

Sectional Committee -X Agricultural Sciences

Chair

Dr. Sneh Lata Singla-Pareek, FNA



Dr. Sneh Lata Singla-Pareek, Group Leader at ICGEB, New Delhi, is a distinguished scientist in Plant Stress Biology and Agricultural Biotechnology. With a Ph.D. from the University of Delhi and visiting fellowships at institutions like the University of North Carolina, Cornell University, and UC Davis, she has made ground-breaking contributions to understanding the abiotic stress tolerance mechanisms and enhancing rice crop yield. Her research has led to the development of high-performing, stress-resilient rice varieties, earning recognition from the seed industry. She has successfully led multiple national and international research projects and has coordinated a Centre of Excellence and bi-national research programs. She has published over 200 research articles and 45 book chapters. A globally recognized expert, she has received numerous awards, including the NAAS Fellowship-2025, SERB-POWER Fellowship, J.C. Bose Gold Medal, DBT-BIRAC Innovator Award, and the Innovative Young Biotechnologist Award. She is a Fellow of INSA and NASI and has been featured in Stanford University's list of the world's top 2% scientists for the three consecutive years. Beyond her research, Dr. Singla-Pareek actively involved in mentoring graduate students and trains professionals from neighboring countries, fostering scientific talent and collaboration in plant biotechnology.



INSA Distinguished Lecture

Plant genomics for climate resilient crops

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Climate change and abiotic stress affects agriculture and crop production adversely. Wheat is a temperate crop and prone to various abiotic stresses. Tolerance to heat stress is a complex phenomenon and controlled by multiple genes. Heat tolerance related gene transcripts were identified based on their putative functions and validated by cDNA macroarray and northern/RT-PCR analysis in wheat. A common response to high temperature stress is the synthesis of Heat Shock Proteins (HSPs). HSP encoding genes are found to be under the control of Heat Shock Factors (HSF), transcription factors that regulate the expression of HSP genes. For spike photosynthesis genome-wide transcriptome exploration revealed the awn showing high expression of genes involved in photosynthesis as compared to other photosynthetic organs in spike including spike, lemma and palea. *A. tauschii* suffered less inhibition of photosystem II efficiency and net photosynthetic rate (Pn). Although *A. tauschii* showed nearly complete recovery of PSII, the adverse effect was more pronounced in *A. speltooides*. Functional characterization of additional transcription factors from *Triticum aestivum* was undertaken, namely TaZnF and TaMADS. The wheat bZIP displays temporal and varietal specific regulation and its overexpression showed enhanced tolerance to salinity, drought and heat stress. TaZnF expression was upregulated under high temperature, salinity, drought and cold stress. In addition, characterization of a heat stress inducible Myo-inositol-1-Phosphate Synthase (TaMIPS) gene from wheat (*Triticum aestivum*) has been undertaken in the T2 generation overexpression lines. The discovery of novel genes, determination of their expression pattern in response to abiotic stress and an improved understanding of their roles in stress adaptation (obtained by functional genomics) will provide the basis of effective engineering strategies leading to greater stress tolerance and management in agriculture. Thus, with the advent of genomics, a new era of plant sciences is beginning which helps not only in gene discovery and functional analysis of novel genes, but also aid in mining efficient alleles for introgression in desired plants for crop improvement and generation of agriproduct diversification.

Speaker's Profile

Professor Paramjit Khurana has contributed extensively in the area of *Seri* biotechnology and Wheat Biotechnology. In wheat, a systems biology approach has been used to investigate the molecular mechanisms regulating auxin-induced somatic embryogenesis. She has done pioneering work on genetic transformation of wheat and mulberry. The development of wheat transgenics over-expressing potato proteinase inhibitor gene conferred tolerance against the Cereal Cyst Nematode in *T. durum*, and that of HVA1 over-expression imparted tolerance towards salinity and drought in *T. aestivum*. Doubled haploid technology to produce transgenics to avoid segregation of introduced traits in wheat has been successfully demonstrated by her group. Transgenics in mulberry have been raised for drought, salinity and biotic stress with HVA1 and osmotin genes, respectively, and transferred to the Central Sericulture Research & Training Institute (CSRTI) at Mysore, and University of Agricultural Sciences (UAS), Bangalore, for field evaluation. In addition, she has also done excellent work on lipopolysaccharide (LPS)-mediated cellular recognition during legume-Rhizobium symbiosis and cell-to-cell communication by use of impermeant macromolecules in living cells. She sequenced the complete chloroplast genome and nuclear of mulberry, and was actively associated with sequencing of rice, tomato and wheat genomes as part of the International Genome Sequencing Conso

Advanced techniques for climate change monitoring in lowland rice using eddy covariance

