New Phytologist Workshop

Molecular mechanisms of light-regulated plant development

11 – 13 December 2025
Indian Institute of Science Education and Research (IISER), Bhopal, India

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15:10 – 15:20	6.5 Ajar Anupam Pradhan, IISER Bhopal, India **A light regulated Arabidopsis MATE transporter regulates the root hair development under low phosphate stress**
15:20 – 15:30	6.6 Pooja Jakhar, IISER Mohali, India **Shedding light on iron nutrition: light mediated regulation of Iron homeostasis in *Arabidopsis thaliana***
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16:20 – 16:40	7.2 Naresh Loudya, Indian Institute of Science, Bengaluru, India **Understanding chloroplast development: identification and characterization of the *CUE6* gene in Arabidopsis**
16:40 – 17:00	7.3 Yogesh Mishra, Banaras Hindu University, India **Do growth chambers mimic nature? A systems biology perspective on plant light responses**
17:00 – 17:10	7.4 Priyanka Mishra, Indian Institute of Science, Bengaluru, India / Royal Holloway, University of London, United Kingdom **An ARF2-GRF5 module, operating early, indicates genetic hierarchy during chloroplast biogenesis**
17:10 – 17:20	7.5 Arpan Mukherjee, IISER Bhopal, India **Functional characterization of BBX15 during early seedling development in Arabidopsis**
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Speaker abstracts

1.1

Function of the COP1/SPA ubiquitin ligase in plant growth and development

Ute Hoecker
University of Cologne, Germany

Light controls plant development throughout the plant life cycle by affecting the protein stability of key transcription factors with a role in plant differentiation. These transcription factors, such as HY5, PAP2 or CONSTANS, share a val-pro (VP) motif that is bound by the E3 ubiquitin ligase COP1/SPA which subsequently polyubiquitinates these transcription factors leading to their degradation. COP1/SPA is mainly active in darkness, and is inactivated by light, thereby allowing an accumulation of the transcription factors only in light-exposed plants. Here, we will present mechanistic insight into the inhibition of COP1/SPA activity by photoreceptors.

Biography

Ute Hoecker is Professor of Plant Sciences at the University of Cologne, Germany. After studying Agricultural Sciences in Germany she moved to the U.S. as a Fulbright fellow. She obtained a Ph.D. in Plant Molecular and Cellular Biology from the University of Florida, USA, working with Don McCarty on ABA signaling in maize seeds. As a postdoctoral researcher in Peter Quail´s lab she started her research in photobiology of Arabidopsis which she continued as an independent group leader at the University of Duesseldorf, Germany, and since 2006 as a professor in Cologne. Ute Hoecker´s research uses genetics and molecular biology to unravel the complex light signalling networks with a particular focus on the control of protein ubiquitination by the COP1/SPA ubiquitin ligase. Her lab uses Arabidopsis and *Physcomitrium patens* (moss) as model species.

1.2

Molecular control of growth and development by the inositol pyrophosphate messengers in land plants

Debabrata Laha
Indian Institute of Science, India

Land plants, being sessile organisms, face specific environmental challenges for survival. To mitigate these challenges, land plants have evolved a complex array of interconnected signaling pathways. One such pathway is the inositol-derived signaling network, specific to all eukaryotes. $InsP_6$, the fully phosphorylated form of inositol, also known as phytic acid, serves as a signaling molecule either directly or as a precursor to inositol pyrophosphate (PP-InsP) messengers. PP-InsPs are diphosphate-containing inositol phosphates (InsPs) that orchestrate diverse aspects of plant physiology, including hormone signaling and nutrient sensing. Moreover, plants with defective PP-InsP metabolism exhibit significant growth and developmental defects. Intriguingly, the molecular mechanisms underlying the physiological processes controlled by PP-InsPs remain largely unexplored in embryophytes. Furthermore, much of what we know about their functional roles derives from research based on the model plant *Arabidopsis thaliana*. It is yet to be explored whether the physiological functions of PP-InsPs are conserved across other clades of land plants. In this meeting, I will discuss the recent efforts by our group to delineate the molecular basis of PP-InsP-controlled growth and development in land plants. Finally, our current understanding on the functional conservation of physiological processes by PP-InsP messengers will also be discussed.

Biography
Dr. Laha pursued his BSc and MSc degree at the Visva Bharati University, Shantiniketan, West Bengal. In 2015, Dr. Laha received his PhD degree at the University of Tuebingen, Germany with Summa cum laude, the highest possible recognition in German academic system. His PhD work was supported by the competitive DAAD fellowship. Dr. Laha initiated his research group at the Department of Biochemistry, IISc in September 2020. Dr. Laha received several national and international recognition at each step of his academic journey including Har Govind Khorana-Innovative Young Biotechnologist Award, Infosys Young Investigator Award, Reinhold and Maria Foundation Outstanding PhD Thesis Award, DFG International Postdoctoral Fellowship and IASc Summer Research Fellowship. Dr. Laha has published over 25 research articles till date in top-tier international journals including *Nature Chemical Biology*, *Plant Cell*, *Plant Physiology*, *Plos Genetics*, *Nature Communications*, *Angewandte Chemie* etc.

1.3

TMK interacts with Phytochrome to regulate light signaling in *Marchantia polymorpha*

Shubhajit Das
Institute of Science and Technology Austria (ISTA), Klosterneuburg, Austria

In the liverwort *Marchantia polymorpha* (Mp), both red (R) and far-red (FR) lights are perceived by a single phytochrome MpPHY. While vegetative growth requires R light, FR light is necessary for reproductive growth. A higher FR/R ratio perception by MpPHY induces gametangiophore development. In dark, MpPHY remains in an inactive, cytoplasmic Pfr form. Both R and/or FR light stimulus converts MpPHY to an active Pr form that translocate into the nucleus where it interacts with PHYTOCHROME INTERACTING FACTOR (MpPIF). While R light activated MpPHY-MpPIF interaction leads to MpPIF degradation, FR activated MpPHY does not degrade MpPIF. MpPHY and MpPIF are positive regulators of reproductive development as their loss-of-function mutants fail to develop gametangiophore. We noticed that loss-of-function of the extracellular auxin receptor MpTMK (TRANSMEMBRANE KINASE) causes a reproductive defect that resembles *Mpphy* and *Mppif* loss-of-function. We found that in *Mptmk* mutant, MpPHY is constitutively nuclear which leads to constant degradation of MpPIF. We show that MpTMK can interact with MpPHY. We propose that potential MpPHY phosphorylation by MpTMK causes a defect in MpPHY dark reversion. Therefore, a constitutively active MpPHY causes constant clearance of MpPIF from nucleus in *Mptmk* mutant, impairing the downstream signaling for reproductive development

1.4

Quantitative analysis of light-dependent gene regulation in Marchantia spores

Zohar Meir ORCID iD
Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria

Light is perhaps the most important signal in plant development, but its direct effects on gene expression are difficult to disentangle. One major challenge is that light quickly induces growth, involving wide transcriptional changes that can obscure the early, specific effects of particular light cues. In addition, different light receptors — each tuned to specific wavelengths and intensities — often function simultaneously within the same cells, making it hard to attribute responses to any single pathway. Finally, light responses typically involve many cell-types with varying sensitivities and growth potentials, making it difficult to interpret how specific cues drive morphogenetic changes across complex plant tissues.

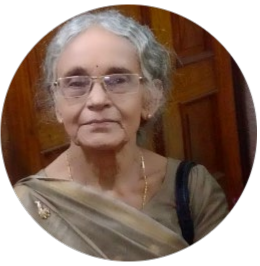
To overcome these challenges, we used *Marchantia polymorpha* spores, single-celled and exposed, as a model to quantify light impact on development. By combining live 3D imaging and single-cell RNA sequencing of nearly 400,000 spores exposed to different light regimes, we discovered a transient state involving activation of multiple light receptors. This state precedes the activation of cell-cycle programs in spores, which are not induced under dark conditions. Our findings reveal a direct link between light and cell-cycle regulation, offering a quantitative framework for studying light responses across diverse biological systems.

1.5

Molecular basis of GA-independent DELLA regulation by the VIH-type inositol pyrophosphate synthase in a non-vascular land plant.

Priyanshi Rana
Indian institute of Science, Bengaluru, India

DELLA proteins act as central hubs integrating endogenous and environmental signals to control plant growth and development. In angiosperms, gibberellins induce DELLA degradation via the GID1 receptor, but bryophytes lack this canonical GA perception system despite encoding DELLA genes. Therefore, the mechanisms of DELLA regulation in these early land plants remained unclear until recently. In my work, we have shown that in the liverwort Marchantia polymorpha, the inositol pyrophosphate messenger InsP8, synthesized by MpVIH controls DELLA stability. Specifically, we found that MpVIH-deficient plants mimic MpDELLA overexpression lines and suppression of MpDELLA in the Mp*vih* plants largely restores growth and developmental defects associated with Mp*vih* plants. These findings reinforce a functional relationship between MpVIH and MpDELLA. Mechanistically, we found that MpVIH-derived InsP8 binds to MpDELLA, induces changes in the secondary structure and promotes proteasomal degradation. These findings uncover a noncanonical mechanism of DELLA regulation, highlighting how metabolic messengers can fine-tune plant developmental responses. Because DELLA proteins also mediate light-regulated growth and development, my research opens up avenues to connect molecular links between hormone, metabolite, and light-regulated pathways in plant development.



1.6

Light impact on plant development and evolution through geological ages – a review

Bharati Nandi
West Bengal State University, India

An integral part of the transition of plants from aquatic environments to land and later to colonize diverse terrestrial habitats, involved their response to changing light intensities and spectra. The Precambrian environment differed dramatically from modern conditions. Key factors that influenced early life's relationship with light included: Reduced sunlight intensity (70-80% luminous) and high UV radiation. Early plants mostly cyanobacteria and consequently other algae adapted to these conditions through ancestral and simple light-sensing mechanisms, evolved sensory systems like phytochrome pathway to perceive light signals enabling adaptations such as changes in pigment for low light environments and the development of photomorphogenic responses that control the growth and development of plants in newly formed environmental niches. Appearance of cryptochromes and DNA photolyase helped the early aquatic plants mostly chlorophytes to move toward or away from a light source to find optimal conditions for photosynthesis and avoid UV damage by their phototaxis mechanism. The evolution of land plants from streptophytes involved the development of regulatory mechanisms, photoreceptor system to cope with the harsher terrestrial environment. This talk will summarize the light dependent evolutionary modifications seen in plants during their transition from the Paleozoic through Mesozoic to Cenozoic era.

Biography
Dr. Bharati Nandi is a distinguished botanist and former faculty member of the Department of Botany at Kalyani University, West Bengal, India. She earned her M.Sc. (1967) and Ph.D. (1975) in Botany from Calcutta University. Dr. Nandi began her teaching career as a part-time lecturer at an undergraduate college under Calcutta University (1970–1974), later serving as a full-time faculty member at Kalyani University from 1983 until her retirement in 2010. Post-retirement, she has been guest faculty at Kalyani University, Calcutta University and currently with West Bengal State University.

1.7

Cryptochrome-mediated blue light signaling controls the division of Marchantia spores

Nikhil Job ORCID iD
Gregor Mendel Institute of Molecular Plant Biology (GMI), Vienna, Austria

The mature plant body of *Marchantia polymorpha* develops from a single cell spore. Development begins with an asymmetric cell division that defines growth axis and establishes cell fate which provides foundation for the subsequent development. Light is required to initiate this cell division, and the molecular mechanism remains unknown.

We discovered that CRYPTOCHROME-mediated blue light signalling promotes first cell division. Mp*cry* loss of function mutants does not divide under blue light and remain as single cells. Using yeast 2 hybrid screening, we identified two transcription factors, MpLOS1 and MpC2H2-1, that physically interact with MpCRY. We hypothesis that MpCRY, MpLOS1 and MpC2H2-1 constitute a regulatory module to promote cell cycle progression. Consistent with this model, spores harboring loss of function alleles of Mp*los1* and Mp*c2h2-1* divide earlier than wild type. These data are consistent with the hypothesis that these transcription factors repress cell cycle progression.

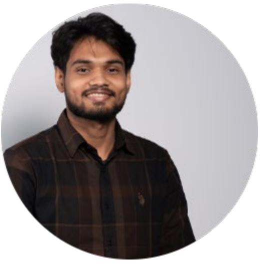
Together, we discovered a previously uncharacterized CRY/LOS1/C2H2-1 transcription module that controls the initiation of first cell division in Marchantia life cycle.

1.8

Mechanistic insights into the role of IPK1 in plant thermomorphogenesis.

Riya Ghosh ORCID iD
Indian Institute of Science, Bengaluru, India

Inositol hexakisphosphate ($InsP_6$), also known as phytic acid, is the fully phosphorylated form of inositol and represents the most abundant inositol phosphate in the studied plant tissues. InsP6 controls a wide range of physiological processes, including plant growth and development. In Arabidopsis thaliana, loss-of-function mutants of IPK1 exhibit multiple growth and developmental abnormalities. However, the molecular mechanisms underlying these physiological processes remain largely unexplored. Whether the role of IPK1-derived $InsP_6$ in regulating plant growth is conserved across land plants is yet to be explored. Our parallel investigation using Marchantia polymorpha, one of the first land plants and the flowering eudicot Arabidopsis thaliana is poised to address some of these open questions. Our findings reveal that the role of IPK1 in growth and development is conserved between these evolutionarily distant species. Furthermore, we demonstrate that the catalytic activity of IPK1 is critical in both species for thermomorphogenesis, an adaptive response of plants to cope up with elevated temperatures. My current ongoing efforts to identify cellular targets of IPK1 are likely to provide mechanistic insights into IPK1-controlled thermomorphogenesis and plant development.



1.9

Identification of regulators of de-novo meristem formation in *Marchantia polymorpha*

Soumavo Dolui
Gregor Mendel Institute of Molecular Plant Biology, Austria

The haploid body of *Marchantia polymorpha* develops from unicellular spores and forms a meristem de novo from which the body of the plant develops. The development of the meristem is not surrounded by parental tissue, like the meristems in embryos of angiosperms, making it a tractable experimental system in which to discover mechanisms of meristem initiation. While much is known about the mechanisms controlling meristem function once initiated, little is known about molecular mechanisms that control the development of meristems from non-meristem cells. This research aims to describe the molecular mechanism that promotes meristem development. Transcriptomic profiling across developmental stages established a pseudotime trajectory of sporeling development, revealing a distinct "transition state", associated with the meristem formation, marked by coordinated activation of several gene modules. Integrating single-cell transcriptomic data with the sporeling time-course dataset provided both temporal and cell-type-specific resolution, showing similar gene expression behaviors across datasets. This combined approach identified a *GRF* transcription factor as a potential regulator of the pre-meristem to meristem switch. Reporter lines for genes expressed specifically in pre-meristem (e.g., *POD38*) and meristem (*LTP-like66*) cells highlight dynamic gene expression shifts. For example, several genes encoding *LIPID TRANSFER PROTEINS* (*LTP*s) serve as markers for distinct cell-types that exist in the pre-meristem population before meristems develop. Our analysis identifies key regulatory signatures underlying meristem initiation, offering new molecular insight into de-novo meristem formation.

2.1

Cracking the phototropin phosphocode: reversible phosphorylation in directional light signalling

John Christie
University of Glasgow, United Kingdom

Plants rely on blue-light photoreceptors known as phototropins to fine-tune growth and photosynthetic efficiency in response to changing light conditions. These serine/threonine kinases initiate signalling at the plasma membrane through dynamic protein phosphorylation, driving directional responses such as phototropism (growth towards blue light) and chloroplast accumulation (repositioning to the upper cell surface under low light). Central to these responses are members of the NPH3/RPT2-like (NRL) family, which act downstream of phototropins. NPH3 is essential for phototropic curvature, while RPT2 and NCH1 coordinate chloroplast positioning. We have shown that phototropins phosphorylate these NRL proteins at a conserved C-terminal motif, and recently identified two Clade L TYPE 2C PROTEIN PHOSPHATASES (PP2Cs) that specifically mediate their dephosphorylation. Loss of these PP2Cs results in sustained NRL phosphorylation, disrupting both phototropic growth and chloroplast movement. These findings uncover a critical layer of regulation in the phototropin signalling network, highlighting reversible phosphorylation as a key mechanism for decoding directional light cues. Moreover, this reversible phosphorylation by Clade L PP2Cs appears to represent an evolutionarily conserved mechanism among phototropin-NRL targets, coordinating diverse light-directed movement responses that are pivotal for plant development and environmental adaptation.

Biography

John obtained his BSc Honours degree in Biochemistry at the University of Glasgow, which stimulated his interest in receptor proteins and cell signalling. He stayed in Glasgow for his PhD studies in Molecular Biology, funded by the Gatsby Charitable Foundation, investigating how UV/blue light regulates the expression of flavonoid biosynthesis genes in plants. He was especially interested in understanding how proteins known as photoreceptors convert photons of light into molecular signals that trigger a multitude of different physiological processes. At this time, little was known about the molecular basis of plant UV/blue light receptors. This fascination led him on an academic career to uncover the molecular identity and photochemical properties of these enigmatic photoreceptor proteins. He completed his postdoctoral position with Winslow Briggs at the Carnegie Institution of Washington, Stanford in 2002 and returned to Glasgow to take up a Royal Society University Research Fellowship to continue his research on natural and synthetic photoreceptor systems where he currently holds a professorship in Photobiology.

2.2

Loss-of-function RUP-variants influence ubiquitin-proteasome system and enhance carotenoid and folate levels in tomato

Yellamaraju Sreelakshmi
University of Hyderabad, India

REPRESSOR OF UV-B PHOTOMORPHOGENESIS (RUP) negatively regulates UV-B signalling, yet its broader physiological roles in crop plants remain largely unexplored. We compared two tomato accessions bearing truncated RUP protein, *rup-1* and *rup-2* (*rup-* variants), with the cultivar Arka Vikas (AV), which harbours the native RUP protein. *rup*-variants seedlings exhibited enhanced tolerance to supplemental UV-B light. Red ripe (RR) fruits of *rup*-variants showed significantly higher carotenoid and folate levels than AV. Introgressing *rup*-variants into AV confirmed that the increased carotenoid accumulation is genetically linked to RUP truncation. Metabolomic profiling revealed a major shift in primary metabolism in *rup*-variants, particularly at the breaker stage, with pronounced reduction in sugars and amino acids. Proteomic analyses of *rup*-variants fruits identified that a significant proportion of differentially expressed proteins belonged to chaperones and ubiquitin-proteasome system (UPS). Our results suggest that RUP modulates metabolic pathways during fruit ripening, and its loss triggers metabolic reprogramming associated with elevated folate/carotenoid levels.

