35TH DPMB ANNUAL SYMPOSIUM
FEBRUARY 23-24, 2023

INTERNATIONAL YEAR OF
MILLETS
2023

Welcome the Mighty

Azadi Ka Amrit Mahotsav

A CENTURY OF ACADEMIC EXCELLENCE
UNIVERSITY OF DELHI
दिल्ली विश्वविद्यालय
निष्ठा धृतिः सत्यम्
YEARS
1922-2022

34th DPMB Annual Symposium 2022

Best speaker (M.Sc.): Kirti Sharma

Best speaker (Ph.D.): Tonu Angaila Chithung

Best Chairperson: Dr. Akanksha Bhatnagar

Best cover page: Shitij Gupta

Best photography: Dr.Vibha Verma (I), Dr. Ridhi Khurana (II), Dr. Neelima Boora (III)

In the Name of Science

Can I have a moment of science, please?
Let's praise the Science Bearer!
The one always on time
DPMB's shine
The one you can't forget
Because the lectures are so fine

Can I have a moment of science, please?
Let's praise the Science Bearer!
The one so bold and charming
Wit so towering
Can't limit with a label
Speaks with a passion so empowering

Can I have a moment of science, please?
Let's praise the Science Bearer!
A fanfare so huge
Calm, composed, captain's grammar rules
Created an empire
Who knew the quiet one is the real Guru

Can I have a moment of science, please?
Let's praise the Science Bearer!
The one with perfect comedic timing
DPMB's darling
We laugh, we learn (so much fun)
This "stressed" one punches the best puns

Can I have a moment of science, please?
Let's praise the Science Bearer!
The one with killer viva questions
And a deftly cultivated sense of humor
This one knows everything
You'll witness when you'll present something

Can I have a moment of science, please?
Let's praise the Science Bearer!
Sit with this one and dissect science
Uses a meticulous, methodical protocol
To clean cobwebs from your mind
Can be intimidating, still worth the fright

Can I have a moment of science, please?
Let's praise the Science Bearer!
Leaves a signature of calcium everywhere
A complex one with a clear worldview
Enter this one's den
Meet a lot of heads with interesting hues

Can I have a moment of science, please?
Let's praise the Science Bearer!
This one exudes excellence
A solution to your programmable fears
Who knew this one's frequent absence
Can strike a chord so fierce

Can I have a moment of science, please?
Let's praise the Science Bearer!
A great mentor
And not just in academics
A safe place when personal problems creep
Go to this one, you'll get the help you need

Can I have a moment of science, please?
Let's praise the Science bearers!
A fascinating pair of two
So dedicated and never rude
I wish these generous teachers sparkle and
Buy a big coffee machine soon

Can I have a moment of science, please?
Let's praise these Science Bearers!
Any praise is less
For these DPMB's pillars

—*Sheena Shah*

Dr. Kamala Sohonie

First Indian woman to receive Ph.D. in a scientific discipline

Several women have challenged society and achieved their dreams throughout history. One of them was Kamala Sohonie, the first Indian woman to earn a Ph.D. in science. Born on June 18, 1911, in Indore, Madhya Pradesh, Dr. Kamala was brought up in a well-educated family. Her father and uncle were amongst the earliest chemistry graduates of the Tata Institute of Sciences (now the Indian Institute of Science, IISc). Science had always piqued Dr. Kamala's curiosity. Her family members were not shocked by her insistence on pursuing chemistry. Following the footsteps of her father and uncle, Kamala entered Bombay Presidency College to pursue an undergraduate degree in physics and chemistry.

She assumed that the next logical step would be to apply for a research fellowship at the IISc, confident that she met the requirements. Her first setback, though, was a resounding rejection. She found that hard to believe, especially since Sir C. V. Raman, the then director of IISc, did not think women were competent enough to pursue research. After being rejected, Dr. Kamala staged a "*satyagraha*" in front of Prof. C. V. Raman's office, which compelled him to admit her on certain conditions. Firstly, she would not be allowed to apply as a regular candidate and would have to stay on probation for the entire first year. Secondly, she would have to work late at night as per the instruction of her guide. Lastly, she would not spoil the environment by being a "distraction" to her male colleagues. She accepted the restrictions despite being openly humiliated by them, thus becoming the first woman admitted to the institute as an MSc. student in 1933. Later, she would explain, "Though Raman was a great scientist, he didn't admit me as a regular student. The bias against women was so bad at that time. What can one expect if even a Nobel Laureate behaves in such a way?" After a year of earning her M.Sc., Dr. Kamala convinced Prof. Raman that she was worthy of continuing as a student, who not only allowed her to stay on as a student but also opened the doors to other women in the institute. His perspective about women changed and he readily admitted many lady students from then on.

Under the supervision of her IISc mentor, Professor Srinivasaiah, Dr. Kamala established herself as an expert in the nutritional components of milk, pulses, and legumes. In 1935, her first paper was published, describing the non-protein nitrogen of nine pulses as essential for enhancing child nutrition.

After completing her M.Sc. in Biochemistry in 1936, she was given the opportunity to work with Dr. Derek Richter's group at Cambridge University in the U.K. Dr. Richter recognized her zeal to do research and provided her a spare table to work during the day where he himself would work at night after she used to leave. When Dr. Richter left to work somewhere else, she joined Dr. Robin Hill's lab, who was conducting similar research on plant tissues. Her research on potatoes led to the identification of the enzyme "Cytochrome C," which plays an essential role in the electron transport chain and is found in plants, human, and animal cells. In contrast to the normal long Ph.D. submissions, she completed her thesis on Cytochrome C in just 14 months, which had only 40 typed pages. She was awarded a Ph.D. in 1939 and thus became the first Indian woman on whom the title of Ph.D. degree was conferred.

After coming back to India, she was appointed Professor and Head of the Biochemistry Department at Lady Harding Medical College in New Delhi. Subsequently, she focused on the benefits of vitamins while serving as Assistant Director at the Nutrition Research Laboratory at Coonoor. After marrying M.V. Sohonie, an actuary, she moved to Mumbai in 1947 and joined the Royal Institute of Science as a Professor in the Department of Biochemistry, where she worked on the nutritional aspects of legumes. On the recommendation of Rajendra Prasad, the then President of India, Dr. Kamala began working on "Neera" (sap collected from the inflorescence of many types of toddy palms). She discovered considerable amounts of vitamin A, vitamin C, and iron in the drink, and demonstrated that these elements can be retained even if the drink was made into jaggery and molasses to increase shelf life. Further research showed that adding Neera as an inexpensive dietary supplement to the diets of undernourished adolescent children and pregnant women from tribal communities, caused significant improvement in their overall health. She earned the Rashtrapati Award for her efforts in this area.

In 1997, she received the National Award of Excellence and Contribution to Science. She passed away in 1998, shortly after collapsing at a felicitation event organized by the Indian Council of Medical Research in New Delhi. Her life serves as a metaphor for women's resilience in overcoming obstacles and proving their worth. In those days, she broke the glass ceiling, and today, women are thriving in the scientific field. While she is no longer with us, her contributions and dedication will continue to inspire scientists in the years to come.