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Mass and energy exchange was studied in lowland flooded rice–rice ecology at ICAR–Central Rice Research Institute, Cuttack, Odisha, using the eddy covariance technique. Mass exchange, including net ecosystem carbon dioxide exchange (NEE), net ecosystem methane exchange (NEME) and water vapour flux was measured during dry and wet cropping seasons and the respective fallow periods. In both cropping seasons, the flooded rice paddy acted as a net CO₂ sink (negative NEE) from the vegetative to early maturity stage. The NEE decreased gradually from the vegetative phase to maximum tillering, then increased slightly during flowering until harvest. The Q10 model is the most appropriate for partitioning NEE into gross primary productivity and ecosystem respiration, compared to the rectangular hyperbolic method. The NEME was higher from active tillering to panicle initiation stages and was controlled by air and soil temperatures, standing water and radiation. Parameters such as actual evapotranspiration and crop coefficients, calculated from eddy covariance data, can be used to improve crop water requirements and irrigation management. Among the energy fluxes, latent heat flux dominates over sensible heat flux in flooded rice ecology. During the fallow seasons, a higher proportion of available heat flux is partitioned into sensible heat due to reduced soil moisture content. Energy balance closure was evaluated using ordinary least squares, energy balance ratio and residual heat flux (RHF), with RHF proving to be the most effective estimation method. On average, RHF was 10.3–12.0% higher in the wet season compared to the dry season. The energy balance in paddy fields shows a greater imbalance during the rainy season, as energy is advected in the fresh rainwater.

Speaker's Profile

Dr. Chatterjee is currently working as a Senior Scientist (Soil Science) at ICAR-Central Rice Research Institute, Cuttack. He did his graduation from BCKV, Mohanpur; Masters from GBPUAT, Pantnagar and PhD from IARI, New Delhi. He achieved 1st rank in ASRB-ARS and joined ICAR RCNEH, Nagaland Centre in 2011. He was awarded NEWS fellowship and visited UKCEH, Edinburgh and INRA, Paris in 2018. Dr. Chatterjee's research focused on monitoring climate change using eddy covariance and adaptation and mitigation strategies using nitrogen management. He is a member of several academies and societies, including Associate of NAAS and WAST, member of INYAS and NASI, and life member and young scientist awardee of ISCA, CMSI and ISSS. He has published more than 65 research papers in reputed journals.

Essential role of soil biodiversity in food, environmental and human health security

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Soil biodiversity provides key ecosystem functions including primary productivity, climate regulation and nutrient cycling. Similarly, crop-associated microbiota, which are mainly recruited from soils, play critical role in the provision of vital host functions including nutrient absorption, provisions of key phytohormones, metabolites, and resilience against biotic (e.g. pathogens and pests) and abiotic (e.g. drought, heatwave) disturbances. Soil biodiversity also plays direct role in plant and human health via reducing exposure to pathogens, suppressing antibiotic resistance gene transfer, and degrading harmful chemicals pollutants from the environments. This presentation will provide overview, empirical data and maps in direct evidence for 1. linkage between soil biodiversity and ecosystem functions including food production at local to global scales, 2. current and future global distribution of pathogens, and 3. critical role of soil biodiversity in suppressing pathogens. The presentation will argue that effective conservation policies of soil biodiversity is integral to improve outcomes for food and environmental security and human health.

Speaker's Profile

Brajesh is a Disguised Professor of Soil biology, at Hawkesbury Institute for the Environment, Western Sydney University. Through his fundamental research, he identifies the quantitative relationships between soil biodiversity and ecosystem/ host functions and how natural/anthropogenic pressures such climate change affect this. His applied research harnesses the knowledge gained in fundamental research to improve agriculture productivity, restoration success and environmental sustainability. Outcomes from his research have informed multiple policy decisions at national and international levels, and he is currently working with multiple government and inter-governmental bodies including as a member of UN- FAO's Intergovernmental Panel on Soil and the Chair of FAO- International Network on Soil Biodiversity (FAO-NETSOB).

Prof Singh has published ~ 340 scientific papers and these have been cited >57,000 times with h' index of 107. He is a Fellow of many academies including the Australian Academy of Science.

