2024

Department of Plant Molecular Biology

University of Delhi South Campus

Estb. 1988

Cover Page

The mature wheat spikes represent the successful culmination of the Wheat Genome Sequencing Project in 2014, an international consortium project where DPMB contributed towards sequencing of the long arm of chromosome 2A. This is the latest in a series of genome sequencing endeavors (starting from Rice in 2005, followed by Tomato in 2012) to which our department has significantly contributed. A graphical representation of a network on the right signifies current and sustained efforts of all the faculty members of the DPMB towards understanding the Gene regulatory networks, Protein-protein interactions and Signaling networks that govern growth and development in plants and affect their ability to withstand abiotic and biotic stress conditions.

Contacts

The Head, Department of Plant Molecular Biology
University of Delhi South Campus, Benito Juarez Marg, New Delhi 110021, INDIA

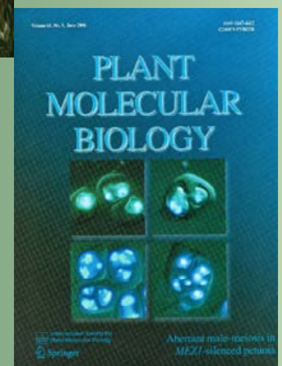
E head@pmb.du.ac.in **T** 011-2411-1208 **W** http://dpmb.ac.in

About

The Department of Plant Molecular Biology was established in 1988 under the Faculty of Interdisciplinary and Applied Sciences to cater to the needs of students in frontier areas of plant biology and to carry out research on Molecular Aspects of Plant Biology and Biotechnology. The Department was enriched by merger of the Unit for Plant Cell and Molecular Biology in 1988 (originally established by the DST), and award of COSIST grant by the UGC (1990-1995). The Department has been recognized for Special Assistance Programme (DRS Phase I to Phase III) by the UGC (2002-2018) to strengthen research/teaching in the area of Functional Genomics. Since its establishment in 1988, Professor S.C. Maheshwari (1988-1992), Professor Akhilesh K. Tyagi (1988, 1992-95, 1998-2001), Professor Jitendra P. Khurana (1995-1998, 2001- 2004, 2014 - 2016), Professor Paramjit Khurana (2004 - 2007, 2016-2019), Professor Anil Grover (2007-2010, 2019-2022), Professor Indranil Dasgupta (2010 - 2013), Professor Madan Mohan (2013 - 2014) and Professor Sanjay Kapoor (2022-till date) have served as Heads of the Department.

The research has been supported by major grants in the form of "Centre for Plant Molecular Biology" and "Genome Initiatives on Sequencing, Gene Discovery and Function" by DBT, in addition to other competitive grants from DST, UGC, European Commission and the Rockefeller Foundation. The faculty is involved in multi–institutional as well as international projects. The research has yielded about 750 publications and a few patents have been filed. Efforts of the faculty have been recognized in the form of fellowships to national/international scientific academies and national/international awards. While providing due emphasis to basic research and training, the Department endeavors to convert knowledge into application for human welfare.

Research Highlights (Journal cover pages)



Research Publications (in numbers)

In last five years (2018-2023)

45.05
Average Citation

78
H-index

228
Publications

Prof. Sanjay Kapoor

Research Interests: Functional Genomics of Reproductive Development in Rice

Following the establishment of floral organ primordia, plants develop male (pollen) and female (embryo sac) gametophytes within the androecium and gynoecium, respectively. The gametes formed therein undergo fertilization to form seeds. To understand the gene regulatory networks that govern the development of these reproductive structures, our lab focuses on two key areas: identifying genetic components and mapping their interactions to construct biologically realistic gene regulatory networks.

We have conducted a comprehensive transcriptome analysis across 30 rice tissue types and developmental stages. This work has revealed co-expressed gene groups that either exhibit similar up-regulation profiles or are expressed in a tissue- or stage-specific manner, thus constituting potential interactomes. By applying a subtractive logic approach, we have shortlisted genes with specific expression profiles, which we further validate through RNAi/miRNA silencing and ectopic expression in transgenic rice and Arabidopsis. To assess their promoter activities, we have used GUS and GFP reporters in transgenic systems.

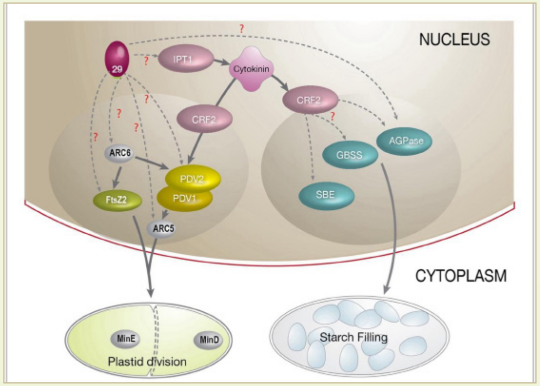
Our research extends to MADS-box transcription factors and RNA interference (RNAi) machinery, with a focus on OsMADS29. This gene plays a significant role in grain filling in rice by regulating hormone homeostasis and starch metabolism. Our findings indicate that M29 targets components in cytokinin biosynthesis/regulatory pathways that are conserved from early land plants to modern monocots and dicots. These suggest that new regulatory components can evolve by interacting with components of ancient biochemical pathways. Additionally, M29 interacts with 19 other MADS-box proteins expressed in seeds, potentially diversifying its targets. Recent data indicate that M29 regulates plastid biogenesis, promoting the differentiation of proplastids into amyloplasts, which appears to have evolved specifically in cereals to support endosperm development. We are now exploring methods to transform non-seed cells into starch-producing cells, aiming to synthesize starch independently from cereal crops.

Our lab is also involved in exploring microspore embryogenesis—a process that accelerates breeding by producing doubled-haploid embryos from haploid cells. Using Brassica napus, we explore the role of histone deacetylase inhibitors in inducing haploid embryogenesis. Employing fluorescence-activated cell sorting (FACS) and multiomics, we aim to identify key genes involved in this process to improve breeding efficiency and enhance crop resilience.

Furthermore, we are examining translation-level regulation during seed development in rice. By integrating Proteome, Small RNome and Polysome analyses, we seek to understand how translational control impacts seed development, potentially contributing to crop productivity and resilience.

Awards and Distinctions

- Prof. R.N. Tandon Memorial Award by the National Academy of Sciences, India (NASI) (2018)
- Editor, Rice (2019 ~)
- Fellow of the National Academy of Sciences, India (December 7, 2013)
- Fellow of Science and Technology Agency Japan (1997-1999)
- JSPS (Japan Society for the Promotion of Science) long-term Post-doctoral fellowship (1995-1997).
- Japanese Government ("Monbusho"—Ministry of Education and Culture) Fellowship (1992-94).



Proposed role of OsMADS29 in regulating plastid division and starch biosynthesis via cytokinins.

Select Publications

1 Verma, V., Boora, N., Nayar, S., Kumar, G., Thapliyal, S., Ankur, … Kapoor, S. (2023). Ca2+-Calmodulin regulates nuclear translocation of the rice seed-specific MADS-box transcription factor OsMADS29. FEBS Journal, 290(14), 3595–3613.

2 Khurana, R., Bhimrajka, S., Sivakrishna Rao, G., Verma, V., Boora, N., Gawande, G., … Kapoor, S. (2022). Characterization of Transcription Regulatory Domains of OsMADS29: Identification of Proximal Auxin-Responsive Domains and a Strong Distal Negative Element. Frontiers in Plant Science, 13(April), 1–17.

3 Boora, N., Verma, V., Khurana, R., Gawande, G., Bhimrajka, S., Chaprana, K., … Kapoor, S. (2021). Determination of Tripartite Interaction between Two Monomers of a MADS-box Transcription Factor and a Calcium Sensor Protein by BiFC-FRET-FLIM Assay. Journal of Visualized Experiments, 178, 1–18.

4 Nayar, S., Kapoor, M., & Kapoor, S. (2014). Post-translational regulation of rice MADS29 function: homodimerization or binary interactions with other seed-expressed MADS proteins modulate its translocation into the nucleus. Journal of Experimental Botany, 65(18), 5339–5350.

5 Nayar, S., Sharma, R., Tyagi, A. K., & Kapoor, S. (2013). Functional delineation of rice MADS29 reveals its role in embryo and endosperm development by affecting hormone homeostasis. Journal of Experimental Botany, 64(14), 4239–4253.

6 Baranwal, V. K., Mikkilineni, V., Zehr, U. B., Tyagi, A. K., & Kapoor, S. (2012). Heterosis: emerging ideas about hybrid vigour. Journal of Experimental Botany, 63(18), 6309–6314.

7 Sharma, R., Agarwal, P., Ray, S., Deveshwar, P., Sharma, P., Sharma, N., … Kapoor, S. (2012). Expression dynamics of metabolic and regulatory components across stages of panicle and seed development in indica rice. Functional & Integrative Genomics, 12(2), 229–248.