Sheena Shah

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Preface

सरस्वति महाभागे विद्ये कमललोचने ।
विद्यारूपे विशालाक्षि विद्यां देहि नमोस्तुते ॥

O Devi Saraswati, the most Auspicious Goddess of Knowledge with Lotus-like Eyes,
An Embodiment of Knowledge with Large Eyes, Kindly Bless me with Knowledge. I Salute you

With the above-said words, we thank God for providing us with the capability and opportunity of being a part of this great institution and family. Being the part of one of the lighthouses of plant science is our greatest joy and pleasure.

With the blessings of God, we are celebrating our 35th annual symposium of the Department of Plant Molecular Biology (DPMB). The department has been organizing this event since 1988 which is mainly formulated by the students at DPMB under the guidance of our esteemed faculties. This symposium includes oral presentations by Doctoral and Master's students and the sessions are chaired by post-doctoral or senior students. Along with academics and research, it also includes fun events and competitions. After two years of Covid, this year, once again it is being organized as a two-day offline event. The five sessions spread over two days will encompass presentations from 20 students discussing various aspects of plant biology. We will start the event with a formal welcome note by Milinda Lahiri followed by Saraswati Vandana (prayer of the Goddess of knowledge, texts, and wisdom).

The first session on **"Plant Growth and development"** includes five talks and will be chaired by **Ms. Ankita Prusty**. This session will start with the paper presentations by one of our Doctoral Students, **Ms. Priya Gambhir** who will talk about her recently accepted research article on methylglyoxal homeostasis during tomato fruit ripening. **Rinki** will discuss the mechanism of fertilization-induced auxin synthesis in the endosperm for seed and fruit development. **Aditya** will talk about the role of MED25 in fruit ripening, followed by **Arjun** who will elaborate on the control of meiotic crossovers. The session will conclude with a presentation on the functional relevance of ERF.F12 in the transition to tomato fruit ripening by **Pooja Solanki**.

Spaced with a tea break, the next session on **"Signal Transduction in plants"** will be chaired by **Dr. Vibha Verma** and will feature four speakers. Starting with our final year M.Sc. student, **Ankit Kumar** will shed light on how reactive oxygen species inhibit nitrate signaling. **Milinda Lahiri** will present the newfound evidence about the role of phytochrome in plant plasticity and survival. **Monika** will talk about the role of calcium ions and auxin in plant regeneration and signaling. The concluding presentation of this session will be by **Amit Kumar** on a new calcium sensor switch that aids plants in better survival in salt stress.

Post lunch we will begin with the third session **"Innovations and Plant Biotechnology"** chaired by **Dr. Tanya Biswas**. Three speakers from our M.Sc. final year batch will present the latest findings of researchers all over the world and bring us up to speed with new trends in plant sciences. **Muskaan Johnson** will introduce us to gene editing technology by grafting. **Ashwani Kumar** will elaborate on COP9 signalosome and **Smrity Jha** will show us the exciting new pink cotton, a better sustainable option for textiles.

The final session for the day will be on **"RNA Biology and epigenetics"** and will be chaired by **Ms. Neelam**. The first talk of this session will be by **Ms. Tonu Angaila Chithung** who will be presenting her findings on the evolution of miRNA biogenesis machinery in plants with a special focus on rice. **Sheena Shah** will be presenting on DNA methylation in gene expression and development. The last presentation of the day will be by **Bhawana Kadyan** who will focus on bi-directional small RNA trafficking and cross-kingdom RNAi in the *Arabidopsis-Botrytis cinerea* pathosystem. The day will conclude with high tea and snacks.

The following day, we will begin with the same enthusiasm and meet for welcome tea. The last session of the symposium on **"Stress Biology"** will be chaired by **Ms. Sanchi Bhimrajka**. The session will comprise five presentations. Beginning with **Sonam Pahuja**, we will get to know about OsCRT3 conformational changes which promote OsCIPK7 binding which ultimately regulates tolerance to chilling. **Nikunj Bhandari** will elaborate on waterlogging stress in plants. **Sneha Pathak** will present findings about HAK5, which provides advantages during potassium deficiency. **Nikita** will discuss the evolutionary arms race between *Phytophthora sojae* and soybean. The final presentation will be by **Deepshikha Sharma** who will focus on HSFA1 which alters the 3D chromatin organization of enhancer-promoter interactions in tomato and HSFA3 is a modulator of heat stress memory-related genes in *Arabidopsis.*

The second day will mark its end with the most awaited event of the symposium, the QUIZ. Following this, there will be a prize distribution program. The symposium will then come to an end with the concluding remarks by the Head of the Department. We all feel honoured to be a member of this organizing committee. It has been an exciting learning experience for all of us in organizing the 35th Annual Symposium of DPMB. The organizing committee comprises of **Dr. Tanya Biswas Sardana, Shivam Sharma, Sanskriti Ravi, Sonam Pahuja, Nikunj Bhandari, Monika, Milinda Lahiri, Ankit Kumar Yadav, Ashwani Kumar, KVSK Arjun Chaudhary, Sheena Shah,** and **Sneha Pathak.**

We sincerely express our gratitude to **Prof. Girdhar Kumar Panday** (Symposium convener) **and Dr. Amit Kumar Singh** (Co-convener) for their guidance and support in organizing this event. We would also like to take this opportunity to thank **Prof. Sanjay Kapoor** (Head of the Department) and all the distinguished faculty members and the staff of the Department for their constant support and guidance. We are highly obliged to our teachers for providing their valuable time and judgment for the cover page, the photography competition, and the Sci-Toons.

Milinda Lahiri

35th DPMB ANNUAL SYMPOSIUM 2023

Day 1: February 23, 2023

Welcome Note **10:00-10:10 AM**

Saraswati Vandana **10:10 -10:15 AM**

Session I: Plant growth and development **10:15-11:30 AM**

Chairperson: Ankita Prusty

1. **Priya Gambhir:** Methylglyoxal homeostasis during tomato fruit ripening (Paper Presentation)
2. **Rinki:** Mechanism of fertilization-induced auxin synthesis in the endosperm for seed and fruit development
3. **Aditya:** Role of MED25 in fruit ripening
4. **K.V.S.K. Arjun Chowdary:** Control of meiotic crossovers
5. **Pooja Solanki:** Functional relevance of ERF.F12 in transition to tomato fruit ripening

 Tea Break **11:30-12:00 PM**

Session II: Signal transduction in plants **12:00-01:00 PM**

Chairperson: Dr. Vibha Verma

6. **Ankit Kumar:** ROS inhibit nitrate signaling
7. **Milinda Lahiri:** Phytochrome: Understanding the molecular basis of plant plasticity and survival
8. **Monika:** Ca^{2+} and auxin have role in plant regeneration and signaling
9. **Amit Kumar:** A new Ca^{2+} sensor switch to help plants better manage salt

