E effectively mitigates BPA-induced oxidative and reproductive stress in male O. niloticus, supporting its potential application as a nutritional intervention strategy in aquaculture systems.

Keywords: Bisphenol A; Vitamin E; Oxidative stress; Reproductive toxicity; Antioxidant enzymes; Nile tilapia; Hematological parameters; Testicular histology; Endocrine disruption

Abstract No: F6

Heat Shock Factor Diversity and Evolution in Aquatic Crustaceans: A Bioinformatic Study

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ABSTRACT

Crustaceans include shrimps, prawns, crabs etc. live wide variety of aquatic habitats and tolerate wide fluctuations in temperature. Heat shock pathway is evolutionary conserved and responsible for thermal adaptation. Heat shock Factor (HSF) is a key transcription factor of the pathway which senses temperature fluctuations and upregulates heat shock protein genes thus enabling organisms to counter stress. The present study is conducted to analyse sequence features, domain organisation, phylogenetic analysis and structure prediction of HSF protein sequences from selected aquatic crustaceans using computational tools. BLAST search using human HSF1 in the genomic database revealed the presence of single copy gene in all animals. Sequence identity among the animals ranges between 34 - 61% (aprox). Domain prediction revealed presence of: winged helix DNA binding or HSF type DNA binding domain in N-terminal in all groups and vertebrate heat shock transcription factor domain towards C-terminal in only higher taxa. Phylogenetic analysis revealed two clusters evolved from a common ancestor and they separated out from human isoforms. Multiple sequence analysis and structure prediction revealed conserved DNA recognition helix and DNA binding residues but wing domain showed variations. Compared to human HSF1 and 2, there is single deletion in wing domain. In conclusion, the present study revealed that there are two types of HSF proteins present in aquatic crustaceans based on domain organisation and phylogeny but with conserved DNA binding domain.

Keywords : Crustacea, Heat Shock Factor, Sequence Analysis, Phylogeny, Structure

Abstract No: F7

Effects of Climate Change on Ramsar Sites and Inland Fisheries Resources in Bihar, India

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ABSTRACT

Climate change is gradually affecting the structure and functioning of wetlands and inland fisheries, especially in climate-sensitive regions like Bihar, India. These sites are extremely significant from biodiversity, fisheries, and livelihood importance. There are six Ramsar wetlands in five districts of Bihar till 2026; Nagi and Nakti Bird Sanctuaries (Jamui), Udaipur Jheel (West Champaran), Gokul Jalashay (Buxar), Kanwar Lake (Begusarai) and Gogabeel lake (Katihar). Secondary climate data (2019-2024) from NASA POWER was used to analyze trends in maximum and minimum temperatures, precipitation, and specific humidity for five districts. The findings show that there is a steady increase in both maximum and minimum temperatures, with irregular rainfall and humidity levels, which directly affect the hydrology and fish habitats. Buxar districts has the average maximum and minimum temperature (T_{max}=47°c; T_{min}=4.11°c), indicating temperature variability. In contrast, Begusarai recorded higher specific humidity, while Katihar showed comparatively greater precipitation. All of these factors were combined into composite vulnerability index. Katihar is recorded the highest vulnerability index (VI=0.5) derived from maximum temperature and minimum temperature, specific humidity, and rainfall. On the basis of these data, Katihar showed the most climatically vulnerable district, followed by Begusarai, West Champaran, Buxar and Jamui showed the lowest relative vulnerability among the five districts. These findings underscore the immediate impetus that Ramsar wetlands and inland fisheries in Bihar have been increasing their sensitivity towards climatic aberrations. Management of fisheries regulation, wetland restoration, smarter water management, and getting local communities more involved to overcome these situations. These steps can build real resilience as the climate keeps changing.

Abstract No: F8

Predicted Land Use Land Cover and Flood Susceptibility Scenario under Future Urban Expansion in Bihar

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ABSTRACT

Land use Land Cover (LULC) change has emerged as a significant, yet often under recognized driver of environmental degradation and flood risk across rapidly urbanizing regions. While floods are often blamed only on heavy rainfall or rivers, the way land is being transformed by rapid urbanization plays an equally important role. Expansion of cities and towns is steadily reducing river water spread area, agricultural land, and forest cover. River channels are getting narrower, vegetation that used to absorb rainwater is vanishing and natural flood plains are getting smaller. Rapid runoff and more frequent and severe flooding are frequently the results of urbanization- induced changes such increasing impervious surface, vegetation loss and encroachment of rivers corridors. Bihar, with its dense network of rivers and low lying terrain, is especially vulnerable to these changes and experiences floods almost every year. Accessing present and predicted future LULC dynamics, especially the potential shrinkage of rivers, agricultural lands and forest areas under continued urban expansion is therefore essential for effective flood risk management. Modern geospatial technologies, including GIS and satellite imagery, make it possible to observe past and present land changes and to prepare prediction maps showing possible future scenarios. Such information can guide better land-use planning, protection of rivers and floodplains, and expansion of green spaces. This abstract highlights the urgent need to recognize LULC change as a key driver of floods and to use geospatial technology as a tool for building safer and more resilient landscapes.

Keywords: LULC, Geospatial technology, Flood, Urbanization, Agricultural land, Bihar

Abstract No: F9

Integrated Bioinformatics and *In-vitro* Evaluation ofAntimicrobial Leads Against *Edwardsiellatarda*

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ABSTRACT

Edwardsiellatarda is a Gram-negative bacterial pathogen causing edwardsiellosis in several cultured fish species, resulting in high mortality, tissue damage, and major economic losses in aquaculture, particularly in catfish and tilapia farming. The persistence of this pathogen in aquatic environments and its increasing resistance to antibiotics highlight the urgent need for alternative therapeutic strategies. This study aimed to identify and validate novel drug targets in *E. tarda* using an integrated bioinformatics and experimental approach, focusing on the peptidoglycan biosynthesis pathway.Two essential enzymes involved in bacterial cell wall synthesis—D-alanine–D-alanine ligase and UDP-N-acetylglucosamine enolpyruvyl transferase (MurA)—were selected as potential drug targets. Protein sequences were retrieved from the NCBI database, and three-dimensional structures were modeled using Swiss-Model and AlphaFold2. Model quality was assessed using SAVES 6.0, PROCHECK, and ERRAT. Virtual screening of 2,512 compounds from Enamine, NCI, and IMPPAT 2.0 databases was conducted using AutoDock Vina. Protein–ligand interactions were analyzed using Discovery Studio Visualizer. The top three compounds were shortlisted based on binding affinity, drug-likeness, and toxicity predictions and evaluated in vitro against *E. tarda* using minimum inhibitory concentration (MIC) assays.AlphaFold2-generated models exhibited superior structural quality. Citronellal showed the highest binding affinity toward D-alanine–D-alanine ligase (−11.1 kcal/mol), while anthraquinone demonstrated optimal binding to MurA (−7.4 kcal/mol). In vitro assays identified citronellol as the most potent compound, with an MIC of 64 µg/ml, followed by neryl acetate (128 µg/ml) and citronellal (800 µg/ml).Citronellol emerges as a promising antimicrobial lead targeting D-alanine–D-alanine ligase, demonstrating the value of integrating in silico screening with experimental validation for developing alternatives to antibiotics in aquaculture.