Biography
My research group utilizes functional genomics to investigate tomato development, with a particular focus on fruit ripening and plant architecture. We are especially interested in how light regulates these processes. By combining genomics and proteomics approaches, we identify, isolate, and characterize novel alleles of candidate genes that influence key traits such as plant and inflorescence architecture, carotenoid and folate accumulation, and the shelf life of tomato fruits.

2.3

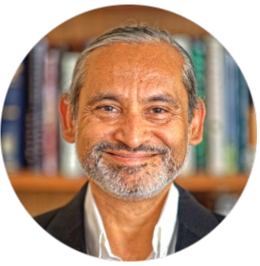
Integrative isotopic and metabolomic profiling illuminates metabolic strategies of UV-B stress adaptation in Arabidopsis

Shyam Masakapalli ORCID iD
Indian Institute of Technology Mandi, India

Ultraviolet-B (UV-B) radiation shapes plant growth and stress adaptation, yet its impact on metabolic dynamics remains poorly resolved. By integrating metabolomics, kinetic $^{13}CO_2$ tracer-based metabolic mapping, and morpho-physiological analyses, we uncovered UV-B–induced metabolic rewiring in *Arabidopsis* wild type and UV-tolerant BBX31 genotypes. While wild type plants exhibited broad metabolic perturbations, BBX31 lines modulated photosynthetic metabolites, reduced TCA cycle intermediates, and enhanced GS/GOGAT and secondary metabolic pathways. $^{13}CO_2$ tracing revealed BBX31-mediated flux redistribution toward phenylpropanoid and GS/GOGAT pathways, supporting the accumulation of protective metabolites such as phenylalanine, oxoproline, and glutamine. Although metabolomics indicated increased branched-chain amino acids (BCAAs) under UV-B, negligible ^{13}C incorporation suggested their origin from pre-existing pools or protein degradation. Notably, exogenous phenylalanine application, identified as a marker metabolite, improved plant tolerance under UV-B. Collectively, these findings highlight BBX31-driven metabolic reprogramming under UV-B stress and offer strategies for targeted metabolite enrichment and metabolic engineering to enhance UV-B resilience in plants.
https://orcid.org/0000-0003-1988-5569

Biography

Shyam K Masakapalli is a Professor and Dean R&D (SRIC) at Indian Institute of Technology Mandi. He served as the founding Chairperson of the School of Biosciences and Bioengineering (2022-24). His core expertise is in the areas of Metabolic Systems Biology of Plants and microbes with focus on cellular metabolism, Metabolomics, 13C Fluxomics, Phytochemistry, cellular bioprocessing and Agrotechnologies. He served as a Board of Editor in ASM Journal mSystems (2023-2025). He supervises PhD, Postdocs, MTech and BTech scholars at Metabolic Systems Biology Lab (MSBL). He also served as a course coordinator of MTech Biotechnology, and Faculty advisor of BTech-MTech Bioengineering that led to successful MTech Biotechnology and BTech Bioengineering programs. He received “Distinguished Teacher Award” at IIT Mandi and executed ~16 prestigious projects funded by ECR-SERB, DBT-BMBF, IMPRINT, SPARC, DBT-FarmerZone, DST-SaiAFARM etc. He has been instrumental in establishing the Botanical Garden at IIT Mandi which is also supporting his quest to identify novel "Himalayan Phytochemicals" for a range of applications. Prof Masakapalli received PhD in Plant Sciences from the University of Oxford (Supervisors: Prof. George Ratcliffe and Dr. Nick Kruger) in 2012. He worked as a Postdoctoral fellow (2011-2015) first at the University of Oxford (with Dr. Lee Sweetlove) and later at the University of Bath, UK (with Prof. David Leak and Prof. Michael Danson) until he joined IIT Mandi in 2015 as Assistant Professor. He did his M.Tech at IIT Kharagpur in the department of Agriculture and Food Engineering in 2007.



2.4

Anesthetic block of phototropism involves disruption of microtubules, revealing critical mechanisms of how anesthesia acts to suppress consciousness in humans

Rajnish Khanna ORCID iD
Carnegie Institution for Science, Stanford, USA. i-Cultiver, Inc., Manteca, USA

Anesthetics used in humans and animals have previously been shown to depress respiration, inhibit plant growth and immobilize leaf movement, in a reversible manner. Animals and plants share a common ancestor 1.6 billion years ago as well as numerous molecular targets associated with structural proteins, signaling pathways and metabolic enzymes. For this reason, it has been proposed that plants could provide a simplified (reduced) experimental system to understand how anesthetics work at the molecular level. We are taking a systematic approach with different concentrations of isoflurane to identify basic mechanisms linked to disruption of specific environmental responses using the model plant *Arabidopsis thaliana* (mouse cress). Arabidopsis plants expressing GFP-TUBULIN showed that isoflurane disrupts microtubule dynamics linked to phototropism and young seedling development. Further, we found that GFP-labeled microtubules in *constitutively photomorphogenic 1* (*cop1*, lacking E3 ubiquitin ligase activity) mutants exhibit tolerance to isoflurane. Plant microtubules are known to play essential roles in responding to environmental stimuli. In central nervous systems, like ours, isoflurane targets multiple sites, but the underlying mechanisms of anesthetics remain a mystery. Furthermore, mechanisms of anesthetic activity may inform us of basic processes involved in consciousness, since all anesthetics block consciousness.

2.5

Illuminating hidden layers of light signalling: functional analysis of PHOTOTROPIN2 promoter via CRISPR/Cas9-mediated editing

Kunnappady Princy ORCID iD
University of Hyderabad, Hyderabad, India

Phototropin 1& *2* are major blue light photoreceptors in higher plants, responsible for functions such as phototropism, chloroplast photorelocation, stomatal opening, leaf flattening, and leaf positioning. While the two photoreceptors exhibit functional redundancy, *phototropin2* is the crucial player under high-fluence conditions. Although their intrinsic functions were studied in depth in Arabidopsis, the regulatory mechanisms and signaling pathways governing these photoreceptors remain less understood in crop plants. Cis-regulatory dissection is an emerging field in reverse-genetics where the functional aspects of elements present upstream of a gene can be studied. In this study, we employed CRISPR/Cas9-mediated cis-regulatory dissection of the tomato *phot2* gene to investigate the contribution of non-coding promoter elements to light-dependent signaling. Targeted editing generated multiple alleles of the *phot2* promoter, enabling functional evaluation of distinct cis-elements. Besides the expected defects in PHOT2-mediated responses, we observed significant pleiotropic phenotypes. Leaf flattening response, phototropism, and chloroplast photorelocation responses were significantly disrupted across all edited lines. Our results demonstrate that non-coding regulatory elements are critical for precise modulation of *phot2* expression and associated physiological functions. Our study reveals previously unrecognized layers of photoreceptor regulation and provides valuable insights with potential applications in crop improvement.

2.6

Role and functions of CONSTANS-LIKE B-Box family transcription factors in UVR8 signaling

Rucha Kulkarni ORCID iD
University of Geneva, Geneva, Switzerland

Plants perceive UV-B radiation through the evolutionarily conserved photoreceptor UV RESISTANCE LOCUS 8 (UVR8). Active UVR8 monomers interact with and inactivate the E3 ubiquitin ligase CONSTITUTIVELY PHOTOMORPHOGENIC 1 (COP1), initiating a transcriptional response. In the green alga *Chlamydomonas reinhardtii*, CrCOP1 inactivation stabilizes downstream targets like CrCONSTANS (CrCO), a key B-box (BBX) family transcription factor mediating photoprotection. In contrast, in *Arabidopsis thaliana* UV-induced photomorphogenic and photoprotective responses are mainly regulated by the bZIP family transcriptional regulators ELONGATED HYPOCOTYL 5 (AtHY5) and HY5 HOMOLOG (AtHYH), whereas the roles of BBX family members seem to be less prominent. Six close homologs of CrCO in *Arabidopsis* — members of structural group I — interact with AtCOP1 and are UV-B-stabilized. However, their single mutants showed no major UV-B phenotypes, suggesting functional redundancy. To test this, I generated higher-order combinatorial mutants. Transcriptomic analyses revealed that At*bbx123456* mutant exhibited reduced UV-B responses and associated specific photomorphogenic phenotypes. To further explore the evolution of CO-like functions under UV-B, CrCO homologs were also examined in *Marchantia polymorpha*. I will present our latest understanding of the roles of CONSTANS homologs in UV-B signalling across the green lineage, bridging molecular mechanisms with evolutionary insight.

3.1

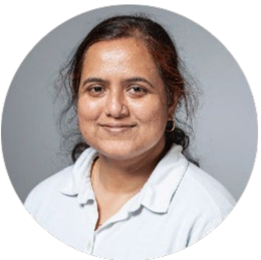
Glutathione at the crossroads: integrating redox and light signals to control ethylene biosynthesis

Riddhi Datta
Postgraduate Department of Botany, Barasat Government College, India

Ethylene biosynthesis is finely regulated through multi-level control of key enzymes 1- aminocyclopropane-1-carboxylate synthase (ACS) and oxidase (ACO). Cellular redox state, particularly glutathione (GSH), and light signaling pathways closely interact to dynamically modulate ethylene production in plants. Glutathione acts as a crucial signaling molecule that transcriptionally upregulates ACS2 and ACS6 via WRKY33 and stabilizes ACO1 at both mRNA and protein levels through S-glutathionylation, enhancing ethylene biosynthesis during stress. Concurrently, the E3 ubiquitin ligase COP1 mediates light-dependent degradation of ACS2/6 proteins in darkness, reducing ethylene synthesis post-translationally. Recent studies reveal that COP1 itself is subject to S-nitrosylation, which inhibits its ubiquitin ligase activity, leading to COP1 repression and promotion of photomorphogenesis. PHYTOCHROME INTERACTING FACTORS (PIFs) further regulate ACS gene transcription in light-responsive manners, integrating additional layers of ethylene regulation. This concerted glutathione–NO–light signaling crosstalk provides a robust molecular framework by which plants balance growth, development, and stress adaptation via precise modulation of ethylene biosynthesis. This talk will discuss the molecular interplay and physiological outcomes of this integrated regulatory network, highlighting the expanding roles of redox post-translational modifications such as Snitrosylation in controlling key signaling hubs like COP1.

Biography

Dr. Riddhi Datta is an Assistant Professor in the Post Graduate Department of Botany at Barasat Government College. She has a Ph.D. in Biological Sciences from CSIR-Indian Institute of Chemical Biology and her research focused on the role of glutathione in mitigating stress response in Arabidopsis thaliana. Her research interests include exploring glutathione-mediated signaling in plants, and understanding how lectins provide abiotic stress tolerance. She has published numerous research papers and a book chapter on these topics. She was a gold medalist in both her Undergraduate and postgraduate studies from University of Calcutta. She has received several awards, including the INSA medal for Young Scientists (2017), Women Excellence Award from the SERB, Government of India (2020), Young Botanist Award from the Indian Botanical Society (2021), Indian National Young Academy of Sciences (INYAS) Membership (2024), and National Academy of Science, India (NASI) membership (2025). Dr. Datta is a science communicator regularly contributing to popular science through various articles published in magazines and newspapers like *Science Reporter*, *The Telegraph*, *The Wire*, and *The Statesman*.



3.2

Decoding the potential of post-translational modifications in fine-tuning plant growth and development

Moumita Srivastava
Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, India

Post-translational modifications (PTMs) function as critical molecular switches, enabling plants to decode environmental cues through intricate signalling networks that fine-tune protein stability, activity, interactions, and localisation. Among these, modification by the small ubiquitin-like modifier (SUMO) has emerged as a key mechanism for rapidly reprogramming molecular pathways during stress responses. SUMO attachment to target proteins occurs through a cascade of enzymatic steps—activation, conjugation, and ligation—closely resembling ubiquitination. Importantly, SUMOylation is reversible: SUMO-specific proteases can remove SUMO moieties from substrates, conferring plasticity to signalling pathways that adapt to fluctuating environments. In this talk, I will discuss how SUMOylation of transcription factors serves as a conduit through which environmental signals modulate hormone signalling, allowing plants to balance growth and development with surgical precision.

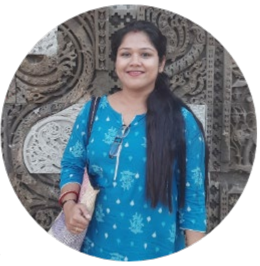
Biography
Dr. Moumita Srivastava is a Scientist-C at the Rajiv Gandhi Centre for Biotechnology (RGCB), Thiruvananthapuram, India. She earned her PhD in Biotechnology from the National Institute of Technology, Durgapur, and has carried out research at Durham University, Rothamsted Research, and Iksuda Therapeutics in the UK. Her laboratory focuses on plant growth and stress biology, with a particular interest in how post-translational modifications (PTMs) regulate signaling crosstalk during environmental stress responses. She is a recipient of the DBT-Ramalingaswami Fellowship and the DST-National Postdoctoral Fellowship, and has published her work in leading journals including *The Plant Cell, PNAS, Current Biology, Journal of Experimental Botany*, and *Plant Cell Reports*.

3.3

Analysis of the COP1/SPA–photoreceptor complex formation in *Arabidopsis thaliana*

Ira Trivedi ORCID iD
Institute for Plant Sciences, University of Cologne, Cologne, Germany

Light is a central regulator of plant development, controlling transitions from germination to flowering. Photoreceptors such as phytochromes and cryptochromes detect specific wavelengths and, upon activation, inhibit the CONSTITUTIVE PHOTOMORPHOGENIC (COP1)/SUPPRESSOR OF PHYA-105 (SPA) complex, a central repressor of light signalling. In darkness, the COP1/SPA complex functions as an E3 ubiquitin ligase, targeting positive regulators of photomorphogenesis for degradation. Although light-induced inhibition of COP1/SPA by photoreceptors is well established, the underlying mechanisms remain only partially understood. A key aspect is the direct interaction of phytochromes with SPA1, which disrupts the COP1–SPA1 association. My research focuses on dissecting this process at multiple levels. Using yeast three-hybrid assays, I identified the SPA1 N-terminus as essential for PhyA-mediated, red-light-enhanced dissociation of COP1–SPA1. Intramolecular FRET-FLIM analyses suggest that phytochrome binding induces conformational changes in SPA1, further destabilizing the complex. To validate these competitive interactions in planta, I am establishing in vivo approaches, including Split-Luciferase and FRET-FLIM. In parallel, I am characterizing the effects of missense mutations in the SPA1 N-terminal domain on complex formation and function. Finally, I am developing proximity labelling strategies to define the COP1/SPA1 proteome, aiming to uncover novel regulators of light signalling.



3.4

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

Annayasa Modak ORCID iD
IISER-Kolkata, Mohanpur, India

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

4.1

Light as an architect: How light quality shapes plant structure

Ullas Pedmale
Cold Spring Harbor Laboratory, USA

Roots and shoots thrive in distinct environments; nevertheless, roots possess the ability to sense adverse environmental conditions encountered by the shoots. The Shade Avoidance Response (SAR), induced by sub-optimal light conditions emanating from nearby vegetation, prompts the rapid growth of stems and petioles to optimize light absorption. However, this response also results in compromised root growth, thereby affecting the overall performance of plants negatively. Despite the pivotal role of roots in plant growth and productivity, there is limited knowledge regarding the mechanisms influencing root growth when shoots detect alterations in light conditions. Recognizing the significance of roots in the broader context of plant development, we aimed to unravel the mechanisms through which vegetative shading impacts root growth. To achieve this, we created a high-resolution spatiotemporal transcriptome map of shade-grown plant roots using single-cell RNA sequencing. This approach allowed us to unveil tissue-specific programs that impede root growth under shade. Our investigation revealed that the epidermal and pericycle cell types exhibited the most pronounced responses to shading. Furthermore, we identified several cell-type-specific transcriptional programs that collaboratively contribute to the inhibition of root growth under shaded conditions. This research enhances our understanding of how roots adapt to environmental cues and provides valuable insights for optimizing plant growth and productivity in varying light environments.

Biography

Dr. Ullas Pedmale is an Associate Professor at Cold Spring Harbor Laboratory, in New York, USA. He leads a research program dedicated to understanding how organisms integrate environmental and endogenous signals to regulate growth and development. Understanding growth not only helps improve agricultural yield but also cancer, which is uncontrolled growth in mammals. Using plants as a model system, his lab investigates how cues such as light, temperature, and nutrient availability interact with intrinsic developmental programs to shape plant architecture and physiology. His multidisciplinary approach combines molecular genetics, genomics, developmental biology, and physiology to uncover fundamental mechanisms of plant adaptation.

4.2

Investigating the role of miR166-HD-ZIP III module in tuber shape, colour and productivity in potato

Anjan Banerjee
IISER Pune, India

Tuberization (potato tuber development) is a highly dynamic and complex process. During inductive photoperiodic condition (short-day), a modified stem (stolon) develops from a belowground part and undergoes through a complex transition process (stolon-to-tuber) and finally develops a mature potato. The above ground shoot generates plethora of signals, which selectively transports from leaves to the below ground developing stolons and trigger tuber development. This process is tightly regulated by a combination of environmental, hormonal, and molecular factors. In past, we have identified several mobile signals (mRNAs, miRNA, TFs) that either positively or negatively regulate tuber development. Based on our small RNA datasets, some of the key miRNA's role has also been explored in stolon-to-tuber transition process. Previously, we showed that *miR156* overexpression (OE) develops profuse aerial stolons and tubers from axillary meristems under short-day (SD) photoperiod but contrary, reduces below-ground tuber yield. Subsequently, we demonstrated that PcG Proteins MSI1 and BMI1 function upstream of *miR156* to regulate aerial tuber formation in potato and emphasized the role of photoperiod and epigenetic mechanism in governing both aerial and belowground tubers. Recently, we have identified a unique functional role of miR166–HD-ZIP III module in potato and its pleiotropic effects on growth and development. Specifically, we observed that *miR166* is essential for regulating key developmental traits including plant height, vascular patterning, leaf curvature, and root architecture. Interestingly, we observed that miR166–HD-ZIP III module alters tuber shape, colour, and overall productivity in potato. I will summarize our efforts in deciphering the role of key miRNAs in potato development.

Biography

Anjan is the Rahul Bajan Chair Professor in the Biology Division of the Indian Institute of Science Education and Research (IISER Pune). He is a Fellow (FNA) of the Indian National Academy of Science, New Delhi. His research interest include Plant developmental biology, Micro RNA (miRNA) and gene regulation, Long distance signalling and plant-pathogen interaction

4.3

Blue light turns on iron uptake: uncovering the CRY–HY5 regulatory network in *Arabidopsis thaliana*

Santosh Satbhai
IISER Mohali, India

Iron (Fe) is an essential micronutrient for nearly all living organisms, and its deficiency poses a major threat to crop productivity and human health. While the mechanisms underlying Fe uptake and accumulation are well characterized, the influence of environmental cues, particularly light, on Fe homeostasis remains largely unexplored. In this study, we demonstrate that blue light enhances Fe accumulation and thereby positively regulates Fe homeostasis in *Arabidopsis thaliana*. Under Fe-limiting conditions, blue light specifically promoted root elongation, whereas red light had no such effect. We identified that this blue light–induced response is mediated by the transcription factor HY5 (Elongated Hypocotyl 5), a member of the basic leucine zipper (bZIP) family of transcription factors. The *HY5* mutants exhibited markedly reduced root elongation and Fe accumulation under blue light compared with wild-type plants grown under Fe-limiting conditions, highlighting the crucial role of HY5 in this process. Furthermore, we show that blue light photoreceptors CRY1 and CRY2 act upstream of HY5 to regulate Fe uptake. Overall, our results reveal that the CRY–HY5 signaling module links light perception to nutrient acquisition through a novel light-dependent mechanism regulating Fe homeostasis. These insights provide a foundation for developing strategies to optimize light environments to enhance Fe uptake and improve the nutritional quality of crops.