Soil health and livelihood centric research: A journey towards sustainable development

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Soils are valuable natural resources and play a significant role in meeting the UN Sustainable Development Goals (SDG). Soil health management and restoration of the depleted soil organic C pool are reliable strategies to mitigate Climate Change and desertification. On the other hand, solid waste utilization as organic fertilizers is a useful proposition to reduce the waste-load in cities, which can substitute the chemical fertilizers in agricultural soils. In these contexts, vermicomposting, composting, and microbe mediated technologies are effective options. This deliberation would reveal major research outcomes on vermicomposting and biofertilizer technologies. Various industrial and urban wastes can be treated and sanitized through vermicomposting into valuable manures and eventually can be utilized for cultivation. As such, the earthworm mediated system is far more efficient than conventional composting techniques regarding enrichment of the finished product. Interestingly, our research exhibited the unique potential of earthworms in removing toxic heavy metals from waste materials through some novel metal binding proteins in their intestines. We have also explored earthworm gut environment and formulated microbial inoculums that has immense potential as prolific biofertilizers for the farming communities. This talk would showcase innovative waste valorization techniques, utilizing earthworm microbial consortia, enable the detoxification of industrial residues and lignocellulosic waste without pre-treatment, exemplifying sustainable waste-to-wealth practices. Moreover, our research on emerging contaminants, including pharmaceuticals and pesticides, emphasizes strategies to mitigate environmental risks, aligning with SDG 6. Overall, our holistic approach integrates biological innovation with sustainability, offering impactful solutions for environmental protection, food security, and climate resilience.

Speaker's Profile

Dr. Satya Sundar Bhattacharya, Professor and Head of the Soil and Agro-Bioengineering Laboratory, Department of Environmental Science, Tezpur University, leads research on plant bioactivity under environmental stress, waste management, soil health, nano-fertilizers, and earthworm microbiology. He has guided 10 Ph.D. scholars and published over 100 papers, books, and chapters, with 80 in high-impact journals (h-index: 38 Google Scholar, 35 Scopus). He holds an Indian patent (2020) on a novel soil conditioner, licensed for use. A former Research Professor at Hanyang University, Korea, he collaborates with Örebro University, Sweden, and received the GYTI Award (2018) and NASI Fellowship (2024).

Integrated multi-omics approaches for climate-smart future crops

Mukesh Jain



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Recent advances in multi-omics approaches have accelerated gene discovery and understanding the molecular basis of important agronomic traits for undertaking translational research. I shall illustrate the use of high-throughput multi-omics technologies in generation of genomic resources and connecting genes and genomic variations to agronomic traits giving examples from a non-model (chickpea) crop plant. We sequenced the genome/transcriptome of chickpea to reveal the gene space, gene regulatory networks and genetic variations associated with important agronomic traits. A comprehensive analysis of transcriptome dynamics during seed development and under drought stress in chickpea cultivars with contrasting seed size and drought response identified a significant proportion of the genes exhibiting cultivar-specific expression patterns. The transcriptional changes in cell cycle, endoreduplication, carbohydrate metabolism and hormone signal transduction pathways were found to determine seed size/weight in the chickpea cultivars. Further, we revealed the regulation of candidate genes via differential DNA methylation and non-coding RNAs. A comprehensive gene expression atlas was developed and demonstrated its applications in functional genomic studies and candidate gene discovery. Our studies provide insights into the molecular signatures and regulatory mechanisms governing key agronomic traits and will surely facilitate various areas of functional and translational genomics research in crop plants for sustainable agriculture and ensure food security.

Speaker's Profile

Dr. Mukesh Jain is currently serving as a Professor at the School of Computational & Integrative Sciences, Jawaharlal Nehru University, New Delhi. He has worked extensively in the areas of Plant Genomics, Biotechnology and Computational Biology, and published more than 140 articles in international journals of high repute with an h-index of 60 and >16000 citations. Prof. Jain is one of the pioneers of next-generation genomics research in plant sciences in India. In addition to the development of several high-value public web resources, his group has made significant contributions in understanding the molecular mechanisms underlying abiotic stress responses and seed development in crop plants. For his outstanding scientific contributions, Prof. Jain has been honored with several awards and Fellowships of the National Academies. Prof. Jain's current research interests include understanding epigenetic and chromatin-level regulation of agronomic traits using integrated multi-omics, single-cell genomics, and systems biology approaches.

Sustainable use of *Oryza glaberrima* and wild species *Oryza coarctata* for management of salinity stress of rice

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Wild species are excellent reservoirs of important genes, many a times that are not found in cultivated gene pool. Canonically rice plant is salt sensitive though few genotypes are salinity tolerant which have been extensively used as donor in salinity breeding program of rice. Thus there is a need to discover alternative favourable alleles/genes that give better salinity tolerant. *Oryza coarctata* is a wild species that can grow up to maximum EC value of 65 ECe (electrical conductivity) dS/m². It is mainly found in the coastal region of South Asian countries. Unfortunately, the conventional crossing of this plant is not very successful with rice. Thus, to find out the cause of low breeding success as well as salinity tolerant mechanisms, we did cytogenetic, genomics, transcriptomics and metabolomics study of this species. While decoding the nuclear genome along with transcriptomic studies gave several novel salt tolerant genes, metabolomics study indicated allantoin a key compound that might be responsible for its salinity tolerance. Further transgenic Arabidopsis plant with over expressed allantoin biosynthesis gene indicated that it renders salinity stress through some hormonal pathways. African rice *Oryza glaberrima* though low yielder yet grow under human neglects. We have found out novel salinity tolerant genes from this species and utilized for developing the coastal salinity tolerant rice variety. A details account of our research finding of this species related to these two species will be delivered in my talk.