Keywords: D-alanine-D-alanine ligase, E. tarda, Anti-bacterial, Citronellol, AlphaFold 2, ERRAT, Enamine, NCBI

Abstract No: F10

Catfish Diversity in Gandak River near Hajipur, Bihar

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ABSTRACT

Catfishes are important benthic scavengers that contribute significantly to freshwater river ecosystems by consuming organic debris and thereby helping to maintain water quality. They also serve as a vital source of high-quality protein for human populations, function as sensitive ecological indicators, and exhibit remarkable tolerance to low dissolved oxygen conditions. In addition to their ecological importance, catfishes support recreational fisheries and are widely used as model organisms in scientific research. In light of these backgrounds, present study assessed the diversity of catfishes in the Gandak River near Hajipur, Bihar. Sampling was conducted over a period of two months from August to September 2025. A total of seven catfish species belonging to one order (Siluriformes), four families, and five genera were recorded during the study period. The family Bagridae was represented by four species viz. *Mystuscavasius, Mystustengara, Mystus vittatus*, and *Sperata aor*. The family Ritidae included *Rita rita*, while Ailiidae was represented by *Clupisomagarua*, and Siluridae by *Wallago attu*. According to the IUCN Red List of Threatened Species, *Mystuscavasius, Mystustengara, Mystus vittatus, Sperataaor, Rita rita, and Clupisomagarua* are categorized as Least Concern (LC), whereas *Wallago attu* is classified as Vulnerable (VU). The findings provide baseline information on catfish diversity in the Gandak River and may aid in future conservation and management strategies.

Keywords: Catfish diversity, Gandak River, Siluriformes, Freshwater fishes, IUCN Red List

Abstract No: F11

Market-Based Assessment of Fish Diversity, Conservation Status, and Economic Importance in Dholi, Bihar

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ABSTRACT

This study presents the first comprehensive assessment of ichthyofaunal diversity at the Dholi fish market in the Burhi Gandak region from January, 2025 to October, 2025**,** documenting 44 fish species across 20 families and 11 orders, primarily sourced from the Burhi Gandak, Bagmati. Order Cypriniformes dominated with 39% of species (15 in Cyprinidae), followed by Siluriformes (21%), reflecting typical patterns in Indian rivers. IUCN statuses indicate 41 species as Least Concern (LC) which is a positive sign of sustainable exploitation, two species are Near Threatened, and *Wallago attu* is Vulnerable which need to be considered. Consumer preferences favor small-sized, fresh fish like *Salmostomabacaila* (Chipwa), prized for flavor and nutrition, offering rich sources of micro nutrient when consumed whole. Seasonal species such as *Setipinnaphasa* and *Cirrhinusreba* peak during monsoons, while low-abundance taxa like *Badis badis* signal potential declines. Indian Major Carps (e.g., *Labeorohita*) and exotics are imported, highlighting local production gaps in the region. Use of fishing gear using cast nets, gillnets, and drag nets, lacking regulatory measures. Among 28 vendors (9 regular fish sellers), daily earnings average ₹5,000–6,000. Market prices span ₹120–1,200/kg, with high-value delicacies like *Macrognathusaral* (₹1,000–1,200/kg) contrasting affordable small indigenous species (₹120–160/kg). Premium carps (*Labeocatla* at ₹330/kg) underscore economic gradients driven by demand, size, and origin. These findings emphasize the market's role in local protein security and livelihoods, urging gear regulations and enhanced local aquaculture for sustainability.

Abstract No: F12

Impact of Habitat Fragmentation and Sedimentation on the Biodiversity of Freshwater Gastropods

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ABSTRACT

This research is to assess how freshwater gastropod populations are being destabilized by the dual threats of habitat fragmentation and rising siltation in river systems. It highlights a chain reaction starting with riparian deforestation, which accelerates soil erosion and blankets the riverbed in excess sediment. This physical alteration is shown to suffocate periphyton the essential food source for grazing molluscs while simultaneously degrading the specific micro-environments required for their spawning and larval survival. By comparing continuous river stretches against those partitioned by barriers, the analysis reveals a marked reduction in biodiversity, characterized by a takeover of hardy, generalist species capable of withstanding poor oxygen levels. Additionally, the research demonstrates that physical obstacles, such as check-dams, sever the connectivity between sub-populations, resulting in genetic isolation due to the inability of species to disperse naturally. Given the vital role these molluscs play in sediment stabilization and nutrient cycling, their depletion threatens the broader aquatic food web. Consequently, the paper argues for the urgent implementation of integrated watershed management and the reinstatement of natural hydrological flows to safeguard the genetic future of these communities.

Keywords: Habitat Fragmentation, Siltation/Sedimentation, Benthic Substrate, Periphyton, Riparian Restoration

Abstract No: F13

Economic Impact of Genomic Technologies on productivity and quality in livestock and aquaculture

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ABSTRACT

Genomic technologies have gained increasing attention in the livestock and aquaculture sectors for their potential to enhance productivity, product quality, and economic efficiency. This review paper synthesizes existing literature on the economic impacts of genomic technologies including genomic selection, marker-assisted breeding, and DNA-based diagnostics on livestock and aquaculture production systems. The focus is on assessing how these technologies influence productivity, cost structures, income generation, and market outcomes. This review indicates that genomic interventions contribute to significant productivity gains by improving growth rates, feed conversion efficiency, disease resistance, and survival rates in animals and fish. These biological improvements translate into economic benefits such as reduced production costs, lower mortality-related losses, and shorter breeding cycles. Enhanced quality traits further enable producers to meet market standards and obtain price premiums, particularly in organized domestic markets and export-oriented value chains. In aquaculture, the application of genomics for disease resistance and stock improvement has been identified as a critical factor in reducing economic risks associated with disease outbreaks. Overall, the review concludes that genomic technologies hold substantial potential to enhance productivity, quality, and sustainability in livestock and aquaculture systems.

Keywords: Genomic technologies, Livestock, Aquaculture, Productivity enhancement, Quality improvement.

Abstract No: F14

Economic impact of advanced processing technologies in animal and fish-based foods

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ABSTRACT

The livestock and fisheries sectors constitute a vital pillar of agri-food systems in developing economies by contributing to food and nutritional security, employment generation, and rural livelihoods. Despite their significance, these sectors continue to face persistent challenges such as high post-harvest losses, quality deterioration, limited processing infrastructure, and weak market integration, which constrain value addition and economic returns. In recent years, advanced processing technologies including chilling and freezing systems, modified atmosphere packaging, bio-preservation, irradiation, and ready-to-eat product processing have emerged as strategic interventions for improving efficiency, product quality, and competitiveness of animal and fish-based food value chains. This review synthesizes existing empirical and policy-oriented literature to examine the economic implications of adopting advanced processing technologies in livestock and fisheries sectors. The analysis focuses on their role in reducing post-harvest losses, enhancing value addition, improving price realization, and strengthening access to domestic and export markets. Evidence from developing and emerging economies indicates that modern processing technologies significantly improve productivity and profitability while stabilizing incomes and generating employment across the value chain. Although high initial capital requirements and operational costs remain major barriers, especially for small-scale processors, the long-term economic benefits consistently outweigh these constraints. The review further highlights the critical role of institutional support, cold-chain infrastructure development, skill enhancement, and targeted policy incentives in facilitating wider technology adoption. Strengthening producer organizations, improving market linkages, and promoting public–private partnerships are identified as key strategies for inclusive growth. Overall, the adoption of advanced processing technologies is essential for building resilient, efficient, and competitive livestock and fisheries value chains, thereby supporting sustainable agri-food system transformation and inclusive economic development.