 Lunch Break **01:00-02:30 PM**

Session III: Innovations and plant biotechnology **02:30-03:15 PM**

Chairperson: Dr. Tanya Biswas

10. **Muskaan Johnson:** Introduction of gene edits by grafting

11. **Ashwani Kumar:** COP9 signalosome

12. **Smrity Jha:** Pink Cotton - A new dye free Cotton

Session IV: RNA biology and epigenetics 03:15-04:00 PM

Chairperson: Neelam

13. **Tonu Angaila Chithung:** Understanding the evolution of miRNA biogenesis machinery in plants with special focus on rice (Paper Presentation)

14. **Sheena Shah:** DNA methylation in gene expression and development

15. **Bhawana Kadyan:** Bi-directional small RNA trafficking and cross-kingdom RNAi in *Arabidopsis-Botrytis cinerea* pathosystem

Group Photograph High Tea **04:00-04:30 PM**

Day 2: February 24, 2023

Welcome Tea **10:00-10:30 AM**

Session V: Stress Biology 10:30-11:45 AM

Chairperson: Sanchi Bhimrajka

16. **Sonam Pahuja:** OsCRT3 conformational changes promote OsCIPK7 binding and regulate tolerance to chilling

17. **Nikunj Bhandari:** Waterlogging stress in plants

18. **Sneha Pathak:** HAK5: The shield for potassium stress in plants

19. **Nikita Gupta:** The evolutionary arms-race between *Phytophthora sojae* and soybean

20. **Deepshikha Sharma:** HSFA1 alters the 3D chromatin organization of enhancer-promoter interactions in tomato and HSFA3 is a modulator of heat stress memory-related genes in *Arabidopsis*

Quiz **11:45-12:45 PM**

Prize distribution by Prof. Sanjay Kapoor (Head of the Department) **12:45-01:00 PM**

Concluding Remarks by Prof. Sanjay Kapoor (Head of the Department) **01:00-01:15 PM**

Lunch **01:15-02:15 PM**

Session I: Plant growth and development

Chairperson: Ankita Prusty

Methylglyoxal homeostasis during tomato fruit ripening

-Balance is the key

Priya Gambhir

Methylglyoxal (MG), a toxic compound produced as a by-product in several cellular processes such as respiration and photosynthesis, is well investigated for its deleterious effects, mainly through glycation of proteins during plant stress responses. However, very little is known about its impact on fruit ripening. In the present study, we report that MG levels are maintained at high level in green tomato fruits, which declines during fruit ripening despite of a respiratory burst during this transition. We demonstrate that this decline is mainly mediated by glutathione-dependent MG detoxification pathway and primarily catalysed by glyoxalase enzyme encoded by *SlGLY14* gene. *SlGLYI4* is a direct target of MADS-RIN and is induced during fruit ripening. Silencing of this gene leads to drastic MG overaccumulation at ripening-stages in the transgenic fruits and interferes with the ripening process. Further investigations show that MG plausibly glycates and inhibits key enzymes such as methionine synthase (MS) and S-adenosyl methionine synthase (SAMS) of ethylene biosynthesis pathway, thereby indirectly affecting fruit pigmentation and cell was metabolism. MG overaccumulation in several non-ripening or inhibited-ripening tomato mutant fruits suggests the tightly regulated MG detoxification process is crucial for normal ripening program. Overall, we underpin a *SlGLYI4*-mediated novel regulatory mechanism of MG detoxification controlling fruit ripening in tomato.

References:

Gambhir, P., Raghuvanshi, U., Parida, A.P., Kujur, S., Sharma, S., Sopory, S.K., Kumar, R., and Sharma, A.K. (2023). Methylglyoxal controls tomato fruit ripening by regulating ethylene biosynthesis. Plant Physiol. **(Accepted).**

Singla-Pareek, S.L., Kaur, C., Kumar, B., Pareek, A., and Sopory, S.K. (2020). Reassessing plant glyoxalases: large family and expanding functions. New Phytol. **227**: 714-721.

Mechanism of fertilization-induced auxin synthesis in the endosperm for seed and fruit development

"Let's play with Auxin"

Rinki

The dominance of flowering plants on earth is owed largely to the evolution of maternal tissues such as fruit and seed coat that protect and disseminate the seeds. The mechanism of how fertilization triggers the development of these specialized maternal tissues is not well understood. A key event is the induction of auxin synthesis in the endosperm, and the mobile auxin subsequently stimulates seed coat and fruit development. However, the regulatory mechanism of auxin synthesis in the endosperm remains unknown. Here, researchers show that a type I MADS box gene AGL62 is required for the activation of auxin synthesis in the endosperm in both *Fragaria vesca*, a diploid strawberry, and in *Arabidopsis*. Several strawberry *FveATHB* genes were identified as downstream targets of FveAGL62 and act to repress auxin biosynthesis. In this work, researchers identify a key mechanism for auxin induction to mediate fertilization success, a finding broadly relevant to flowering plants. Fertilization triggers seed and fruit development through the induction of AGL62 that leads to auxin synthesis in the endosperm. However, pollination/fertilization-induced auxin synthesis is not exclusive to the endosperm and may occur in other sporophytic tissues as is supported by reports of independent auxin synthesis in the seed integuments. Subsequently, newly synthesized auxin not only initiates post-fertilization development *in situ* but also is transported to other seed and floral tissues to coordinate and sustain the post-fertilization development. Comparative functional analysis of AGL62 in other plant species will reveal both conserved and species-specific mechanisms for the induction of post-fertilization developmental programs.

Reference:

Guo, L., Luo, X., Li, M., Joldersma, D., Plunkert, M., and Liu, Z. (2022). Mechanism of fertilization-induced auxin synthesis in the endosperm for seed and fruit development. Nat. Commun. **13**: 3985.

Role of MED25 in fruit ripening

Friend of ripening

Aditya

Fleshy fruit ripening is precise and well-coordinated process, involving changes in fruit's texture, colour, flavour, and other qualitative characteristics. The coordinated expression of thousands of ripening-related genes, including structural genes, which encode enzymes directly engaged in various phases of fruit ripening, and regulatory genes, which control gene expression. The transcription factors ETHYLENE INSENSITIVE3 (EIN3)/EIN3-LIKE (EIL) are essential for fruit ripening since they are the master controllers of the ethylene signalling pathway. A severe non-ripening phenotype is produced when the *EIL* genes in tomatoes are silenced or knocked out. Numerous transcription factors necessary for ripening have been discovered in addition to EILs. The *ripening-inhibitor* (*rin*) mutant, which was one of them, completely failed to ripen, indicating that RIN is a crucially important positive regulator of fruit ripening. Mediator subunit MED25 physically interacts with ETHYLENE-INSENSITIVE 3 (EIN3)/EIN3-LIKE (EIL), thereby synchronises an ethylene-dependent transcriptional program for the regulation of ripening-induced gene expression. MED25 forms a transcriptional module with EILs to regulate the expression of ripening-related regulatory as well as structural genes through promoter binding. To maintain ethylene homeostasis during fruit ripening, the EIL1-MED25 module synchronises transcriptional pathways with both positive and negative feedback, as well as its downstream regulators.