Speaker's Profile

Dr. Mondal is a Principal Scientist at ICAR-NIPB, New Delhi and working on pre-breeding of rice, wild species of rice and tea genomics. He has decoded the genome of Indian tea and wild species of rice (*Oryza coarctata*). He is the recipient of several scientific awards including the fellows of NASI, NAAS, ISPG, Indian Botanical Society, PTCA. Guided 11 Ph. D. students including one Nigerian student. He helped to create 2 self-help groups and mentored a farmer's organization of Sundarbans, West Bengal to get the Genome savior Award-2016. He is Editors of 4 journals and members of several scientific committee. He has written three Books and has more than 100 research papers. He has, 5 copy rights, filed 4 Indian patents and registered 12 germplasm at NBPGR. Some of his elite lines of rice under varietal trail for salinity tolerant.

Innovating cotton research for augmenting yield and quality

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The epidermal cells of cotton ovules that commit to developing fibres provide an intriguing model for studying genetics and epigenetics, which is also a focus of my laboratory. We have demonstrated that cotton histone deacetylase 5 (HDA5) plays a positive role in regulating cotton fibre development. Inhibiting histone acetylase activity through treatment with Anacardic acid (AA), a p300/PCAF inhibitor, in in-vitro ovule cultures promotes the development of cotton fibbers. Transcriptome and ChIP-seq analyses have revealed that AA enhances fiber yield by increasing the expression of genes in the auxin pathway while suppressing the expression of cell cycle genes. Furthermore, foliar application of AA on developing flowers and bolls significantly improved cotton yield across multiple genotypes and locations. Multi-location AICRP trials conducted over two years confirmed a yield enhancement of 5-30% in cotton, leading to technology development and commercialization. Another major challenge in cotton hybrid production is the reliance on hand emasculation or ms5ms6-based genetic male sterility systems. Male sterility and fertility restoration are crucial for successful F1 seed production. We have developed a novel reversible male sterility strategy achieved through the spatiotemporal modulation of anther tapetum degeneration. This provides a controllable and efficient approach for harnessing hybrid vigour in cotton. Additionally, we generated large-scale genomic resources and re-sequenced 320 *Gossypium hirsutum* genotypes, identifying over 3.2 million SNPs and Indels. Genome-wide association studies (GWAS) identified more than 250 significant markers associated with key traits, including fiber yield and quality, stress tolerance, plant architecture, and flowering time. These high-quality polymorphic SNPs and trait-associated markers were utilized to develop a 120K cotton SNP chip, facilitating molecular-assisted breeding and association-based mapping for agronomically important traits in cotton.

Speaker's Profile

Dr Sawant works as the Chief Scientist at CSIR-NBRI, Lucknow, and his group has made significant contributions to cotton research. The lab's research focuses on transcriptional regulation and epigenetic mechanisms of fiber development. His group is utilising innovative technologies and genomic resources to enhance cotton for improved lint yield and quality. His group identified Anacardic acid as a novel growth-promoting molecule that enhances cotton fibre yield and quality. This innovation has been granted a US patent, and the technology is now commercialised. The 120K cotton SNP Chip has been developed for marker-assisted breeding in cotton varieties, and the Chip has been licensed. Dr Sawant's lab developed a novel reversible male sterility strategy for the development of F₁ cotton hybrids.

Plant microbiome engineering for climate resilient agriculture

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A crop's productivity is an outcome of the multitude of interactions between the plant, soil and its environment. The plant is no longer considered an individual entity, but is a part of a holobiont, with indispensable association with the microbiome. The plant microbiome contributes to the plant's fitness by various mechanisms. The rhizosphere is a special zone surrounding the plant roots, harbouring a huge microbial diversity that is recruited by the plant. To address the challenges faced by agriculture worldwide, viz. increasing population and deterioration arable land (due to climate change), plant growth promoting rhizobacteria (PGPR) have been employed for enhancing soil fertility and crop productivity since decades.