Keywords: Advanced processing technologies, livestock and fisheries economics, value addition, post-harvest losses, agri-food value chains

Abstract No: F15

Innovative Non-Thermal Approaches for Fish Preservation: Pulsed Electric Field (PEF) Technology

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ABSTRACT

With the current trend of prioritising sustainability, food safety, and minimal processing as key elements in the development of the seafood industry, Pulsed Electric Field (PEF) technology has become one of the potential science-driven solutions for innovative seafood preservation and processing. PEF is a non-thermal processing technique that has immense potential to improve microbial safety as well as preserve the quality of heat-sensitive food components like proteins, omega-3 fatty acids, vitamins and sensory properties. The mechanism operates by applying short bursts of high-voltage electric pulses that cause the electroporation process of the microbial cell membranes, resulting in the subsequent effective microbial inactivation without producing the adverse impacts of thermal processing. PEF maintains the nutritional and organoleptic characteristics of seafood products due to its ability to operate at near-ambient temperatures. In treatment, the food materials are put into a controlled chamber with electrodes and optimisation of electrical parameters like the intensity of voltage, the length of pulse and electrode spacing to permeabilize the cell membranes and improve mass transfer. This mechanism accelerates the diffusion of salts, water, and solutes during processes such as salting, marination, and drying, thereby reducing processing time and energy consumption. Moreover, the industrial utility of PEF can be increased by synergistic combination with the newly developed technologies, such as enzymatic hydrolysis, cold plasma, ultrasound, and rapid solvent extraction. Its green features, especially in terms of low energy and water consumption, are in line with the objectives of food processing sustainability. The abstract highlights the fact that, PEF has significant potential to enhance texture, shelf life, food safety, and to extract value-added bioproducts, which makes it a key technology in the next-generation, sustainable seafood processing systems.

Keywords: Pulsed Electric Field, sustainable seafood preservation, non-thermal processing, electroporation, microbial inactivation, Shelf-life extension

Abstract No: F16

Climate-Resilient Fisheries Management Strategies for Beels of the Gangetic Plains

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ABSTRACT

Beels, seasonally inundated floodplain wetlands and oxbow lakes of the Gangetic Plains, are among the most productive inland open water ecosystems in South Asia, supporting rich fish biodiversity and sustaining thousands of small-scale fishing households. However, accelerating climate change is altering the hydrological and ecological foundations of these wetlands. Rising temperatures, erratic monsoon patterns, shortened hydroperiods, and increasing frequency of extreme flood and drought events are disrupting river-wetland connectivity, modifying nutrient dynamics, and affecting fish breeding cycles. These changes have led to shifts in species composition, reduced recruitment success of Indian Major Carps, proliferation of hardy and invasive species, and growing instability in fish yield.

This abstract outline a comprehensive framework for climate-resilient fisheries management tailored to beels of the Gangetic Plains. The approach integrates hydrological restoration, climate-smart stocking strategies, habitat and biodiversity conservation, participatory co-management, and climate information systems. Emphasis is placed on maintaining ecological connectivity, protecting spawning refugia, promoting indigenous climate-tolerant species, and strengthening community-based governance institutions. The framework further advocates for the incorporation of wetland fisheries into state climate adaptation plans, disaster risk reduction strategies, and ecosystem-based management policies.

By aligning ecological sustainability with livelihood security, climate-resilient management can enhance adaptive capacity while safeguarding biodiversity and fishery productivity. The abstract underscores the need for interdisciplinary research, long-term ecological monitoring, and policy convergence to ensure that beel fisheries remain viable under emerging climate uncertainties. Strengthening resilience in these floodplain systems is not only critical for regional food and nutritional security but also essential for sustaining the socio-ecological integrity of the Gangetic basin.

Keywords: Beel fisheries, Climate resilience, Floodplain wetlands, Ecosystem-based management, River-wetland connectivity, Adaptive co-management

SPBB-SPRINGER YOUNG SCIENTIST AWARD-2026

Abstract No: SSA1

Molecular Dissection of CcCEN-like 2 Reveals Its Key Role in Floral Transition and Plant Architecture in Pigeon Pea

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ABSTRACT

Pigeon pea (Cajanus cajan L.) is a climate-smart, protein-rich pulse crop; however, indeterminate growth habit and non-synchronous flowering pose major challenges to yield stability and breeding efficiency. Deciphering the molecular regulation of floral transition is therefore critical for developing determinate and early-flowering ideotypes under changing climatic conditions. In the present study, a genome-wide comparative genomics approach was employed to identify floral pathway orthologs in pigeon pea. A total of 412 floral orthologs were identified, including 148 genes associated with floral meristem identity, photoperiod, and circadian clock pathways. Evolutionary analyses revealed strong purifying selection (Ka/Ks) and restricted gene duplication, supported by synteny analysis. Phylogenetic analysis of phosphatidylethanolamine-binding protein (PEBP) family members indicated a close association between flowering regulation and plant architecture. Expression profiling in contrasting determinate and indeterminate genotypes highlighted CcCEN-like 2, an anti-florigen paralog closely related to Arabidopsis AtTFL1 and tomato SP5G, as a key regulator. Constitutive overexpression of CcCEN-like 2 in tobacco resulted in delayed flowering (26–32 days), pronounced vegetative growth, and reduced reproductive output, accompanied by strong down-regulation of floral inducer genes APETALA1 and LEAFY. Conversely, RNAi-mediated silencing of CcCEN-like 2 in pigeon pea produced compact phenotypes with reduced vegetative vigour, confirming its role as a floral repressor. Collectively, these findings establish CcCEN-like 2 as a pivotal regulator of floral transition and plant architecture and highlight its potential as a molecular target for breeding determinate pigeon pea cultivars.

Keywords : Pigeon pea; Flowering time regulation; Anti-florigen; CEN/TFL1; PEBP family; Climate-resilient breeding

Abstract No: SSA2

Integrative genome-wide association, transcriptome, and metabolome analyses identify genetic determinants of high total soluble solids in Onion (Allium cepa L.)

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ABSTRACT

The dehydration industry requires onion cultivars with high total soluble solids (TSS=15 °Bx) to ensure superior processing quality. In this study, we employed an integrative genomics approach to identify genetic determinants underlying TSS variation in onion. Genotyping-by-sequencing (GBS) generated 7,734 high-quality SNPs, which were analyzed using multiple GWAS models (GLM, MLM, MLMM, FarmCPU, and BLINK). A highly significant SNP, SCAJJJL010074204.1_52690, was consistently associated with TSS content and explained up to 65% of the phenotypic variation. Integration of GWAS results with transcriptome profiling of high-TSS (HTSS) and low-TSS (LTSS) lines revealed that the SNP co-localized with two differentially expressed transcripts, E1.U.164657 and E1.U.58798, encoding ATP synthase subunit alpha. Genes within the ±50 kb flanking region showed strong upregulation in HTSS lines, including DNA/RNA polymerases, myosin-kinesin ATPases, pentatricopeptide repeat proteins, heat shock protein 70, plastidal glycolate/glycerate translocator, and electron transfer flavoprotein subunit beta. RNA-seq analysis further indicated enhanced expression of ATP synthase (26 genes) and carbohydrate metabolism–related genes (65 genes) in HTSS lines. Metabolomic profiling corroborated these findings, revealing elevated carbohydrate metabolism in HTSS genotypes. Collectively, the SNP SCAJJJL010074204.1_52690, ATP synthase subunit alpha–encoding transcripts, and elite HTSS lines (S74, S75, and S76) represent valuable resources for onion improvement. These findings provide strong targets for marker-assisted selection and suggest that targeted genome editing to convert the C allele to the T allele at this SNP locus may further enhance TSS and processing quality in onion.

