



2018



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

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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- till date), Professor Anil Grover

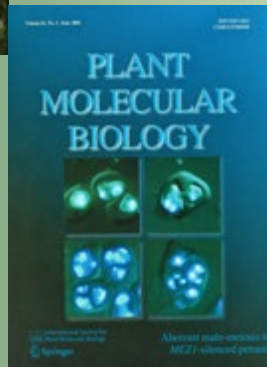


(2007-2010), Professor Indranil Dasgupta (2010 - 2013), and Professor Madan Mohan (2013 - 2014) have served as Heads of the Department.

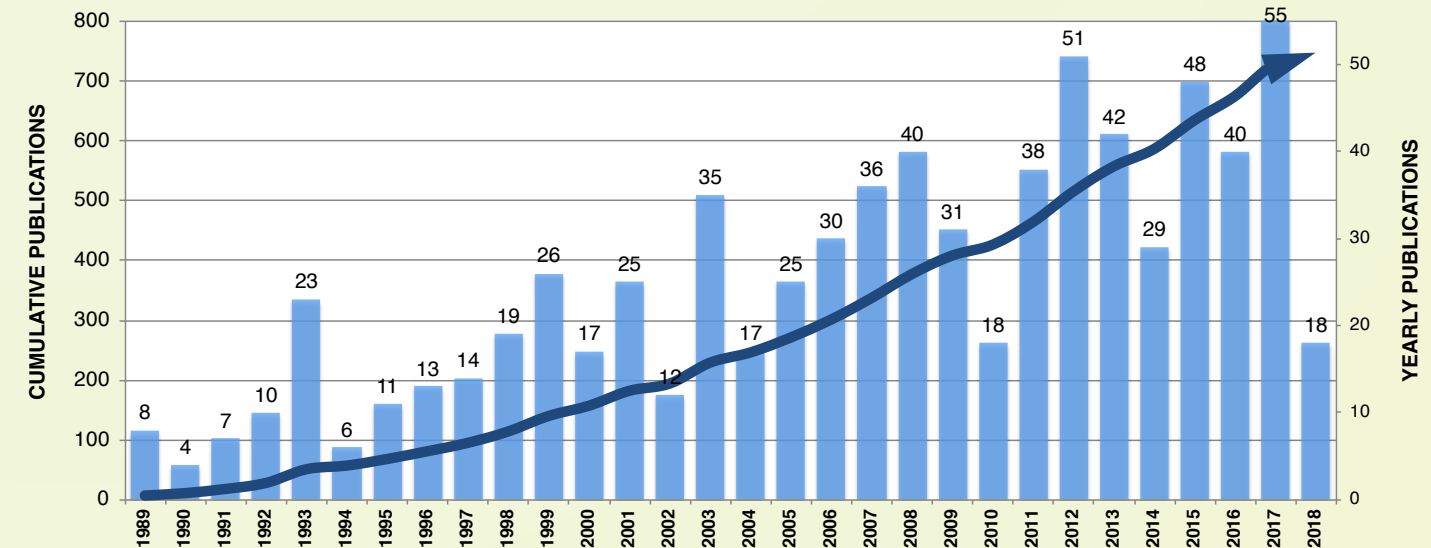
The research has been supported by major grants in the form of “Centre for Plant Molecular Biology” and “Genome Initiatives on Sequencing, Gene Discovery and Function” by DBT, in addition to other competitive grants from DST, UGC, European Commission and the Rockefeller

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 for basic research and training, the Department endeavors to convert knowledge into application for

Research Highlights (Journal cover pages)



Research Publications (in numbers)



In last five years (2012-2017)

261

Research articles in peer-reviewed journals

26

Book Chapters

5

4259

Citations

Prof. Akhilesh K. Tyagi

Research Interests

Major research interests of the group relate to **photosynthesis/phototransduction, stress/reproductive biology, genome analysis and genetic enhancement**. Lead role has been played in major research efforts India has undertaken in Plant Science, which include Centre for Plant Molecular Biology at Delhi University, Indian Initiative for Rice Genome Sequencing, Indian Initiative on Tomato Genome Sequencing, Network Project on Rice Functional Genomics, Centre of Excellence in Biotechnology, Next Generation Challenge Program in Chickpea Genomics and Analysis of Diversity in Yield Components. This has led to generation of genome-wide information from important crop plants like rice, tomato and chickpea, representing three major groups of plants, i.e. cereals, vegetables and pulses, responsible for our food and nutritional security.