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Control of meiotic crossovers

Unzipping the serpent mating!

K.V.S.K. Arjun Chowdary

Crossovers and chromosome segregation are the two major hallmarks of meiosis. Recombination process involves double strand breaks, 5'–3' resection, strand invasion D-loop formation, DNA synthesis, double Holliday junction formation and resolution. Recombination rates are plastic across the genome, sex, stress and developmental stages of the plant. Crossovers are obstructed from occurring close to each other by a phenomenon called CO interference. What controls them is a classic subject to investigate! Meiotic crossovers were studied using HEI10^{oe} and *zyp1* mutant lines in which HEI10 is a known ZMM protein (also known as synapsis initiation complex) of class 1 crossovers (COs) and *ZYP1* encodes for the transverse filament of synaptonemal complex (SC), respectively. Overexpression of HEI10 led to an increase in class 1 crossovers but some CO interference persisted. Although, the *zyp1* mutation caused an increase in class 1 COs, it abolished CO-interference. In the double mutants, CO rate increases a lot. A mutation in the SC component increased the diffusion of HEI10 and resulting in more foci as predicted by the diffusion-based coarsening process. In short, Class 1 COs per unit length of SC are limited by HEI10 dose and ZYP1-mediated CO-interference.

References:

Durand, S., Lian, Q., Jing, J., Ernst, M., Grelon, M., Zwicker, D., and Mercier, R. (2022). Joint control of meiotic crossover patterning by the synaptonemal complex and HEI10 dosage. Nat. Commun. **13**: 5999.

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Morgan, C., Fozard, J. A., Hartley, M., Henderson, I. R., Bomblies, K., and Howard, M. (2021). Diffusion-mediated HEI10 coarsening can explain meiotic crossover positioning in *Arabidopsis*. Nat. Commun. **12**: 4674.

Functional relevance of ERF.F12 in transition to tomato fruit ripening

A tale of red to green

Pooja Solanki

Fruit ripening is most likely controlled by a complex network of phytohormones. Ethylene is one of the phytohormones that has long been recognised as the primary catalyst for climacteric fruit ripening. By blocking ethylene production or signal transduction via mutation or downregulation of key genes of ethylene biosynthesis or signalling pathways efficiently blocks the ripening process. ERFs are post-ethylene signalling components that play significant roles in controlling their expression. Epigenetic modifications such as DNA methylation, RNA methylation, and histone modifications also play important roles in climacteric fruit ripening. The roles of both transcription factors and epigenetic modifications in regulating fruit ripening are mostly ethylene-dependent, further emphasizing the central role of ethylene in regulating climacteric ripening. *SlERF.F12*, an ERF gene that produces a protein with an EAR motif and whose expression levels sharply drop during the transition to ripening, is a prime contender to be a key player in the regulation of this process. By enlisting the co-repressor TOPLESS protein 2 (TPL2) and the histone deacetylases (HDAs) HDA1/HDA3, SlERF.F12 inhibits the beginning of tomato fruit ripening through its C-terminal EAR motif. SlERF.F12 interacts with the co-repressor TPL2 and recruits HDAs to form a tripartite complex actively represses transcription of ripening genes by decreasing the level of the permissive histone acetylation marks H3K9Ac and H3K27Ac at their promoter regions. The roles of both transcription factors and epigenetic modifications in regulating fruit ripening are mostly ethylene-dependent, further emphasizing the central role of ethylene in regulating climacteric ripening.

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Session II: Signal transduction in plants

Chairperson: Dr. Vibha Verma

ROS inhibit nitrate signaling

Nitrate veils ROS

Ankit Kumar

Nitrate is a macronutrient as well as a signaling molecule that controls plant metabolism, growth, and crop yield. Reactive oxygen species (ROS), which are by-products of aerobic metabolism and were previously studied for their detrimental effects, have emerged as significant regulators of plant growth and development as well as plant responses to stress. Nitrogen deficiency causes the build-up of ROS. Chemical compounds that inhibited ROS build-up prevented the activation of gene expression involved with the nitrate-starvation response. However, the interplay between nitrate and ROS signaling in plant development remained unclear. The recent developments shed some light on understanding the involvement of ROS. A study showed that growth-related transcription factors HOMOLOG OF BRASSINOSTEROID ENHANCED EXPRESSION2 INTERACTING WITH IBH1 (HBI1) and its three closest homologs (HBIs) in *Arabidopsis* were induced in the presence of nitrate through NLP6 and NLP7. Nitrate treatment induced the nuclear localisation of NLP7, which reduced the accumulation of H_2O_2. This shuttling process is acting as a feedback regulatory loop in sensing nitrate signals. In a similar way, another study reported that the GARP (Golden2, ARR-B, Psr1) transcription factors were expressed in the presence of nitrate and worked by inhibiting nitrate transporters (NRT2.4 and NRT2.5), recyclers and ROS accumulation. Whereas in the absence of nitrate, ROS accumulated and activated the expression of transporters and recyclers. Hence, these studies conclude that ROS is a potential messenger for nitrogen starvation response.

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Phytochrome: Understanding the molecular basis of plant plasticity and survival

Morning Shows the Day

Milinda Lahiri

Phytochromes are chief regulators of growth plasticity, an essential characteristic that ascertains plants to adapt to the changing environment. Phytochrome has been shown to affect numerous physiological and developmental processes in the early stages, and now with growing evidence, probably in adult stages as well. Moreover, phytochrome may regulate plant responses during a wide range of environmental fluctuations by mediating transcription, post-transcriptional, and translation regulations. It is noteworthy that among all the phytochromes known in *Arabidopsis*, phytochrome B is the most extensively studied at a functional level. Nevertheless, the emerging role of other phytochrome members in this aspect is of paramount interest as it provides a control mechanism for biomass distribution and, in turn, control of crop yield. In addition to well-established local molecular effects, it also mediates several long-distance functions. Additionally, it seems to be an important regulator of carbon distribution, biomass production, and metabolic status at the seedling stage that allows a trade-off during shade conditions, regulating the growth of the plant well to the seed-setting stage. Shade Survival Syndrome, an important mechanism that allows plants to be able to grow strategically in areas of heavy crowding and canopy shade is also under strict regulation of the signals perceived by phytochrome. It is believed that the information assimilated by phytochromes is used to achieve an optimal balance to improve the survivability and continuity of species in crowded locations both at an inter- and intra-species level.