Keywords: high total soluble solid content (HTSS); low total soluble solid content (LTSS), genotyping-by-sequencing (GBS), carbohydrate metabolism, chloroplast ATP synthase, SNP, transcriptome

Abstract No: SSA3

Over-expression of AtMYB12 transcription factor improves flavonol content and salt stress tolerance in transgenic soybean (Glycine max (L.) Merrill)

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ABSTRACT

Soybean (Glycine max (L.) Merrill) belongs to Fabaceae family, contains 40% proteins and 20% oil. In the present study, the AtMYB12 transcription factor was cloned into pCAMBIA 1301 and introduced into soybean cv. JS335 using Agrobacterium tumefaciens strain EHA105 to improve flavonol content and enhances salt tolerance. The putative transformants showed gus expression in mature leaves, trifoliate leaves, and stem. The presence of AtMYB12 was confirmed through PCR, resulting in an amplicon size of 786 bp. The seeds of transgenic plants exhibited significantly higher levels of total phenolics, flavonoids, antioxidant activity compared to the non-transformed plants HPLC analysis confirmed increased rutin (1.5-fold) and quercetin (1.3-fold) in AtMYB12-transformed seeds. transgenic soybean plants exhibited successful integration of the AtMYB12 transgene, resulting in significantly elevated expression of key flavonol biosynthetic genes across different seed developmental stages. Furthermore, the study aimed to enhance salt tolerance in soybean by overexpressing AtMYB12. The transgenic plants subjected to salt stress exhibited significant improvements in morphological features, photosynthetic pigments, and leaf relative water content compared to non-transformed plants under salt stress. Over-expression of AtMYB12 mitigated membrane damage, increased enzymatic antioxidant activities, osmoprotectants, polyphenolics, flavonoids, and upregulated genes associated with flavonol biosynthesis, abscisic acid biosynthesis, proline biosynthesis, and ion transport mechanisms under salt stress conditions. These findings underscore the potential of AtMYB12 in mitigating salt stress and enhancing soybean resilience. Overall, AtMYB12 emerges as a promising candidate for simultaneously improving flavonol content and salt tolerance in soybean.

Key words : Soybean; AtMYB12; Over-expression; Flavonols; Salt stress

Abstract No: SSA4

Metabolite and Enzyme-Based Characterization of Rancidity Behaviour in Pearl Millet Flour for Nutritional Evaluation

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ABSTRACT

Pearl millet (PM), recognised as a nutrient-rich and climate-resilient nutri-cereal, continues to gain attention for its health benefits. Yet, its wider use is limited by rapid rancidity in stored flour. To understand this issue, we evaluated contrasting PM genotypes and examined the biochemical determinants of rancidity. A positive association was observed between linoleic acid content and lipoxygenase (LOX) activity, confirming their central role in rancidity development. Total phenolic content (TPC) also showed a positive correlation with polyphenol oxidase (PPO) and peroxidase (POX) activities, both of which contribute to browning and influence antioxidant behaviour. Significant variations were further identified in C-glycosyl flavones, compounds responsible for off-flavour formation and colour changes. The study also assessed the effectiveness of physical treatments in suppressing rancidity-inducing enzymes and their impact on nutritional quality. Hydrothermal treatment was most effective in reducing enzymatic activity, but it also reduced phenolics, flavonoids, and antioxidant potential. In contrast, microwave and infrared treatments enhanced these nutritional attributes. Nutritional characteristics varied markedly across treatments. Hydrothermal processing, while effective in lowering rancidity, altered starch digestibility by reducing rapidly digestible starch (RDS) and increasing slowly digestible starch (SDS) and resistant starch. However, it also reduced the bioaccessibility of phenolics and essential minerals, such as iron and zinc, compared with microwave and infrared methods. Overall, the results highlight the value of biochemical markers for selecting low-rancidity PM lines and provide insights into optimising processing strategies. These findings support the development of minimally rancid, nutritionally superior pearl millet flour for researchers and food processing industries.

Keywords: C-glycosyl flavones, Micronutrients, Lipoxygenase, Rancidity, Shelf-life

Abstract No: SSA5

Genomic evidence identifies TFL1 as a key regulator of flowering and determinacy in Pigeonpea

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ABSTRACT

Pigeonpea exhibits substantial diversity for days to flowering (DTF) across its germplasm collections. Its major varieties are of medium to late maturity duration and possess higher yield potential than early-flowering genotypes. Although yield and floral induction are not mutually exclusive, they are governed by independent genetic pathways. Identification of genes/markers regulating flowering time could therefore facilitate the development of early-maturing, high-yielding pigeonpea varieties with minimal yield penalty. We employed integrated genomics approaches, including GWAS, QTL mapping, QTL-seq, and expression profiling, to identify genomic regions/markers associated with DTF and determinacy in pigeonpea. Phenotypic analysis of an F_2 population derived from an early × late flowering cross revealed linkage between DTF and determinacy, with determinacy showing monogenic inheritance. QTL mapping identified eight QTLs for DTF and four QTLs for determinacy. Concurrently, QTL-seq analysis detected a major linked QTL for both traits on chromosome 3, harbouring a 10 bp deletion in the first exon of the *TERMINAL FLOWER 1 (TFL1)* gene. Comparative analysis revealed two common QTL regions on chromosomes 3 and 10 across QTL mapping and QTL-seq approaches. Association analysis of these QTL regions identified 18 robust marker–trait associations supported by strong linkage disequilibrium. Based on Arabidopsis ortholog annotations, 78 candidate genes were prioritised that clustered into autonomous, photoperiodic, and epigenetic regulatory pathways upon protein-protein interaction analysis. Fine mapping using a *TFL1*-specific deletion marker and six new SSR markers narrowed the major QTL on chromosome 3 to a 243,363 bp interval, explaining 36.47% of the phenotypic variance. Expression analysis indicated that the *TFL1* deletion disrupts protein function rather than transcript abundance, leading to determinacy and altered flowering time. Overall, the *TFL1* gene-specific deletion represents a key genetic determinant of flowering time and growth habit in pigeonpea and provides a valuable functional marker for marker-assisted breeding.

Keywords: Days to flowering, Determinacy, GWAS, Pleiotropic gene, TFL1

Abstract No: SSA6

Metabolic Drivers of Rancidity-Induced Bitterness in Pearl Millet Flour

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ABSTRACT

Pearl millet (Pennisetum glaucum) flour is highly susceptible to rapid hydrolytic and oxidative rancidity, leading to early bitterness development and reduced shelf life, which limits its consumer acceptance and industrial utilization. The present study employed an integrated, multi-scale analytical framework to elucidate metabolite drivers underlying rancidity-associated bitterness. Flour samples prepared from a composite of twelve pearl millet genotypes were aged under dark household-like conditions for up to 30 days after milling. Biochemical indices confirmed progressive rancidity development, while untargeted UHPLC-HRMS-based metabolomics revealed extensive storage-induced metabolic reprogramming. Comparative analysis identified 110 differentially expressed metabolites associated with ageing, predominantly linked to lipid hydrolysis, oxidation, and secondary degradation pathways. Notably, storage led to the accumulation of bitterness-associated metabolites including medium-chain and oxidized fatty acids (e.g., hexanoic acid, nonanoic acid, 9-oxo-onanoic acid), lipid-derived aldehydes and ketones, and phenolic degradation products. To establish sensory relevance, these metabolites were subjected to structure-based molecular docking against the broadly tuned human bitter taste receptor TAS2R14, followed by ligand efficiency scoring and interaction fingerprinting to resolve receptor–ligand interaction patterns. This integrative filtering strategy refined the metabolite space to a focused panel of 15 high-confidence bitterness-linked markers, including oxidized fatty acids and phenolic derivatives exhibiting favorable binding energies and conserved interaction fingerprints within the TAS2R14 binding pocket. Collectively, the study bridges biochemical confirmation with metabolomics-driven molecular interaction analysis to provide mechanistic insight into rancidity-induced bitterness in pearl millet flour. The proposed workflow offers a robust framework for identifying sensory-relevant rancidity markers and advancing shelf-life evaluation in cereal-based food systems.