Precise molecular model/phylogeny-based annotation/expression profiling of highly significant gene families representing transcription factors, signal transduction components, protein processing components and RNA interference-associated proteins, controlling crucial plant processes, has been done. The genome-wide transcriptome profile during reproduction and stress is being associated with pathway analysis to unravel intricate net-works. Seed/anther-specific genes coding for MADS, MED, HAP, bZIP, ZOS, PK, HLH and GW2 proteins have been used to decipher their function by raising overexpression

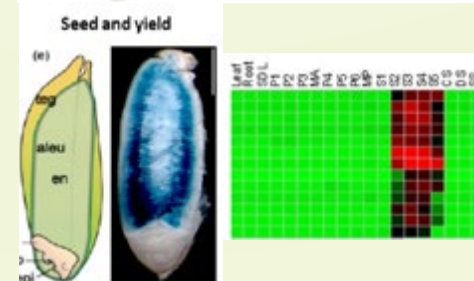
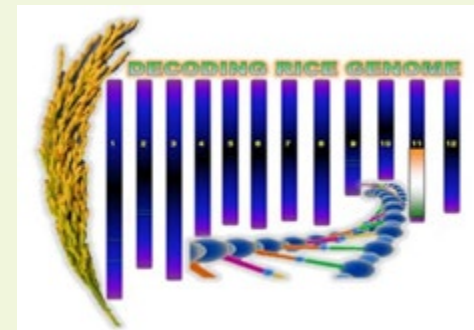
and knockdown transgenics with specific reference to target traits. Anther- and seed-specific promoters (*OSIPK*, *OSIFBOX*, *OSIHLH*, *OSIPP3*, *OSIPA*, *OSIZOS*) have also been evaluated in transgenic systems to provide components for modulation of useful processes like male sterility and nutritional value, respectively. A novel stress-associated protein (SAP) gene family has been discovered in plants. For water-deficit response, selected *SAP*, *TCP* and *RLCK* genes have been evaluated for capacity to confer water-deficit stress tolerance/sensitivity. Stress-inducible promoters (*NBS-Str1* and *BLEC-Str8*) have been evaluated in rice. Molecular genetic approaches involving DNA marker, association, linkage, & bi-parental map as also haplotype have been used to identify genes/QTLs controlling seed traits and other architectural traits of agronomic value in chickpea and rice.

This work is highly relevant to understand dynamic aspects of the function of biological systems and also to generate appropriate options for genetic enhancement of crop plants. In fact, the knowledge about plant genomes is already being used to breed improved varieties of rice, tomato and chickpea in India and world-wide. Over-all, >250 publications of international repute have been generated with GS H-index of 63 and 15000 citations. This research is largely an outcome of investigations of national/international collaborators and >120 Post-Doctoral, Doctoral, Master, Fellow and Trainee researchers.



Awards and Distinctions

- President, National Academy of Sciences, India (2015-2016).
- Director, National Institute of Plant Genome Research, New Delhi (2009-2016).
- Fellow, National (FNASc, FASc, FNAAS, FNA) and international (FTWAS) Science Academies.
- JC Bose National Fellowship Award, DST, Government of India, 2007-2021.
- GM Modi Award for Innovative Science & Technology, 2017.
- Shri Om Prakash Bhasin Award for Science and Technology, 2011.
- BP Pal Memorial Award, ISCA, 2008.
- Birbal Sahni Medal 2006, IBS, 2006.
- NASI – Reliance Industries Platinum Jubilee Award, NASI, 2006.
- National Bioscience Award, DBT, Govt. of India, New Delhi, 1999.