8 Kapoor, M., Arora, R., Lama, T., Nijhawan, A., Khurana, J. P., Tyagi, A. K., & Kapoor, S. (2008). Genome-wide identification, organization and phylogenetic analysis of Dicer-like, Argonaute and RNA-dependent RNA Polymerase gene families and their expression analysis during reproductive development and stress in rice. BMC Genomics, 9(1), 451.

9 Arora, R., Agarwal, P., Ray, S., Singh, A. K., Singh, V. P., Tyagi, A. K., & Kapoor, S. (2007). MADS-box gene family in rice: genome-wide identification, organization and expression profiling during reproductive development and stress. BMC Genomics, 8(1), 242.

10 Kapoor, S., & Sugiura, M. (1999). Identification of Two Essential Sequence Elements in the Nonconsensus Type II PatpB-290 Plastid Promoter by Using Plastid Transcription Extracts from Cultured Tobacco BY-2 Cells. The Plant Cell, 11(9), 1799–1810.

11 Kapoor, S., Kobayashi, A., & Takatsuji, H. (2002). Silencing of the Tapetum-Specific Zinc Finger Gene TAZ1 Causes Premature Degeneration of Tapetum and Pollen Abortion in Petunia. The Plant Cell, 14(10), 2353–2367.

The Team


Dr. Amit Dwivedi
Inspire Faculty


Dr. Vibha Verma
Maharishi Kanad
PDF


Dr. Shivam Sharma
PDF


Aradhana Agarwal
PhD Student


Chhavi Bharadwaj
Project Fellow


Prashansa Sharma
Intern


Haney Gupta
Technical Assistant


Sudhir Kumar
Growth room
Attendent

Prof. Girdhar K. Pandey

Research Areas: Calcium-mediated Signaling, Functional Genomics of Stress Signaling, and Stress Adaptation in Plants

Responding to external stimuli and facilitating dynamic changes in cellular homeostasis is key to plant survival. Being sessile in nature and facing multifactor stresses such as temperature, drought, salinity, and biotic invasions in the environment, plants have evolutionarily developed and conserved intricate system of cellular signaling and cross-talk to sense, respond and mount adaptive response for survival. Calcium is a multifaceted ubiquitous molecule orchestrating multiple signaling pathways in all eukaryotes, physiological or developmental processes. Intracellular transient calcium spikes, also known as specific "Ca2+ signatures, often follow stress perception, which is specific in eliciting characteristic downstream responses to combat stress effectively. An entire calcium signaling toolkit is dedicated to maintaining calcium transients, sensing them, and relaying the signal through post-translational modifications, most commonly protein phosphorylation and dephosphorylation, and restoring resting calcium concentrations.

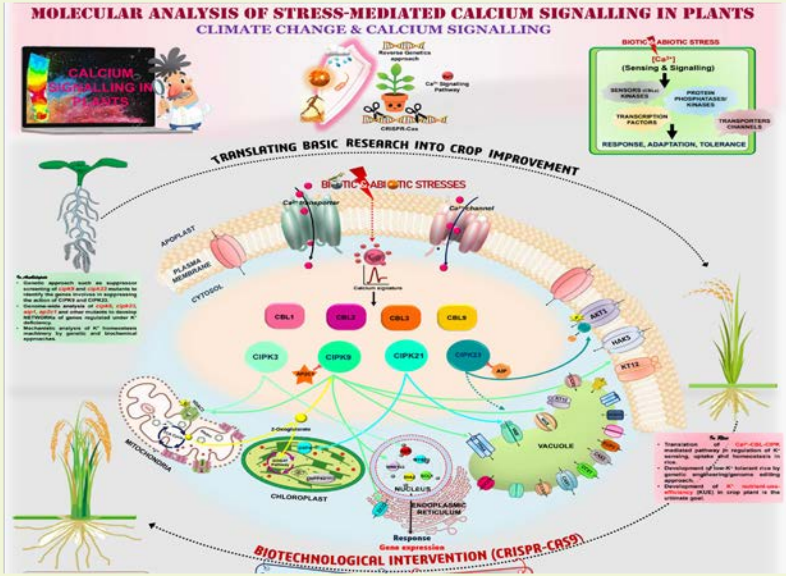
At present, we are in the midst of extensively characterizing several crucial sensors, such as CBL1, CBL2, CBL3 and CBL9, and their partner kinases, such as CIPK3, CIPK9, CIPK21 and CIPK23 under different abiotic and biotic stresses and identifying their phosphorylating targets, specifically potassium channels and transporters under low nutrient stress, calcium exchangers under abiotic stresses in model plant system Arabidopsis thaliana.

Our group is also engaged in translational extrapolation of models deduced in Arabidopsis to crop plants such as rice to generate transgenic plants with enhanced stress resilience with little to no effect on crop productivity. The interaction of several pathways converging /diverging at critical "hubs" is being investigated by using the advanced tools of genetic and functional genomics, where several networks can be mapped collectively. Molecular and genetic manipulation of key/master regulators is the prime focus, which carries immense potential for the agricultural biotechnology sector.

Awards and Distinctions

- Prof. Shri Ranjan Memorial Award, National Academy of Sciences, India (NASI)
- J.J. Chinoy Gold Medal Award, Indian Society of Plant Physiology, New Delhi, India
- Fellow, National Agricultural Academy of Sciences (NAAS), New Delhi
- Fellow, National Academy of Sciences, India (NASI)
- National Bioscience Award, DBT, India
- Foreign Expert Award, Jiangsu Academy of Agricultural Sciences, Nanjing, China
- Visiting Professor, Jiangsu Academy of Agricultural Sciences, Nanjing, China
- Visiting Professor, College of Life Sciences, Capital Normal University, Beijing, China
- INSA-DFG fellowship
- DBT-CREST Award
- Far Eastern Regional Research Organization (FERRO) award, USDA, USA

The Team



Select Publications

1 Singh N, Ravi B, Saini LK, Pandey GK (2023) Voltage-dependent anion channel 3 (VDAC3) mediates P. syringae induced ABA-SA signaling crosstalk in Arabidopsis thaliana. Plant Physiology and Biochemistry, 12;206:108237. doi: 10.1016/j.plaphy.2023.108237.

2 Saini LK, Sharma M, Ravi B, Ghosh S, Pahuja S, Singh N, Pandey GK (2023) Overexpression of ARM repeat/U-box containing E3 ligase, PUB2 positively regulates growth and oxidative stress response in Arabidopsis. Biochemical Journal, 480 (9), 555-571.

3 Sanyal SK, Sharma K, Bisht D, Sharma S, Sushmita K, Kateriya S, Pandey GK (2023) Role of calcium sensor protein module CBL-CIPK in abiotic stress and light signaling responses in green algae. International Journal of Biological Macromolecules 237, 124163.

4 Kanwar P, Sanyal SK, Mahiwal S, Ravi B, Kaur K, Fernandes JL, Yadav AK, Tokas I, Srivastava AK, Suprasanna P, Pandey GK. (2021) CIPK9 targets VDAC3 and modulates oxidative stress responses in Arabidopsis. Plant Journal, 109(1):241-260 doi: 10.1111/tpj.15572. PMID: 34748255.

5 Kumar M, Sharma K, Yadav AK, Kanchan K, Baghel M, Kateriya S, Pandey GK (2020) Genome wide identification and biochemical characterization of Calcineurin B-like calcium sensor proteins in Chlamydomonas reinhardtii. Biochemical Journal, 477(10):1879-1892. doi: 10.1042/BCJ20190960.

6 Sanyal SK, Kanwar P, Fernandes JL, Mahiwal S, Yadav AK, Samtani H, Srivastava AK, Suprasanna P, Pandey GK (2020) Arabidopsis Mitochondrial Voltage-Dependent Anion Channels Are Involved in Maintaining Reactive Oxygen Species Homeostasis, Oxidative and Salt Stress Tolerance in Yeast. Frontier in Plant Science, 11:50. doi: 10.3389/fpls.2020.00050.

7 Yadav AK, Jha SK, Sanyal SK, Luan S, Pandey GK. (2018) Arabidopsis Calcineurin B-like proteins differentially regulate phosphorylation activity of CBL-interacting protein kinase 9. Biochemical Journal, 475(16):2621-2636.

8 Singh A, Yadav AK, Kaur K, Sanyal SK, Jha SK, Fernandes JL, Sharma P, Tokas I, Pandey A, Luan S, Pandey GK (2018) Protein Phosphatase 2C, AP2C1 Interacts with and Negatively Regulates the Function of CIPK9 under Potassium Deficient Conditions in Arabidopsis. Journal of Experimental Botany, 69(16):4003-4015.

9 Shankar A, Fernandes JL, Kaur K, Sharma M, Kundu S, Pandey GK (2018) Rice Phytoglobin regulate responses under low mineral nutrients and abiotic stresses in Arabidopsis thaliana. Plant Cell Environment 41(1):215-230.