Keywords: Rancidity; Bitterness; Pearl millet flour; Metabolomics; TAS2R14 docking; Interaction fingerprinting; Lipid oxidation metabolites

Abstract No: SSA7

Transcriptomics Decoding of Desiccation Tolerance and Host Exploitation in Anguina tritici

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ABSTRACT

Transcriptome profiling of anhydrobiotic, revived, and adult stages of the wheat seed gall nematode Anguina tritici revealed key molecular mechanisms underlying desiccation tolerance and host parasitism. Using Illumina NovaSeq 6000 sequencing, high-quality read alignments were obtained from all samples, resulting in a robust draft transcriptome. The combined final assembly spanned 133.2 Mb, comprising 105,606 transcripts, representing a substantial genomic resource for understanding stress adaptation and pathogenicity in this nematode. Functional annotation and pathway enrichment highlighted the MAPK, mTOR, FoxO, and longevity-regulating pathways as central components of stress adaptation and developmental regulation. Genes linked to stress response and survival, including heat shock proteins, peroxisomal catalase, nuclear hormone receptor domains, and homologues of DAF-2 and DAF-21, indicate conserved mechanisms associated with dauer formation, oxidative stress mitigation, and metabolic regulation. Critical signaling components such as MPK-1, RSKN-1, and RAC serine/threonine kinase further emphasize coordinated cellular responses to dehydration. Effector analysis identified proteins associated with pathogenicity, including 14-3-3 proteins, SNARE-like proteins, laminin-like proteins, pectate lyase, and glycoside hydrolase family 18 enzymes, suggesting roles in host cell wall degradation, intracellular trafficking, nutrient acquisition, and host invasion. Differential expression analysis demonstrated stage-specific upregulation of stress-responsive genes during anhydrobiosis and developmental/metabolic genes in adults, with qRT-PCR validation confirming transcriptomic trends.

Together, these findings provide a comprehensive molecular framework for understanding anhydrobiosis and parasitism in A. tritici, and identify potential genetic and signaling targets for nematode management and crop protection strategies. Keywords: Wheat seed gall nematode, Anhydrobiosis, Transcriptome, Parasitism

Theme: Plant Metabolomics & Systems Biology

Objective: To understand the bionomics of the nematode, including life cycle duration and above ground parasitism in relation to wheat growth. To investigate the biorhythm and survival strategies of Anguina tritici, the wheat seed gall nematode, particularly its exceptional ability to survive for decades in a dormant (anhydrobiotic) state. To generate and analyze the first transcriptome assembly of A. tritici in order to identify genes and pathways associated with parasitism, stress tolerance, and longevity.

Methodology

Seed galls of wheat infected with Anguina tritici were collected, and second-stage juveniles (J2) were isolated for biological and molecular studies. Bionomic observations were conducted to understand the nematode's life cycle, host–parasite synchronization, and the influence of growing degree days on development. The survival strategy of the nematode in the anhydrobiotic J2 stage within seed galls during the off-season was also examined. For molecular analysis, nematode samples representing active and anhydrobiotic stages were prepared, and total RNA was extracted, followed by quality and quantity assessment. High-quality RNA was used for library preparation and transcriptome sequencing using the Illumina NovaSeq platform. Raw sequence reads underwent quality control, adapter trimming, and filtering to obtain clean reads. De novo transcriptome assembly was performed to generate the final transcript dataset, which was evaluated using BUSCO against the Nematoda database to assess completeness. Functional annotation of assembled transcripts was carried out using sequence similarity searches, Gene Ontology classification, and KEGG pathway mapping. Differential gene expression analysis was performed to identify stage-specific genes. Further analysis was focused on identifying genes and pathways associated with parasitism, survival, and stress tolerance.

Key Findings

The study revealed that the life cycle of Anguina tritici ranges from 90 to 140 days or longer, closely synchronized with wheat growth and influenced by growing degree days. The nematode survives adverse off-season conditions in the anhydrobiotic J2 stage within seed galls, enabling long-term persistence. The first transcriptome assembly of A. tritici generated 133.2 Mb of sequence data comprising 105,606 transcripts, with 80.3% completeness based on BUSCO analysis. Functional annotation and differential expression analysis identified genes encoding glycolases, lyases, hydrolases, 14-3-3 proteins, and SNARE-like effectors, which are associated with aboveground parasitism in wheat stem pith, floral primordia, and seed endosperm tissues. Homologues of CBR-DAF-2 and CBR-DAF-21 suggest the involvement of dauer formation and longevity pathways in survival. Additionally, key stress-related signaling pathways, including MAPK, ErbB, FoxO, and mTOR, were identified, with heat shock proteins and protein kinases playing central roles in stress tolerance. Overall, the study provides foundational molecular insights into the parasitic adaptation and long-term desiccation survival mechanisms of A. tritici

Abstract No: SSA8

Enhancing Helicoverpa armigera resistance in Potato through RNAi-Bt combinatorial approach

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ABSTRACT

Helicoverpa armigera (Lepidoptera: Noctuidae) is a major agricultural pest causing severe yield losses.Excessive reliance on synthetic insecticides has led to resistance, pest resurgence, environmentalconcerns, and risks to human and non-target health. Although Bt crops provided initial success, resistantstrains emerged, necessitating alternative strategies such as host-delivered RNAi (HD-RNAi) andchimericBt proteins. This research aimed to evaluate a combined approach using a construct containinga chimeric Bt protein, Cry1AcF, derived from domain swapping, and artificial microRNA (multi-amiRs)targeting key insect genes, acetylcholinesterase1 (Ace1) and 20-hydroxy ecdysone receptor (EcR),crucial in signal transduction and molting in H. armigera. Potato crop underwent transformation usingthe pCAMBIA2300::multi-amiR+Bt vector through Agrobacterium-mediated genetic transformation,followed by analysis to confirm transgenic nature and efficacy against H. armigera. The confirmationprocess involved various molecular analyses like PCR and RT-PCR amplification using gene-specificprimers, Southern blotting for gene integration, northern blotting for amiRNA expression, and lateralflow strip (LFS) Test for Bt protein expression. Short-duration bioassays with second-instar larvaerevealed significant damage and increased mortality rates among larvae fed on transgenic lines.Extended bioassays till the pupal stage demonstrated notable growth retardation, abnormal development,prolonged pupal stage, and reduced weights in larvae and pupae fed on transgenic leaves. Adultsoriginating from transgenic lines exhibited substantial deformities, especially in wing structures,affecting their mobility and flight capabilities. Real-time PCR analysis demonstrated significantsuppression of target genes in larvae, pupae, and adults fed on potato transgenic leaves. Additionally,certain larvae that died during the bioassay, displaying disrupted midgut tissues, were directly linked tothe expression of the Cry1AcF gene present in the transgenic lines. Therefore, the current studyrevealed a substantial impact of Multi-amiR+Bt on controlling H. armigera, demonstrating its potentialas an immensely valuable approach for establishing durable resistance against insect pests in otherimportant crops.