Biography

Dr. Santosh Satbhai is an Associate Professor in the Department of Biological Sciences at the Indian Institute of Science Education and Research (IISER) Mohali. He earned his PhD in Plant Genetics from Nagoya University (Japan) and pursued postdoctoral research at world-renowned institutes, including the Gregor Mendel Institute (Vienna) and the SALK Institute (San Diego). His current research focuses on understanding root development and plant responses to environmental signals using genetic, genomic, and biochemical approaches. Dr. Satbhai has published extensively in reputed international journals and contributes actively to the plant biology community. His work aims to unravel how plants integrate developmental cues with environmental information to optimise growth and survival.

4.4

Balancing cell renewal and immunity: cytokinin regulation of root cap function

Eswarayya Ramireddy
IISER Tirupati, India

The root system plays a vital role in below-ground communication with microbes and neighbouring plants, with the root cap serving as the primary interface with the soil. Despite its small size, the root cap is critical for sensing environmental cues, supporting beneficial microbial interactions, and preventing pathogen invasion. A precise balance between cell division, differentiation, and death is essential for its function, as deviations disrupt root growth and communication. Our research investigates how cytokinin regulates this balance in root cap tissue. By reducing cytokinin levels, we demonstrated its necessity in coordinating cell renewal and programmed cell death. Interestingly, many soil-borne pathogens and insects manipulate cytokinin status and signalling at the root tip to gain entry. Using tissue-specific proteomics, we identified root cap–specific Jacalin-Associated Lectins (JALs) as key regulators of stress and immunity. Some JALs mediate salt-induced ER stress, while others influence pathogen interactions. Their expression is oppositely regulated by auxin and cytokinin, linking hormonal control to both root architecture and immune responses. Functional studies revealed that certain JALs act as susceptibility genes in *Ralstonia solanacearum*-mediated bacterial wilt. In my presentation, I will highlight the cytokinin's regulation of root cap growth and development. In addition, I will discuss root cell-type specific immune responses to soil-borne pathogens and the signalling networks involved at the cellular level. Furthermore, I will discuss our attempts to translate this basic research to crop plants to combat soil-borne pathogens.

Biography
Eswarayya (Eswar) Ramireddy is a faculty member in Biology at IISER Tirupati, where he leads the Plant Functional Genomics Lab. His research focuses on the molecular and genetic mechanisms that shape root system architecture and on engineering root traits to enhance crop performance under both abiotic and biotic stresses. His group works with key crop species such as tomato, rice, and finger millet, with a strong emphasis on translating fundamental discoveries “lab-to-land” to achieve tangible agronomic gains.

4.5

Epigenetic and molecular mechanisms of iron deficiency response: implications for light-regulated development in plants

Surjit Singh ORCID iD
Sister Nivedita University, Kolkata, India

Plant productivity is fundamentally constrained by the complex and dynamic interplay between light signals and micronutrient availability, particularly iron (Fe). Understanding this molecular crosstalk and developmental plasticity is critical for engineering high-yielding, climate-resilient crops.

My doctoral and postdoctoral work established that plants utilize an epigenetic 'memory' system to integrate these two signals. Specifically, in *Arabidopsis thaliana*, we demonstrated that Histone H3 Lysine-4 Trimethylation (H3K4me3) controls the expression of *GRF11* and that the transcriptional regulator NON-RESPONSE TO Fe DEFICIENCY 2 (NRF2) acts as a central hub, precisely coupling cellular iron status with light-driven developmental transitions like flowering time.

These discoveries provide the first clear molecular evidence that nutrient stress imprints a chromatin-based memory, allowing plants to adjust their developmental pace to maximize fitness under suboptimal Fe and light conditions.

We are now actively translating this mechanistic insight to the staple crop, rice. Our current efforts involve characterizing and manipulating candidate chromatin modifiers to genetically reprogram the iron-light sensing module. This translational strategy aims to unlock improved Nutrient Use Efficiency (NUE) and stress resilience in paddy systems, directly addressing challenges in global food security.

This presentation will facilitate discussion on integrating light and nutrient signaling, offering novel, epigenetically-driven strategies for manipulating crop development and enhancing productivity under challenging environmental conditions.

Biography

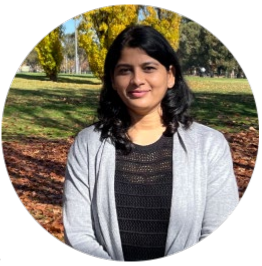
Dr. Surjit Singh is an Assistant Professor (Grade III) in the Department of Biotechnology at Sister Nivedita University, Kolkata, India. He holds a Ph.D. in Biotechnology from the Taiwan International Graduate Program – Molecular and Biological Agricultural Sciences, jointly conducted by Academia Sinica and National Chung Hsing University, Taiwan. His doctoral research elucidated the role of NON-RESPONSE TO Fe DEFICIENCY2/EARLY FLOWERING8 in regulating iron homeostasis and flowering time in Arabidopsis thaliana. Following his Ph.D., Dr. Singh pursued a Postdoctoral Fellowship at the Agricultural Biotechnology Research Center (ABRC), Academia Sinica, focusing on the molecular mechanisms of nutrient signaling and stress response in plants. His current research interests encompass plant physiology, stress biology, molecular genetics, and high-throughput genomics, with a particular emphasis on nutrient homeostasis and sustainable agriculture. Dr. Singh has published extensively in high-impact journals, including *New Phytologist, Chemosphere, Scientific Reports*, and *Journal of Hazardous Materials*, and has contributed several review articles and book chapters as a corresponding author. He is the recipient of multiple awards, such as the Academia Sinica Postdoctoral Fellowship and several outstanding poster presentation awards. He is currently the Principal Investigator of a DST-SERB-SRG-funded research project (2024–2026) on histone methylation-mediated regulation of iron deficiency responses in rice. In addition to his research, Dr. Singh is actively involved in academic mentoring, departmental administration, and organizing scientific conferences. He also serves as a reviewer and editorial board member for reputed international journals, contributing to the advancement of plant and environmental biotechnology research.

4.6

Light promotes and dark inhibits aluminium resistance in Arabidopsis

Debojyoti Kar
Indian Institute of Science Education and Research Bhopal, Bhopal, India

Aluminium (Al^{3+}) ions under acid soil are a major threat to crop production. Aluminium (Al) toxicity inhibits primary root elongation, however if light regulates this process is not known. We found that light, especially blue light, promotes Al resistance by lowering internal Al accumulation in the roots. Blue light enhances HY5 and STOP1 accumulation in Al treated roots. HY5 induces *ALMT1* and *MATE* expression by directly binding to their promoter and enhances carboxylate exudation to exclude Al. In darkness, the aluminium (Al)-mediated root growth inhibition is enhanced. COP1 physically interacts with STOP1 and degrades it to inhibit Al resistance in the dark. The accumulation of HY5 in the roots of Al-exposed plants is also downregulated in a COP1-dependent manner in the dark. *hy5* and *cop1* seedlings showhypersensitive and hyposensitive response to Al respectively, validating the role of these light signalling regulators in modulating Al resistance. Taken together, this study suggests that light promotes Al resistance by enhancing HY5 and STOP1 accumulation, whereas these proteins are degraded in the dark in a COP1-dependent manner to inhibit Al resistance. The light and dark mediated modulation of carboxylate exudation, might offer a unique way of balancing Al resistance and growth.



5.1

Priming-mediated molecular circuits regulating plant stress responses

Annapurna Devi Allu
IISER Tirupati, India

Climate change is advancing at an unprecedented pace, subjecting plants to increasingly frequent and intense episodes of heat stress. This poses a significant threat to global agriculture, food security, and ecosystem stability. Acquired thermotolerance, where prior exposure to mild, non-lethal heat stress (priming) enhances plant survival during subsequent severe stress, offers a promising adaptive strategy. Our findings suggest that this enhanced resilience is mediated by the establishment of robust cellular homeostasis. Recent research has revealed that acquired thermotolerance is governed by a complex regulatory network involving transcriptional, epigenetic, post-transcriptional, and metabolic pathways. However, the mechanisms by which priming-induced signals are sensed, processed, and integrated into these regulatory frameworks remain poorly understood. In our study, we explore how priming cues reshape transcriptional regulatory networks, enabling plants to reprogram gene expression and mount an effective stress response. Uncovering these regulatory mechanisms is key to both advancing fundamental plant biology and enabling the development of climate-resilient crops for sustainable agriculture.

Biography
Anu obtained her PhD in Molecular Biology from the University of Potsdam and the Max-Planck Institute of Molecular Plant Physiology, Germany, in 2014. She continued as a postdoctoral research fellow in the same “Gene-Regulatory Networks” research group at the Max-Planck Institute of Molecular Plant Physiology and the University of Potsdam, Germany, until January 2016. Later, she worked as a postdoctoral researcher at the University of Melbourne, Australia, before joining the Commonwealth Scientific and Industrial Research Organisation (CSIRO), ACT, Australia. After spending one year at CSIRO, she joined the Indian Institute of Science Education and Research (IISER) Tirupati in November 2018 as Assistant Professor in Biology, and now she is an Associate Professor in Biology and Associate Dean of International Relations at IISER Tirupati.

5.2

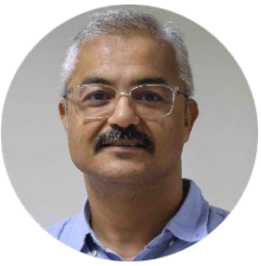
A novel insight into light and temperature mediated plant development by Auxin Binding Protein 1

Kishore Panigrahi
NISER, Bhubaneswar, India

The role of Auxin mediated responses through Auxin Binding Protein 1 (ABP1) has remained controversial. Although several studies over decades have shown its involvement in processes like cell elongation, root bending, leaf venation, membrane hyperpolarization etc., a relatively recent report from Mark Estelle's group, using CRISPR/CAS gene editing has claimed that ABP1 has no role under standard growth conditions in *Arabidopsis*. The earlier works were supported by a T-DNA insertional embryo lethal mutant lines of ABP1. Although we agree and confirmed his claims to be correct fully, here we investigated further its possible role in other specific light and temperature regime during *Arabidopsis* development. In the current presentation, the novel role of ABP1 will be discussed from some of our unpublished data. We found a distinct role of ABP1 under red light-enriched and colder growth paradigms in *Arabidopsis*.

Biography

Dr. Kishore CS Panigrahi, Associate Professor in NISER, India. He also served as a Guest Professor and Mercator Fellow DGF, Germany at the Heinrich Heine University, Dusseldorf in 2022. He completed his PhD focusing on G-protein signaling in Funaria under the guidance of Prof. M.M. Johri from TIFR in 1998. After working as a Postdoc at the University of Lausanne, Switzerland, the University of Freiburg, Germany and as a Group leader at the Max-Planck Institute, Koln, Germany, he joined NISER in Dec 2009 as a permanent faculty member. At NISER, he has been instrumental in setting up a state-of-the-art facility for plant light signalling research. His group at NISER works to understand flowering time regulation, circadian clock and light-mediated developmental responses in Arabidopsis, rice, moss and Mung bean. He is also interested in drawing a molecular evolutionary paradigm in understanding light and hormone perception. He has served as the programme coordinator for the international cooperation programmes such as ERASMUS k107 with Croatia and also with MPIPZ and DAAD, Germany. He is honoured with the Global Faculty Award from Frei University Berlin, 2025, Germany.



5.3

Aggregate remodeling JDPs of *Arabidopsis thaliana*

Chandan Sahi ORCID iD
IISER Bhopal, Bhopal, India

Protein homeostasis is vital for survival under heat stress. While Hsp70s are central regulators of this process, the role of their J-domain protein (JDP) co-chaperones in plants is not well defined. We identified eight *Arabidopsis thaliana* orthologs of the yeast Class II JDP Sis1, six of which associate with heat-induced aggregates and co-localize with the disaggregase Hsp101. Using yeast prions as model substrates, these JDPs displayed distinct aggregate-remodeling activities, highlighting their evolutionary conservation and specialization. Among them, AtDjB3 emerged as a key regulator of HSR. Loss of *AtDjB3* impaired Hsc70-1 recruitment to aggregates, retaining HsfA1d in the cytoplasm and reducing its promoter occupancy at heat-inducible genes. Consistently, *atdjb3* mutants were thermosensitive, while AtDjB3 overexpression enhanced survival at 37°C. Our findings reveal that plants harbor multiple conserved JDPs with specialized disaggregation functions and establish AtDjB3 as a dual-function co-chaperone that promotes both aggregate clearance and Hsf-dependent transcriptional activation during heat stress.
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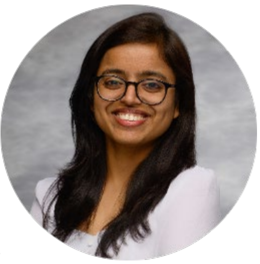
Biography

Dr. Chandan Sahi is an Associate Professor in the Department of Biological Sciences at the Indian Institute of Science Education and Research (IISER) Bhopal, where he also serves as Associate Dean, Research & Development. He earned his B.Sc. (Botany Hons) and M.Sc. in Plant Molecular Biology from the University of Delhi (South Campus), followed by a Ph.D. in Plant Molecular Biology from the same university. He pursued postdoctoral research and later worked as a Research Associate and Assistant Scientist at the University of Wisconsin–Madison before joining IISER Bhopal. His research focuses on stress biology and molecular chaperones, with particular emphasis on Hsp40s, also known as J-domain proteins, and their partnership with Hsp70s in plants, exploring their molecular specificity and evolutionary diversification. At IISER Bhopal, he leads the Chaperone and Stress Biology Laboratory.



5.4

Role of BBX protein as a molecular player in PIF4-HY5 crosstalk during Thermomorphogenesis

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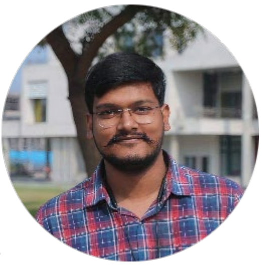
Plants are subjected to various climatic extremes during their growth, which influence their development. One of the most common effects of climate change is the increase in ambient temperatures, which plants are currently experiencing due to global warming. Numerous studies have shown that elevated temperatures impact plant morphology as they adapt to the warm environment. The phenotypic changes induced by higher ambient temperatures include increased hypocotyl length during early development, hyponastic leaf growth, longer primary roots, and earlier flowering. This phenomenon of morphological adaptation to high temperatures is known as thermomorphogenesis. PIF4 is considered the central regulator in this signaling pathway that promotes the expression of cell elongation genes. Previous studies also showed that HY5 is a negative regulator of genes promoting thermomorphogensis and COP1 upon sensing high temperature translocate in the nucleus and degrades HY5. In this study, we found that BBX28 protein gets induced by high ambient temperature and promotes cell elongation downstream to PIF4. Our findings indicate that under high ambient temperature, BBX28 acts similar to COP1 and inhibits HY5 to repress signaling of the plant hormone auxin, which results in the promotion of cell elongation and contributes to hypocotyl growth.



5.5

Unravelling the dynamics of plant circadian rhythms: integrating light intensity and temperature effects for seasonal adaptation in Arabidopsis

Shashank Kumar Singh ORCID iD
Indian Institute of Technology Gandhinagar, Gandhinagar, India

Circadian rhythms are self-sustained oscillations that allow plants to align their physiology and development with daily and seasonal cycles. In *Arabidopsis*, these rhythms arise from an intricate network of transcriptional and translational feedback loops. These loops consist of transcription factors such as CCA1, LHY, PRRs, TOC1, LUX, ELF3, and ELF4, as well as post-translational regulators including GI, ZTL, COP1, and photoreceptors. This network integrates multiple environmental signals, with light and temperature being the most prominent, influencing the clock's timing and stability.

In this study, we present an ODE-based mathematical model (M1) built on earlier frameworks, extended with newly identified regulatory interactions and components, and explicitly incorporating light (intensity and photoperiod) and temperature as entrainment signals. The model captures plant circadian dynamics under various light–dark cycles and thermocycles, reproducing characteristic changes in period, phase, and amplitude. By combining light and temperature regulation, the framework provides a way to investigate how the circadian system adapts to daily and seasonal changes and to fluctuating environments.

This work provides a systematic framework for linking environmental signals with circadian regulation and developmental outcomes. It offers a foundation for identifying critical interactions stabilising rhythmicity and guiding experimental efforts to understand plant adaptation to fluctuating environments.

5.6

Photoreceptor-mediated regulation of starch metabolism and crop productivity

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Light is a fundamental signal perceived by photoreceptors that regulate plant growth, metabolism, and stress adaptation. These proteins act as molecular sensors which couple environmental cues to regulatory networks. Deciphering the role of photoreceptors in such plant regulatory mechanisms is essential for effort aimed at optimising carbon allocation and improved crop productivity. We implemented an integrated experimental and analytical approach for understanding photoreceptor-mediated regulation of plant processes that can affect productivity. We assessed the impact of phytochrome deficiency on transitory starch metabolism in tomato through starch quantification and gene expression profiling under controlled light conditions. Our experimental analyses with tomato *phyA* and *phyB1* mutants showed that phytochrome deficiency impaired transitory starch metabolism coupled with altered expression of key genes involved in starch metabolism. Complementary review analyses synthesized findings on the manipulation of light environments to regulate photoreceptor activity as a tool for improved crop productivity, and on genetic engineering and optogenetic strategies to reprogram light signalling for crop improvement. Here, we connect mechanistic insights into photoreceptor-regulated starch metabolism with strategies for crop improvement, involving the integration of experimental evidence, light management, and receptor engineering as a framework to exploit light signalling for sustainable, climate-resilient agriculture.