10 Pandey GK, Kanwar P, Singh A, Steinhorst L, Pandey A, Yadav AK, Tokas I, Sanyal S, Beom- Kim B-G, Lee SC, Cheong YH, Kudla J, Luan S (2015) CBL-interacting protein kinase, CIPK21, regulates osmotic and salt stress responses in Arabidopsis. Plant Physiology, 169(1):780-92.

Prof. Saurabh Raghuvanshi

Research Areas: MicroRNA mediated Plant Stress Response, Biocuration and Big Data Analytics

MicroRNA mediated regulatory schemas in plants Our group is working on an integrated approach of comparative genomics on different dimensions of genome, epigenome (DNA methylation & histone modification) and transcriptome (including miRNome) to understand the evolution of drought tolerance response in rice. We are especially interested in miRNA mediated regulatory networks in rice and have elucidated several miRNA gene mediated regulatory schemas that may be involved in regulating plant stress response. It was also possible to identify and characterize regulatory networks that behave in a completely opposite manner in contrasting rice cultivars under similar drought stress conditions. Further our group has also identified >100 novel miRNA genes in rice, some of which are involved in basic processes like flower development and stress response.

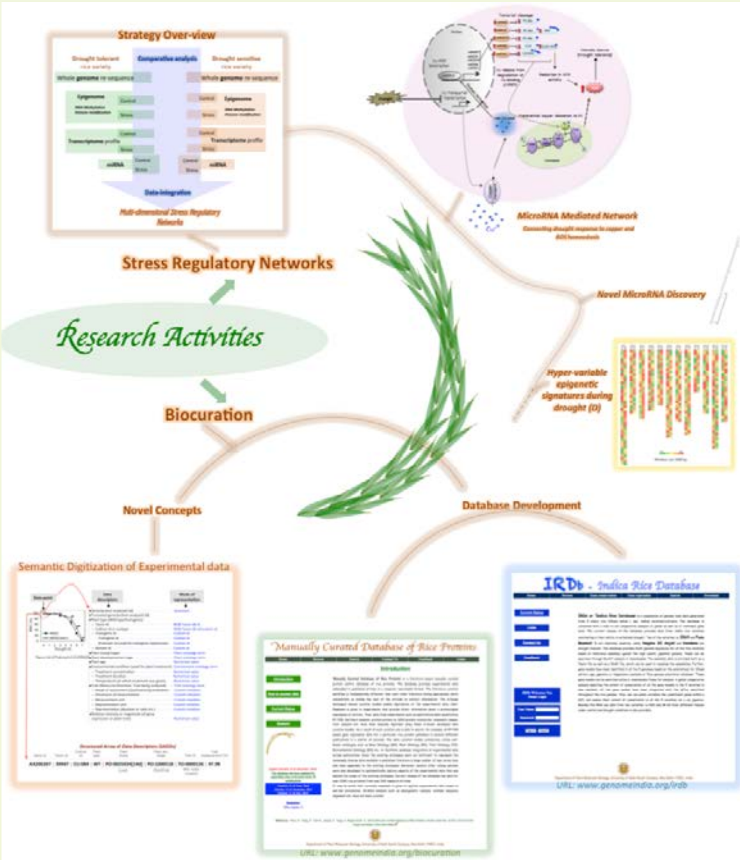
Biocuration and database development: On the other hand, our group is also actively involved in 'Biocuration' and database development wherein we have developed novel curation and digitization data models. Understanding complex plant trait requires a 'systems' level understanding, which can only be achieved though seamless data integration. However, most of the published experimental data (research publications) is presented in a very heterogeneous format (images, graphs etc.) that is not amenable to computerized search and integration.

Further, as Project Lead Prof. Saurabh Raghuvanshi established the first life science data repository of India i.e. the Indian Biological Data Center (ibdc.rcb.res.in) at RCB, Faridabad, India. As per the BiotechPRIDE guidelines of Dept. of Biotechnology, Govt. of India, it is mandated to archive, curate and dissipate life science data sets generated across the nation.

Major milestone

- Rice genome sequencing: 1st eukaryotic genome sequencing project of India. (Established the data analytics lab and performed the assemblies and annotation).
- Mycobacterium indicus pranii genome sequence:1st microbial genome sequencing project of India. (Established the data analytics lab and performed the assemblies and annotation).
- Development of experimental data digitization formats
- Identification of cultivar specific microRNA regulatory modules in rice.
- Indian Biological Data Center: 1st Life science data repository of India (as Project lead).

The Team



Select Publications

1 Balyan, S., Kumar, M., Mutum, R.D., Raghuvanshi, U., Agarwal, P., Mathur, S., and Raghuvanshi, S. (2017). Identification of miRNA-mediated drought responsive multi-tiered regulatory network in drought tolerant rice, Nagina 22. Sci. Rep. 7: 15446.

2 Gour, P., Garg, P., Jain, R., Joseph, S. V., Tyagi, A.K., and Raghuvanshi, S. (2014a). Manually curated database of rice proteins. Nucleic Acids Res. 42: 1214–1221.

3 Gour, P., Garg, P., Jain, R., Joseph, S. V., Tyagi, A.K., and Raghuvanshi, S. (2014b). Manually curated database of rice proteins. Nucleic Acids Res. 42.

4 Itoh, T. et al. (2007). Curated genome annotation of Oryza sativa ssp . japonica and comparative genome analysis with Arabidopsis thaliana. Genome Res.: 175–183.

5 Mutum, R.D., Balyan, S.C., Kansal, S., Agarwal, P., Kumar, S., Kumar, M., and Raghuvanshi, S. (2013). Evolution of variety-specific regulatory schema for expression of osa-miR408 in indica rice varieties under drought stress. FEBS J. 280: 1717–1730.

6 Mutum, R.D., Kumar, S., Balyan, S., Kansal, S., Mathur, S., and Raghuvanshi, S. (2016). Identification of novel miRNAs from drought tolerant rice variety Nagina 22. Sci. Rep. 6: 30786.

7 Saini, V., Raghuvanshi, S., Khurana, J.P., Ahmed, N., Hasnain, S.E., Tyagi, A.K., and Tyagi, A.K. (2012a). Massive gene acquisitions in Mycobacterium indicus pranii provide a perspective on mycobacterial evolution. Nucleic Acids Res. 40: 10832–10850.

8 Saini, V., Raghuvanshi, S., Khurana, J.P., Ahmed, N., Hasnain, S.E., Tyagi, A.K., and Tyagi, A.K. (2012b). Massive gene acquisitions in Mycobacterium indicus pranii provide a perspective on mycobacterial evolution. Nucleic Acids Res. 40: 10832–10850.

9 Tanaka, T. et al. (2007). The Rice Annotation Project Database (RAP-DB): 2008 update. Nucleic Acids Res. 36: D1028–D1033.

10 International Rice Genome Sequencing Project (2005). The map-based sequence of the rice genome. Nature 436: 793–800.

Prof. Surekha Katiyar-Agarwal

Research Interests

Understanding the Molecular Basis of Stress Tolerance in Plants, with Emphasis on Membrane Proteins and Transcription Factors:

Plants face a wide range of environmental challenges and respond to these unfavourable conditions at the biochemical, molecular, and physiological levels. Our laboratory focuses on understanding the molecular changes that occur in plants under stress. Small RNAs have emerged as key regulators of not only plant development but also of stress responses. Our group is actively involved in genome-wide discovery of small RNAs in economically important crops such as wheat, mustard, potato, chickpea and rice. Efforts are being made to decipher the role of these small RNAs in stress tolerance in plants. In addition, we are also investigating the molecular and physiological function of stress-associated gene families, including tetraspanins and Heat Shock Transcription Factors (HSFs). Tetraspanins, integral transmembrane proteins, facilitate the organization of 'microdomain webs' at the cell surface, influencing signalling pathways. Our research has shown that tetraspanin genes are differentially expressed in various tissues and diverse abiotic stresses in rice. Altering the expression of TET5 in rice leads to distinct changes in plant development and responses to drought and salinity stress. Current efforts are focused on identifying the interacting partners of TET5, which would provide further insights into the mechanisms of stress tolerance in rice.