Keywords: Helicoverpa armigera, Bt protein, Potato, RNAi, durable resistance

Abstract No: SSA9

Phenotypic and anatomical validation of tomato grafts compatibility with differentsolanaceous rootstocks

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ABSTRACT

Grafting plays an essential role in tomato for improving the crops resilience to biotic stresses and abiotic stresses, which results in the higher yields and healthier plants. Grafting allows to use resistant rootstocks to overcome soil borne diseases like bacterial wilt and adverse environmental conditions, thereby providing the sustainable production. This study investigates the compatibility of tomato cv. Sahoo as scion with selected solanaceous rootstocks, emphasizing graft union success, grafted seedlings vigour and subsequent plant performance. The experiment was conducted during the rainy winter season of 2024-25 by adopting the cleft grafting method. The experiment was laid down with completely randomized design with 26 different rootstocks in 3 replications and the traits like plant height, number of total roots, root length, percentage of graft compatibility and plant vigour index were recorded after 15 days of grafting. Sahoo grafted onto the Bluestar rootstock significantly recorded the highest percentage of graft compatibility (91.30 %) followed by Solato (85.10 %), Solmel (81.93 %) and Utkal Anushree (80.70 %). The lowest percentage of graft was seen in tomato rootstocks Saksham (3.03 %), Utkal Kumari (3.63%), Utkal Jyoti (5.70 %) and in chilli rootstocks also less graft compatibility was recorded. Although Yodha (16.93 cm) and Sbjh-5005 (16.67 cm) recorded the highest grafted height but the graft compatibility is less. Maximum number of total roots (94.33) was observed in Solmel and the highest root length (20.70 cm) and plant vigour index (2421.28) was recorded in Solato grafted with Sahoo. Along with these traits microscopic examination revealed that active callus formation that are differentiating into new vascular tissue leads to successful union of the grafts which is mostly seen in between the brinjal rootstocks and tomato scion. Different important statistical tools such as PCA, combine correlation and clustering with heatmap analysis justified the consideration of traits & genotypes and supported selection of genotypes for grafting in tomato for controlling bacterial wilt and increasing productivity.

Keywords : Grafting, rootstock-scion compatibility, microscopic examination, bacterial wilt, low moisture stress

Abstract No: SSA10

Effect of Non-Thermal Pretreatment and Convective Drying on Bioactive Compounds, Antioxidant Capacity, Microstructure, FTIR, and Sensory Quality Attributes of Litchi

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Abstract

This study optimized ultrasound-assisted osmotic dehydration (USOD) of litchi quarters using response surface methodology with a Box-Behnken design to maximize water loss and minimize solid gain. Independent variables were ultrasound amplitude (20-40%), sonication time (10-30 min), and sucrose concentration (20-60% w/w), using a 4:1 solution-to-fruit ratio. Water loss and solid gain ranged from 8.45-28.87% and 2.17-6.73%, respectively. Optimal conditions (34.79% amplitude, 30 min, 40% sucrose) predicted 23.76% water loss and 3.89% solid gain, with second-order regression models showing good fit. The effect of USOD pretreatment followed by convective drying at 60°C was evaluated in comparison with untreated samples. USOD-pretreated samples showed significantly ($P < 0.05$) higher lightness (L^* 46.69), lower moisture content (11% dry basis) and water activity (0.40), greater phenolic retention (10.72 mg GAE/g DW), higher flavonoid content (3.17 mg QE/g DW), and enhanced DPPH scavenging activity (65.47%). In addition, these samples exhibited significantly ($P < 0.05$) lower hardness (4.7 N), higher rehydration ratio (2.89), lower shrinkage (72.13%), and superior sensory acceptability (7.4). Scanning electron microscopy revealed noticeable microstructural alterations in USOD-pretreated samples compared with fresh and control samples, while FTIR analysis confirmed greater antioxidant retention in USOD-pretreated dried litchi quarters.

Keywords: Litchi, Ultrasound assisted osmotic dehydration, Total Phenolic Content, Total Flavonoid Content, DPPH scavenging activity, SEM, FTIR.

Abstract No: SSA11

Screening for low phosphorus tolerance and nitrogen use efficiency in rice biparental population under acidic soil of North Eastern Hill Region

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ABSTRACT

Soils in North-East India are acidic with metal toxicity and macro nutrient deficiencies specially for nitrogen (N) and phosphorus (P). This necessitates identification of genotypes and molecular targets which would impart high yield in a sustainable manner. Hence, in present study, we evaluated a biparental population ULRC36 (Shahsarang x KMR3) for two seasons (F 10 , F 11) under acidic lowland and upland (approx. pH 5.4) conditions. The experiment was carried out under low phosphorus and low nitrogen condition in augmented randomized complete block design with five blocks and nine checks. The morphological traits like tiller number at 60DAT (TN60), plant height (PH), number of tillers (TN), number of panicles (PN), length of the panicle (PL), panicle weight (PW), biological yield (BY) and grain yield per plant (GYPP) were recorded. Traits like BY (0.92), PN (0.58) and PW (0.58) were found highly correlated with GYPP at 0.1% level of significance. Based on yield contributing traits, 15 lines representing two extreme pools viz. superior (12.43-23.93g of GYPP) and inferior lines (1.77-3.40g of GYPP), were screened for low P tolerance and nitrogen use efficiency by exposing seven days old seedlings for 14 days using modified Yoshida solution with four treatments and three replications. Parameters like root length, shoot length, root fresh weight, shoot fresh weight, root dry weight and shoot dry weight were recorded on both normal and treated seedlings on 14 th day of treatment. ULRC36-68, ULRC36-103-1 and ULRC36-263-2 were identified as superior performing lines both under hydroponics and field evaluation. A set of 43 gene based molecular markers were used to check allelic status, out of which 11 markers were found polymorphic. Marker trait association revealed association of markers RM12550, RM12557, RM12558, FR033-3, RM13209 and RM1365 with yield contributing traits under lowland, upland and hydroponics conditions. The markers and the superior performing lines identified can be used for crop improvement program to achieve high grain yield under nutrient deficient conditions.