6.1

Light-dependent regulation of secondary metabolism by HY5: a conserved mechanism across plant species

Prabodh Trivedi
CSIR-CIMAP, Lucknow, India

Plants produce a vast array of metabolites essential for growth and development. While primary metabolites support fundamental physiological processes such as germination, photosynthesis, and reproduction, secondary metabolites serve critical ecological roles, enabling plants to withstand diverse biotic and abiotic stresses. Although the biosynthetic pathways of these compounds are well characterized, their regulation by environmental cues, particularly light, remains less understood. Light triggers extensive transcriptional reprogramming in plants, influencing up to 35% of the genome through the action of transcription factors that bind to light-responsive elements (LREs) in gene promoters. Among these, ELONGATED HYPOCOTYL 5 (HY5), a bZIP transcription factor, acts as a master regulator of photomorphogenesis and secondary metabolism. Our studies reveal that HY5 extends its regulatory function beyond flavonoid biosynthesis to govern terpenoid and alkaloid production. In *Arabidopsis thaliana*, AtHY5 directly binds to the *AtSQS1* promoter, repressing squalene biosynthesis in a light-dependent manner. In *Nicotiana tabacum*, CRISPR/Cas9-mediated knockout ($NtHY5^{CR}$) and overexpression lines demonstrated that HY5 moves from shoot to root, regulating nicotine biosynthesis by activating root-expressed genes. Similarly, in *Solanum lycopersicum*, SlHY5 binds to G-box motifs in promoters of structural and regulatory genes involved in steroidal glycoalkaloid (SGA) biosynthesis. SlHY5 knockout mutants exhibited reduced SGA accumulation and increased pathogen susceptibility, whereas overexpression enhanced defense and flavonoid production. Collectively, these findings establish HY5 as a conserved regulator of light-dependent secondary metabolism across plant species, linking photomorphogenic signaling with metabolic reprogramming and stress adaptation.

Keywords: ELONGATED HYPOCOTYL 5; Light signalling; Secondary metabolism; Terpenoid and alkaloid biosynthesis; Transcriptional regulation

Biography

Dr. Prabodh Kumar Trivedi obtained his Ph.D. in 1994 from the CSIR-National Botanical Research Institute (CSIR-NBRI), specializing in chloroplast genomics. Following the completion of his doctoral research, he joined CSIR-NBRI as a Scientist and steadily advanced through various scientific and leadership roles. With over three decades of research experience in the field of plant genomics and biotechnology, Dr. Trivedi has made significant contributions to understanding and improving plant systems at the molecular level. He currently serves as the Director of CSIR-Central Institute of Medicinal and Aromatic Plants (CSIR-CIMAP), Lucknow, a premier research institute dedicated to the development of medicinal and aromatic plants for societal and industrial benefit. In addition, Dr. Trivedi is the Theme Director of the AgriNutriBiotech theme of CSIR and the Mission Director of CSIR's flagship project, the Aroma Mission, which aims to boost the cultivation, processing, and value addition of aromatic crops across India, thereby enhancing rural livelihoods and promoting sustainable agriculture.

6.2

A combination of regulatory processes driving anthocyanin accumulation in *Abg* tomato mutant

Himabindu Kilambi
NISER, India

Tomato fruit development and ripening is a complex process accompanied by several changes in pigment metabolism, accumulation of nutrient and flavor compounds that attribute to the overall fruit quality and nutritional value. Anthocyanins and carotenoids are light induced, effective nutritional antioxidants that are accumulated in the fruits, and contribute to mitigate the nutritional deficiencies for the people around the globe. In tomato Aubergine (*Abg* mutant), the fruit accumulates high levels of anthocyanin in comparison with Ailsa Craig (AC) wild type control. A MBW complex of transcription factors are responsible for the fruit color in *Abg*, but the regulation of the anthocyanin pathway and molecular factors affecting both carotenoid and anthocyanin is not well understood in this mutant. Through proteomic analysis, in *Abg* mutant fruits, we could identify increased abundance of proteins related to RNA and protein processing mechanisms in addition to the proteins regulating lipid metabolism and transport, which might be associated with enhanced pigment content. Targeted metabolomics analysis revealed increased accumulation of Cyanidin in the *Abg* fruit peel. Multiomics approaches are in progress to reveal the interplay of several regulators in this mutant that might lead to increase in nutritional quality of tomato fruits.

Biography
Dr. K Himabindu Vasuki, is an early career Plant Biologist and has worked with tomato, a model for fleshy fruit ripening as well as Arabidopsis, the gold standard reference, for several plant processes including metabolism and transport. She is an Assistant Professor in the School of Biological Sciences at NISER where she is attempting to understand the mechanism of fruit pigmentation, the accumulation of flavanoids in tomato varieties. Dr. Himabindu has unsurpassed research experience on tomato fruit ripening, where she could dissect a handful of candidates responsible for carotenoid accumulation in the fruits. Dr. Himabindu has been awarded with DST Inspire Faculty award, India and Tel Aviv International Post Doctoral Fellowship & honored as visiting scientist, Weizmann Institute to pursue her research in hormone metabolism and transport. Dr. Himabindu could successfully identify the unprecedented interactions between plant hormone transport-secondary metabolites-stress in Arabidopsis and Tomato during her post doctoral research. Dr. Himabindu's current research focuses on regulation of fruit flavanoids and investigating their role beyond stress adaptation towards enrichment.

6.3

BRL3 at the crossroads of growth and climate adaptation

Aditi Gupta
CSIR-NBRI, Lucknow, India

Brassinosteroid (BR) signaling is essential for plant growth and environmental adaptation. While the BRASSINOSTEROID-INSENSITIVE 1 (BRI1) receptor is well characterized, the functions of its cell/tissue specific homologs, BRL1 and BRL3, remain less understood. In Arabidopsis, we show that BRL3 is a key regulator of growth acclimation towards various environmental cues such as elevated temperature, photoperiod length, water availability etc. Loss of BRL3 impairs thermoresponsive elongation, and BRL3 signaling through BES1 modulates BR-responsive genes controlling growth, hormone balance, and stress adaptation. Tissue-specific complementation demonstrates that BRL3 activity in phloem companion cells is sufficient to restore thermomorphogenic responses. Transcriptomic analysis reveals that BRL3 orchestrates growth–stress trade-offs under stress conditions. These findings uncover a previously unrecognized phloem-localized BR signaling mechanism that fine-tunes thermal adaptation and extends the current understanding of BR receptor specificity, offering insights relevant to engineering climate-resilient crops.

Biography

Dr. Aditi Gupta is a Senior Scientist at the CSIR-National Botanical Research Institute (NBRI), Lucknow, where she leads research on how plants sense and adapt to their environment through complex signaling networks. Her research explores plant signaling mechanisms that underpin growth and environmental adaptation, with a particular focus on brassinosteroid receptor kinases and their roles in stress resilience. Dr. Gupta obtained her Ph.D. from National Institute for Plant Genome Research (NIPGR), New Delhi, where she elucidated the molecular cross-talk between sugar signaling and the steroid hormones in regulating early seedling development and fitness in Arabidopsis thaliana. As a postdoctoral researcher at the Centre for Research in Agricultural Genomics (CRAG), Barcelona, she uncovered new mechanisms linking brassinosteroid signaling with plant adaptation to drought and heat. She is a recipient of the INSA Medal for Young Scientist, NASI Young Scientist Platinum Jubilee Award, and the DST-INSPIRE Faculty Award. Her group integrates molecular genetics, physiology, and functional genomics to uncover new regulatory nodes in plant signaling networks aiming to develop climate-smart, high-yielding, and nutritionally robust crops.

6.4

Light-dependent modulation of secondary plant product biosynthesis and host-associated rhizospheric microbiome in plants

Akanksha Singh ORCID iD
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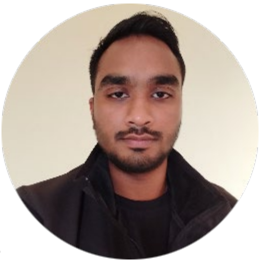
Plants continuously navigate their alliance with associated microbiomes to balance the intrinsic regulatory networks with changing environmental factors. Our study dissects the role of ELONGATED HYPOCOTYL 5 (HY5), a central transcription factor of light signalling in fine tuning photosynthesis, flavonoid expression, microbial recruitment and soil function under contrasting light and dark conditions using Wild type (WT), HY5 overexpression (SlHY5OX), and CRISPR knockdown (*SlHY5*^{CR}) lines of tomato at different time intervals. At 24 h, microbial diversity varied little across treatments, but by 72 h a marked shift emerged in darkness, with WT plants recruiting the highest diversity; likely compensating for reduced photosynthesis. Similarly, the *SlHY5*^{CR} lines showed reduced microbial diversity in light but a sharp increase with pronounced alkalinity in darkness, indicating greater microbial dependence when HY5 is impaired. Conversely, SlHY5OX lines exhibited a stable diversity pattern across both light and dark conditions, suggesting a reduced reliance on microbial interactions. The observations paralleled with flavonoid gene expression profile with HY5OX lines strongly inducing flavonoid pathway genes in light while *SlHY5*^{CR} lines counterbalanced under dark. Together, the results highlight the regulatory role of HY5 in maintaining a balance between light driven photosynthesis, flavonoid metabolism and microbial cooperation for shaping plant ecological resilience.

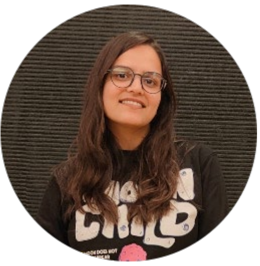


6.5

A light regulated Arabidopsis MATE transporter regulates the root hair development under low phosphate stress

Ajar Anupam Pradhan ORCID iD
Indian Institute of Science Education and Research, Bhopal, Bhopal, India

Light perception by the photoreceptors regulates the early seedling photomorphogenesis in land plants. The mechanism governing the early seedling establishment is well characterized in Arabidopsis, while the root photomorphogenesis is yet to be completely characterized. Recent studies have identified the role of light signaling factors e.g. - ELONGATED HYPOCOTYL 5 (HY5), to positively regulate the root hair development in coordination with the phytohormone auxin. We identified a light activated Multidrug and Toxic compound Extrusion (MATE) transporter MATE5, which is expressed in the root epidermal cells upon and positively regulates the root hair development. The promoter of *MATE5* contains G-box elements where HY5 binds and regulates its expression in response to light signaling and genetically HY5 acts upstream of MATE5. HY5 is reported to take part in the cross talk between light signaling and nutrient uptake, we also identified *MATE5* is inducible under low phosphate stress and HY5 gets enriched in the G-box in response to low phosphate as well to regulate the enhancement in the root hair production. Our study identified a novel light signaling mediated pathway regulating a MATE transporter to modulate the root hair development under low phosphate stress.



6.6

Shedding light on iron nutrition: light mediated regulation of Iron homeostasis in *Arabidopsis thaliana*

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Indian Institute of Science Education and Research, Mohali, Mohali, Punjab, India

Iron (Fe) is an essential element for almost all living organisms and its deficiency severely impacts crop productivity and human health. While the mechanisms underlying iron uptake and accumulation are well studied, the role of light in modulating iron homeostasis remains poorly understood. In this study we report that blue light enhances iron accumulation thereby positively regulating iron homeostasis in *Arabidopsis thaliana*. Under iron deficient conditions, root elongation is promoted specifically in blue light but not in red light. We further reveal that the transcription factor HY5 (Elongated Hypocotyl 5), mediates this blue light-driven response. The *hy5* mutants showed reduced root elongation under Fe limiting conditions and lower iron accumulation under blue light as compared to wild-type plants. Our findings suggest a pivotal role of HY5 in light mediated Fe uptake in plants. We further show that blue light photoreceptors CRY1 and CRY2 act upstream to HY5 to regulate iron uptake in Arabidopsis. Our work highlights a novel light-mediated regulatory mechanism for Fe acquisition. These insights offer promising avenues for optimizing light conditions to enhance Fe uptake and improve the nutritional quality of crops.

Keywords: Blue light signaling; Photoreceptors; Iron homeostasis; Root Development; HY5; Nutrient-Light interaction

7.1

The RDUF1/RDUF2 E3-ubiquitin ligases promote seedling photomorphogenesis via inhibiting PIF3/PIF4 activity in Arabidopsis

Sreeramaiah N Gangappa ORCID iD
IISER Kolkata, Mohanpur, India

Light exerts a profound influence on plant growth and development. The E3 ubiquitin ligases RING DOMAIN OF UNKNOWN FUNCTION 1117 1 (RDUF1) and RDUF2 function as positive regulators of photomorphogenesis by establishing a positive feedback loop with the key transcription factor HY5. Here, we identified an HY5-independent mechanism through which RDUF1 and RDUF2 promote seedling photomorphogenesis in Arabidopsis. We found that RDUF1 and RDUF2 suppress PHYTOCHROME INTERACTING FACTOR 3 (PIF3) and PIF4 activity. Genetic studies indicate that RDUF1 and RDUF2 function likely upstream to PIF3 and PIF4, as the hypocotyl lengths of *pif3pif4rduf1* and *pif3pif4rduf2* triple mutants resemble those in the *pif3pif4* double mutants. Further, our protein-protein interactions data confirmed direct physical interactions between RDUF1/RDUF2 and PIF3/PIF4. Moreover, biochemical experiments showed that RDUF1/RDUF2 promote the ubiquitination and subsequent degradation of PIF3 and PIF4 proteins, leading to their destabilization. In turn, reverse transcription quantitative PCR (RT-qPCR) and DNA-protein binding assays revealed that PIF3 and PIF4 directly recognize the G-box light-responsive element (LRE) in the promoters of *RDUF1* and *RDUF2* genes, thereby inhibiting their transcription, indicating a negative feedback loop to inhibit RDUF1/RDUF2 activity. Together, these findings establish the molecular link between RDUF1/RDUF2 with PIF3/PIF4, and also demonstrates PIF3/PIF4 as likely novel substrates for RDUF1/RDUF2-mediated ubiquitination and degradation, facilitating seedling photomorphogenesis in Arabidopsis.
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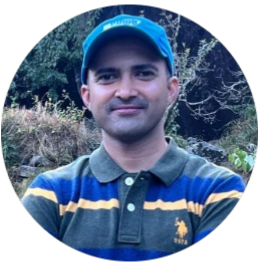
Biography

Dr. Sreeramaiah N. Gangappa is an Assistant Professor at the Indian Institute of Science Education and Research Kolkata (IISER Kolkata), West Bengal, India. He obtained his PhD from the National Institute of Plant Genome Research, New Delhi, India, followed by a postdoctoral fellowship at the University of Gothenburg (Gothenburg, Sweden) from 2009 to 2012 to work on the role of BBX proteins in light-mediated seedling development. Later, he moved to the John Innes Centre (Norwich, UK) with the prestigious Marie Skłodowska-Curie Fellowship to understand the temperature signaling mechanisms coordinating growth-defense trade-off in Arabidopsis until 2018, before moving to IISER Kolkata as an Independent faculty. Light and temperature are the critical ecological cues controlling plant growth, reproduction and fitness. The effect of light on plant growth and development, and the signaling integration mechanisms are well elucidated. However, the temperature integration mechanisms are poorly understood. Moreover, the cross-talk between light and temperature signaling is largely unexplored. Increasing seasonal temperatures due to global warming significantly impact plant health, resulting in poor yield and compromised disease resistance. Our lab is interested in understanding the mechanistic basis of temperature signalling mechanisms, temperature-light signalling cross-talk, and temperature-mediated regulation of growth and defence responses in Arabidopsis and crops.



7.2

Understanding chloroplast development: identification and characterization of the *CUE6* gene in Arabidopsis

Naresh Loudya
Indian Institute of Science, Bengaluru, India

Chloroplast biogenesis is tightly regulated by coordinated crosstalk between nuclear and chloroplast genomes, influenced by developmental cues and environmental factors such as light. This coordination ensures the transition of undifferentiated proplastids into photosynthetically active chloroplasts. Among various nucleus-encoded factors, multiple proteins of the tetratricopeptide repeat (TPR) family are essential for chloroplast development; however, the function of many remains unclear. In *Arabidopsis*, the chloroplast-defective mutant *cue6*, identified through forward genetic screening, exhibits a combination of virescence and reticulate leaf phenotypes and impaired vegetative growth. Phenotypic and cellular analyses of *cue6* revealed a diminished chloroplast compartment, particularly during early stages of development. Bulk segregant analysis and whole-genome sequencing identified a point mutation in a nuclear gene encoding a chloroplast-targeted TPR protein. A comparative transcriptome profiling in *cue6* showed upregulation of non-photosynthetic and downregulation of photosynthesis-related genes in both the nucleus and the chloroplast, indicative of a “juvenile” developmental state. Additionally, the *cue6* plastids showed significantly reduced mRNA editing efficiency in photosynthesis-related transcripts, while editing was enhanced at known sites in housekeeping gene transcripts. Taken together, our findings suggest that *CUE6* plays a critical role in plastid biogenesis. We are currently conducting further studies to elucidate its molecular function in chloroplast development.

Biography

Dr. Naresh Loudya is an Assistant Professor in the Department of Microbiology and Cell Biology at the Indian Institute of Science (IISc), Bengaluru. After completing a master's in Plant Biotechnology in India, he was awarded a PhD from Royal Holloway, University of London, under the guidance of Prof. Enrique López-Juez and Prof. Paul Jarvis (University of Oxford). Before joining IISc in 2022, he worked as a Postdoctoral Research Associate at Royal Holloway, in a joint project with the universities of Cambridge and Oxford. Dr. Loudya’s previous research has made significant contributions to understanding the series of molecular events underlying plastid development, the mechanism of protein import at the chloroplast inner membrane, and the true role of plastid-to-nucleus communication (“retrograde signalling”). His research group at IISc focuses on investigating early plastid biogenesis and how defects in plastids are communicated to the nucleus.

7.3

Do growth chambers mimic nature? A systems biology perspective on plant light responses

Yogesh Mishra
Banaras Hindu University, India

Plants display remarkable phenotypic plasticity, enabling acclimation to fluctuating environmental conditions. To investigate these adaptive responses, we compared *Arabidopsis thaliana* plants grown in the field with those cultivated under controlled low (LL, 30 µmol quanta m^{-2} s^{-1}), normal (NL, 300 µmol quanta m^{-2} s^{-1}), and high light (HL, 600 µmol quanta m^{-2} s^{-1}) conditions. Field-grown plants differed markedly from laboratory-grown plants in leaf morphology, pigment composition, photosystem components, and stress-related proteins. Indoor plants exhibited larger leaves with altered shapes, reduced xanthophyll pigments, increased Lhcb1 and Lhcb2 levels, and absence of early-light-induced proteins (ELIPs), leading to diminished non-photochemical quenching (NPQ). By contrast, field-grown plants showed enhanced capacity for state transitions and higher mortality in mutants lacking ELIPs, suggesting their role in natural acclimation. Metabolomic profiling revealed light-intensity–dependent accumulation of sugars, tricarboxylic acid (TCA) intermediates, and amino acids, with distinct biphasic and circadian responses when NL plants were shifted to field conditions. To further dissect acclimatory mechanisms, we analysed chloroplast stroma proteomes using 2D-DIGE and mass spectrometry. Fifty-eight proteins were differentially expressed, including those involved in the Calvin–Benson cycle, plastid metabolism, photorespiration, and RNA metabolism. Notably, seven uncharacterized proteins accumulated specifically in field-grown plants, and mutants of three proteins (a senescence-associated protein, AT1G74940, and two unknowns, AT5G05180 and AT3G15605) exhibited higher mortality under field conditions. These findings emphasize the importance of "field-omics" approaches in uncovering novel molecular players of acclimation and highlight that analyses confined to controlled conditions may underestimate the true adaptive potential of plants in nature.