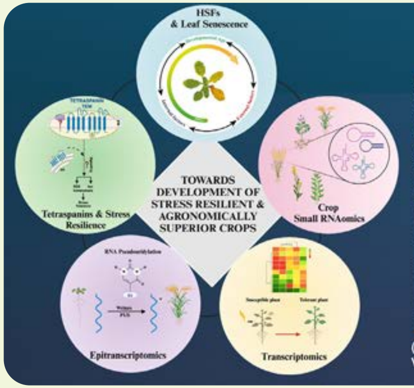
Investigating the Regulation of Senescence in Plants, with Emphasis on Heat Shock Factors and Small RNAs: Leaf senescence is a complex, yet highly orchestrated, stage of plant development, involving age-dependent degeneration ultimately leading to death. In agricultural aspects, leaf senescence is thought to limit the yield in crops, and it is a major cause of post-harvest spoilage of vegetable crops. Moreover, abiotic stresses accelerate senescence in plants leading to enormous negative agro-economic impact. Our group is involved in unravelling the gene reprogramming changes that occur in flag leaf senescence and coleoptile senescence in rice. We have performed transcriptome analyses (both RNA-seq and small RNA-seq) of flag leaf and coleoptile senescence in rice. Efforts are being made to elucidate the components and pathways regulating rice leaf senescence. Interestingly, several members of HSF family in rice are differentially expressed at different stages of flag leaf, coleoptile and dark-induced senescence. Functional characterization of members of HSF family in rice and Arabidopsis is being carried out concerning their role in regulating leaf senescence.

Exploring the Role of Epitranscriptome Changes in Defining Stress Response in Plants, with Emphasis on Pseudouridylation: Cellular RNAs are essential in biological systems, not only as structural components or messengers or translators but also as regulators of gene expression. Modification of RNAs significantly impacts their attributes, such as stability, conformation, intracellular transport, translational efficiency, fidelity, turnover, interactions, and overall function. Pseudouridylation of RNAs dominates the modification landscape across organisms and is therefore considered as the 'fifth nucleotide'. Our research involves understanding the biological function of pseudouridine synthases (PUS), the writers of pseudouridylation, in regulating growth, development, and stress responses in both Arabidopsis and rice.

Our overarching aim is to understand the molecular basis of plant development and stress tolerance, and how these processes are regulated. The knowledge generated from our research will contribute to engineering crop plants with superior agronomic traits, enhanced stress resilience, and improved productivity, supporting sustainable food security.

Awards and Distinctions

- Innovative Young Biotechnologist Award (IYBA)-2012 by Department of Biotechnology, India



OUR POWERHOUSE

(L-R) Bisma Batool, Nikunj Bhandari, Dharmendra Shishodia, Milinda Lahiri, Inderjit Kaur, Surekha Katiyar-Agarwal, Jayati Pathak, Vidisha Saxena, Yashika Dhingra, Nandini Killa, Ismail Yasir

Select Publications

1 Mani B, Kaur I, Dhingra Y, Saxena V, Krishna GK, Kumar R, Chinnusamy V, Agarwal M, Katiyar-Agarwal S. 2024. Tetraspanin 5 orchestrates resilience to salt stress through the regulation of ion and reactive oxygen species homeostasis in rice. Plant Biotechnol doi: 10.1111/pbi.14476

2 Kumari A, Sharma P, Rani M, Laxmi V, Sahil, Sahi C, Satturu V, Katiyar-Agarwal S, Agarwal M. 2024. Meta-QTL and ortho analysis unravel the genetic architecture and key candidate genes for cold tolerance at seedling stage in rice. Physiology and Molecular Biology of Plants. https://doi.org/10.1007/s12298-024-01412-1

3 Dhingra Y, Gupta S, Gupta V, Agarwal M, Katiyar-Agarwal S. 2023. The emerging role of epitranscriptome in shaping stress responses in plants. Plant Cell Reports. 42(10):1531-1555 10.1007/s00299-023-03046-1

4 Dhingra Y, Lahiri M, Bhandari N, Kaur I, Gupta S, Agarwal M, Katiyar-Agarwal S. 2023. Genome-wide identification, characterization, and expression analysis unveil the roles of pseudouridine synthase (PUS) family proteins in rice development and stress response. Physiology and Molecular Biology of Plants. 29(12):1981-2004) https://doi.org/10.1007/s12298-023-01396-4

5 Sasi JM, Cheeni VK, Kukreja B, Budhwar R, Shukla RN, Agarwal M, Katiyar-Agarwal S. 2022. Integrated transcriptomics and miRNAomics provide insights into the complex multi-tiered regulatory networks associated with coleoptile senescence in rice. Front. Plant Sci. 13:985402 https://doi.org/10.3389/fpls.2022.985402

6 Sasi JM, Gupta S, Singh A, Kujur A, Agarwal M, Katiyar-Agarwal S. 2022. Know when and how to die: Gaining insights into the molecular regulation of leaf senescence. Physiology and Molecular Biology of Plants. 28(8):1515-1534 https://doi.org/10.1007/s12298-022-01224-1

7 McLoughlin, F., Basha E, Fowler ME, Kim M, Bordowitz, Katiyar-Agarwal S, Vierling E. 2016. Class I and II small heat-shock proteins protect protein translation factors during heat stress. Plant Physiol. 172(2):1221-1236. 10.1104/pp.16.00536

8 Bhardwaj AR, Joshi G, Kukreja B, Malik V, Arora P, Pandey R, Shukla RN, Bankar KG, Katiyar-Agarwal S, Goel S, Jagannath A, Kumar A, Agarwal M. 2015. Global insights into high temperature and drought stress regulated genes by RNA-Seq in economically important oilseed crop Brassica juncea. BMC Plant Biol 15:9

9 Pandey R, Joshi G, Bhardwaj AR, Agarwal M, Katiyar-Agarwal S. 2014. A Comprehensive Genome-wide Study on Tissue-specific and Abiotic Stress-specific miRNAs in Triticum aestivum. 2014. PLoS ONE 9(4):e95800

10 Zhang X, Zhao H, Gao S, Wang WC, Katiyar-Agarwal S, Huang HD, Raikhel N, Jin H. 2011. Arabidopsis Argonaute 2 Regulates Innate Immunity via miRNA393(*)-Mediated Silencing of a Golgi-Localized SNARE Gene, MEMB12. Molecular Cell 42(3):356-66.

11 Katiyar-Agarwal S and Jin H. 2010. Role of small RNAs in host-microbe interactions. Annu. Rev. Phytopathol. 48:225-246

12 Katiyar-Agarwal S, Gao S, Vivian-Smith A and Jin H. 2007. A novel class of bacteria-induced small RNAs in Arabidopsis. Genes and Development 21:3123-3134

13 Katiyar-Agarwal S, Morgan R, Dahlbeck D, Borsani O, Villegas A, Zhu J-K, Staskawicz B, Jin H. 2006. A Pathogen-Inducible Endogenous siRNA In Plant Immunity. Proc Natl Acad Sci USA 103 (47):1802-18007

Prof. Mradu Gupta (on deputation)

Research Interests

•Understanding the basic concepts of Ayurvedic medicine, diagnosis and treatment of diseases using Ayurvedic drugs.

•Pharmacognosy, macro and microscopic studies of medicinal plants parts used for prevention & treatment of diseases.

•Phytochemical standardization of chemical compounds of medicinal plants using chromatography, spectroscopy & quality control parameters.

•Various types of acute, sub-acute & chronic toxicity studies using oral and vaginal types of Ayurvedic formulations in rodents

•Analysis of pharmacological activities of medicinal plants and formulations using modern scientific methods.

•Clinical studies of Ayurvedic formulations using patients suffering from various diseases such as fever, arthritis, pain, diabetes, skin, gastric and liver diseases etc. in the OPD & IPD of the hospital.

Research Experience

Possessing over 17 years research experience in the field of pharmacognosy, phytochemistry, acute, sub-acute & chronic toxicity studies, efficacy of pharmacological properties such as anti-inflammatory, analgesic, antipyretic, antiarthritis, antidiabetic, anti-leucorrheal, neuroprotective, spermatogenesis and wound healing activities. Vast experience of handling sophisticated instruments such as TLC, HPTLC, HPLC, UV -VIS and FTIR spectroscopy, GC-MS, Eliza, Laminar flow, PCR, Electrophoresis and other instruments used for pharmacognostical analysis. Conducted a large number of animal experiments in rodents following the rules of Institutional Animal Ethics Committee under CPCSEA for animal house to establish the efficacy of new Ayurvedic drugs. Directly supervised the clinical trial of medicinal plants using oral and vaginal routes in the form of ointment and medicated oils following the norms of Biomedical research committee & Institutional clinical trial committee prescribed by ICMR. Performed detailed clinical evaluation of research Ayurvedic drugs on human subjects having diseases such as diabetes, skin infections, wounds, arthritis, fever, pain, deficient lactation, semen disorders, vaginal discharge disorders and stress up to the level of clinical trial stage II along while using Haematological, LFT, Lipid Profile and Hormonal biochemistry tests following the standard guidelines of AYUSH and ICMR.