However, amendment with PGPR suffers from various limitations including the compromised efficacy and survival of the introduced strains under field conditions. Engineering the rhizosphere microbiome to enhance plant's fitness and resilience has emerged as a promising approach to agricultural sustainability. The group's success stories in rhizosphere engineering by top-down and bottom-up approaches, and their translation from lab to field, will be presented. Case studies will be discussed wherein an in depth understanding of soil-plant-microbiome nexus has been gained, followed by harnessing the microbiome for stress mitigation using different model crops.

Speaker's Profile

Shilpi Sharma is a Chair Professor at Department of Biochemical Engineering and Biotechnology, at IIT Delhi. An alumnus of the Department of Botany, BHU, she completed her Ph.D. from Ludwig Maximilian University, Germany, followed by postdoc at the Helmholtz Centre, Munich. She is an environmental microbiologist tailoring plant-microbe interactions for attaining Food Security and Agricultural Sustainability. She has authored >120 international publications and 20 chapters. She has been bestowed upon several coveted awards by the Indian Botanical Society, AMI, BRSI, and "She is: 75 Women in STEAM", an honour conferred by Government of India and British High Commission. She is the inaugural winner of the TATA Transformation Prize in Food Security, and Exemplary Women Leadership award, IIT Delhi. She is also the Fellow of the National Academy of Sciences.

From Genes to Farmers' Doorsteps: Molecular Innovations Empowering India's Dairy Value Chain

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Dairy value chain in India, the world's top milk producer for more than two decades, is a solution to nation's food insecurity. However, certain intricate problems in dairy production, processing, quality and safety as well as public health, limit the competitiveness of dairy value chain to a global level. Particularly, reproductive problems such as late maturity, accurate estrus and ovulation identification, abortion, retention of placenta, uterine infections and mastitis cause huge economic losses nearly Rs. 40-50,000 crores annually. Our efforts in translational and basic research provided innovative and simple solutions to these problems. For instance, the molecular endocrinology of buffalo aromatase, the key gene in estrogen biosynthesis, was explored. Further, we developed Buffalo Salivascope, a simple salivary fern pattern-based estrus identification method and a peptide based nanobiosensor strip for ovulation prediction at farmers' doorsteps. Similarly, LAMP colour reactions were developed for detecting *Ureaplasma diversum* for screening dairy animals with sub-clinical uterine diseases, and to identify xenobiotics in milk samples. To make dairy industry further remunerative, we recognized the emerging value-added components of milk, milk extracellular vesicles (mEVs) and delineated their molecular repertoire. Effective therapeutic and delivery potential of mEVs was also demonstrated by encapsulating mEVs either with miRNA or curcumin or antibiotics, for treating mastitis, in cancer cell lines and in vivo bioavailability studies. These integrated molecular, and mEVs based innovations collectively demonstrate a transformative potential to strengthen India's dairy value chain with direct translational impact at farmer, industry and public health levels.

Speaker's Profile

Dr. Dheer Singh, Director and Vice-Chancellor, ICAR-National Dairy Research Institute, Karnal, is a distinguished biochemist, Fellow of National Academy of Sciences (FNASc) and Fellow of National Academy of Agricultural Sciences, India. He significantly contributed to resolving buffalo reproductive problems by delineating the buffalo Cyp19A1 gene molecular biology and developing proofs of concept for ovulation prediction and field-applicable methods for estrus detection to increase conception rate and profitable buffalo rearing. He also characterized milk exosomes and demonstrated their potential as delivery vehicles for nutraceuticals and drugs. He published more than 100 research papers in reputed national and international journals.

Plant metabolic engineering and bioprocess technology for value addition

SK Yadav



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We have significantly contributed in the areas of biotechnology and metabolic engineering for crop improvement and bioprocess technology for the production of value-added products. Understood the caffeine metabolic pathway in tea with respect to seasonal and developmental conditions. Developed low-caffeine *Kangra jat* tea and seed less/ low-seeded fruits through gene silencing. Provided first evidence of epigenetic regulation of flavonoid biosynthesis and antioxidant pathway during salinity stress, molecular regulation of steviol glycosides in stevia, glyoxalase pathway and its role in providing stress tolerance to crop plants. Molecular insights into the picroside biosynthetic pathway have suggested that PkGPPS.SSU interacts with two PkGGPPS to form heteromeric GPPS in *Picrorhiza kurroa*. We have developed nanoformulations of plant bioactives catechins, picrorhiza, stevioside, betulin, etc. to improve their efficacy, stability and bioavailability. Also developed edible coatings from waste biomass for shelf-life enhancement of fruits and vegetables, an economical process for extraction of pectin from black carrot pomace and identified an ethanol tolerant microbial strain for acetic acid production from biomass. An efficient process has also been developed for the production of bacterial cellulose. A direct process has been developed for recovery of nano-silica and lignin from paddy straw and bagasse agro-waste. Processes have been developed for the synthesis of high-value and low-calorie rare sugars like D-tagatose, D- ribose, D-talose and functional molecules.