Biography

Dr. Yogesh Mishra is a plant molecular biologist with a research focus on the molecular stress biology of plants and cyanobacteria. He earned his Ph.D. from Banaras Hindu University (BHU), Varanasi, India, where he studied the molecular responses of *Anabaena doliolum* to heat and UV-B stress. He conducted postdoctoral research at the Umeå Plant Science Centre, Sweden, with Prof. Stefan Jansson, applying systems biology to explore light-regulated processes in Arabidopsis thaliana. He further specialized in abiotic stress signal transduction under the mentorship of Prof. Csaba Koncz at the Max Planck Institute for Plant Breeding Research (MPIPZ), Cologne, Germany. Currently, Dr. Mishra leads an independent research group in the Department of Botany at BHU. His team investigates mechanisms of abiotic stress tolerance and signaling in Anabaena sp. PCC 7120, *Dumortiera hirsuta* (a liverwort), and Arabidopsis thaliana, using integrated molecular and systems biology approaches.

7.4

An ARF2-GRF5 module, operating early, indicates genetic hierarchy during chloroplast biogenesis

Priyanka Mishra
Indian Institute of Science, Bangalore, India. Royal Holloway, University of London, Egham, United Kingdom

GLK1 and GLK2 transcription factors drive photosynthesis-associated nuclear (PhAN) gene expression, their simultaneous loss in Arabidopsis results in pale, underdeveloped chloroplasts. Our understanding of early regulation of chloroplast development is less defined. Mutagenesis of a *glk1 glk2* mutant identified *suppressor of glks* (*sgl*) *2*, *sgl2*, which restored chlorophyll levels, PhAN gene expression, thylakoid stacking, and chloroplast volume in mesophyll and bundle-sheath cells. *sgl2* was caused by loss of *AUXIN RESPONSE FACTOR2* (*ARF2*). In *glk1 glk2*, where *glk1* is knock-down allele, low but detectable *GLK1* expression was elevated in $arf2^{sgl2}$ *glk1 glk2*, while suppression was reduced *in glk1-2 glk2-2*KO alleles, revealing part of the action of $arf2^{sgl2}$ occurs through GLK1.

Overexpression of *Growth Regulating Factor 5* (*GRF5*), negatively regulated by *ARF2*, also rescued chlorophyll levels in *glk1 glk2*, suggesting *ARF2* and *GRF5* function as a transcription module. Presumed orthologs of *ARF2* and *GRF5* are expressed very early in developing cereal leaves, during plastid proliferation and assembly, while *GLK* expression peaks later, during greening. Overall, this demonstrates *ARF2* as a negative switch modulating GRF5 early in chloroplast development, acting upstream of GLKs. regulating them directly or indirectly. We propose a transcriptional hierarchy with feed-forward regulation during chloroplast biogenesis in developing leaves.

7.5

Functional characterization of BBX15 during early seedling development in Arabidopsis

Arpan Mukherjee ORCID iD
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The integration of multiple signaling pathways is crucial for coordinating growth and adaptation of plants under changing environmental conditions. Optimal growth during the early stages determines the resilience potential of a plant. Exogenous light and endogenous hormone signals influence the switch from heterotrophic to photoautotrophic growth and subsequent development. Arabidopsis B-box domain proteins are light-responsive transcription factors which regulates various physiological processes during early seedling development, including germination, photomorphogenesis, flowering, thermomorphogenesis, and shade-avoidance. We identified that a B-box containing protein BBX15 exhibits differential total chlorophyll level, delayed in cotyledon opening as well as changes in cell expansion in its loss-of-function mutants and overexpressing lines. Gene expression analysis of several chlorophyll biosynthesis regulators in loss-of-function and overexpressors of BBX15 indicates it as a negative regulator of chlorophyll biosynthesis. Furthermore, the loss-of-function mutant shows elongated petiolar growth under low light condition. We also observed a gradual increase in transcript and protein abundance of BBX15 in cotyledon on dark to light transition. Overall, our data suggests the light activation of BBX15 modulates downstream factors which regulate cotyledon opening, greening, and expansion.

7.6

Plastidial-oxylipins mediated priming couples light acclimation and defence governing plant development

Ritu Godara ORCID iD
CSIR-IHBT, Palampur, India

Plants are constantly challenged by simultaneous biotic and abiotic stresses, necessitating integrated signaling networks to ensure survival. A common consequence of numerous stresses, including high light and pathogen infection, is the damage to the photosynthetic apparatus, leading to the overproduction of reactive oxygen species (ROS) within chloroplasts. Overproduced ROS then oxidize biomolecules of the photosynthetic apparatus, including lipids and proteins, and damage them. Oxidation of biomolecules drives the peroxidation of unsaturated fatty acids in thylakoid galactolipids, yielding lipid hydroperoxides and cyclic peroxyl radicals. These primary products decompose into reactive electrophilic species (RES), while coordinated lipoxygenase activity generates oxylipins, including 12-oxo-phytodienoic acid and jasmonic acid. Notably, volatile RES with α, β-unsaturated carbonyl moieties are proposed to translocate from chloroplasts to other cellular compartments and the apoplast, potentially acting as mobile signals that prime local and systemic defence responses. Our research elucidates how light stress and pathogen attack converge on chloroplast lipid peroxidation to produce oxylipin signals, which systemically prime photoprotective and immune responses. I aim to present these findings at this meeting to engage with leaders in light signalling and dissect the molecular mechanisms underlying this light-defence synergy.

8.1

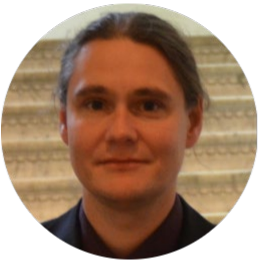
CRY2-interacting CIB mediates photoperiodic control of bud break in hybrid aspen trees

Rishikesh Bhalerao
Umea Plant Science Center, Sweden

The timing of spring budbreak is crucial for survival and productivity in temperate and boreal forest trees. The timing of bud break must be tightly regulated since precocious bud break exposes the plants to severe damage from snap frosts in spring, while delayed bud break reduces the length of growing season. Temperature and photoperiod are the main environmental cues controlling the timing of bud break. Whereas the role of temperature in bud break is well studied, the molecular basis of photoperiodic regulation of bud break remains elusive. Here we address this gap in regulation of bud break using genetic and pharmacological approaches in model tree hybrid aspen. We identify a photoperiod-regulated CIB transcription factor and its interactor CRY2 as antagonistically acting regulators of bud break. CIB promotes bud break via GA biosynthesis. Moreover, cold induced, dormancy regulating transcription factors LIM1 and tree ortholog of florigen component, FT1, redundantly promote CIB expression revealing a link between dormancy regulation and bud break. Our results thus reveal a genetic network mediating photoperiodic control of bud break and previously unrecognized role of CIB in integrating temperature and photoperiodic cues to ensure reliable timing of spring bud break, a major adaptive trait in the trees.

Biography

Rishikesh Bhalerao received his Ph. D in 1993 from Umea University. Following his Ph. D, he did his Post-doc with Csaba Koncz at the Max-Planck Institute in Cologne. He returned to Sweden in 1997 and started his own research group shortly afterwards at The Swedish University of Agricultural Sciences (SLU). Rishi is a full professor at SLU and the major focus of his work is understanding how seasonal cues such photoperiod and temperature control annual growth cycle of trees using hybrid aspen as a model. Rishi was elected as EMBO member in 2023 and selected as Wallenberg scholar in 2024.



8.2

Circadian coordination of growth and development

Antony Dodd
John Innes Centre, Norwich, United Kingdom

Circadian clocks align biological processes with 24 h fluctuations in environmental conditions. In plants, this is thought to increase organismal fitness, ensure responses to the abiotic and biotic environment are appropriate for the time of day, and have widespread impacts upon the daily coordination of metabolism, physiology, and development. Furthermore, the circadian clock is crucial for monitoring the seasonal changes in photoperiod that underlie developmental events such as the transition to flowering. The group investigates circadian regulation under both controlled environments and under field conditions. In this presentation I shall show recent advances from the group that use Arabidopsis as an experimental model to link circadian programs to the coordination of metabolism and growth.

Biography

Antony Dodd is a research group leader, and Head of Cell and Developmental Biology, at the John Innes Centre, UK. His group focuses on circadian regulation, using both plants and bacteria as model systems. Some current research interests include roles for circadian clocks in natural plant populations, circadian organization of metabolism, and the intersection between daily and seasonal timing in the regulation of plant development. He is also part of the European Union-funded programme MicroClock, which investigates the circadian clock in *Bacillus subtilis*. Antony’s PhD was on 24 h cycles of metabolic regulation in CAM plants, he was a post-doc at the University of Cambridge, and established his own lab at the University of York and University of Bristol, before joining the John Innes Centre in 2019.

8.3

Genetic framework mediating the photoperiodic control of shoot architecture development and seasonal growth in perennial plants

Jay Prakash Maurya ORCID iD
Banaras Hindu University, Varanasi, India

Shoot branching is an important aspect of light-regulated shoot architecture development in plants. In contrast with annuals, branching in perennials native to temperate and boreal regions must be coordinated with seasonal growth cycles. How branching is coordinated with seasonal growth is poorly understood. We identified key components of the genetic network that controls branching and its regulation by seasonal cues like photoperiod in the model tree hybrid aspen. Our results demonstrate that branching and its control by seasonal cue is mediated by mutually antagonistic action of aspen orthologs of flowering regulators *TERMINAL FLOWER 1* (*TFL1*) and *APETALA1* (*LIKE APETALA 1/LAP1*). *LAP1* promotes branching through local action in axillary buds. *LAP1* acts in cytokinin dependent manner, stimulating expression of the cell cycle regulator *AIL1* and suppressing *BRC1* (*BRANCHED1*) expression to promote branching. Short photoperiod and low temperature, the major seasonal cues heralding winter, suppress branching by simultaneous activation of *TFL1* and repression of the *LAP1* pathway. Our results thus reveal the genetic network mediating control of branching and its regulation by environmental cues facilitating integration of branching with seasonal growth control in perennial trees.

Biography

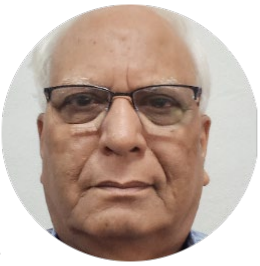
Dr. Jay Prakash Maurya is an Assistant Professor in the Department of Botany at Banaras Hindu University, India, where he leads the Plant Development and Molecular Biology (PDMB) research group. His research focuses on understanding how environmental cues such as light and temperature regulate plant developmental processes. Using Arabidopsis and potato as model systems, his group investigates the molecular mechanisms underlying dormancy, seed germination, and storage organ formation. By integrating developmental biology with biochemistry and molecular genetics, his work aims to uncover fundamental principles of various aspects of plant development and growth regulation.

8.4

Integration of light and temperature signals by *AtFPF* drives floral transition in Arabidopsis

Sukriti ORCID iD
CSIR-IHBT, Palampur, India

The transition from vegetative to flowering is a key developmental process in plants, regulated by complex interactions between light and temperature signals. Our research focuses on the Arabidopsis Flowering Promoting Factor (FPF) gene, a plant-specific, intron less gene encoding small proteins lacking known functional domains. Phenotypic analysis of CRISPR-generated *AtFPF* mutants revealed delayed flowering, while overexpression lines flowered earlier, although the underlying regulatory mechanisms remain unclear. Previously thought to be meristem-specific, our promoter analysis shows that AtFPF is initially expressed in leaves during early development and gradually shifts to the meristem during floral transition, likely via the vasculature. This dynamic pattern suggests additional environmental regulation, potentially through light, as a related homolog, AtFLP1, was recently shown to respond to red/far-red light independently of FT in both Arabidopsis and cotton. Moreover, our studies in saffron suggest that AtFPF expression may also be responsive to temperature cues. Together, these findings support a model in which AtFPF integrates both light and temperature signals to regulate flowering. Elucidating the underlying mechanisms of AtFPF function including its upstream regulators, interacting partners, and downstream targets will provide valuable insights for engineering plants with optimized flowering responses to changing climates and environmental conditions.



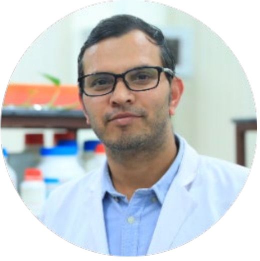
8.5

Decoding the genetic basis of the tomato root-suppressed (Rs) mutant by integrated genomics and metabolomics

Rameshwar Sharma
University of Hyderabad, India

The tomato *Rs* mutant, induced by radiation, exhibits a severe inhibition of primary root elongation in both dark- and light-grown seedlings. Adult plants display a dwarfed stature, highly serrated leaves, aberrant floral organs, and convoluted fruits. Application of a hydrogen sulfide (H_2S) donor moderately stimulated root elongation in *Rs* seedlings, hinting at a potential disruption in sulfur metabolism or signaling. Comprehensive metabolomic analysis revealed that *Rs* seedlings and adult plants possess a unique metabolic profile strongly resembling that of sulfur-deficient plants. To decipher the genetic basis of this phenotype, we employed whole-genome sequencing of the mutant and generated a MutMap population. As *Rs* is a radiation-induced mutant, we utilised a specific variant analysis pipeline to identify single-nucleotide polymorphisms and insertions/deletions (indels) within both genes and promoter regions.
This genomic data was integrated with public tomato transcriptome databases to shortlist genes with expression profiles consistent with the observed phenotypes. Through this strategy, we have identified a set of putative candidate genes that are the prime suspects responsible for the pleiotropic *Rs* phenotype.

Biography
Professor Rameshwar Sharma is a retired plant scientist from the University of Hyderabad, where he worked from 1978 to 2020. He earned his PhD in Plant Photobiology in 1978 from Jawaharlal Nehru University. For the past three decades, his research has focused on using the tomato as a model system to understand plant development. His work combines forward and reverse genetics, including genome editing, to study developmental mutants, fruit ripening, and carotenoid biosynthesis. Professor Sharma has been an Alexander von Humboldt Fellow in Germany, a JSPS Visiting Professor in Japan, and a Visiting Professor in Finland. He has authored over 120 research publications and has led several major projects funded by agencies like the Department of Biotechnology (DBT) and the International Atomic Energy Agency (IAEA), with a focus on tomato genome mutation and biofortification.



8.6

Investigating stress sensors in chloroplasts and their signaling mechanisms, shaping responses toward light and related stressors in non-model plants

Vivek Dogra ORCID iD, Sumanta Mohapatra ORCID iD
CSIR-IHBT, Palampur, India

Environmental perturbations, especially light alone or in combination with other stresses, often negatively impact the photosynthetic electron transport, resulting in increased reactive oxygen species (ROS) production in the chloroplast. This leads to oxidative damage to various biomolecules. The cellular system utilizes ROS or ROS-generated metabolites to instigate signaling pathways, resulting in acclimation, growth inhibition, or programmed cell death (PCD) for sustaining stress. Various stress-generated or stress-activated signaling components and downstream pathways are identified in model plants; however, they are largely unexplored in non-model plants. Recently, we identified an evolutionarily conserved chloroplast-localized enzyme, polyphenol oxidase (PPO), that oxidizes catechins into theaflavins (TFs) in *Camellia sinensis* (Tea), as a stress sensor and its catalyzed products as signaling molecules. The PPO undergoes a stress (ROS)-induced proteolytic activation and initiates an oxidized flavonoid-mediated stress signaling under drought and high light/cold stresses. PPO activation and TFs accumulation were linked to the activation of UPR (unfolded protein response)-like response, which was reinforced by virus-induced silencing and overexpression of PPO, and direct feeding of TFs in tea plants. Pharmacological treatments revealed that TFs interact with HSP90, activating a canonical IRE-bZIP60-dependent ER stress pathway resulting in PCD. Similar proteolytic activation of PPO and subsequent instigation of stress signaling in other plant species (tomato and wheat) demonstrated that PPO acts as an evolutionarily conserved stress sensor, integrating light with other stressors and instigating an inter-organelle communication in plants.

References:

Mohapatra S, Mishra A, Godara R, Bali S, Twinkle, Kumar A, Kumar R, Kumar N, Kumar P, Acharya V, Dogra V. Oxidative stress-induced proteolytic activation of polyphenol oxidase triggers an oxidized flavonoids-mediated stress signaling in *Camellia sinensis*. bioRxiv. 2025:2025-09.
https://orcid.org/0000-0003-1853-8274

Biography

Dr. Dogra is a Principal Scientist at CSIR-IHBT, Palampur where he started his independent research group in 2020. Earlier, he worked as postdoc fellow at Shanghai Center for Plant Stress Biology, Shanghai for almost 6 years. He is a recipient of DBT Ramalingaswamy re-entry fellowship (2020-2025). His research focusses on plant adaptation and stress signaling mechanisms under changing climate, in both model and non-model pants especially those inhabiting high altitudes.

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8.7

Metabolic responses of red and green A*maranthus tricolor* to distinct light wavelengths

Shweta Pawar
IIT Mandi, MANDI, India

Light is a key regulator of plant growth, metabolism, and physiology. Understanding how *Amaranthus* responds to distinct light wavelengths provides both mechanistic insights into metabolic adaptation and opportunities to enhance nutritional quality. In this study, two *Amaranthus tricolor* varieties (red and green) were exposed to eight wavelengths spanning 400-700 nm. Gas Chromatography- Mass Spectrometry (GC-MS) profiling revealed wavelength-dependent shifts in amino acids, phenols, sugars, organic acids, and fatty acids. In red *Amaranthus*, essential amino acids, including branched-chain amino acids (BCAAs) and phenylalanine, were significantly enriched under amber and far-red light compared to photosynthetically active radiation (PAR). In green *Amaranthus*, essential amino acid profiles resembled those of the red variety, but lysine and threonine were uniquely elevated under amber and far-red light. Notably, phenolic compounds such as ferulic acid and caffeic acid accumulated under blue and green light in green *Amaranthus*, a genotype typically characterized by lower phenolic levels than the red variety. These results indicate genotype-specific metabolic rewiring, likely mediated by photoreceptor-regulated phenylpropanoid pathways. Overall, our findings underscore the potential of wavelength-specific light regimes to selectively enhance bioactive and nutritional metabolites in *Amaranthus*, offering strategies to improve its value under controlled cultivation systems.