Awards and Patents

- Received the Kaviraj Bagla Kumar Mazumdar prize for 1999 from Calcutta University for obtaining highest marks in the M. D. (Ayurveda) examination of 1999 in the entire batch.
- Received the first position in the entire batch in the Junior Course in Bengali at the Ramakrishna Mission Institute of Culture, School of languages, Kolkata, January- June, 2002.
- Received the first position in the entire batch in the Senior Course in Bengali at the Ramakrishna Mission Institute of Culture, School of languages, Kolkata, July- December, 2002.
- Granted Patent No. 388853 dated 19.11.2015 as the inventor by the Controller General of Patents, Designs and Trade Marks, Government of India for "Poly Herbal Formulation" on the basis of Application No. 1180/KOL/2015 filed on 19.11.2015 by the Department of Science & Technology, Government of West Bengal and the Institute of Post Graduate Ayurvedic Education & Research, Kolkata under Health & Family Welfare Department, Government of West Bengal

Pharmacognosy- macro and micro analysis of plant parts and its powder form for identification in the lab & museum

Select Publications

1 Mradu Gupta, Anumita Dey and Sushmita Majumder, "Evaluation of antioxidant property of selected regional medicinal plants", 2022, International Journal of Pharmaceutical Sci. and Res., 13 (6): 2367-2379

2 Mradu Gupta, Sushmita Majumdar, Suchetna Banerjee, Suhrita Pal and Tanushree Mondal, "A double-blind randomized clinical trial of novel Ayurvedic muco-adhesive extended-release vaginal tablet (NA) for treatment of leucorrhea, 2020, International Journal of Clinical Obstetrics and Gynaecology, 4(2): 324-333

3 Mradu Gupta and A. K. Mondal, "Clinical spermatogenic assessment of aqueous extract of Yashthimadhu (Glycyrrhiza glabra Linn.) in the treatment of male reproductive disorders, 2020, International journal of Medical and Health Res., 6(6): 42-48

4 Mradu Gupta and A. K. Mondal, "Clinical evaluation of aphrodisiac activity of a novel Ayurvedic formulation for treatment of male sexual disorders", 2020, International Journal of Research in Medical Science, 8: 2515-23

5 Mradu Gupta and A. K. Mondal, "Clinical assessment of herbal formulation in reducing oxidative stress causing spermatogenetic disorders using the ROS, d- ROMs and MDA tests", 2020, International Journal of Medical and Biomedical Studies, 4(7): 119-124

6 Mradu Gupta and A. K. Mondal, "A pre-clinical study for pharmacognostical and chemical standardization of aqueous and alcoholic extracts of Ayurvedic spermatogenetic formulation using Spectroscopy & Chromatography (including GC- MS) methods", 2020, J. of Pharmacognosy and Phytochemistry, 9(4): 1284-1296

7 Mradu Gupta, Sushmita Majumdar, Suchetana Banerjee, Anumita Dey and Sabari Sengupta, "Experimental evaluation of wound healing activity of Ayurvedic antimicrobial formulations using In vivo animal excision and incision methods", 2020, International Research Journal of Pharmacy, 11(11): 41-48

8 Mradu Gupta, Riya Dutta and Saswati Sasmal, "Standardization of the Hydro- Alcoholic Extract of Ayurvedic Vaginal Formulation (NA) by using Chromatography (HPTLC, HPLC) and Spectroscopy (UV-VIS &FTIR &GC-MS) Methods", 2020, International Journal of Pharmaceutical Sci. and Research, 11(1): 312-327

Published Books

9 Comparative Analysis on Pharmacognosy, Phytochemical, Chromatography (HPTLC, HPLC) and Spectroscopy (UV-Vis and FTIR) of root, stem and leaf of medicinal plants for authentication, Dr. Mradu Gupta, ISBN;978-93-90777-xx-x, Volume I, pages; 342, First Edition: 2024, Publishers Chaukhambha Orientalia, Varanasi (UP).

Published Chapters in Books

10 Mradu Gupta, "In vitro Impact Assessment of Aqueous Extract of Sida cordifolia Linn. upon Rat Spermatozoa Parameters", Emerging Research in Medical Sciences Vol. 1, Chapter 7, Print ISBN: 978-93-89246-66-7, eBook ISBN: 978-93-89246-67-4, DOI: 10.9734/bpi/erms/v1

11 Mradu Gupta, "In vivo Antioxidant Activity of Sida cordifolia Linn. in K2Cr2O7 Induced Oxidative Stress by Measurement of Reactive Oxygen Species Levels in Rats", New Insights into Disease and Pathogen Research, Vol.3, Chapter 9, Print ISBN: 978- 93-89562-36-1, eBook ISBN: 978-93-89562-37-8, DOI: 10.9734/bpi/nidpr /v3

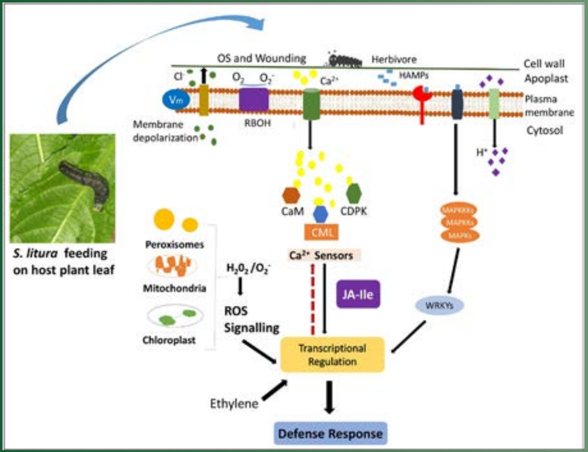
Dr. Archana Singh (Associate Prof.)

Research Interests

Plants, being immobile, make tempting targets for pests and pathogens. However, they have developed sophisticated defense mechanisms to ward off herbivores and pathogenic invaders. They employ both direct and indirect defenses, including physical barriers, defensive chemicals, extrafloral nectars, and volatile compounds. Plants employ two types of defense mechanisms based on the timing of deployment: constitutive and induced defenses. Compared to constitutive defenses, inducible defenses are more efficient and long-lasting as plants maintain a fine-tuned regulatory system to balance defense and growth.

Understanding the mechanism of induced plant defense against herbivores and pathogens can be achieved through functional genomics approaches. Our laboratory's primary objective is to unravel the molecular intricacies of induced plant defense.

We employ transcriptomic, proteomic, metabolomic techniques, bioinformatics tools, and we also conduct in *silico*, in vitro, and transgenic analyses to functionally characterize defense-related genes. Our research primarily focuses on three plant species: *Glycine max*, *Cicer arietinum*, and *Zea mays*, and their interactions with insect herbivores and pathogens. Our aim is to identify and characterize candidate genes that play pivotal roles in plant defense against pests and pathogens. This knowledge can pave the way for innovative strategies to enhance crop resistance through targeted genetic modifications, leading to more cost-effective, environmentally friendly, and sustainable pest and pathogen management.



Deciphering herbivory-induced early signaling events (calcium signaling, ROS generation, activation of MAPK Pathway).

Awards and Distinctions

- IoE Fellow, School of Climate Change and Sustainability, Institution of Eminence, University of Delhi.
- EMBO Fellow, by European Molecular Biology Organization, Meyerhofstrasse Heidelberg, Germany.
- Raman Fellow, by University Grant Commission (UGC).
- Member, Editorial Board, Scientific Reports.
- Member, Editorial Board, Frontiers in Plant Sciences.

The Team

Selected Publications

1. Singh S, Singh IK, **Singh A**. Comparative Proteome Analysis of Spodoptera litura-infested *Zea mays* Reveals a Robust Defense Strategy Targeting Insect Peritrophic Membrane. Plant Physiology and Biochemistry. 2024 Jun 13:108835
2. Mahmood S, Singh IK, **Singh A**. ABCB19 transporter: fostering brassinosteroid transport through membrane flexibility. Trends in Plant Science. 2024 Jun 28.
3. Taneja M, Yajnik KN, Kumari M, Singh IK, **Singh A**. Deciphering MAP kinase pathway in *Cicer arietinum* upon *Helicoverpa armigera*-infestation. Plant Stress. 2024 Sep 1;13:100527.
4. **Singh A***, Singh S, Singh R, Kumar S, Singh SK, Singh IK* (2021). Dynamics of *Zea mays* transcriptome in response to a polyphagous herbivore, Spodoptera litura. Functional & Integrative Genomics, 21, 571–592.
5. **Singh** A, Kumar A, Hartley S*, Singh IK* (2020). Silicon: its ameliorative effect on plant defense against herbivory. Journal of Experimental Botany, 71(21), 6730–6743.
6. Singh S, **Singh A***, Kumar S, Mittal P, Singh IK* (2020). Protease inhibitors: recent advancement in its usage as a potential biocontrol agent for insect pest management. Insect Science, 27(2), 186–201.
7. **Singh A***, Jain D, Tyagi C, Singh S, Kumar S, Singh IK* (2018). *In silico* prediction of active site and in vitro DNase and RNase activities of Helicoverpa-inducible pathogenesis related-4 protein from Cicer arietinum. International Journal of Biological Macromolecules, 113, 869–880
8. **Singh A**, Tyagi C, Nath O, Singh IK* (2018). Helicoverpa-inducible Thioredoxin h from *Cicer arietinum*: structural modeling and potential targets. International Journal of Biological Macromolecules, 109, 231–243.
9. **Singh A**, Lim GH, Kachroo P* (2017). Transport of chemical signals in systemic acquired resistance. Journal of Integrative Plant Biology, 59(5), 336–344.
10. **Singh A**, Singh IK, Verma PK* (2008). Differential transcript accumulation in *Cicer arietinum* L. in response to a chewing insect Helicoverpa armigera and defence regulators correlate with reduced insect performance. Journal of Experimental Botany, 59(9), 2379–2392.