Key words: Acidic soil, Allelic status, Rice

Abstract No: SSA12

A MYB96-SWEET15 regulatory module contributes to drought stress adaptation in Arabidopsis thaliana

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ABSTRACT

MYB transcription factors (TFs) are among plants' most prominent gene families, conserved across plant lineages from simple algae to complex dicots. AtMYB96, an R2R3-MYB TF binds to the MYB-recognition element (MREs) in the target gene's promoter and regulates the expression. Drought is the most prevalent abiotic stress among others and negatively impacts plant productivity and yield. Our study focused on the functional characterization of AtMYB96 and its regulation of the sugar transport target SWEET15 in enhancing plant stress tolerance. The expression analysis showed substantial induction of MYB96 expression under drought and abscisic acid treatment. To support this, the promoter activity of AtMYB96 was observed to increase GUS expression under PEG-induced stress, especially in guard cells. The generated AtMYB96 OE lines exhibited dwarf and reduced lateral root phenotypes, as well as hypersensitivity to ABA. The AtMYB96 OE lines displayed a high survival rate in drought at the vegetative stage, whereas the mutant was more drought-susceptible. The efficient photosynthetic machinery (evidenced by high Phi2) and reduced reactive oxygen species in OE lines under drought stress support the crucial role of AtMYB96 in enhancing drought tolerance. We performed metabolomic analysis, which revealed elevated levels of sugars in OE lines. Transcriptomic analysis and whole-genome binding site scanning were performed, revealing significant expression of sugar transporters, particularly SWEET15. The confocal imaging showed plasma membrane localization of the gene. The TF-target validation experiments, including EMSA, ChIP, and transactivation assays, revealed that MYB96 directly binds and activates the SWEET15 gene. Additionally, the drought experiment showed that drought sensitivity and ABA insensitivity in the sweet15 mutant were the same as those observed in the myb96 mutant. Overall, the results indicate that AtMYB96 activates its downstream target, SWEET15, potentially increasing sugar content and enhancing drought resilience in the plant.

Keywords: Drought, Transcription factor, MYB TF, Sugar transport, TF-target

Abstract No: SSA13

Genetic Dissection of Root Architecture and Acid Phosphatase Activity Underlying Phosphorus-Use Efficiency in Indian Mustard (*Brassica juncea* L. Czern& Coss)

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ABSTRACT

Phosphorus (P) deficiency remains a major constraint to crop productivity and nutritional security, particularly under climate-induced limitations on fertilizer use. Indian mustard (*Brassica juncea* L. Czern& Coss), a key oilseed crop of India, exhibits low phosphorus-use efficiency (PUE), and the genetic coordination between root-mediated phosphorus acquisition and internal phosphorus utilization is not fully understood. The present study elucidates the integrated role of root architectural traits and acid phosphatase activity in governing PUE in Indian mustard using combined phenotypic and genomic approaches. A diversity fixed foundation set comprising 280 genetically diverse genotypes was evaluated under three phosphorus regimes-low (5 µM), normal (250 µM), and high (1 mM)-in a controlled hydroponic system. Phosphorus limitation induced pronounced modifications in root system architecture, including increased total root length, root volume, lateral root proliferation, and a 52-56% increase in root-to-shoot ratio, reflecting enhanced exploratory capacity under P stress. Simultaneously, phosphorus deficiency led to a 67% increase in root acid phosphatase activity and a 58% increase in leaf acid phosphatase activity, indicating enhanced phosphorus mobilization and internal recycling. Across all phosphorus levels, leaf acid phosphatase activity consistently exceeded root activity, highlighting the predominance of intracellular phosphorus remobilization in sustaining growth under P stress. Genome-wide association analysis using 3,72,285 SNP markers identified 44 significant marker-trait associations across 14 genomic regions, several of which were common to both root architectural traits and acid phosphatase activity. Functional annotation revealed candidate genes associated with phosphorus hydrolysis, root development, and nutrient signaling, including purple acid phosphatases, phospholipases, and auxin-responsive regulators. Based on combined root and biochemical efficiency, JM-06016, IM-170, Kranti, and JT-1 were identified as phosphorus-efficient genotypes. Overall, integrating biochemical traits with GWAS elucidates key molecular mechanisms underlying phosphorus-use efficiency in mustard and provides robust genomic targets for marker-assisted breeding to reduce fertilizer dependence and enhance nutritional security under climate change.

Keywords : *Brassica juncea*; Phosphorus-use efficiency; Root architecture; Acid phosphatase; GWAS

Abstract No: SSA14

Design and Field Validation of Synthetic Microbial Communities to Improve Wheat Growth and Yield

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ABSTRACT

The agricultural biologicals market, growing at a CAGR of over 8%, is projected to reach $4.5 billion by 2032. Microbiome research is enhancing plant-microbe interactions to increase plant nutrition through various mechanisms. Manipulating these microbes through pairwise community construction followed by integration with non-microbial biostimulants can significantly improve crop nutrition and protection. In this study, significant plant growth-promoting traits (PGPts) and community-forming traits (CFts) were identified among selectedmorphotypes. Out of 292 isolates, 40, 81 and 57 were screened for nitrogen fixation, phosphorus, and potassiumsolubilization, respectively. Among other nutrients, zinc and calcium solubilization were noted in 31 and 63 isolates, respectively. In community forming characteristics out of 292 isolates 55were showing positive for EPS production, in motility 234 isolates were showing positive for motility test and 83 were good performers, whereas for biofilm 39 isolates were performed better and 24 isolates were better in PHB production. Synthetic microbial communities (SMs) were constructed by identifying key abundant genera (Ab) from submitted metagenomic data. Four SMs were developed: SM1 (PGPtisolates+Ab), SM2 (CFtisolates+Ab), SM3 (both traits' isolates+Ab), and SM4 (both traits only). Non-microbial biostimulants, Humic Acid (HA) and Seaweed Extract (SWE), were integrated at optimal concentrations of 0.2% and 1%, respectively.Field experiments confirmed enhancements in shoot length, flag leaf length, productive tillers, and earhead length in SM3+HA.SM3+HA found 34% increase in the plant biomass compared to the negative control followed by SynBio of SM1 and SM4 with HA. Photosynthetic rate and chlorophyll content were also significantly improved. Whereas yield was increased by 24.87% in SM3+HA compared to the RDF. Metagenome analysis revealed shifts in rhizospheric soil diversity with the treatments having key abundant genera, and maximum diversity was observed with SM3. This study underscores the potential of synthetic microbial communities integrated with biostimulants to enhance plant growth, offering a sustainable agricultural approach.

Keywords: Community, Plant growth promoters, Microbiome, Biostimulant, Biofertilizer

Abstract No: SSA15

Genomics-assisted development of novel quality protein popcorn hybrids through marker-assisted introgression of *o2* and *o16* genes and their differential effects on phenotype and quality

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ABSTRACT

Popcorn, is a high-value specialty cornhighly favored for popping quality, whole-grain nutritional properties, and low glycemic index. Globally, the popcorn market was valued USD 14.12 billion in 2024, with substantial popularity as a healthy, ready-to-eat snack. Despite its potential, its endosperm protein, like other maize types, is nutritionally inferior due to predominance of lysine and tryptophan-deficient zeins. Moreover, genetic improvement in popcorn remains constrained, as enhancement of nutritional quality is a complex and challenging process that must simultaneously preserve endosperm hardness and popping quality. These limitations have resulted in development of only limited number of nutritionally superior hybrids and increased import dependence. Therefore, genomics-assisted introgression of *opaque2* (*o2*) and *opaque16* (*o16*) genes was employed for nutritional enhancement of superior popcorn hybrids *viz*., Pusa Popcorn Hybrid-1 and Pusa Popcorn Hybrid-2. With the use of flint donors (*o2o2/o16o16*), simultaneous selection for high endosperm modification was emphasised to recover popcorn-like fully poppable kernels with highly vitreous and hard endosperm. The two-backcross generation marker-assisted backcross breeding involved foreground selection for *o2* and *o16*, and background selection for recovery of recurrent parent genome, using whole-genome distributed simple sequence repeat markers. This multifaceted selection resulted in identification of *o2* and *o16* lines, with high background recovery (>95.30% in BC_2F_2) and fully recovered popping quality, kernel vitreousness, and hardness. The study identified differential effects of *o2* and *o16* on lysine, tryptophan and endosperm hardness. The enhanced inbred lines showed a substantial improvement in nutritional quality, with average lysine content increased by 2.78-fold (*o2o216o16*), 1.99-fold ($o2o2o16^{+}o16^{+}$), and 1.68-fold ($o2^{+}o2^{+}o16o16$), and tryptophan: 3.49-fold (*o2o216o16*), 2.35-fold ($o2o2o16^{+}o16^{+}$), and 1.98-fold ($o2^{+}o2^{+}o16o16$). Similarly, the hybrids exhibited enhanced average