Speaker's Profile

He has contributed significantly in the area of biotechnology and bioprocessing for crop improvement and production of value-added molecules. He has already published more than 220 research papers, 19 patents, 4 books, 38000 citations, 65 h-index. He is fellow of INSA, NASI, NAAS, RSB. He is recipient of National Bioscience Award, NASI-Reliance Industries Platinum Jubilee Award, and "Recognition Award" by NAAS. He is an Honorary Member of PTCA. He has also been conferred INSA-YSA, 2008; NASI-Platinum Jubilee YSA, 2009; CSIR-YSA, 2010; NAAS-Associate, 2013; Prof. Hira Lal Chakravarty Memorial Award of ISCA, 2012-2013; Haryana Yuva Vigyan Ratna Award, Haryana Govt., 2011-12.



Genome wide profiling and functional characterization studies reveal role of PGPR-responsive miRNAs in drought stress tolerance in plants

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Pseudomonas putida strain MTCC5279 (RA), a plant growth promoting rhizobacteria improves plant growth and development and stress tolerance by colonizing their root surface. Further, along with several stress responsive genes, microRNAs are also well known for their crucial involvement in drought stress response. Considering the above, identification and expression profiling of small RNAs in chickpea roots was carried in the presence of *P. putida* RA inoculation under drought stress through high-throughput sequencing. A total of 923 conserved and 216 novel miRNAs from all four libraries were identified. 431 and 332 conserved miRNAs; and 60 and 39 novel miRNAs were found to be differentially expressed in RA and drought with RA-inoculated plants, respectively. At-miR393a-5p in *Arabidopsis thaliana* homologous system was functionally characterised for its role in growth and development. Our results indicated that At-miR393a-5p overexpressing *Arabidopsis* exhibited diverse plant growth and development attributes, such as increased shoot length, primary root length, biomass, number of lateral branches and number of siliques as compared to the Col-0 wild type plants. Additionally, all the overexpressing lines have improved water status, cell membrane integrity, proline accumulation and super oxide dismutase activity under drought stress. Another study revealed that RA-responsive Car-miR166 plays beneficial stress-mitigating roles under drought in transgenic *Arabidopsis* and chickpea plants. The results reported that the transgenic lines showed a positive interaction of miR166 with PGPR, resulting in drought stress mitigation and better plant survival in harsh drought conditions, paving the way for further characterization and utilization of miRNAs in crop improvement programmes.

Speaker's Profile

Dr Charu Lata is Principal Scientist and Associate Professor (AcSIR) at CSIR-NIScPR, New Delhi. Dr Lata pursued Ph.D. from NIPGR (JNU) in foxtail millet genomics. Later, she joined ICAR-NIPB as INSPIRE Faculty Fellow, and then as a Scientist at CSIR-NBRI, Lucknow. She moved to CSIR-NIScPR, New Delhi in 2019. Her research interest has been in the field of crop improvements especially abiotic stress responses and tolerance in crop plants. She has primarily focused in the research areas pertaining to the elucidation of mechanisms regulating abiotic stress tolerance in legumes and cereal crops through transcriptomics, small RNA profiling, and functional characterization studies. Dr Lata is also a recipient of several prestigious awards and honours.

Addressing livestock health and food safety using cutting edge molecular tools

Rajib Deb

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The livestock sector plays a pivotal role in strengthening India's economy by contributing significantly to food security, rural livelihood, and agricultural sustainability. Ensuring the health of livestock is critical for enhancing productivity, profitability, and the overall safety of animal-derived foods. Food safety, particularly in livestock products such as milk and meat, remains a major concern due to issues like adulteration and contamination, which not only pose serious risks to public health but also raise concerns related to religious taboos. Rapid and accurate disease diagnosis is a cornerstone of livestock health management, enabling timely intervention and effective disease control. The application of advanced molecular diagnostic tools offers unprecedented precision and speed in detecting major bacterial and viral pathogens affecting livestock. Moreover, vaccination remains the most reliable strategy for disease prevention; hence, the development of indigenous vaccines using local pathogen isolates is essential for achieving region-specific protection. This presentation will highlight recent advancements in molecular approaches for livestock disease diagnosis and species-specific food adulteration detection. Efforts toward the development of an indigenous vaccine candidate against Indian isolates of porcine viral diseases will be discussed, along with insights into host-pathogen interactions in emerging diseases like African swine fever. These innovative molecular interventions promise to revolutionize livestock health management and food safety assurance, aligning with the goal of sustainable agriculture in India.