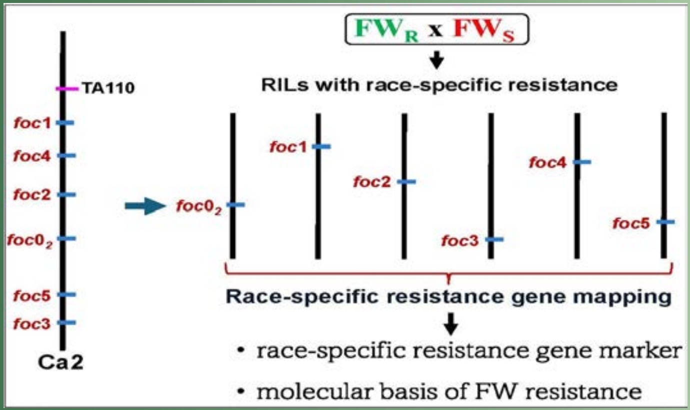
Dr. Kamal Kumar (Assistant Prof.)

Research Interests

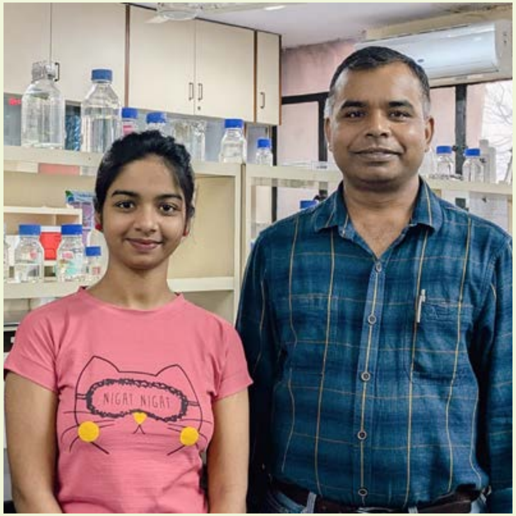
Our laboratory, in collaboration with other research groups, focuses on fine-mapping and utilizing naturally evolved allelic variations to develop climate-resilient, pathogen-resistant, and high-yielding crop varieties. Our goal is to uncover the biological significance of these genetic variations at the molecular level and incorporate the beneficial traits into widely cultivated legume crops. In cases where genetic variability is limited or desirable alleles are absent, we are developing genome-editing and transgenic protocols to address these challenges.

Our research is primarily on three important legume crops: chickpea (*Cicer arietinum*), mung bean (*Vigna radiata*), and cluster bean or guar (*Cyamopsis tetragonoloba*). In chickpea, we are working to identify loci responsible for fusarium wilt resistance (FWR) by using differential lines resistant to various races of *Fusarium oxysporium f.sp. ciceri*. We aim to pinpoint race-specific FWR loci within a targeted genomic region of the desi chickpea accession WR315 by comparing these differential lines genomic and RNA sequences. The development of race-specific resistance gene-associated markers will be significantly helpful in marker-assisted backcrossing (MABC) programs.

Guar has been largely neglected in research despite its significant role in industries such as hydraulic drilling, pharmaceuticals, and textiles. Our research aims to enhance seed or endosperm size, thereby increasing guar gum yield per seed. Additionally, we are investigating the regulation of galactomannan biosynthesis genes during pod development. In mung bean, our focus is on identifying the genes that regulate heat-stress tolerance and prevent flower shedding. We welcome researchers who share an interest in these areas to engage in discussions and explore opportunities for future collaborations.



The Team



Select Publications

1 Singh R, Kumar K, Purayannur S, Verma PK (2023). Genomics-assisted genetics of complex regions from chickpea chromosome 4 reveals two candidate genes for Ascochyta blight resistance. Plant Science 334, 111781.

2 Singh SK, Shree A, Verma S, Singh K, Kumar K, Srivastava V, Singh R, Saxena S, Singh AP, Pandey A, Verma PK (2023). The nuclear effector ArPEC25 from the necrotrophic fungus Ascochyta rabiei targets the chickpea transcription factor CaβLIM1a and negatively modulates lignin biosynthesis, increasing host susceptibility. Plant Cell 35(3), 1134–1159.

3 Singh R*, Kumar K*, Bharadwaj C, Verma PK (2022). Broadening the horizon of crop research: a decade of advancements in plant molecular genetics to divulge phenotype governing genes. Planta 255(2), 46. (*Joint first authors)

4 Sinha M, Shree A, Singh K, Kumar K, Singh SK, Kumar V, Verma PK (2021). Modulation of fungal virulence through CRZ1 regulated F-BAR dependent actin remodeling and endocytosis in chickpea infecting phytopathogen Ascochyta rabiei. PLoS Genetics 17(5), e1009137.

5 Maurya R, Singh Y, Sinha M, Singh K, Mishra P, Singh SK, Verma S, Prabha K, Kumar K*, Verma PK* (2020). Transcript profiling reveals potential regulators for oxidative stress response of a necrotrophic chickpea pathogen *Ascochyta rabiei*. 3Biotech 10,117. (*Joint corresponding authors)

6 Kumar K*,Purayannur S*, Kaladhar VC, Parida SK, Verma PK (2018). mQTL-seq and classical mapping implicates the role of an AT-HOOK MOTIF CONTAINING NUCLEAR LOCALIZED (AHL) family gene in Ascochyta blight resistance of chickpea. Plant, Cell & Environment 42, 2128–2140. (*Joint first authors)

7 Purayannur S*, Kumar K*, Kaladhar VC*, Verma PK (2017). Phylogenomic analysis of MKKs and MAPKs from 16 legumes and detection of interacting pairs in chickpea divulge MAPK signalling modules. Scientific Reports 7, 5026. (*Joint first authors)

8 Kumar K, Srivastava V, Purayannur S, Kaladhar VC, Cheruvu PJ, Verma PK (2016). WRKY domain-encoding genes of a crop legume chickpea (*Cicer arietinum*): Comparative analysis with *Medicago truncatula* WRKY family and characterization of group-III gene(s). DNA Research 23(3), 225–239.

9 Kumar K, Yadav S, Purayannur S, Verma PK (2013). An alternative approach in Gateway cloning when the bacterial antibiotic selection cassettes of the entry clone and destination vector are the same. Molecular Biotechnology 54, 133–140.

10 Yadav S, Kushwaha HR, Kumar K, Verma PK (2012). Comparative structural modelling of a monothiol GRX from chickpea: insight in iron-sulphur cluster assembly. International Journal of Biological Macromolecules 51, 266–273.

Dr. Amit Kumar Singh (Assistant Prof.)

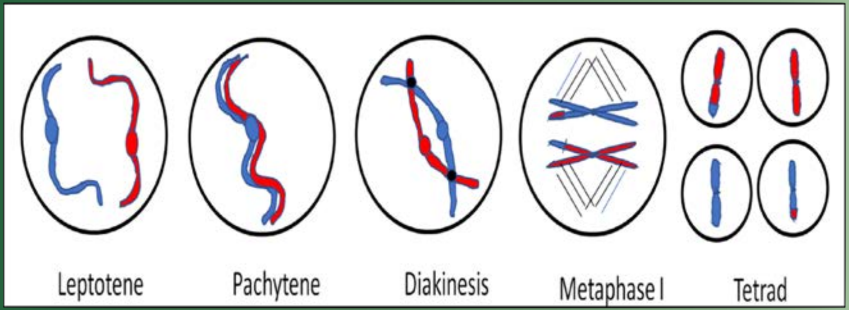
Research Interests

Plants being sessile in nature are exposed to various environmental stresses (heat, cold, drought, UV, flood, salt etc.) which decrease their productivity and yield. Every 1°C rise in global temperature can decrease major crop production by 0.6 ~ 8.9%. In the male reproductive organ, climate change can lead to male sterility which causes an adverse effect on food yield and crop production. To cope with these environmental stresses, plants employ various gene regulatory mechanisms, including epigenetic changes. Although extreme environmental stress decreases crop yield, a few studies report priming with moderate stress can result in higher crop yield. Plants can memorize the stress conditions with the help of epigenetic modification to adapt better and these memories can be passed to next generation. Thus, we aspire to elucidate molecular mechanism by which plant response and remember environmental stress.