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Ca^{2+} and auxin have role in plant regeneration and signaling

Life is better with true friends

Monika

Under appropriate culture conditions, the somatic cells of the plants have a capacity to regenerate an organ or the whole plant. During *in vitro* plant regeneration, there is an induction of the pluripotent mass of cells called callus and during this process of regeneration there is ectopic activation of the root formation due to the phytohormone auxin which is important for both root and shoot regeneration. Reports suggest that in *Arabidopsis*, calcium signaling module CALMODULIN IQ-MOTIF CONTAINING PROTEIN (CaM-IQM) interacts with auxin signaling module to regulate the lateral root and callus formation. Loss-of-function of CaM-IQM results in dampening in auxin responsiveness which leads to retardation of auxin induced callus and lateral root formation. IQM is a calcium independent Calmodulin Binding Protein with an IQ motif. CaM-IQM complexes interact with the auxin signaling repressor INDOLE-3-ACETIC ACID INDUCIBLE (IAA) in Ca^{2+} dependent manner. Indeed CaM-IQM interacts with IAA-ARFs which have a molecular interplay with Ca^{2+} and auxin signaling during plant regeneration and development. When CaM6 interacts with IAA19 it destabilizes the interaction of IAA19 with ARF7 and thus, regulates the callus formation regulated by auxin.

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A new Ca^{2+} sensor switch to help plants better manage salt

The stronger the opponent, the stronger the defence shielding

Amit Kumar

Plant growth can be hampered by soil that contains an excessive amount of sodium (Na^+). In *Arabidopsis*, the formation of a "sodium-sensing niche" is attributed to the fact that Na^+ stress is responsible for the activation of primary calcium (Ca^{2+}) signals in a certain cell group that is located within the root differentiation zone. For plants to detect and recover from salt stress, primary calcium signalling is extremely necessary. The amplitude of this primary Ca^{2+} signal and the speed of the Ca^{2+} wave that arises both increase dose-dependently with increasing Na^+ concentrations, giving quantifiable information about the stress intensity. In addition to this, they describe a Ca^{2+}-sensing mechanism that is responsible for measuring the severity of the stress in order to mount appropriate responses regarding salt detoxification. This is made possible by a Ca^{2+}-sensor-switch mechanism, in which different amplitudes of Ca^{2+} signals trigger activation of the SOS3/CBL4 and CBL8 sensors, differentially. Despite of the fact that the SOS3/CBL4-SOS2/CIPK24-SOS1 axis is responsible for the basal salt tolerance, the CBL8-SOS2/CIPK24-SOS1 module is not activated until a significant amount of salt stress is experienced. Therefore, Ca^{2+}-mediated translation of Na^+ stress intensity into SOS1 Na^+/H^+ antiporter activity makes it easier to fine-tune the sodium extrusion capacity for the purpose of optimising the cell's tolerance to severe salt stress.

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Session III: Innovations and plant biotechnology

Dr. Tanya Biswas

Introduction of gene edits by grafting

CRISPR/Cas9 a powerful tool for genome editing

Muskaan Johnson

Genome editing (GE) technology has brought revolution in the field of biological research as it has equipped us with the ability to precisely edit the genome of living organisms. CRISPR/Cas9 is one such GE tool which is employed to induce targeted modification(s) in plants. Due to its high efficiency, ease of use, and accuracy it has become one of the popular genome editing tools. However, there are certain limitations associated with CRISPR/Cas9 system. Plant GE technology based on CRISPR/Cas9 depends upon *Agrobacterium tumefaciens* mediated transfer or direct gene transfer, using cultured plant tissues. There are many plant species which are either recalcitrant to transformation or show inefficient regeneration, therefore, grafting of WT scion on a donor transgenic rootstock serves as the best solution to this technical problem. Another issue associated with CRISPR/Cas9 system is the lengthy process of outcrossing, which is required to eliminate CRISPR/Cas9-associated sequences to generate transgene-free, gene-edited plant lines. This issue has been resolved with the help of a grafting-based system where the *Cas9* and guide RNA transcripts were fused to TLS (tRNA-like sequences) motifs that move RNAs from transgenic rootstocks to grafted wild-type shoots (scions) so as to achieve heritable gene editing. Hence, graft-mobile gene editing system enables the production of transgene-free offspring in one generation without the need for transgene elimination.

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COP9 signalosome

From plants to cancer treatment

Ashwani Kumar

COP9 signalosome (CSN) is an evolutionarily conserved protein complex found in plants as well as animals and it is involved in diversity of functions. It is composed of eight subunits (from CSN1 to CSN8). COP9 signalosome inhibits E3 ubiquitin ligase activity of CRLs by promoting the cleavage of NEDD8-CUL1 conjugate (also conceptualized as deneddylation). The metalloprotease motif of CSN5 is responsible for its deneddylation activity. It was first isolated from cauliflower. In plants, it is known to be repressor of light regulated development in dark. Homozygous mutants of *CSN* were failed to reach maturation and flowering stage thus suggested its fundamental role in development. Other than development CSN also takes part in hormone signalling in plants, for instance, it directly interacts with SCF^{TIR1} during auxin signaling and helps substrate degradation of SCF^{TIR1}. Similarly, hypomorphic mutants *csn5a-1* and *csn1-10* showed delayed seed germination mediated by ABA biosynthesis. CSN also mediates ethylene response by interacting with EER5. *CSN* mutants are delayed in G2 phase progression in *Arabidopsis* which accompanied by DNA damage response pathway. Delayed in expression of cold responsive genes in *CSN* mutant has been shown. In heat stress also CSN has been found to influence the expression of stress related memory genes. CSN5 promotes tumorigenesis by promoting degradation of substrates like p27, p53. In many types of human malignancies, *CSN5* overexpression has been implicated. For treatment purpose, CSN has been targeted by inhibitors like curcumin and emodin. Similarly, CSN5i3, another inhibitor of CSN5, found to suppress the tumor growth of human xenograft in mice.

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Pink Cotton – A new dye free Cotton

Future eco-friendly dresses will be colored naturally pink

Smrity Jha

Cotton is a dominant natural fiber which account for majority of textile globally. The color of the cotton fiber is dyed post-production. Therefore, large number of synthetic dyes from textile industry released into the environment causes harm to the health of humans and other organisms. The eco-friendly alternatives for coloring the cotton are thus the need of the hour. An alternative of producing 'Pink Cotton' is to engineer natural betalain pigment of beet root in cotton fibers. Two recent reports show that production of genetically engineered pink cotton is on the cards. Li et al. (2023) transformed Coker 315-11 cultivar of cotton with *DODA1* and *CYP76AD1* gene from *Beta vulgaris* and *DOPA5GT* gene from *Mirabilis jalapa*, driven by either 35S CaMV promoter and Itp3 mid-late-stage cotton fiber-specific promoter. The pattern of betalain production differed between transgenic of these two promoters. In transgenic lines of fiber-specific promoter, there was successful production of pink fibers in contrast to transgenic transformed under the control of constitutive promoter which produced white fibers like wild type. However, in fiber-specific transgenic lines, the pink color faded away in final days of boll maturation due to degradation of betalain during final maturation stage. Ge et al. (2022) transformed modern elite variety Zhongmian49 with *CYP76AD1*, *DODA* and *GT* genes from *Beta vulgaris*, driven by 35S CaMV promoter and fiber specific E6 promoter. The transgenic lines accumulated betalain. However, in this case also, pink color did not persist in mature fibers in the transgenic lines. These reports demonstrate that in future, it will be possible to have superior yield and pink fiber color that can be maintained at near maturity. This technology will have huge commercial value.