Select Publications

- 1 Ranjan, R., Khurana, R., Malik, N., Badoni, S., Parida, S.K., Kapoor, S. and Tyagi, A.K. (2017). bHLH142 regulates various metabolic pathways-related genes to affect pollen development and anther dehiscence in rice. *Scientific Reports* 7: 43397.
- 2 Malik, N., Agarwal, P. and Tyagi, A.K. (2017). Emerging functions of multi-protein complex Mediator with special emphasis on plants. *Critical Rev. Biochem. Mol. Biol.* 52: 475-502.
- 3 Malik, N., Dwivedi, N., Singh, A.K., Parida, S.K., Agarwal, P., Thakur, J.K. and Tyagi, A.K. (2016). An integrated genomic strategy delineates candidate Mediator genes regulating grain size and weight in rice. *Scientific Reports* 6: 23253.
- 4 Jain, M., Misra, G., Patel, R., Priya, P., Jhanwar, S., Khan, A., Shah, N., Singh, V., Garg, R., Jeena, G., Yadav, M., Kant, C., Sharma, P., Yadav, G., Bhatia, S., *Tyagi, A. and *Chattopadhyay, D. (2013). A draft genome sequence of the pulse crop chickpea (*Cicer arietinum* L.). *Plant Journal* 74: 715-729. (*joint corresponding authors).
- 5 The Tomato Genome Consortium (TGC*). (2012). The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* 485: 635-641. (*Co-authored as Coordinator of the Indian Initiative on Tomato Genome Sequencing).
- 6 Mathur, S., Vyas, S., Kapoor, S. and Tyagi, A.K. (2011). The mediator complex in plants: structure, phylogeny and expression profiling of representative genes in a dicot (*Arabidopsis thaliana*) and a monocot (*Oryza sativa*) during reproduction and stress. *Plant Physiol.* 157: 1609-1627.
- 7 Giri, J., Vij, S., Dansana, P.K. and Tyagi, A. (2011). Rice A20/AN1 zinc-finger containing stress-associated proteins (SAP1/11) and a receptor-like cytoplasmic kinase (OsRLCK253) interact via A20 zinc-finger and confer abiotic stress tolerance in transgenic *Arabidopsis* plants. *New Phytol.* 191: 721-732.
- 8 Kathuria, H., Giri, J., Nataraja, K.N., Murata, N., Udayakumar, M. and Tyagi, A.K. (2009). Glycinebetaine-induced water-stress tolerance in *codA*-expressing transgenic indica rice is associated with up-regulation of several stress responsive genes. *Plant Biotech. Journal* 7: 512-526.
- 9 The International Rice Genome Sequencing Project*. (2005). The map-based sequence of the rice genome. *Nature* 436: 793-800. (*Co-authored as Coordinator of the Indian Initiative for Rice Genome Sequencing).
- 10 Mukhopadhyay, A., Vij, S. and Tyagi, A.K. (2004). Over-expression of a zinc-finger protein gene from rice confers tolerance to cold, dehydration, and salt stress in transgenic tobacco. *Proc. Natl Acad. Sci. USA* 101: 6309-6314.

Prof. Jitendra P. Khurana

Research Interests

Our group has contributed extensively to the area of light perception and signal transduction mechanisms in plants. Some of the initial works on Arabidopsis mutants led to the identification of the blue light receptor, phototropin1, which in fact remained elusive for over a century. Some other novel mutants characterized include *bls1* and *cnr1*, which are defective in light, hormone and sugar signaling. The genes encoding blue light receptors, *CRY1* and *CRY2* from Brassica napus and *CRY2* from rice have been functionally validated in transgenics for their role in regulating plant height and flowering time. Microarray analysis of these transgenics has revealed that *CRY1* regulates plant height largely by modulating the expression of genes involved in GA biosynthesis, auxin signalling and cell wall modification enzymes.

In the past over 15 years, our group has actively participated in sequencing rice, tomato and wheat genomes as part of the International Consortia. Using genome sequence resources, we have phylogenetically analyzed and characterized several rice gene families, including auxin-inducible *AUX/IAA*, *SAUR* and *GH3* gene families, cytokinin-inducible Response Regulator (*RR*) genes, and those encoding F-box proteins (involved in 26S proteasome-mediated protein degradation) and the basic leucine zipper (*bZIP*) transcription factors.

We have identified an interacting partner of one of these *AUX/IAA* proteins and demonstrated its role

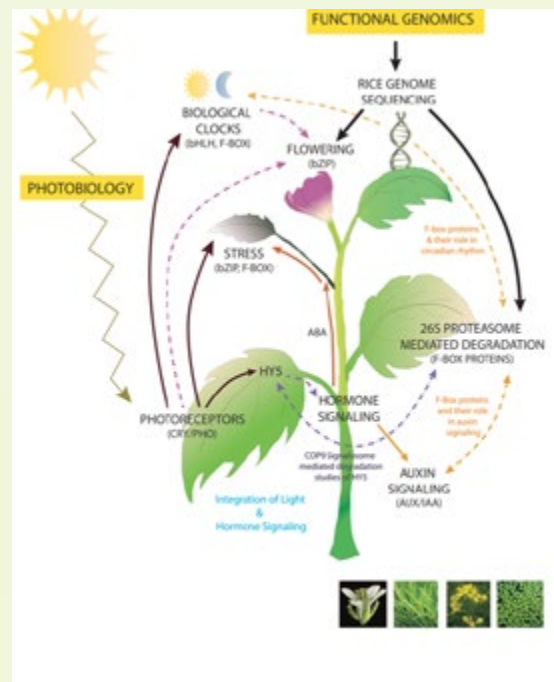
in stress signalling. We have elucidated the role of *OsFBK1*, encoding a component of E3 ligase, in lignin biosynthesis by regulating turnover of cinnamoyl-CoA reductase during anther and root development in rice. Among the rice *bZIP* protein coding genes, *OsbZIP48*, orthologous to *HY5* of Arabidopsis could functionally complement *hy5* mutant of Arabidopsis. Strikingly, it caused semi-dwarfism when over-expressed in rice and its T-DNA insertion mutant was seedling lethal. In contrast to *AtHY5*, *OsbZIP48* protein was found to be stable in dark. Thus, it appears that *OsbZIP48* has undergone neofunctionalization during the course of evolution in rice.