Histone methylation and other histone modifications play crucial roles in epigenetic regulation of stressed plants. Histone H3K4 tri-methylation and H3K36 tri-methylation corresponds to active transcription of gene throughout the genome. They are also associated with various biotic and abiotic stresses. However, their role during plant reproduction is not well known. CSN5, a subunit of eight protein COP9 signalosome complex (CSN) plays significant role in the repair of recombination-induced DSB during Drosophila oogenesis. It is required for resetting transcriptional stress memory after recurrent heat stress. Further, in Drosophila it is essential for meiotic progression. However, its role during meiosis in plant is not explored much. Thus, we wish to understand the role of epigenetics and COP9 Signalosome in plant reproduction and adaptation during abiotic stress.

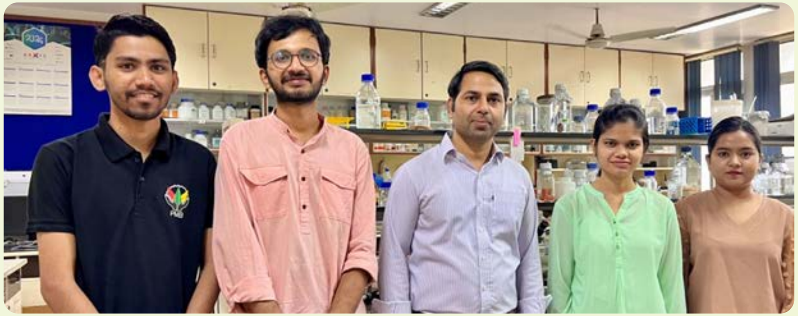
Fellowships & Awards

- Scholarship from India-Japan Cooperative Science Programme (IJCSP) in 2010



Epigenetic and abiotic factors affecting meiosis and plant reproduction

The Team



Select Publications

1 Bhushan, S., A.K. Singh, Y. Thakur, and R. Baskar (2023). Persistence of parental age effect on somatic mutation rates across generations in Arabidopsis. BMC Plant Biology, 23, 152. doi: 10.1186/s12870-023-04150-w. (IF 2021: 5.26)

2 Singh, A.K.*, S. Dhanapal, A. Finkelshtein and D.A. Chamovitz (2021). CSN5A subunit of COP9 signalosome is required for resetting transcriptional stress memory after recurrent heat stress in Arabidopsis. Biomolecules, 11, 668. doi: 10.3390/biom11050668. *Corresponding author. (IF 2021: 6.064)

3 Jogawat, A, B. Yadav, N.A. Chhaya, N. Lakra, P. Kumari, A.K. Singh, and O.P. Narayan (2021). Crosstalk between phytohormones and secondary metabolites in the drought stress tolerance of crop plants. Physiologia Plantarum, 172, 1106-1132. doi: 10.1111/ppl.13328. (IF 2021: 5.081)

4 Saini, R, A.K. Singh, G. Hyde, and R Baskar (2020). Levels of heterochiasmy during Arabidopsis development as reported by Fluorescent Tagged Lines. G3: Genes Genomes Genetics, 10, 2103-2110. (IF 2021: 3.542)

5 Singh, A.K., S. Dhanapal, and B.S. Yadav (2020). The dynamic responses of plant physiology and metabolism during environmental stress progression. Molecular Biology Reports, 47, 1459–1470. doi: 10.1007/s11033-019-05198-4. (IF 2021: 2.742)

6 Singh, A.K., B.S. Yadav, S. Dhanapal, M. Berliner, A. Finkelshtein, and D.A. Chamovitz (2019). CSN5A subunit of COP9 signalosome temporally buffers response to heat in Arabidopsis. Biomolecules, 9, 805. doi: 10.3390/biom9120805. (IF 2021: 6.064)

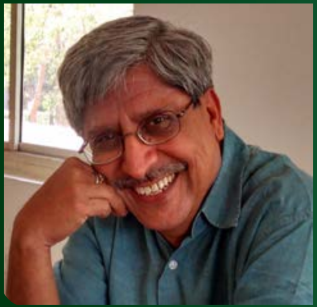
7 Singh, A.K.* and D.A. Chamovitz (2019). Role of Cop9 signalosome subunits in the environmental and hormonal balance of plant. Biomolecules, 9, 224. doi: 10.3390/biom9060224. *Corresponding author. (IF 2021: 6.064)

8 Saini, R*, A.K. Singh*, S. Dhanapal, T.H. Saeed, G.J. Hyde, and R. Baskar (2017). Brief temperature stress during reproductive stage alters meiotic recombination and somatic mutation rates in the progeny of Arabidopsis. BMC Plant Biology, 17, 103. doi: 10.1186/s12870-017-1051-1. *Joint first authors. (IF 2021: 5.26)

9 Shah, J. M., A.M. Ramakrishnan, A.K. Singh, S. Ramachandran, U. Unnikrishnan, A. Jayshankar, N. Balasundaram, S. Dhanapal, G. Hyde, and R. Baskar (2015). Suppression of different classes of somatic mutations in Arabidopsis by vir gene-expressing Agrobacterium strains. BMC Plant Biology, 15, 210. doi: 10.1186/s12870-015-0595-1. (IF 2021: 5.26)

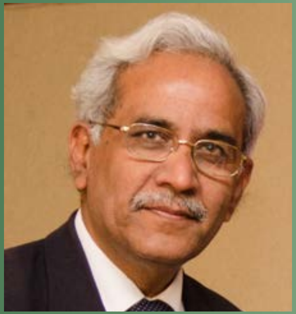
10 Singh, A.K., T. Bashir, C. Sailor, V. Gurumoorthy, A.M. Ramakrishnan, S. Dhanapal, U. Grossniklaus, and R. Baskar (2015). Parental age affects somatic mutation rates in the progeny of flowering plants. Plant Physiology, 168, 247-257. (IF 2021: 8.005)

Superannuated Faculty



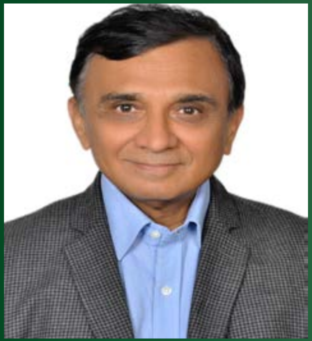
Prof. Madan Mohan
*(2006-2018)

Prof. Jitendra P. Khurana
*(1988-2019)



Prof. Akhilesh K. Tyagi
*(1988-2021)

Prof. Paramjit Khurana
*(1988-2021)



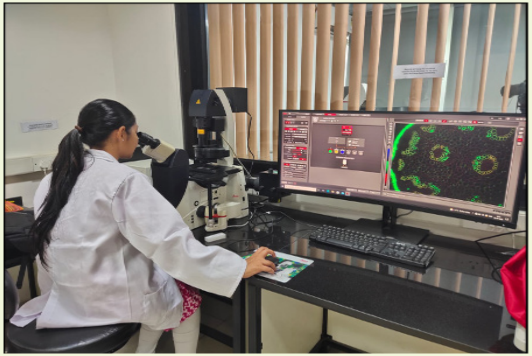
Prof. Anil Grover
*(1989-2023)

Prof. Indranil Dasgupta
*(1996-2023)

Prof. Arun K. Sharma
*(1997-2024)

* Duration of Service

CIF at DPMB



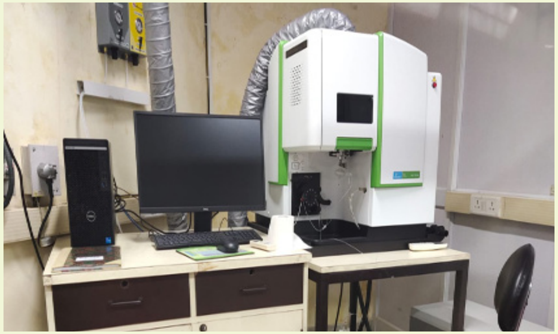
imaging Facility

High Performance Computing (HPC) System

Plant Growth Room

Growth Chambers

Green Houses



ICP-OES

Life at DPMB

M.Sc. Classroom

Sports Day

Farewell Party

Excursion Trip

Rangoli Competition

International Conference

Annual Symposium

DPMB ALUMINI

Overview of Indian Research Institutions/Private Organizations wherein DPMB Alumini are employed

DPMB ALUMINI

Overview of International Research Institutions/Private Organizations wherein DPMB Alumini are employed