Speaker's Profile

Dr Rajib Deb, PhD at present working as Senior Scientist at ICAR-National Research Centre on Pig, Guwahati, Assam. Currently his area of research is on the area of piggery health sector emphasizing on development of molecular diagnostic tools, vaccine candidates, understanding the host-pathogen interaction and immunological criteria associated with viral pathogenesis in the line of development of successful therapeutic gadgets and antimicrobial resistant.

Integrating genomics and biotechnology for climate-resilient and resource-efficient direct-seeded rice systems

Nitika Sandhu

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Direct Seeded Rice (DSR) is emerging as a transformative solution to address the urgent challenges of groundwater depletion, labour scarcity, methane emissions, and production stagnation in rice-based systems. However, its large-scale adoption is constrained by poor seedling emergence under deep sowing, early-stage abiotic stress tolerance, iron deficiency, and weed competition. My research integrates genomics-driven breeding, high-throughput phenotyping, and advanced molecular tools such as QTL mapping, genome wide association studies, genomic selection, haplotype-based selection, and CRISPR/Cas9-led functional gene validation to develop climate-resilient, resource-efficient rice cultivars tailored for DSR ecosystems. Significant progress has been made in dissecting genomic regions associated with traits improving adaptation of rice under DSR. Traits include anaerobic germination, early seedling vigor, early and uniform germination from deep sowing depth, mesocotyl elongation, submergence, flood and drought tolerance, root traits improving nutrient uptake, grain yield under DSR, weed competitiveness, herbicide tolerance, lodging resistance, grain quality, and biotic stress tolerance/resistance. Elite introgression and pre-breeding lines have been developed and field-evaluated across multi-locations in India, demonstrating enhanced establishment, nutrient-use efficiency, and yield stability under water-deficit, direct-seeded conditions. Beyond this, the research emphasizes translation to farmer fields through marker-assisted selection, trait-based varietal pipelines, and farmer-centric validation. Ongoing efforts include genome editing for seedling vigor, herbicide tolerance and the development of AI-enabled predictive tools for stress diagnostics and agronomic decision support. This integrated genomics-to-field pathway aims to accelerate the deployment of next-generation DSR rice cultivars, positioning India as global leaders in climate-smart, sustainable rice intensification.

Speaker's Profile

Dr. Nitika Sandhu is a molecular geneticist specializing in direct-seeded rice (DSR). Her pioneering research in next-generation sequencing-based trait mapping has identified 17 QTLs associated with enhanced DSR adaptation, now applied in genomics-assisted breeding programs for developing climate-resilient rice varieties. As an early-career researcher, she has published 55 research papers in reputed international journals, 14 book chapters, and one book, and has registered eight DSR-adapted breeding lines with NBPGRI and eight gene sequences with NCBI. She has secured five national and one international research project from DBT/DST (India) and UKRI (UK), respectively, contributing significantly to rice improvement and sustainable agriculture.

Innovative products/processes and solutions for Indian food industry & consumers

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To offer curcumin in easy, convenient, daily use food format, two novel nutraceutical products: 'curcumin functionalized/fortified cream powder and milk powder' were developed. Instant liquid cream and curcumin latte/milk can be reconstituted which revealed high sensory acceptability. Effect of processing conditions on powder functionalities, particle size, morphology, curcumin bioavailability, fluorescence, anti-cancer properties and cytotoxicity were studied. Results showed that CP and MP had significantly higher yield (85 and 81.3%). TEM confirmed curcumin particles to be in the nano-scale (50–250nm) compared to initial 2000nm curcumin size. In-vitro simulated digestion followed by Caco-2 cells uptake showed significantly high (CP: 95.01%; MP: 89.7%) curcumin bioavailability. CP and MP exhibited potent anticancer activity (100-2700µg/mL) by significantly inhibiting hepatic cancer (HepG2) cells with no cytotoxicity (MTT assay). Further, almond protein hydrolysate powder (APHP) was developed from almond meal through enzymatic hydrolysis using alcalase. APHP had all essential amino acids with 92.05mg BCAA/g protein and 0.44 PDCAAS score. APHP was shown to have significant immunostimulatory activity at 900 mg/kg bw in mice model wherein it had significantly high lymphocyte proliferation, NK cell activity (YAC-1 cells), peritoneal macrophage phagocytosis and IL-6 & IL-10 levels compared to the control; it also neutralized delayed type hypersensitivity (DTH) reaction induced by DNCB. APHP shown to be fortified (15%) in pea protein-based supplement with favourable sensory profiling. A low-cost meat storage structure requiring no direct electricity was developed using PCM to ensure hygienic meat for Indian consumers. Spoilage, pathogenic microbes were 1000 times less than FSSAI limits & meat is safe from physical contaminants: dust, flies.