lysine and tryptophan levels (.89-fold (*o2o216o16*), 2.09-fold ($o2o2o16^{+}o16^{+}$), 1.80-fold ($o2^{+}o2^{+}o16o16$), and 3.84-fold (*o2o216o16*), 2.56-fold ($o2o2o16^{+}o16^{+}$), and 2.21-fold ($o2^{+}o2^{+}o16o16$). The nutritionally enhanced hybrids have significant potential in addressing malnutrition, reducing import dependence, and new varietal development.

Keywords: popcorn, *opaque2*, *opaque16*, nutritional improvement, marker-assisted introgression, specialty corn breeding

Abstract No: SSA16

Brassinosteroid-Regulated Physiological and Transcriptomic Networks Confer Heat Stress Tolerance in Finger Millet

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ABSTRACT

Escalating global temperatures associated with climate change are increasingly threatening crop productivity, particularly in climate-resilient yet underexploited cereals such as finger millet (*Eleusine coracana* L.), which are vital for food and nutritional security in semi-arid regions. Developing mechanistically informed approaches to enhance thermotolerance is therefore essential. This study systematically examined the physiological, developmental, and transcriptomic responses of the finger millet genotype RAU 8 to acute heat stress and assessed the effectiveness of seed priming with the 24-epibrassinolide (EBR). Heat stress screening identified 45 °C for 3 h as a critical lethal threshold, resulting in severe disruption of cellular homeostasis and approximately 90% mortality within 5-7 days. In contrast, EBR-primed seedlings showed significantly improved survival, maintained leaf turgidity and chlorophyll stability, and exhibited reduced heat-induced injury, while growth under non-stress conditions remained unaffected. EBR treatment also enhanced root system architecture, characterised by increased primary root elongation, greater lateral root density, and sustained root vigour, thereby supporting improved water and nutrient acquisition under heat stress. Transcriptome profiling revealed extensive EBR-mediated reprogramming of the heat stress response. Compared with heat-stressed controls, EBR-treated seedlings displayed increased transcriptomic complexity, improved de novo assembly quality, and higher functional annotation rates. Gene ontology and KEGG analyses showed enrichment of pathways related to stress signalling, protein folding and quality control, antioxidant defence, amino acid biosynthesis, and DNA replication and repair, coupled with suppression of energy-intensive housekeeping processes. Differential expression analysis identified 3,330 heat-responsive genes, including strong induction of heat shock proteins, molecular chaperones, ubiquitin-proteasome

components, and major transcription factor families. MapMan analysis further confirmed coordinated modulation of metabolism, hormone signalling, photosynthesis, and redox homeostasis. Collectively, these results demonstrate that EBR priming enhances thermotolerance through integrated physiological improvement and adaptive transcriptomic reprogramming, offering a scalable strategy to improve millet resilience under climate-induced heat stress.

Keywords 24-epibrassinolide, Thermotolerance, Transcriptome sequencing, Heat shock proteins, Climate resilient, Stress physiology

Abstract No: SSA17

Machine LearningDriven Prediction of Deletions and Duplications in Plant Genome

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ABSTRACT

Structural variations (CNVs), including deletions and duplications, represent a major source of large-scale variation in plant genomes (>1000bp) and are known to influence agronomically important traits. Accurate classification of CNV types remains challenging due to genome size, high repeat content, and heterogeneous sequencing coverage commonly observed in plant genomes. In this study, we present a Gradient Boosting-based machine learning framework for the prediction and classification of CNV types- deletions, duplications, and non-CNV regions in plant genomes.

The proposed approach utilizesfeatures derived from sequencing depth profiles, nucleotide composition, and coverage-related statistics that capture key characteristics of CNV regions. The model was trained using a high-confidence dataset comprising both experimentally validated and computationally curated CNVs, ensuring robustness across diverse genomic contexts. Performance evaluation was conducted across multiple CNV size ranges and varying training set sizes to assess model stability and generalization capability.

The Gradient Boosting model demonstrated strong and consistent performance, achieving an overall classification accuracy of 89.27%, with precision, recall, and F1-score values of 89.3%, and a receiver operating characteristic area under the curve (AUC) of 0.9783. These results highlight the reliability of the proposed framework in distinguishing CNV types in complex plant genomes. This method focuses on accurately classifying CNV types from pre-identified genomic regions, thereby complementing existing CNV detection pipelines.The approach offers a scalable and efficient solution for CNV classification, with potential applications in plant genomics, breeding, and evolutionary studies.

Keywords : Machine Learning, Plant Genomics, Structural Variation, Deletion, Duplication

Abstract No: SSA18

Morpho-Molecular Determinants unlock the Heat Stress Resilience mechanism in Wheat and Their Implications for Grain Biofortification

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ABSTRACT

Global temperatures are rising and winter durations are shortening, exposing wheat to terminal heat stress. As a staple crop providing nearly 55% of global carbohydrates and about 20% of dietary calories, sustaining wheat production is essential for ensuring food and nutritional security for the growing world population. The present study evaluated the impact of heat stress induced by delayed sowing on morpho-physiological performance over two growing seasons. Significant effects of genotype, treatment, and year were observed for most agronomic traits, indicating strong genetic and environmental influences. Late sowing accelerated crop phenology, significantly reducing days to heading, anthesis, and maturity, reflecting heat-induced shortening of the growth and grain-filling period. Stress tolerance indices revealed substantial genotypic variation, with Chirya-3 exhibiting the highest stability and tolerance across both years, while RAUW-111, RG-2, and HD2967 maintained relatively high productivity but showed greater sensitivity, and IC-212185 emerged as the most susceptible genotype. Grain biochemical analysis demonstrated genotype-specific responses to stress, with significant reductions in iron, starch, and protein content in selected genotypes, whereas zinc, amylose, and phytate remained comparatively stable. The relative expression of heat shock protein-related genes during the grain-filling stage under heat stress further revealed clear genotype-specific differences. Hsp90, a molecular chaperone involved in protein folding and stabilization of stress-responsive proteins, was upregulated in most genotypes, with stronger induction in HD2967, Chirya-3, and IC-212185, while SunStar showed marked downregulation, indicating a weaker stress response. Hsp-Sti, a co-chaperone linking Hsp70 and Hsp90, was strongly induced across genotypes but remained lower in SunStar. HypDnaJ, a member of the Hsp40 family, was downregulated in all genotypes, with greater suppression in SunStar. ClpB1 showed strong induction in HD2967, IC-212185, and Chirya-3 but minimal induction in SunStar, indicating differential activation of heat-responsive chaperone systems under stress conditions.

Keywards : Terminal heat, Stress tolerance, Grain biochemical, Gene expression

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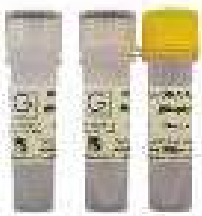

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