Stanford University

HARVARD MEDICAL SCHOOL

MICHIGAN STATE UNIVERSITY

UNIVERSITÄT BERN

WASHINGTON STATE UNIVERSITY

UNIVERSITY OF ALBERTA

THE ROCKEFELLER UNIVERSITY
Science for the benefit of humanity

TEXAS TECH UNIVERSITY HEALTH SCIENCES CENTER EL PASO

LSU LOUISIANA STATE UNIVERSITY

UNIVERSITY OF DELAWARE

UNIL UNIVERSITE DE LAUSANNE

UMEÅ UNIVERSITET

University of Basel BIOZENTRUM The Center for Molecular Life Sciences

UNIVERSITY OF GEORGIA
Griffin Campus

STATE UNIVERSITY OF NEW YORK TO LEARN TO SEARCH TO SERVE 1948

UFC UNIVERSITÉ DE FRANCHE-COMTÉ

RUTGERS THE STATE UNIVERSITY OF NEW JERSEY

NUS National University of Singapore

NANYANG TECHNOLOGICAL UNIVERSITY SINGAPORE

TEXAS A&M UNIVERSITY

UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN

UNIVERSITY OF CALIFORNIA

hhu Heinrich Heine Universität Düsseldorf

DPMB ALUMINI

Overview of International Research Institutions wherein DPMB Alumini are employed

LMU KLINIKUM DER UNIVERSITÄT MÜNCHEN

UF UNIVERSITY of FLORIDA

FRIEDRICH-SCHILLER-UNIVERSITÄT JENA

Ben-Gurion University of the Negev

IOWA STATE UNIVERSITY OF SCIENCE AND TECHNOLOGY

THE UNIVERSITY OF CHICAGO 1890

INDIANA UNIVERSITY

SALK INSTITUTE FOR BIOLOGICAL STUDIES

Max Planck Institute of Molecular Plant Physiology

Institute of Molecular and Cell Biology IMCB

John Innes Centre Unlocking Nature's Diversity

Massachusetts General Hospital Founding Member, Mass General Brigham

Agricultural Research Organization Volcani Center

MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH

NYU Grossman School of Medicine

Singapore Institute for Clinical Sciences SICS

BIO-RAD

Alnylam PHARMACEUTICALS

syngenta

Simplot

ROTHAMSTED RESEARCH

MONSANTO

CORTEVA agriscience

BTI BOYCE THOMPSON INSTITUTE

Administrative Structure of the Department

Head of the Department :

Prof. Sanjay Kapoor

Teaching Faculty :

Prof. Girdhar Kumar Pandey
Prof. Saurabh Raghuvanshi
Prof. Surekha Katiyar-Agarwal
Prof. Mradu Gupta
Assoc. Prof. Archana Singh
Asstt. Prof. Kamal Kumar
Asstt. Prof. Amit Kumar Singh

Non-teaching Staff :

Technical Staff

Mr Prakash Chandra - Technical Officer
Ms. Renu Dhawan - Technical Assistant (Computer)
Mr Bhuvan Singh Negi - Technical Assistant (Computer)

Scientific Staff

Ms. Neelam Bedi - Junior Scientific Officer

Lower Subordinate Staff

Mr Raksh Pal - Plant Growth Room Attendant

Academic Programmes

M.Sc. in Plant Molecular Biology and Biotechnology

No. of Seats: 25

(Admitting students from CUET and DBT GAT-B streams from 2023-24 onwards)

The M.Sc. Course in Plant Molecular Biology and Biotechnology (PMBB) at Plant Molecular Biology Department (PMB), University of Delhi South Campus (UDSC) has been designed to expose students to the latest developments in the exciting and burgeoning areas of modern Plant Sciences. This course aims to prepare students to take research in Plant Molecular Biology and allied areas as a possible career option as well as to enable generation of manpower for the emerging Plant Biotechnology industry.

The Course comprises Classroom Teaching, Laboratory Practicals, and Tutorials in the form of Seminars and a Dissertation. Students are offered a total of 10 core, four Discipline Specific Elective (DSE) and one Open Elective Theory papers alongwith three Laboratory Practicals papers. In the fourth semester, every student is given an opportunity to join a research lab to work on unique research problems. The aim of this exercise is to expose our students to rigour of planning, designing and executing the experimental plan for a given research problem, followed by presenting the results in the form of a dissertation.

Admission to M.Sc. Program in Plant Molecular Biology and Biotechnology (PMBB) involves written entrance examinations CUET (PG) and GAT-B. Based on the performance in the written examination, a total of 15 and 10 students are selected from CUET(PG) and GAT-B streams, respectively, as per university reservation rules.

For the session starting in July, applications can be submitted through the DU PG Admission Portal by the end of May (*please check DU website for exact dates*).

Doctor of Philosophy in Plant Molecular Biology

No. of Seats: Variable (10-15)

Over the years DPMB's Ph.D. program has produced a number of researchers, teachers and professionals who have had major impact on the area of Plant Science Research and teaching in India and abroad. The DPMB faculty is considered among the best in Plant Biology Research in India.

Moreover, being in the heart of the Capital of India and close proximity of several high ranking University's and National Institutes involved in Life Science Research, DPMB provides a unique learning experience that extends well beyond the boundaries of laboratories and classrooms.

The Department of Plant Molecular Biology, UDSC invites applications for Full Time Ph.D. programme twice (in June and in December) for a limited number of seats in each academic year. The broad research areas offered are: Functional Genomics, Epigenomics, Gene Regulatory Networks, Molecular Basis of Plant Reproduction and Yield, Post-harvest Biotechnology, Abiotic Stress Biology, Role of Small RNAs, Signal Transduction, Plant Virology, Database Curation and Networking.

For details regarding the eligibility criteria and selection procedure for admission to the DPMB Ph.D. program please refer to the departmental website http://www.dpmb.ac.in.

Ph.D. Scholars

Sl. No.	Name of Scholar	Date of Registration	Home State	Prior degree(Degree Before PhD)	Prior Degree Institute Name
1	Nikunj Bhandari	9.2.2023	Uttrakhand	M.Sc.	Jamia Millia Islamia. Delhi
2	Monika	9.2.2023	Haryana	M.Sc.	MDU Rohtak
3	Tanashvi Seth	25.9.2023	Delhi	M.Sc.	JNU, Delhi
4	Yogita Thakur	26.9.2023	Himachal Pradesh	M.Sc.	Himachal Pradesh Univ.
5	Aradhana Aggarwal	25.9.2023	Haryana	M.Sc.	GB Univ.
6	Vidisha Saxena	25.9.2023	Delhi	M.Sc.	Univ. of Delhi
7	Aakriti Singh	25.9.2023	Uttar Pradesh	M.Sc.	Univ. of Delhi
8	Prity Kumari Sahu	25.9.2023	Jharkhand	M.Sc.	Ranchi Univ. , Jharkhand
9	Anushka	25.9.2023	Uttar Pradesh	M.Sc.	CCSU, Meerut
10	Amit Kumar	12.1.2022	Bihar	M.Sc.	Univ. of Delhi

Ph.D. Scholars

Sl. No.	Name of Scholar	Date of Registration	Home State	Prior degree(Degree Before PhD)	Prior Degree Institute Name
11	Sonam Pahuja	17.2.2021	Haryana	M.Sc.	Banaras Hindu Univ.
12	Tonu Angalia Chithung	11.10.2019	Manipur	M.Sc.	Univ. of Delhi South Campus
13	Diksha Bisht	11.10.2019	*Delhi*	M.Sc.	Central Univ. of Punjab
14	Neelam	13.5.2019	Delhi	M.Sc.	Univ. of Delhi South Campus
15	Lokesh Kumar Saini	8.5.2019	Rajasthan	M.Sc.	Univ. of Rajasthan
16	Inderjit Kaur	22.4.2019	Delhi	M.Sc.	Mumbai Univ.
17	Yashika Dhingra	23.10.18	Haryana	M.Sc.	Univ. of Delhi
18	Soma Ghosh	23.10.18	Haryana	M.Sc.	Univ. of Delhi
19	Rohit Kumar	23.10.18	Delhi	M.Sc.	Univ. of Delhi
20	Gayatri Tripathi	23.10.18	Delhi	M.Sc.	Univ. of Delhi

Ph.D. Scholars

Sl. No.	Name of Scholar	Date of Registration	Home State	Prior degree(Degree Before PhD)	Prior Degree Institute Name
21	Sanskriti Ravi	15.3.2018	Delhi	M.Tech.	Delhi Technological Univ.
22	Vishal Vashisth	15.3.2018	Delhi	M.Sc.	Univ. of Delhi
23	Shivam Sharma	15.3.2018	Uttar Pradesh	M.Sc.	Univ. of Delhi South Campus
24	Arunima Singh	23.10.18	Uttar Pradesh	M.Sc.	Banasthali Vidyapith
25	Chanchal Singhal	23.10.18	Ghaziabad	M.Sc.	CCS Univ., Meerut

The University of Delhi Logo
Redesigned in
High Resolution Vector Graphics
by Prof. Sanjay Kapoor

The PMB Logo
Conceptualized by
Dr. Mrinalini Chawla and Ms. Vibha Verma &
Designed by Prof. Sanjay Kapoor

Disclaimer

This brochure has been conceptualized, designed and compiled by Prof. Sanjay Kapoor with inputs from all faculty members of the Department of Plant Molecular Biology, UDSC. The royalty free images, which were subsequently modified, used to develop the cover were obtained from https://pngtree.com.

Notes

PMB Group in 2024