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Session IV: RNA biology and epigenetics

Chairperson: Neelam

Understanding the evolution of miRNA biogenesis machinery in plants with special focus on rice

It takes a village to raise a child

Tonu Angaila Chithung

miRNA biogenesis process is an intricate and complex event consisting of many proteins working in a highly coordinated fashion. Most of these proteins have been studied in *Arabidopsis*; however, their orthologs and functions have not been explored in other plant species. In the present study, we have manually curated all the experimentally verified information present in the literature regarding these proteins and found a total of 98 genes involved in miRNA biogenesis in *Arabidopsis*. The conservation pattern of these proteins was identified in other plant species ranging from dicots to lower organisms, and we found that a major proportion of proteins involved in the pri-miRNA processing are conserved. However, nearly 20% of the genes, mostly involved in either transcription or functioning of the miRNAs, were absent in the lower organisms. Further, we manually curated a regulatory network of the core components of the biogenesis process and found that nearly half (46%) of the proteins interact with them, indicating that the processing step is perhaps the most under surveillance/regulation. We have subsequently attempted to characterize the orthologs identified in *Oryza sativa*, on the basis of transcriptome and epigenetic modifications under field drought conditions in order to assess the impact of drought on the process. We found several participating genes to be differentially expressed and/or epigenetically methylated under drought, although the core components like DCL1, SE, and HYL1 remain unaffected by the stress itself. The study enhances our present understanding of the biogenesis process and its regulation.

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DNA methylation in gene expression and development

Meet the methylation-free plants!

Sheena Shah

DNA methylation is an epigenetic process in which a methyl group is added to DNA, which often alters gene function and influences gene expression. The addition of methyl groups to bases within the DNA helix is controlled by a family of enzymes called DNA methyltransferases. Plants have five known methyltransferases: METHYLTRANSFERASE 1 (MET1), CHROMOMETHYLASE 2 (CMT2), CMT3, DOMAINS REARRANGED METHYLTRANSFERASE 1 (DRM1) and DRM2. These methyltransferases are found to exhibit differential activity on cytosines in different sequence contexts. To fully investigate the extent of this epigenetic mark's control over gene regulation and plant development, DNA methylation-free *Arabidopsis* plants were created in a recent study in which the genes encoding all known functional DNA methyltransferases were mutated (a quintuple-knockout mutant known as *mddcc*). As expected, *mddcc* mutants showed severe developmental defects, extreme growth retardation and failed to flower. However, their survival span was found to be longer as compared to other genotypes (WT, *ddcc,* and *met1-9*) in long-day conditions. This suggests that DNA methylation might be necessary for *Arabidopsis* development but dispensable for its survival. The findings further indicated that DNA methylation controls gene expression in a dose-dependent manner and that functional redundancy is limited between CG and non-CG methylation in the regulation of gene expression. Thus, the *mddcc* mutant helped to assess the impact of DNA methylation on the regulation of gene expression and development in plants.

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Bi-directional small RNA trafficking and cross-kingdom RNAi in *Arabidopsis-Botrytis cinerea* pathosystem

Defending the fort through small RNAs

Bhawana Kadyan

Small RNAs (sRNAs) regulate vital biological processes in living organisms by regulating gene expression through modulation of transcription, target RNA stability, and mRNA translational. Surprisingly, sRNAs are also transmitted from fungi to plants and vice-versa. The significance of this cross-kingdom sRNA transfer was decoded in the *Arabidopsis-Botrytis* pathosystem where the gray mold disease causative agent, *Botrytis cinerea*, transfer small RNAs (*Bc*-sRNAs) to target *Arabidopsis thaliana* RNAs involved in host defence. The functional significance of these Bs-sRNAs can be inferred from the fact that *B. cinerea dcl1 dcl2* double mutant strain has reduced virulence and *A. thaliana ago1* mutant plants exhibit reduced susceptibility. Thus, *B. cinerea* hijacks the host RNA interference (RNAi) machinery to suppress plant immunity. Vice-versa, *Arabidopsis* secretes exosomes to deliver host sRNAs into fungal cells to silence virulence-related genes. Similar to mammalian tetraspanins, AtTET8-and AtTET9-associated exosomes help in transferring host sRNAs into fungal cells. The *Arabidopsis* trans-acting siRNAs and hetero-chromatic siRNAs biogenesis-impaired mutant plants are more susceptible to *B. cinerea* as compared with the wild type. These findings break the classical notion that chemicals and proteins only act as virulence effectors for phytopathogenic organisms.

In agricultural biotechnology, cross-kingdom RNA transfer is used to generate pathogen-tolerant plants through host-induced gene silencing (HIGS). A detailed study of this sRNA transfer machinery will help in generating technologies to deliver RNAs at desired cell types both in plants and animals.

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Session V: Stress Biology

Chairperson: Sanchi Bhimrajka

OsCRT3 conformational changes promote OsCIPK7 binding and regulate tolerance to chilling

OsCRT7 to rice: "Don't worry, I can keep you from getting cold."

Sonam Pahuja

Chilling stress is a major abiotic stress that adversely affects vegetative as well as reproductive stages of rice (*Oryza sativa*) growth, thereby reduces yield, quality, and productivity. Being a staple food, there is a need to dissect the molecular, physiological, and genetic mechanisms behind this chilling injury caused by global climate change in rice. The principal foundation for improving the freezing tolerance trait is the ability to detect cold to activate signal networks or to breed cultivars with elite cold-tolerant varieties. The recent research shed some light on the complex signaling network behind this cold stress. The study showed that the endoplasmic reticulum (ER)-localized Calreticulin 3 (OsCRT3) of rice undergoes conformational and secondary structural changes in response to cold stress, strengthening its association and improving its binding affinity with CBL-interacting protein kinase 7 (OsCIPK7), thereby increasing its kinase activity. As a result of cold stress, OsCRT3 promotes elevation in cytosolic calcium levels, which is sensed by Calcineurin B-Like protein 7/8 (OsCBL7/8) that interacts with OsCIPK7 on the plasma membrane. Together, these findings point to a cold-sensing mechanism that involves a new complex network composed of OsCRT3, OsCIPK7, Ca^{2+}, and its sensors OsCBL7/8 which enables rice to tolerate cold temperatures.