Keywords: *Amaranthus*, metabolite profiling, GC-MS, light wavelength

9.2

Mechanism Controlling Vascular Pattern Fidelity in Wounded Leaves

Kalika Prasad
IISER, Pune, India

The formation of vascular networks in plants has long fascinated biologists and is elegantly explained by the canalization hypothesis, first proposed by Sachs. This model suggests that the directional flow of auxin reinforces its own transport routes, thereby guiding vascular differentiation. In wounded tissues, such as pea epicotyls, a narrow file of vascular cells often forms a loop that bypasses the injured region, restoring continuity. While stems and epicotyls display linear vascular paths, leaves develop intricate, highly polarized vein networks. How these complex patterns emerge from initially homogeneous tissues remains a long-standing question. Classical studies have shown that auxin flux and transport dynamics provide a self-organizing mechanism for vein patterning. Yet, even in the absence of known PIN auxin transporters, veins still form, though abnormally, implying that intercellular transport alone cannot fully explain vascular fidelity. Emerging evidence indicates that auxin signaling—the ability of cells to perceive and respond to auxin - plays a key role in coordinating polarity and vein formation, especially when transport is impaired. Vein regeneration remains remarkably robust, highlighting the contribution of signaling-based feedbacks. When young leaves are wounded and their midvein disrupted, new vascular strands regenerate from nearby tissue. One might expect these strands to fuse with adjacent veins or create new branching patterns, yet they consistently reconnect to the parental midvein, forming a loop that bypasses the wound - strikingly similar to Sachs' classic observation in epicotyls. This invariant pattern raises a fundamental question: how do only a few cells within a large field reprogram to form precise vascular strands? Our study explores how mechanical cues integrate with hormonal signaling to activate vascular regeneration and maintain pattern fidelity, and how these mechano-biochemical responses may be influenced by external cues such as light.

Biography

Kalika's group investigates the fundamental mechanisms underlying regeneration and developmental plasticity in plants. After earning his Ph.D. from the Indian Institute of Science, Bangalore, he pursued an EMBO postdoctoral fellowship at Utrecht University. His group at IISER Pune explores how mechanical, geometric and biochemical cues coordinate self-organized morphogenesis in plant regeneration. A Fellow of Indian Science Academies, INSA, IASc, and NASI, he serves on the Editorial Boards of *Developmental Biology* and *Plant Communications*.

9.3

Redox-regulated Aux/IAA multimerisation modulates auxin responses

Dipan Roy ORCID iD
Durham University, Durham, United Kingdom

Reactive oxygen species (ROS) function as key signals in plant adaptation to environmental stresses, such as drought. Roots respond to transient water unavailability by temporarily ceasing branching through the acclimative response xerobranching.

In this study, we report how a xerobranching stimulus triggers rapid changes of ROS levels in root nuclei, triggering redox- dependent multimerization of the auxin repressor protein

IAA3. Mutations in specific cysteine residues of IAA3 disrupt redox-mediated multimerization and interaction with co-repressor TPl, thereby attenuating IAA3-mediated target gene repression. Other AuX/IAA proteins also vary in their redox-mediated multimerization, which reveals a regulatory mechanism that connects dynamic changes in cellular redox status to auxin signaling. Our study reveals how ROS, auxin, and water availability intersect and shape root adaptive responses, thereby maintaining phenotypic plasticity in plants.

9.4

Molecular insights into developmental adaptations to the environment

Ikram Blilou
KAUST, Saudi Arabia

Plants exhibit remarkable developmental plasticity, enabling them to survive and flourish under ever-changing environmental conditions. In this talk, I will present recent discoveries on how key root developmental regulators integrate environmental and developmental signals to balance growth and defense responses in Arabidopsis and tomato, particularly under biotic stress.
I will also explore root developmental adaptations in desert plants, focusing on the unique strategies employed by species such as date palm and mangrove to withstand extreme salinity, heat, and drought. By analyzing their root systems at both anatomical and molecular levels, we uncover novel mechanisms that underpin their resilience. These insights are now being leveraged to engineer crops with enhanced tolerance to salinity and climate-induced stress, offering promising avenues for agriculture in a warming world

Biography

Dr Ikram Blilou is a Professor leading the Plant Cell and Developmental Biology laboratory within the Division of Biological Environmental Science and Engineering at King Abdullah University of Science and Technology. Her PhD studies, at the University of Granada in Spain, focused on molecular mechanisms in plant defense during early responses to symbiotic mycorrhiza. After graduating, she moved to the Netherlands for postdoctoral research at Utrecht University, where she studied cell-cycle regulation and polar auxin transport. After completing her postdoctoral work, she was appointed as an assistant professor in the Department of Molecular Genetics at Utrecht University in 2003, where she established a line of research focusing on mechanisms regulating protein movement in plant roots. In 2006, she was awarded the prestigious Dutch VIDI and Aspasia grant and was promoted to the rank of associate professor. In 2012, she moved along with her department to Wageningen University where she continued studying root development in Arabidopsis. In 2017, she moved to KAUST where she is currently leading several research projects including stem cell regulation in model plants focusing on transcription factor networks as well as understanding how plants cope in desert environment. Her team uses multidisciplinary approaches, including high-resolution microscopy, tissue culture and plant transformation, genome editing technologies, and transcriptional assays. The team also implements deep learning and computer vision to analyze and quantify dynamic processes in vivo, ranging from protein associations to pathogen invasion, disease detection, and growth quantification.

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2	Kuheli Chalak	Indian Institute of Science	Turnover of inositol pyrophosphate messengers fine-tunes growth and development in *Marchantia polymorpha*
3	Ashish Chauhan	Indian Institute of Technology Mandi	Nutri-metabolomics of lettuce varieties under photosynthetically active radiations
4	Swagatam Das	IISER Bhopal	BBX15 as a central integrator of light and hormonal signals in early seedling development
5	Shambhavi Dwivedi	CSIR-CIMAP	NtHY5 acts systemically to control light-responsive nicotine transport in tobacco
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8	Sumit Jamwal	CSIR-Indian Institute of Integrative Medicines	Xanthophyll-mediated photoprotective mechanism of *Lepidium latifolium L.*, a sleeper weed from Ladakh Himalayas
9	Amit Kumar	C.S.I.R - Institute of Himalayan Bioresource Technology	Light spectrum mediated physiological and molecular responses in *Valeriana jatamansi*
10	Anjali Kumari	IISER Bhopal	Molecular insights into BBX-mediated light-responsive seedling development in *Arabidopsis thaliana*
11	Akankshya Mahapatra	Indian Institute of Science Education and Research Bhopal	Role of light signaling in root hair development

12	Ratikanta Mohapatra	Orissa University of Agriculture and Technology	Prolonged shade tolerance and its complex genomic and micro-RNA regulation in rice
13	Khushi Motwani	Indian Institute of Science Education and Research	To investigate the role of a BBX protein in cotyledon opening
14	Akshay Nair	IISER Tirupati	Short-term high light stress analysis through differential methylation identifies root architecture and cell size responses
15	Ganesh Mahadeo Nawkar	DYPBBI, Dr. D. Y. Patil Vidyapeeth	Red-colored plants: a tool to study the effect of absorbance on phototropic response
16	Dhureen Patel	Indian Institute of Science Education and Research, Bhopal	A B-BOX protein mediates hydrotropic movement of roots in *Arabidopsis thaliana*
17	Padmaja Rai	National Institute of Plant Genome Research (NIPGR)	Synergistic role of silicon and hydrogen sulfide in safeguarding light-regulated photosynthetic performance and stress tolerance in rice under copper oxide nanoparticle toxicity
18	Somdatta Roy	IISER Bhopal	Light-regulating factors control the aluminium-mediated tropic response in Arabidopsis thaliana
19	Dipali Sahu	Indian Institute of Science Education and Research	Identifying the light regulated gene involved in root development in tomato
20	Pallabi Saha	Indian Institute of Science Education and Research	Light-dependent activation of NAC transcription factor promotes seedling establishment in Arabidopsis
21	Samarth Samarth	University of Canterbury	Temporal and seasonal transcriptomic shifts in *Fagus sylvatica* surrounding summer solstice
22	Pranab Santara	Indian Institute of Science Education and Research, Bhopal	Impact of light on aluminium stress tolerance in *Arabidopsis Thaliana*
23	Devlina Sarkar	University of Calcutta	Deciphering temporal dynamics of metabolic reprogramming in guard and mesophyll cells during the C3-to-CAM transition
24	Anagha Sasidharan	Indian Institute of Science Education and Research Bhopal	Role of a light signalling transcription factor in regulating thermomorphogenesis

25	Lata Sharma	Jai Narain Vyas University	Nitric oxide (N=O) & Heme Oxygenase 1 cross-talk and regulation of FCR activity to improve Iron (Fe) uptake and biofortification in Triticum aestivum
26	Shagun Sharma	Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Himachal Pradesh, India	Light regulated developmental reprogramming drives in vitro regeneration of the endangered medicinal herb Fritillaria roylei Hook.
27	Vinay Sharma	ICRISAT, HQ, Patancheru	Light-regulated genes involved in drought tolerance in groundnut
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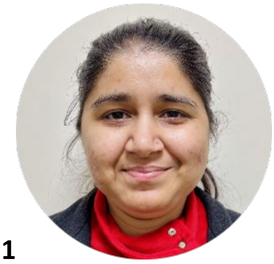
29	Neha Singh	Indian Institute of Science Education and Research Bhopal	Functional characterization of Arabidopsis B-box domain proteins under high-intensity light stress
30	Shikha Suyal	IISER Bhopal	Role of a BBX protein in regulation of early seedling development
31	Sapna Thakur	CSIR-IHBT	Investigating plastid RNA processing dynamics under high light stress in C3 and C4 model crops
32	Yogita Thakur	Indian Institute of Technology, Mandi	Kinetic $^{13}CO_2$ tracing reveals central metabolic reprogramming during light-dark transitions and UV-B stress in *Brassica napus*
33	Gyan Datta Tripathi	IIT Delhi, India	Role of melatonin against nano-stress in tomato plant
34	Kavuri Venkateswara Rao	IISER Bhopal	BBX_NV maintains gravitropic set-point angle of lateral roots in *Arabidopsis thaliana*
35	Julia Zalder	KU Leuven	Optimizing dynamic LED lighting for sustainable crop cultivation

Poster Abstracts



Poster 1

Light-mediated regulation of the WRKY family involved in sclareol production in *Salvia sclarea* L.

Shafali Bhasin
CSIR -Indian Institute of Integrative medicine, Jammu, India. Acsir, Ghaziabad, India

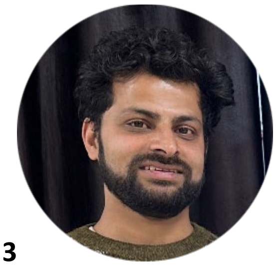
Salvia sclarea is an aromatic plant valued for its therapeutic and nutraceutical benefits worldwide. It is an important oil crop, mainly cultivated for sclareol, a diterpene used to produce Ambroxide. Sclareol is synthesised through the MVA (mevalonate) pathway, which contributes 1-1.5% to the total essential oil content in the aerial parts. Given the limited biosynthesis of sclareol within these plants, there exists a necessity to enhance both the essential oil yield and sclareol content. Therefore, presenting urge to investigate the regulation and biosynthesis of this metabolite. The present study was conducted to elucidate the biosynthesis and regulation under light stress. The WRKY family, known for its role in regulating plant metabolism under stress conditions, was the focus of this analysis. A genome-wide identification of Sswrky genes was performed, followed by characterisation and phylogenetic analysis of the identified SsWRKYs in Salvia sclarea. SsWRKY genes were identified and classified into three groups. Gene homology and synteny analyses conducted to explore evolutionary trends. The plants were subjected to light stress, which led to an enhancement in sclareol levels, alongside an assessment of gene expression and other parameters. This study focuses on the regulation of terpenes, particularly sclareol, in *Salvia sclarea* under light stress.

Poster 2

Turnover of inositol pyrophosphate messengers fine-tunes growth and development in *Marchantia polymorpha*

Kuheli Chalak
Indian Institute of Science, Bengaluru, India

Inositol pyrophosphates (PP-InsPs) are eukaryote- specific second messengers that regulate diverse cellular processes, including immunity, nutrient sensing, and hormone signalling pathways in plants. These energy-rich messengers exhibit high sensitivity to the cellular phosphate status, suggesting that the synthesis and degradation of PP-InsPs are tightly controlled within the cells. Notably, the molecular basis of PP-InsP hydrolysis in plants remains largely unexplored. We reported the functional characterization of MpDDP1, a diadenosine and diphosphoinositol polyphosphate phosphohydrolase encoded by the genome of the liverwort, *Marchantia polymorpha*. We show that MpDDP1 functions as a PP-InsP phosphohydrolase in different heterologous organisms. Consistent with this finding, *M. polymorpha* plants defective in MpDDP1 exhibit elevated levels of 1/3-InsP$_7$ and 1/3,5- InsP$_8$, highlighting the contribution of MpDDP1 in regulating PP-InsP homeostasis *in planta*. Furthermore, our study revealed that MpDDP1 controls thallus development and vegetative reproduction in *M. polymorpha*. Collectively, our study provides insights into the regulation of specific PP-InsP messengers by DDP1-type phosphohydrolases in land plants, highlighting a potential role for these enzymes in modulating broader physiological processes such as stress responses, nutrient signalling, or development.



Poster 3

Nutri-metabolomics of lettuce varieties under photosynthetically active radiations

Ashish Chauhan
Indian Institute of Technology Mandi, Mandi, India

There are several Lettuce varieties with distinct growth phenotypes. While few are desirable for consumption due to their organoleptic properties, others may have phytochemical/nutritional properties amenable to other applications. Studies on comprehensive analysis of nutritional, metabolic, and pathway level changes in lettuce varieties at different growth stages and under different light conditions remain limited. In this study, nutri-metabolomics of seven different lettuce varieties grown in a controlled indoor setup under white LED PAR lights and harvested at two edible stages is investigated. While biochemical assays captured the nutritional properties, GC-MS was used for metabolite profiling.
Our results showed that, in all the lettuce varieties, higher accumulation of organic acids and secondary metabolites occurred in 30 days, while proteins, carbohydrates, and lipids were higher at 60 days. Lettuce varieties at 60 days also showed higher accumulation of essential fatty acids like linolenic and linoleic acids. Other unique nutri-metabolic properties of different varieties were also captured and will be emphasised. These findings highlight stage specific nutritional variations under controlled indoor lights and direct us toward light quality manipulation for tailoring nutritional content. Light induced metabolism under different LED wavelengths is being further explored to develop “Designer Lettuce” enriched with targeted metabolites.

Poster 4

BBX15 as a central integrator of light and hormonal signals in early seedling development

Swagatam Das
IISER Bhopal, Bhopal, India

Light signaling is central to the transition from skotomorphogenesis to photomorphogenesis, yet how it integrates with hormonal and stress pathways to optimize early seedling development remains unclear. We investigated the role of the transcription factor *BBX15* in *Arabidopsis thaliana* as a regulatory node connecting light and phytohormonal cues. Using genetic, biochemical, and molecular approaches, we show that *BBX15* functions as a context-dependent regulator of cotyledon development. Under normal photoperiods or short dark exposures, BBX15 represses chlorophyll biosynthesis genes and restricts cotyledon greening, whereas during prolonged darkness or high ABA treatment, *BBX15* enhances greening, indicating a stress-adaptive role. *BBX15* also limits protochlorophyllide accumulation, restricts cotyledon opening, and reduces ROS during de-etiolation, contributing to photoprotection. Expression analyses reveal cross-talk with *HY5, GLKs, PIFs*, and phytohormones (ABA, ethylene, brassinosteroids), suggesting multiple feedback loops. Collectively, our study identifies *BBX15* as a key integrator of light and hormonal signals, balancing growth and stress resilience to optimize seedling establishment. These findings highlight *BBX15* as a potential developmental checkpoint and open avenues for exploring the evolution of light–hormone integration mechanisms across plants.

Poster 5

NtHY5 acts systemically to control light-responsive nicotine transport in tobacco

Shambhavi Dwivedi
CSIR-CIMAP, Lucknow, India

Nicotine, the primary alkaloid in *Nicotiana* species, accounts for over 90% of total alkaloids and is the main addictive compound in tobacco, contributing to ~8 million deaths annually. To reduce health risks, lowering nicotine levels is a key objective. This study identifies NtHY5, a light-responsive bZIP transcription factor, as a regulator of nicotine transport in tobacco. CRISPR/Cas9-mediated knockout mutants of NtHY5 showed a significant reduction in the expression of genes involved in the nicotine transport, resulting in a marked decrease in nicotine content leaf tissue. Conversely, overexpression lines of NtHY5 exhibited higher transcript levels of these transport genes, leading to enhanced nicotine accumulation. Computational analysis of the promoters (*NtNUP1, NtJAT1, NtJAT2 and NtMATE*) suggested the presence of G-boxes near the transcription start site. Further validation through DNA-protein interaction studies confirmed that HY5 interacts with these light-responsive G-box motifs in the promoters of these genes, promoting nicotine transport. The grafting experiments with wild-type, $NtHY5^{CR}$, NtHY5OX and the transporter mutant lines collectively suggested that NtHY5 moves from shoot to root, where it activates root HY5 and regulates light-dependent nicotine transport in tobacco. Additionally, CRISPR/Cas9-edited mutants of key nicotine transporters also showed altered flavonol and anthocyanin accumulation, emphasizing metabolic interconnectivity in plants.

Poster 6

Role of BBX protein in cotyledon greening

Sanika Ghadage
Indian Institute of Science Education and Research, Bhopal, India

During their growth and development, plants go through various stages. Plant development initiates from germination or radical emergence and ends in reproductive or floral initiation and seeds formation. Plant growth can be categorized into two parts, early and late development. Early plant development primarily involves seedling establishment, which can be further divided into distinct processes such as hypocotyl elongation, cotyledon opening and greening, and root development. Each of these developmental phases is tightly regulated by both the quality and quantity of light. The phenomenon of early seedling development under light is known as photomorphogenesis. Several light signaling factors like HY5, COP1, PIFs, BBXs, are important part of this phenomenon and play major role in regulating the overall development. During our study we found one of the BBX proteins to play a major role in cotyledon greening and photooxidation during dark to light shift. We found that our mutant has more protochlorophyllide content and hence more ROS levels upon keeping in extended dark period. We also found our protein can physically interact with PIF1, a major regulator of cotyledon greening to regulate this process.