Speaker's Profile

Dr. Prarabdh C. Badgujar is a Associate Professor at Dept. of Food Science and Technology, National Institute of Food Technology Entrepreneurship and Management, Kundli (NIFTEM-K), Sonapat, Haryana. His research areas include food toxicology and efficacy studies; Nutraceuticals & functional foods formulations; Protein hydrolysates & Bioactive peptides. He has handled research projects worth 5.2 Crore till date and has transferred 2 technologies to the Industries. He has received 4 Indian patents & 2 copyrights 58 published papers with 1520 citations & h-index of 22. He has guided 4 Ph.D., 27 Master's students. He is recipient of DST-INSPIRE Fellowship, Summer Research Fellowship by IAS, Bangalore, International fellowships by JICA, Govt of Japan & 'MASHAV Scholarship' by Govt. of Israel.

Phytochemicals in food safety and sustainability

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Food safety is one of the critical components of global food sustainability and well aligned with United Nations Sustainable Development Goals (SDGs), particularly SDG 2 (zero hunger) and SDG 3 (good health and well-being). Fungal contamination in agri-food commodities is one of the major causes of food spoilage linked with breaching the food safety and security leads to fatal disease and negatively affects the trades. Among different storage fungi, *Aspergillus flavus* and its associated toxin (aflatoxin B 1) have been considered as the most resilient fungi and mycotoxin in agricultural food commodities. In this talk, I shall present a brief overview on our research work, how the integration of recent techno-scientific innovation especially mathematical modeling, omics approaches and nanotechnology could be used to formulate the novel phytochemicals-based antifungal agents to combat the fungal spoilage, aflatoxin B 1 contamination and emergence of resistance, and to achieve the global food safety and sustainability.

Speaker's Profile

Dr. Bhanu Prakash is currently working as an Associate Professor of Botany at Department of Botany, Banaras Hindu University, Varanasi. His group has explored the preservative and functional characterization of plant-based chemicals. Given his scientific contributions, he has received several prestigious awards such as

- ❖ *Associates (2020): National Academy of Agricultural Sciences (NAAS-New Delhi), India.*
- ❖ *NASI-Young Scientist Platinum Jubilee Award (2017): The National Academy of Sciences, (NASI), India.*
- ❖ *Elected Life member MNASc (2018), National Academy of Science (NASI), Prayagraj, Uttar Pradesh, India.*
- ❖ *Prof Gurcharan Singh Bains Award (2021) Association of Food Scientists & Technologists (Mysore, Karnataka, India).*

Indigenous Next-generation Precision genome editing tools for crop improvement

Kutubuddin Ali Molla

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Genome editing has revolutionized modern biosciences and biotechnology by enabling targeted and precise modification of genetic sequences. While CRISPR–Cas9 and Cas12a systems have become the cornerstone of genome engineering in eukaryotes, their commercial application in India remains limited due to intellectual property (IP) constraints. To address this, our laboratory at ICAR–CRRI focuses on developing indigenous and IP-free genome editing tools for plant research and crop improvement. Moving beyond conventional CRISPR platforms, I will introduce a transposon-associated TnpB system—a compact, programmable, and next-generation genome editor that our group has successfully established for eukaryotic genome editing. In parallel, we are advancing base editing and prime editing technologies to achieve single-nucleotide substitutions and precise, small DNA insertions or deletions without inducing double-strand breaks or requiring donor templates. Drawing from our ongoing research, I will present case studies on (i) base-edited rice with enhanced resistance to major diseases, and (ii) prime-edited rice lines carrying a C4-like phosphoenolpyruvate carboxylase (PEPC) variant that exhibits early flowering and improved photosynthetic efficiency. We further discovered that these prime-edited lines are enriched in zinc, iron, and protein (ZIP) in grains—marking a significant step toward achieving biofortification and nutritional security goals. The presentation will conclude with a brief outlook on our latest efforts to integrate AI-generated proteins in the rational design and optimization of novel genome editors.

Speaker's Profile

Dr. Kutubuddin Molla is a Senior Scientist at ICAR–National Rice Research Institute, Cuttack, India, specializing in genome editing for crop improvement. A Ph.D. from the University of Calcutta and a Fulbright Postdoctoral Fellow at Penn State University, he has developed indigenous genome editing tools, including a compact TnpB system, base editors, and prime editors. His innovations are used in over 35 laboratories worldwide. Dr. Molla has received several honors, including the INSA Medal for Young Scientist (2020) and INSA Associate Fellowship (2025). He was recently selected as a 'Next Generation Leader' for the Asilomar 50th Anniversary Summit, USA.