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Waterlogging stress in plants

Seems like someone had too much to drink…

Nikunj Bhandari

Water is crucial for all the living organisms on earth. However, excess water can also become a source of stress and harm. This is especially true in agriculture, where waterlogging due to irregular rainfall patterns and flooding can lead to reduced crop yields and sometimes complete crop failures. It is a major abiotic stress for plants as it interferes with the metabolism, respiration, and developmental processes. The initial setback to the plants can be attributed to the insufficient supply of oxygen to the roots, which escalates to accumulation of toxic metabolites from anaerobic respiration and harmful levels of reactive oxygen species (ROS), leading to restricted growth and development. Some plant species from the wetlands such as *Oryza* and *Rhizophora* have morphological and anatomical adaptations (adventitious roots and aerenchyma) to survive in such conditions, whereas certain plants modulate their cellular processes to survive. The well-documented responses to waterlogging are associated with activated antioxidant defense system and altered hormone signaling pathways. Besides, several transcriptional factors (TFs) are also differentially expressed, indicating their involvement in the waterlogging response. All this information towards understanding the molecular basis of submergence response can be explored to develop strategies for addressing the challenge of waterlogging stress in plants.

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HAK5: The shield for potassium stress in plants

MYB77, enhancing the high affinity K^+ uptake of roots via HAK5

Sneha Pathak

Potassium (K^+) is an essential macronutrient for plants. Its acquisition by the root from the soil solution is a crucial process for plant growth and development. K^+ deficiency causes shorter root hairs, leaf chlorosis, and less K^+ accumulation in the whole plant and shoot. At very low external K^+ concentrations (<20 μM) the high-affinity K^+ transporter HAK5, acts as a major contributor for K^+ uptake. Under K^+ deficiency, genes regulated at the transcriptional level is limited, including those encoding K^+ transporters, regulatory factors and signalling components. MYB77 positively regulates the expression of *HAK5*, by binding to the *HAK5* promoter and enhances high-affinity K^+ uptake of roots. Among the 26 members of the *Arabidopsis* CIPK protein kinase family, CIPK1 is the most efficient activator of *HAK5*. Moreover, a fine-tuned regulation between HAK5 and AKT1 activities are the major contributors of root K^+ uptake. Taken together, a complex regulatory network controls the high-affinity K^+ transporter and root potassium uptake.

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The evolutionary arms-race between *Phytophthora sojae* and soybean

Weapons in the arsenal of oomycete to dodge host plant

Nikita Gupta

Phytophthora sojae is one of the most damaging plant pathogens of soybean. Over two decades of research on this oomycete-legume interaction has revealed various molecular facets of virulence and counter defence mechanisms used by pathogen and host, respectively. Recent studies focus on *P. sojae*-secreted apoplastic endoglucanase, PsXEG1, and its recognition as a pathogen-associated molecular pattern (PAMP) by response to XEG1 (RXEG1) complex, and subsequent suppression of this PAMP-triggered immunity (PTI) by cytoplasmic effectors. This interaction supports the coevolutionary zig-zag-zig model of plant–microbe interactions. The virulence activity of PsXEG1 is countered by plant-secreted glucanase inhibitor protein, GmGIP1, which is sequestered by the high-affinity paralogous decoy secreted by *P. sojae*. The N-glycosylation of PsXEG1 represents an additional layer of this coevolutionary struggle, protecting PsXEG1 against a host apoplastic aspartic protease, GmAP5, that targets PsXEG1. The cytoplasmic RXLR effectors of *P. sojae* suppress cell death, oxidative burst production, and defence gene induction triggered by PsXEG1 in plants. The resistant soybean plants counteract this PTI-suppression by recognizing the RXLR effectors directly or indirectly through resistance genes. Thus, *P. sojae-Glycine max* interaction model is interesting for research and teaching. The lessons learnt from this system would help in understanding other host-pathogen interactions and raising resistant/tolerant crop plants.

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HSFA1 alters the 3D chromatin organization of enhancer-promoter interactions in Tomato and HSFA3 is a modulator of heat stress memory-related genes in *Arabidopsis*

3D understanding of the heat stress response…

Deepshikha Sharma

Plants, being sessile, have evolved sophisticated ways to modulate their gene expression in response to heat stress (HS). Recent research has unveiled two interesting facets of HS-associated gene expression. Firstly, in higher eukaryotes, heterochromatin is mainly composed of transposable elements (TEs) silenced by epigenetic mechanisms. However, HS disrupt the silencing of certain heterochromatin associated TEs. HS drives the expression of HS responsive genes (mainly Hsps) via transcription factors (TF) like heat shock factors (HSFs). Recent work shows that one such factor, *HSFA1*, alters the 3D chromatin organization of enhancer-promoter interactions and modulates HS responses. 3D chromatin architecture dynamically controls the access of REs (regulatory elements) to their target genes by promoting or inhibiting RE-promoter interactions. Most of studies in plants have focused on deciphering the role of TFs in 3D chromatin architecture and gene regulation under steady-state conditions. In this study, a multidimensional study combining stress at different time points was carried out for deciphering the molecular mechanisms involved in establishing distal RE-promoter interactions. Secondly, acquired thermo-tolerance actively maintained over several days (HS memory) and involves the sustained induction of memory related genes. It is shown that *FORGETTER3/HEAT SHOCK TRANSCRIPTION FACTOR A3* (*FGT3/HSFA3*) is specifically required for physiological HS memory and maintaining high memory-gene expression during the recovery phase following a HS exposure. HSFA3 mediates HS memory by direct transcriptional activation of memory related genes after return to normal growth temperatures.

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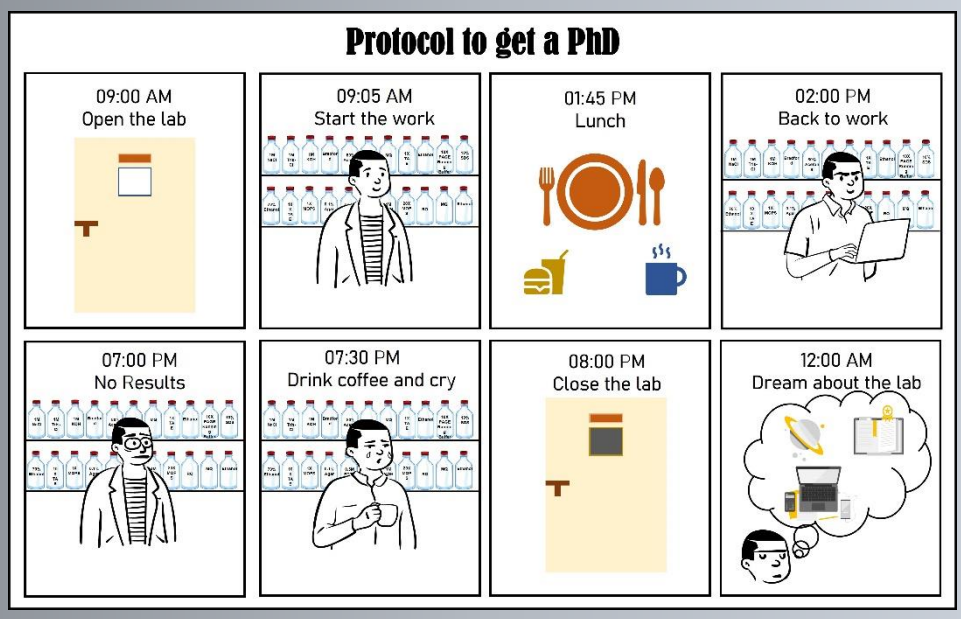
Science Toons