Poster 7

Light stress adaptation: Ultraviolet-B induced modulations of growth, physiological mechanisms, antioxidant activity and essential oil composition of *Ocimum americanum L.*

Vanlalhriatpuii Hmar
Mizoram University, Aizawl, India

Ocimum americanum L. (American or lime basil), an annual herb of the Lamiaceae family, holds notable medicinal value, with traditional use in treating cough, respiratory disorders, rheumatism, and renal ailments. With global climate change and stratospheric ozone depletion increasing UV-B radiation, understanding the responses of medicinal plants is crucial. This study examined the effects of elevated UV-B (eUV-B; 38.8 KJ/m^2) on growth, physiology, antioxidant status, and essential oil composition of O. americanum at 30, 60, and 90 days after transplantation. Plant growth, photosynthetic pigments, and physiological traits declined significantly under eUV-B, while total phenolics increased. eUV-B triggered the accumulation of reactive oxygen species (ROS), including superoxide radicals and hydrogen peroxide, leading to membrane damage and solute leakage, confirmed by histochemical localization. Antioxidant enzymes (SOD, CAT, APX, GR) showed significantly higher activity, indicating activation of defense mechanisms. GC-MS analysis revealed increased levels of specialized metabolites such as caryophyllene and β-ocimene, compounds with known anticonvulsant, antifungal, antitumor, and pest-resistance properties. These results suggest that O. americanum mitigates UV-B stress by boosting antioxidant defense and enhancing the biosynthesis of protective monoterpenes and sesquiterpenes. Overall, while eUV-B impairs growth and physiological functions, it promotes the accumulation of bioactive metabolites with adaptive significance.

Poster 8

Xanthophyll-mediated photoprotective mechanism of *Lepidium latifolium L.*, a sleeper weed from Ladakh Himalayas

Sumit Jamwal
CSIR-Indian Institute of Integrative Medicines, Jammu, India

At high altitudes, the climate is unpredictable, from cloudy to clear, bright sunny weather, which makes fluctuation of light a common feature. As a result, light becomes a limiting factor, which impairs plant growth and development, leading to photoinhibition and photodamage. Plants at high altitudes have developed many stress-tolerance mechanisms to withstand harsh environments, where xanthophyll cycle-mediated non-photochemical quenching (NPQ) is one of the important photoprotective mechanisms adapted by plants to cope with the excess light stress.During its growth in the unfavorable conditions of the trans-Himalayan region of Ladakh, *Lepidium latifolium* showed rigorous adaptive behavior among other native plant species. In the present study, we have investigated the comparative analysis of the xanthophyll cycle among four native plants found in the Nyoma valley of Ladakh. The expression level of VDE was higher in *Lepidium latifolium*, which strongly correlates with high xanthophyll cycle pigments and the energy dissipation mechanism with higher NPQ compared to other plants. Also, transgenesis studies validate the role of the VDE enzyme in the model organism, the *Arabidopsis thaliana* plant, which helps the model plant maintain its non-photochemical quenching kinetics. Crop plants may benefit from this tactic to help them adapt to their changing surroundings.

Poster 9

Light spectrum mediated physiological and molecular responses in V*aleriana jatamansi*

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Valeriana jatamansi Jones is an important Himalayan medicinal herb valued for its bioactive metabolites. The precise manipulation of LED light quality and conditions acts as a powerful tool to sculpt plant growth, fine-tune photosynthetic performance, and boost phytochemical biosynthesis in controlled *in vitro* systems. In this study, the influence of yellow, red, blue, and white (control) LED lights on growth, physiology, secondary metabolite production, and gene expression in *in vitro* raised *V. jatamansi* was systematically assessed. Blue, red, and yellow light increased shoot length by 1.49-, 1.53-, and 1.99-fold, respectively, compared with white light. Red light promoted the maximum fresh weight in both leaf and root tissues. Chlorophyll fluorescence parameters indicated stable photosynthetic efficiency across all light conditions. Root tissue showed 1.14-, 1.40-, and 1.68-fold higher valtrate content accumulation under yellow, blue, and red-light conditions, respectively, compared with white light. Furthermore, qRT-PCR analysis found significant upregulation of iridoid biosynthetic pathway genes *(GES, G10H,* and *7DLS)* under yellow and white light. This study demonstrates the potential of LED lights to optimize growth and boost bioactive metabolite production in *V. jatamansi*, supporting sustainable conservation and scalable pharmaceutical applications under controlled *in vitro* conditions.

Poster 10

Molecular insights into BBX-mediated light-responsive seedling development in *Arabidopsis thaliana*

Anjali Kumari
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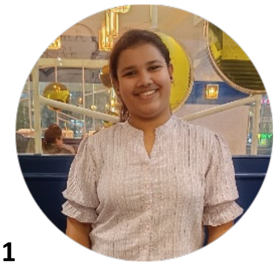
Integration of signal transduction pathways is critical for plants to balance growth against environmental fluctuations. Light is one of the most essential environmental signals that determines this transition, and in response plants have developed photoreceptors and downstream regulators which enable them to integrate light signalling with growth promotion or inhibition. My current research is to deduce the function of a key BBX protein in *Arabidopsis thaliana* during de-etiolation. I am involved in generating the CRISPR/Cas9-generated knockout mutants and overexpression lines for its functional characterization. The project comprises phenotypic analysis under different light qualities along with gene expression studies of regulators of germination and cotyledon greening. Preliminary results suggest that this BBX protein may regulate chlorophyll accumulation, hypocotyl elongation and tissue-specific growth responses, and its transcripts showed diurnal fluctuations in response to dark to light transition. Here, we seek to gain insight into the molecular mechanism by which BBX proteins combine with light signaling to modulate seedling development in response to a fluctuating environment.



Poster 11

Role of light signaling in root hair development

Akankshya Mahapatra
Indian Institute of Science Education and Research Bhopal, Bhopal, India

Root hairs are small, cylindrical extensions from the epidermal cells which helps to increase the surface area for water and nutrient uptake. They also help in plant anchorage and microbe interactions. Like most developmental phenomenon, root hair development is also dependent on the availability of light. In the presence of light, root hair development parameters show an increase than when light is absent. In this study, we aimed to characterize the role of light signaling and its components in root hair development. We identified that the dark and light have effect on the root hair development. We further tried to find out how light quality and quantity will have impact on the root hairs and underlying genetics to explain it. Our preliminary experiments tell us that light may have a role in root hair elongation but which light may have a major impact and the mechanism underlying this effect still need to be addressed.

Poster 12

Prolonged shade tolerance and its complex genomic and micro-RNA regulation in rice

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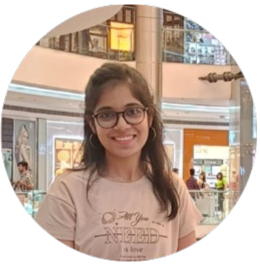
Present work bears importance due to the present unpredictable climatic conditions, associated low-light, cloudy days and its impact on grain filling in rice. This study integrates differential expression of micro-RNA during prolonged-shade (20-days) with their cleaved targets through degradome study and correlating it gene expression using the microarray analysis to reveals complex regulatory action of miRNA during low-light stress in Swarnaprabha rice. The study revealed the up-regulation of most of the ethylene and cytokinin pathway genes in shade grown panicles. This study identifies cleavage-specific interaction of 16 miRNAs and 21 target pairs, whose actions contribute significantly to the shade tolerance phenotype and sustainable yield of Swarnaprabha rice under prolonged low-light stress. Significant up-regulation of *ETHYLENE RESPONSE ELEMENT BINDING PROTEIN-2*, *MOTHER OF FLOWERING TIME 1*, and *SHORT PANICLE1* genes in shade grown panicles was seen. Prominent among them are: *miR5493-OsSLAC* and *miR5144-OsLOG1* for enhanced panicle size, *miR5493-OsBRITTLE1-1* for grain formation, *miR6245-OsCsIF9* for stem mechanical strength, *miR5487-OsGns9* and *miR168b-OsCP1* for pollen development, and *miR172b-OsbHLH153* for hyponasty. The study demonstrates neutrally, uniquely expressed micro-RNAs can contribute to molecular regulation of shade tolerance by differential binding and altering the differential expression of their targets, that are involved in light and different hormone signalling pathways.



Poster 13

To investigate the role of a BBX protein in cotyledon opening

Khushi Motwani
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A seed that has been buried in the ground undergoes skotomorphogenesis marked by hypocotyl elongation, a closed apical hook to protect the apical meristem, and closed unexpanded cotyledons. Upon exposure to light, there is transcriptional reprogramming that drives opening of the apical hook, inhibition of hypocotyl elongation, and unfolding and expansion of the cotyledon. Light elicits different growth responses in different organs of plants. These organ-specific responses are prominently displayed during de-etiolation. Cotyledon opening is a key morphological change that occurs in seedlings during de-etiolation.

Light and brassinosteroid (BR) are two central stimuli that regulate plant photomorphogenesis. Brassinosteroid is a steroid hormone known to inhibit opening of cotyledon and promoting skotomorphogenesis, whereas light promotes cotyledon opening and photomorphogenesis. We are currently investigating the role of a BBX transcription factor in regulating cotyledon opening. Our initial results suggest that BBXa is upregulated under light, and it promotes cotyledon opening. We are interested in understanding the molecular interplay of the BR pathway and BBXa in regulating cotyledon opening via PIFs and SAUR genes.

Poster 14

Short-term high light stress analysis through differential methylation identifies root architecture and cell size responses

Akshay Nair
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DNA methylation repatterning is an epigenomic component of plant stress response, but the extent that methylome data can elucidate changes in plant growth following stress onset is not known. We applied high-resolution DNA methylation analysis to decode plant responses to short- and long-term high light stress and, integrating with gene expression data, attempted to predict components of plant growth response. We identified 105 differentially methylated genes (DMGs) following 1 h of high light treatment and 193 DMGs following 1 week of intermittent high light treatment. Two distinct methylome-predicted plant growth responses to high light treatment could be confirmed by linking methylome changes in auxin response pathways to observed changes in root architecture and methylome changes in cell cycle pathway components to endoreduplication and palisade cell enlargement. We observed methylome changes in a cyclic GMP-dependent protein kinase in association with high light stress signalling. The ability to associate intragenic methylation repatterning with predictable plant phenotypic outcomes after a limited period of high light treatment allows for data-based early prediction of plant growth responses. The approach also permits the dissection of gene networks underpinning plant growth adjustments during environmental change to uncover dynamic phenotype determinants.

Poster 15

Red-colored plants: a tool to study the effect of absorbance on phototropic response

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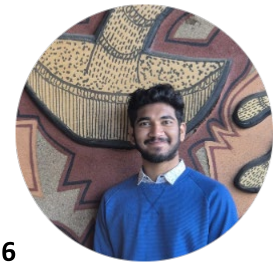
Phototropism, the growth of plants toward light, is essential for optimizing photosynthesis and ensuring proper development. In hypocotyls, air channels play a critical role in scattering light to create a gradient, which is sensed by blue light photoreceptors (phototropins) to guide directional growth. In the *Arabidopsis abcg5* mutant, where air channels are compromised, we investigated whether colored pigments could compensate for the loss of light scattering and still establish a functional light gradient. As a tool, we used RUBY lines, which express a synthetic enzyme cassette that produces the red pigment betalain in the WT and *abcg5* backgrounds. Betalain absorbs maximally in the green region (~530–540 nm) with a smaller peak in the blue region (~420–430 nm). To test whether pigment absorption could provide an alternative mechanism for light gradient formation, we generated independent RUBY-expressing lines with varying betalain levels, as well as tissue-specific lines (epidermis, cortex, and stele). Unexpectedly, red-colored plants displayed stronger defects in phototropic bending. This impairment was linked to their reduced growth rate, highlighting that phototropism is fundamentally a growth-dependent response. Future work will focus on optimizing the growth of red-colored plants to clarify the specific contribution of light absorption to phototropism.



Poster 16

A B-BOX protein mediates hydrotropic movement of roots in *Arabidopsis thaliana*

Dhureen Patel
Indian Institute of Science Education and Research, Bhopal, Bhopal, India

Hydrotropism of roots is a trait that plants have adapted to effectively forage for water. Here, the root growth is mediated in a way such that it grows in the direction of a higher water potential. Higher cytokinin accumulation on the side with lower water compared to the side with higher water potential is essential for the hydrotropic response. MIZ1 is known to regulate the downstream pathway of cytokinin signalling, involving certain ARRs. Further, MIZ1 expression has been reported to be regulated by light-mediated signalling factors involving HY5, and phytochromes A and B. There is little known about the light-mediated hydrotropism. Here, we found a B-BOX transcription factor that regulates hydrotropism of roots, possibly via MIZ1. Our studies using hydrostimulant assays have revealed that mutations enhance hydrotropic movement of the primary root, while their overexpressors have roots insensitive to the water gradient. BBX has also been observed to regulate *HY5* levels, thereby linking light-mediated signalling to hydrotropic response involving MIZ1. Also, we have observed interaction between BBX and the cytokinin downstream response regulator ARR5. Taken together, BBX is a potential regulator for hydrotropism. Here, I will discuss the role of BBX in mediating the light-mediated hydrotropism.

Poster 17

Synergistic role of silicon and hydrogen sulfide in safeguarding light-regulated photosynthetic performance and stress tolerance in rice under copper oxide nanoparticle toxicity

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Nanoparticle pollution seriously threatens crop productivity, with copper oxide nanoparticles (CuO NPs) known to impair photosynthesis, disrupt redox balance, and inhibit growth. This study investigated whether exogenous hydrogen sulfide (H_2S) application, in combination with silicon (Si), could alleviate CuO NP-induced stress in rice (*Oryza sativa L.*) seedlings. Fifteen-day-old seedlings were treated with CuO NPs, either alone or supplemented with Si and NaHS (H_2S donor).

CuO NPs exposure reduced growth, chlorophyll a, chlorophyll b, and carotenoids, while photosystem II efficiency (Fv/Fm, PIABS) also declined. Energy flux analysis revealed increased dissipation (DIo/RC) and decreased electron transport (ETo/RC). In contrast, Si + H_2S supplementation restored pigment levels, improved chlorophyll fluorescence parameters, and ensured balanced energy partitioning. Enhanced antioxidant enzyme activities and non-enzymatic components further strengthened oxidative stress tolerance. Gene expression analyses confirmed up-regulation of antioxidant genes, silicon transporters (*Lsi1, Lsi2*), and auxin transporters (*PIN5, PIN10*), suggesting integrated regulation of stress defense and development.

Overall, results demonstrate that H_2S underpins the beneficial role of Si via activation of the ascorbate–glutathione cycle. This synergistic strategy safeguards light-regulated photosynthetic performance and promotes crop resilience, offering potential applications for sustainable agriculture under nanoparticle-polluted environments.

Poster 18

Light-regulating factors control the aluminium-mediated tropic response in *Arabidopsis thaliana*

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The world's 50% of arable land consists of acidic soil, which is a major concern for agriculture. Aluminium, the third most abundant element on earth, dissociates into trivalent cationic form in acidic soil (pH<5) and this increase in Al^{3+} ion, also known as aluminium toxicity, affects the plant primarily by inhibiting root growth. It also causes inhibition in ATP production, enhances ROS and DNA damage, inhibits germination, and thus poses a great threat to crop productivity. The ability of a plant to penetrate into deeper layers of the soil also depends on an intact root cap with statoliths in root columella cells, maintaining the root gravitational growth axis.

In our study, we found that aluminium toxicity causes a directional bending response due to non-maintenance of the gravitational axis. Gravitropic response in the root is primarily maintained by gravity-sensing amyloplasts, present in root columella cells. This starch reduction-mediated agravitropic response is also regulated by light. We observed that this aluminium toxicity-regulated skewing response is more pronounced in the dark than in the light. We further want to check how the starch reduction behaves under dark conditions and the underlying reasons behind the increased bending angle of the root in dark conditions.

Poster 19

Identifying the light regulated gene involved in root development in tomato

Dipali Sahu
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Tomato (*Solanum lycopersicum* L.) is a vital crop known for its high nutritional value and is the most widely consumed vegetable worldwide. The tomato plant features a taproot system consisting of a primary root, lateral roots, and root hairs, forming the root architecture together. The roots play a crucial role in acquiring water and nutrients, significantly influencing plant growth, development, flowering, and fruit production. Previous research has shown that light positively influences root development in *Arabidopsis thaliana*. *HY5* is a key light-regulating transcription factor that promotes the expression of genes involved in root development. Similarly, I am investigating the genes that govern root development in tomatoes and their connection to SlHY5 and plant photoreceptors. Currently, I am exploring the possible interactions between root development genes and SlHY5 using techniques such as the Yeast Two-Hybrid Assay (Y2H), Bimolecular Fluorescence Complementation (BiFC), and Pull-Down assays. Additionally, I am learning how to create CRISPR/Cas9 mutant lines in tomatoes, along with other molecular techniques and aspects of plant genetics.

Poster 20

Light-dependent activation of NAC transcription factor promotes seedling establishment in Arabidopsis

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Seed germination and early seedling development are critical stages in the plant life cycle, regulated by various exogenous and endogenous factors. Among these, abscisic acid (ABA), a key endogenous regulator, and light, an important exogenous factor, play essential roles in controlling these processes. In addition, maintaining genome stability is vital for successful seed germination and seedling establishment. ABA is well known for its role in maintaining seed dormancy and delaying germination. Elevated ABA levels have been shown to inhibit DNA replication and cell division, resulting in growth retardation. Several studies have also demonstrated that high ABA concentrations suppress plant growth by interfering with these basic cellular processes. Moreover, ABA treatment increases the sensitivity of major loss-of-function mutants in double-strand break (DSB) repair genes. On the other hand, recent research has revealed an important link between light signalling components and the DNA damage response (DDR) pathway. It has also been shown that the seed DDR promotes germination by activating DNA repair mechanisms, triggering cell cycle checkpoints, and delaying programmed cell death. Therefore, we aim to explore the connection between ABA, light, and the DNA damage response pathway during seed germination and early seedling establishment.

Poster 21

Temporal and seasonal transcriptomic shifts in *Fagus sylvatica* surrounding summer solstice

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University of Canterbury, New Zealand

Plants have evolved a complex machinery to sense and communicate with their external environment, integrating multiple cues including daylength, light intensity, temperature and various mechanical stimuli. Multiple studies have recently suggested that the summer solstice may serve as a universal signal for regulating major physiological processes in plants. However, the molecular network by which summer solstice can trigger these physiological changes remain unstudied. To address this research gap, we investigated seasonal and temporal transcriptional shifts in *Fagus sylvatica* around the summer solstice. We observed a marked shift in plant responses, transitioning from growth-related processes to stress-associated after the solstice with significant changes in the expression of genes associated with flavonoid biosynthesis, antioxidants, photosynthesis machinery and phytohormone regulation. A significant shift in the number of circadian-controlled genes was also observed after the summer solstice. While most circadian clock genes maintained their amplitude and rhythmicity, *FsELF3*, a homolog of the Arabidopsis *Early Flowering 3* (*ELF3*) gene exhibited delayed amplitude and phase following the solstice. Our *in silico* analysis further confirmed the identity of FsELF3 and its ability to form biocondensate, thus, providing a framework of how plants can perceive the summer solstice signal to initiate downstream physiological processes.

Poster 22

Impact of light on aluminium stress tolerance in A*rabidopsis Thaliana*

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Aluminum (Al) toxicity is a major barrier to crop productivity in acidic soils, primarily affecting root growth and nutrient uptake. At a soil pH below 5, aluminosilicates dissociate into Al^{3+}ions, and solubilizes in the soil solution. It accumulates in root tip cells, leading to stunted roots. It disrupts cell division, elongation, reduced water and nutrient absorption. At the molecular level, Al interferes with nuclear DNA causing double strand breaks, mitochondria, the plasma membrane, and the cell wall loosening.

Our study highlights a protective role of light against Al toxicity. Arabidopsis seedlings exposed to Al show significantly improved primary root growth under light compared to dark conditions, with lower Al^{3+} accumulation in root tissues. This suggests that light mediates a protective mechanism that reduces Al uptake or its toxic effects.

We are currently exploring how light-regulated transcription factors and their downstream genes respond to Al stress under different light spectra. These findings suggest that environmental signals like light can modulate stress responses and nutrient acquisition, offering a promising direction for improving crop resilience in acidic soils.

Poster 23

Deciphering temporal dynamics of metabolic reprogramming in guard and mesophyll cells during the C_3-to-CAM transition

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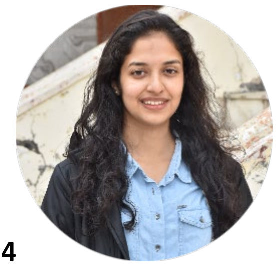
University of Calcutta, Kolkata, India

Crassulacean Acid Metabolism (CAM) plants survive in arid environments by shifting the time of stomatal opening from day to night, minimizing the transpirational water loss (Wickell *et al*., 2021). Engineering this mechanism into C_3 crops can offer a strategy to tackle global warming and ensure food security (Lim *et al*., 2025). This requires identification of metabolic enzymes and transporters whose activities change during the C_3-to-CAM transition not only in mesophyll cell (MC) but also in guard cell (GC), as reprogramming of GC metabolism is crucial for altering stomatal rhythm and thereby regulating the timing of CO_2 uptake. To address this, we developed a six-phase GC-MC diel metabolic model, integrating diel fluctuations in temperature and relative humidity. Simulations using Flux Balance Analysis predicted the C_3-to-CAM transition with gradual reduction in transpirational water loss and captured the changes in temporal enzymatic and transporter activities during the transition in both GC and MC (Sarkar & Kundu, 2025). CAM is further hypothesized to evolve from C_3 ~20-30 million years ago, when $[CO_2]_a$ declined, aridity increased, and temperature decreased (Sage *et al*., 2023). Simulations under these changing atmospheric conditions confirm that both reduced $[CO_2]_a$ and increased aridity may act as evolutionary drivers of CAM.



Poster 24

Role of a light signalling transcription factor in regulating thermomorphogenesis

Anagha Sasidharan
Indian Institute of Science Education and Research Bhopal, Bhopal, India

Plants are sessile autotrophic organisms which thrive on earth by integrating several external and internal cues for their successful development. During the life cycle, climatic extremities are one of the major factors that plants are exposed to, among which high ambient temperature is a factor which can alter plant responses and development. The morphological changes undergone by plants in response to high ambient temperature, is termed as thermomorphogenesis. Through this study we propose a light-regulated transcription factor in promoting hypocotyl elongation during warm conditions. PIF4, a bHLH transcription factor, is known to directly bind and promote the transcription of auxin signalling genes like *SAURs* and *IAAs* to promote hypocotyl elongation. HY5, a central regulator of light signaling, also acts as a negative regulator of thermomorphogenesis by inhibiting the expression of auxin signaling genes. Through our study we found that PIF4 promotes the expression of our protein under high ambient temperature. Our findings also indicate that our protein might inhibits repressive binding of HY5, on the promoter of auxin signalling genes downstream to PIF4, to promote hypocotyl elongation.

Poster 25

Nitric oxide (N=O) & Heme Oxygenase 1 cross-talk and regulation of FCR activity to improve Iron (Fe) uptake and biofortification in Triticum aestivum

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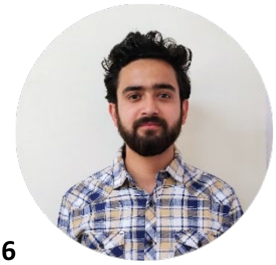
Jai Narain Vyas University, Jodhpur, Rajasthan, India

Nitric oxide (NO) has emerged as a multifunctional signalling molecule that interacts with light-mediated cascades to control several processes such as seed germination, photomorphogenesis, photosynthetic regulation, stomatal behaviour, and stress adaptation. Yet its role in nutrient acquisition, particularly iron (Fe), remains less explored in monocot plants. This study investigates the role of NO in regulating Fe uptake and associated biochemical responses in wheat (*Triticum aestivum*). Fe deficiency restricts crop growth and nutritional quality, making efficient Fe acquisition vital for food security. Wheat seedlings were grown under Fe-deficient (5 µM Fe-EDTA) and Fe-sufficient (100 µM Fe-EDTA) conditions, with or without sodium nitroprusside (SNP, 100 µM) as an NO donor. SNP supplementation under Fe deficiency significantly enhanced ferric chelate reductase (FCR) activity and strongly upregulated heme oxygenase 1 (HO 1) activity. Since HO 1-derived signalling molecules such as carbon monoxide and biliverdin can synergise with NO, this NO–HO 1 interaction appears to play a key role in enhancing Fe mobilisation and accumulation in roots and shoots. These findings highlight NO and HO as interconnected regulators of Fe homeostasis, opening the possibility that their interaction with light signalling could be utilised for Fe biofortification and crop improvement.



Poster 26

Light regulated developmental reprogramming drives *in vitro* regeneration of the endangered medicinal herb *Fritillaria roylei* Hook.

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Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Himachal Pradesh, Solan, India

Light is a central environmental signal that reprograms plant cell fate, driving the transition from dedifferentiated tissues to organized organs. In the endangered Himalayan herb *Fritillaria roylei Hook*., callus induction was achieved at 15°C and 25°C with 4.0 mg/L picloram and 2.0 mg/L thidiazuron, yielding 100% undifferentiated callus. In the absence of light, this callus remained morphogenetically arrested, maintaining a proliferative but unorganized state. Upon exposure to light, however, a developmental switch was initiated callus tissues began chlorophyll biosynthesis, acquired photosynthetic competence and underwent redifferentiation marked by greening, bulblet initiation and progression through somatic embryogenesis to complete plantlets. This suggests activation of light-responsive photoreceptors (e.g., phytochromes, cryptochromes) and downstream signaling cascades that regulate plastid differentiation, auxin-cytokinin cross-talk and expression of organogenesis-related genes. Moreover, light combined with elevated sucrose concentration (6.0%) and auxin-cytokinin supplementation (1.0 mg/L NAA + 1.0 mg/L kinetin) significantly enhanced morphogenesis, achieving 14.1 bulblets/explant and 90.98% regeneration. These findings indicate that while temperature and hormones initiate callus formation, light provides the critical developmental cue for organogenesis, chloroplast development, and full plant regeneration. Understanding these light-regulated molecular-insights offers valuable insights for improving propagation and aiding conservation of *F. roylei*, a critically endangered species.

Poster 27

Light-regulated genes involved in drought tolerance in groundnut

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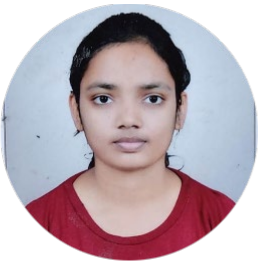
Groundnut is primarily grown in semi-arid tropical regions, where drought is a common abiotic stress. Despite its importance, the genetic mechanisms underlying drought tolerance remain poorly understood. This study used a multi-parent advanced generation inter-cross (MAGIC) population, evaluated across five seasons at two locations, to investigate drought tolerance. A genome-wide association study (GWAS) combining phenotypic data on drought-related traits and 10,556 SNPs identified 37 significant marker-trait associations (MTAs), explaining 0.91-9.82% of phenotypic variance. Notably, 26 MTAs were concentrated on four chromosomes (Ah03, Ah07, Ah10, Ah18), suggesting key genomic regions for drought tolerance. Candidate genes linked to leaf senescence (NAC transcription factor), flowering (B3 domain transcription factor, Ulp1 protease, Ankyrin repeat protein), chlorophyll biosynthesis (FAR1 protein), stomatal regulation (Rop guanine nucleotide exchange factor), and yield traits (Fasciclin-like arabinogalactan proteins) were identified near these MTAs. These genes play critical roles in light-regulated processes, such as chlorophyll synthesis and stomatal function, highlighting their importance in plant development under drought stress. The findings provide a foundation for future gene validation and marker development, enabling genomics-assisted breeding of drought-resistant groundnut varieties, contributing to climate-resilient agriculture.

Poster 28

Light-mediated regulation of miRNA biogenesis in plants

Aastha Shromona
CSIR-CIMAP, Lucknow, India

In recent years, miRNAs have emerged as pivotal regulators of plant development through post-transcriptional gene silencing. Previous reports point to the regulation of several miRNAs by light through ELONGATED HYPOCOTYL5(HY5), well-established as a key regulator of a myriad of photomorphogenetic processes. We postulated that the upregulation of miRNAs maybe driven by the interaction of HY5 with the genes involved in the miRNA biogenesis process. The canonical process of miRNA biogenesis begins with the formation of primary transcripts. These are then acted upon by the RNase-III-like activity of DCL to form miRNA-miRNA* duplex, followed by the AGOs which cleave it to form mature miRNAs. Among these genes, *in-silico* analyses revealed the presence of LREs (Light Responsive Elements) in the promoters of *DCL1*, *DCL2*, *AGO1* and *AGO2* genes of both Arabidopsis and Tomato. The expression of these genes was influenced by a time-dependent dark-to-light transition in the WT, Overexpression and mutant plants of *AtHY5* and *SlHY5*, suggesting the involvement of HY5. DNA-protein interaction assays also revealed very strong interaction between HY5 and promoters of these genes. All these results pointed to the positive influence of HY5 on the expression of these genes, consequently influencing the miRNA biogenesis process.



Poster 29

Functional characterization of Arabidopsis B-box domain proteins under high-intensity light stress

Neha Singh
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Light aids as the primary signal that influences the switch from heterotrophic to photoautotrophic growth and subsequent development. High-intensity light (HL) can cause imbalances in energy distribution between photosystems, leading to photoinhibition and reduced photosynthetic efficiency. Plants accumulate reactive oxygen species (ROS) for signaling and oxidative damage. To mitigate these effects, plants use protective mechanisms like ROS scavenging, anthocyanin biosynthesis, chloroplast repositioning, and stomatal regulation. Gene expression regulation is a rapid response to HL stress.. Our lab is mostly focused on the genetic and molecular studies of a family of light-regulated transcription factors BBXs, which contain one or two zinc-ligating B-box domains at their N-terminal (Vaishak et al., 2019). While BBX proteins have been thoroughly investigated in photomorphogenesis pathway, it’s regulation under HL conditions remain poorly understood. Based on the recent HL specific transcriptomic data (Huang et al., 2019), I have selected B-box domain proteins which are differentially expressed under HL stress and recovery condition. Promoter activity and transcript abundance suggests high light regulation of those *BBXs* in a spatio-temporal manner. Further, we aim to understand through genetic, molecular and biochemical data the activation and suppression of these *BBXs* and their downstream targets under HL stress and recovery condition.

Poster 30

Role of a BBX protein in regulation of early seedling development

Shikha Suyal
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Cotyledon opening and expansion is a crucial morphological change during de-etiolation as opened and expanded cotyledon makes maximum utilization of sunlight to produce food and energy through photosynthesis.

Changes in light quality directly affect the growth and development of plants. The ratio of red (R) to far-red (FR) wavelength is decreased due to the presence of neighbouring vegetation. This leads to developmental changes in the plants referred to as shade avoidance response. These responses include inhibition of seed germination, reduced cotyledon expansion, elongation of hypocotyls and petioles, hyponasty and reduced branching. The molecular control of the shade avoidance mechanism is of immense interest to plant biologists since it can have direct impact on cropping density and yield.

We have identified BBXa, a member of group I of BBX family that positively regulates light induced cotyledon opening and expansion. It is also highly upregulated under shade. Our initial analysis suggests that it form a gene regulatory network with COP1 and PIFs to optimize cotyledon expansion. We are currently investigating the role of this BBX protein in regulating cotyledon opening and expansion during de-etiolation and under shade avoidance responses.

Poster 31

Investigating plastid RNA processing dynamics under high light stress in C3 and C4 model crops

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As the climate is changing, weather patterns are shifting and high altitudes are becoming more prone to higher solar radiations. Excess light energy that cannot be used in photosynthesis cause oxidative damage to cellular components especially in chloroplast and impair photosynthetic machinery. Light modulates chloroplast gene expression and activates light signalling. However, chloroplasts often transcribe genes as polycistronic units limiting their transcriptional regulation. Therefore, post-transcriptional RNA processing including splicing and editing, is a critical mechanism that regulate chloroplast gene expression and ensure the production of functional photosynthetic proteins. RNA processing involves i) editing in chloroplast transcripts typically, deamination of specific cytidine (C) bases to uridines (Us) and ii) splicing of transcripts which underlines the formation of different isoforms from the same transcript. Disruptions in RNA processing have been linked to impaired chloroplast function and increased susceptibility to environmental stressors including high-light and temperature, underscoring the importance of this process in plant growth and development. In the present study, we have identified and characterized novel RNA-editing sites in *Setaria italica* as well as investigated the comparative dynamics of RNA-editing and splicing in *Arabidopsis thaliana* and *S italica* under high-light stress.

Poster 32

Kinetic $^{13}CO_2$ tracing reveals central metabolic reprogramming during light-dark transitions and UV-B stress in *Brassica napus*

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Stable isotopic (^{13}C) labelling is a powerful approach for metabolic mapping in plants and for probing metabolic flux phenotypes. Kinetic transitions following $^{13}CO_2$ fixation during the light phase, and their subsequent redistribution in the dark phase, provide fundamental insights into carbon allocation and stress-induced metabolic reprogramming. However, accurate fragment-level mapping of labelled metabolites requires a robust reference repository, which has so far been lacking. To address this gap, we developed a curated, plant-specific Mass-Isotopomer Fragment Repository (^{13}C-MIFR v1.0) containing TMS and/or TBDMS derivatised amino acids, organic acids, fatty acids, sugars, sugar alcohols and a few secondary metabolite fragments. This resource can aid plant metabolic scientists in carrying out isotopic studies. Using $^{13}CO_2$ labelling, we examined kinetic transitions in central metabolites of *Brassica napus* var. *sheetal* seedlings under standard light-dark growth cycles. Gas Chromatography-Mass Spectrometry (GC-MS)-based mass isotopomer analysis revealed temporal metabolic re-adjustments in central metabolism. Insights from light-to-dark transitions highlighted dynamic reprogramming of carbon fluxes, and ongoing analyses aim to resolve these temporal shifts at finer resolution. Further, under UV-B stress, elevated ^{13}C incorporation was observed in phenylalanine, isoleucine, valine, β-alanine, and GABA at early and mid-time points, indicating a prioritisation of stress-response metabolic adjustments over growth.

Poster 33

Role of melatonin against nano-stress in tomato plant

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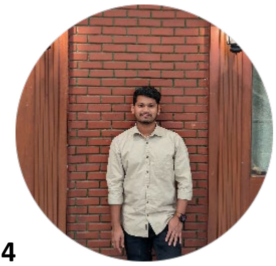
Copper oxide Nanoparticles (CuO NPs) have been used in the various industries ranging from pharma to solar including agrochemicals. These NPs have been reported for its negative and beneficial effect on the plants. The antimicrobial activities of CuO NPs are the major constraint behind its direct application in agriculture. On the other hand, accumulation of the CuO NPs in the environment also ends up in the soil due to indirect release of industrial byproducts and wastes. The interaction of CuO NPs with the plant's rhizosphere may cause a negative impact on the plant in the form of the nano-stress in roots and other parts of plants. Researchers are exploring various strategies to mitigate the nano-stress in plants by introducing phytochemicals to the modification of nanoparticles with multiple methods like green synthesis methods and capping agents. In the study, the usages of melatonin as the mitigating agent in the CuO NPs stress have been explored. Melatonin has been widely researched for the mitigating the abiotic stress by chelating the formation of ROS. Our results showed that the application of melatonin to the plants not only lowered the accumulation of NPs but reduced the ROS formation also.

Keywords- Plant-stress, CuO NPs, ROS, Melatonin



Poster 34

BBX_NV maintains gravitropic set-point angle of lateral roots in *Arabidopsis thaliana*

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Gravity is one of the critical environmental cues regulating plant growth and development. Plants sense the gravity to tune their orientation to ensure that the root grows downward into the soil for efficient absorption of water, minerals, and other nutrients. The lateral roots maintain an angle from the gravitational axis referred as gravitropic set-point angle (GSA) to ensure optimum uptake of nutrients. To maintain the GSA two opposite forces, act upward and downward on the growing lateral roots. Previous studies have indicated that distribution of the phytohormone auxin determines the GSA. The *LAZY* family genes play critical role in the asymmetric distribution of auxin to maintain the GSA. The molecular mechanism regulating the expression of the *LAZY* genes is less understood. The bZIP transcription factor HY5 positively regulates the transcription of *LAZY4* to maintain GSA. *hy5* mutants develop larger growth angle of lateral roots indicating that HY5 is required to keep the lateral roots downward. We identified a B-BOX transcription factor that negatively regulates *HY5*and *LAZYs* to modulate auxin distribution in the lateral roots and pull the lateral roots upward. This poster will discuss the identification and characterization of the role of BBX_NV in regulating GSA.

Poster 35

Optimizing dynamic LED lighting for sustainable crop cultivation

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Energy-efficient lighting strategies are essential for sustainable horticulture. Inspired by natural light dynamics, we investigate two innovative LED treatments, twilight transitions and slow-pulsating light, to reduce energy consumption without compromising crop performance. Twilight treatments simulate gradual shifts between light and dark, potentially engaging circadian rhythms and photoreceptor-mediated pathways, while slow-pulsating light alternates extended light pulses with dark intervals, aiming to mitigate photosynthetic overexcitation and sustain carbon assimilation.

Trials in tomato and cucumber under greenhouse conditions have shown promising physiological responses. To uncover the underlying mechanisms, we focus on tomato as a model crop, growing plants under controlled environments and monitoring real-time physiological parameters. We will perform biochemical, transcriptomic, and proteomic analyses at multiple time points to dissect the regulatory networks involved. This integrative approach aims to refine dynamic lighting strategies based on plant-intrinsic responses, advancing our understanding of how crops adapt to fluctuating light environments and natural photoperiods. Ultimately, our findings will support the development of energy-efficient cultivation systems and deepen insights into the molecular processes underlying light adaptation.