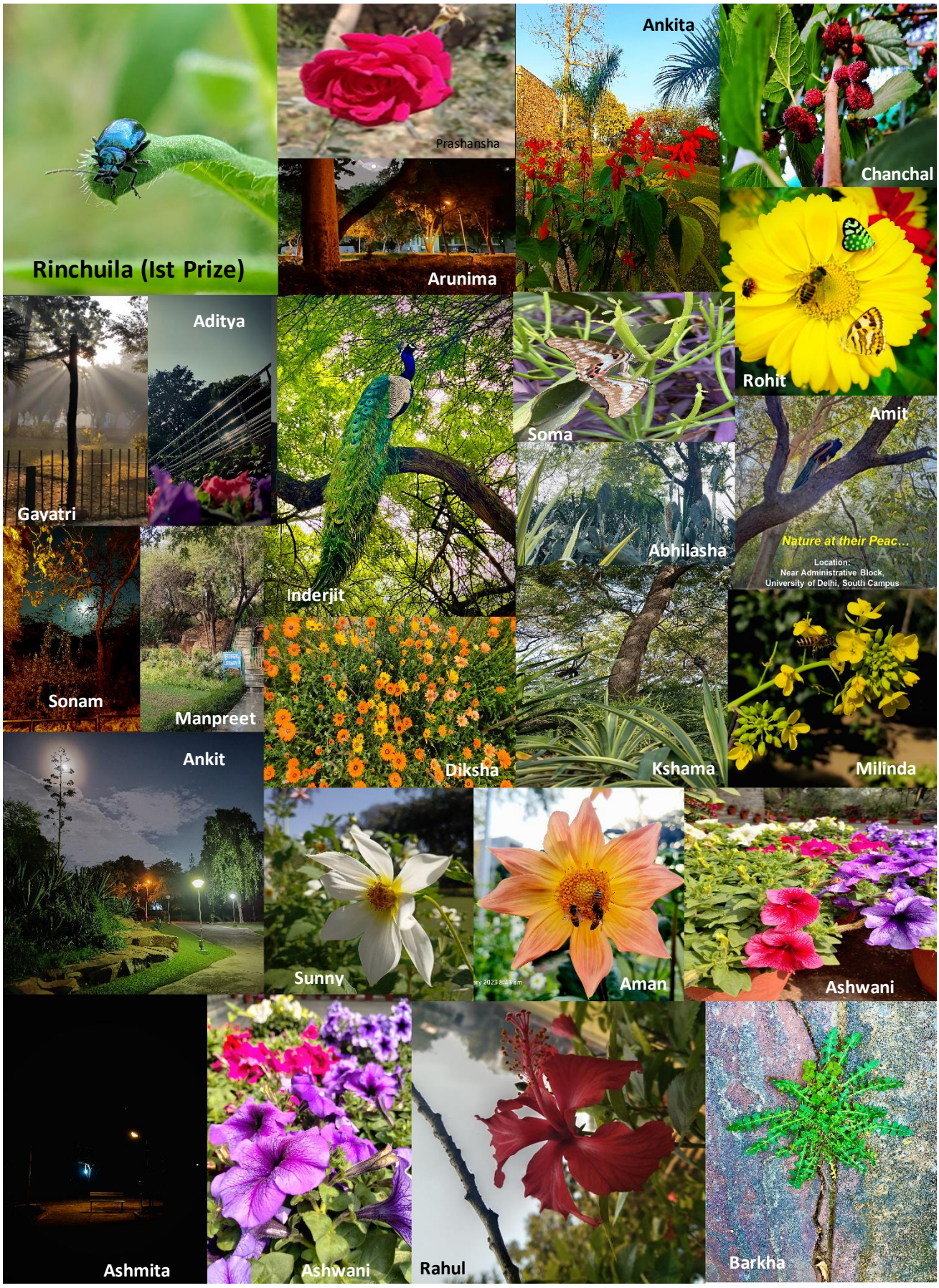
Jaspreet Kaur

Gayatri Tripathi



Gayatri Tripathi

Photography Competition



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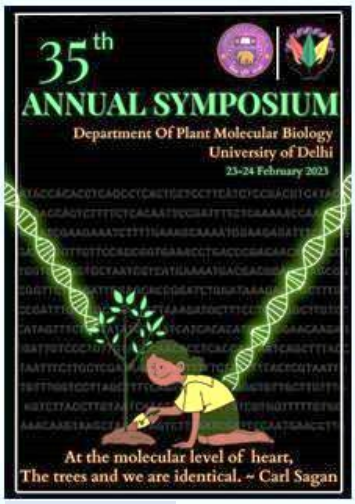
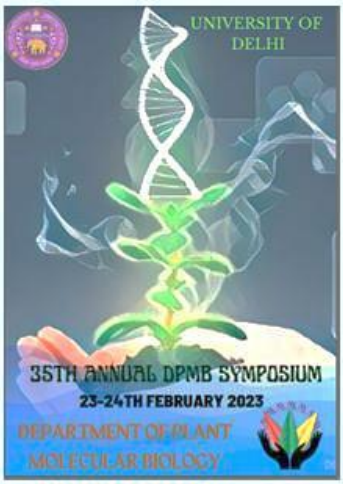
ORGANIZING COMMITTEE 2023

Aditya

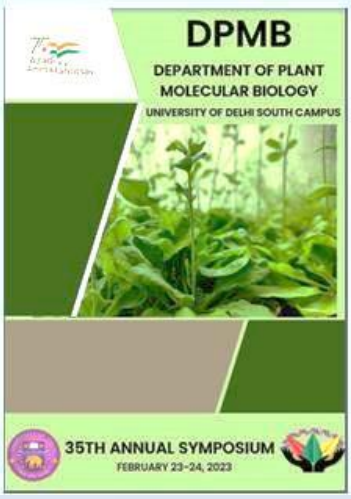


Prashansa



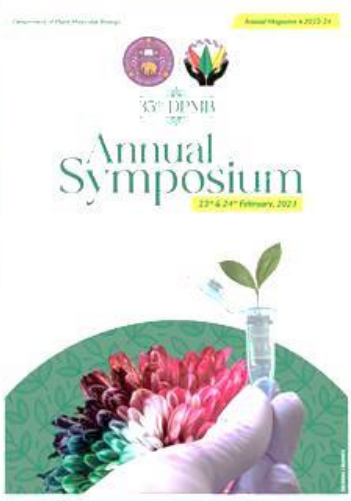
Ankita

Ankit



Gayatri

Amit



Sunny

Milinda

The UN General Assembly approves a resolution presented by India, designating 2023 as the "International year of millets" with the goal of increasing public awareness of the advantages of the grains for human health and their adaptability to climate change. It is intriguing to know how these "tiny grains" pack a big nutritional punch and support the globe in combating its challenges.

--KVSK Arjun Chowdary