We have also characterized a rice gene encoding polycomb group/*SET* domain proteins. This gene could restore telomere silencing in a yeast mutant, indicating functional conservation of gene repression mechanisms in eukaryotic chromatin. In addition, genes encoding topoisomerase 6 (*TOP6A1*, *A2*, *A3* and *TOP6B*), a subclass of topoisomerase II, have been characterized from rice. When rice *TOP6A1*, *TOP6A3* and *TOP6B* genes were over-expressed in Arabidopsis (as a model system), all the genes independently conferred tolerance to abiotic stress, suggesting their use in transgenic manipulation for stress tolerance in crop plants like rice.



Awards and Distinctions

- Fellow of the Indian National Science Academy, New Delhi
- Fellow of Indian Academy of Sciences, Bangalore
- Fellow of the National Academy of Sciences, India
- Fellow of the National Academy of Agricultural Sciences, India
- Fellow of The World Academy of Sciences (TWAS), Trieste, Italy
- Tata Innovation Fellowship by the Department of Biotechnology, Government of India (2010-2013)
- Prof. Birbal Sahni Medal by the Indian Botanical Society (2011)
- J.C. Bose National Fellowship by the Science and Engineering Research Board (SERB), Government of India (2013-2018)
- Goyal Prize (in Life Sciences) by the Goyal Foundation, Kurukshetra University, Haryana (2017)
- Shri Om Prakash Bhasin Award (in Biotechnology) by the Om Prakash Bhasin Foundation, New Delhi (2017)



The Team



Select Publications

- 1 Borah, P., and Khurana, J.P. (2018). The OsFBK1 E3 ligase subunit affects anther and root secondary cell wall thickenings by mediating turn-over of a cinnamoyl-CoA reductase. *Plant Physiology* 176: 2148–2165.
- 2 Burman, N., Bhatnagar, A., and Khurana, J.P. (2018). OsbZIP48, orthologous to AtHY5, exerts pleiotropic effects in light-regulated plant development. *Plant Physiology* 176: 1262-1285 (In Focus Issue "Energy: Light and Oxygen").
- 3 The International Wheat Genome Sequencing Consortium (IWGSC) (2014). A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. *Science* 345: 1251788-1 to 1251788-11.
- 4 Sharma, P., Chatterjee, M., Burman, N., and Khurana, J.P. (2014). Cryptochrome 1 regulates growth and development in Brassica through alteration in the expression of genes involved in light, phytohormone and stress signaling. *Plant Cell Environ.* 37: 961-977.
- 5 The Tomato Genome Sequencing Consortium (2012). The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* 485: 635-641. (Authored as one of the Principal Investigators).
- 6 Jain, M., and Khurana, J.P. (2009). An expression compendium of auxin-responsive genes during reproductive development and abiotic stress in rice. *FEBS J.* 276: 3148-3162.
- 7 Nijhawan, A., Jain, M., Tyagi, A.K., and Khurana, J.P. (2008). A genomic survey and gene expression analysis of basic leucine zipper (*bZIP*) transcription factor family in rice. *Plant Physiology* 146: 333-350.
- 8 Jain, M., Nijhawan, A., Arora, R., Agarwal, P., Ray, S., Sharma, P., Kapoor, S., Tyagi, A.K., and Khurana, J.P. (2007). F-box proteins in rice. Genome-wide analysis, classification, temporal and spatial gene expression during panicle and seed development, and regulation by light and abiotic stress. *Plant Physiology* 143: 1467-1483.
- 9 Chatterjee, M., Sharma, P., and Khurana, J.P. (2006). CRYPTOCHROME 1 from Brassica napus is upregulated by blue light and controls hypocotyl/stem growth and anthocyanin accumulation. *Plant Physiology* 141: 61-74.
- 10 International Rice Genome Sequencing Program (2005). The map-based sequence of the rice genome. *Nature* 436: 793-800.

Prof. Paramjit Khurana

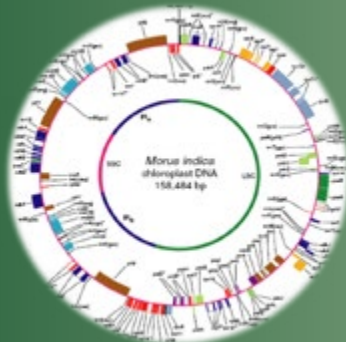
Research Interests

Our work revolves around understanding the processes of Plant Embryogenesis and Heat Stress Tolerance in Wheat, and Mulberry Genomics, Gene Function Identification and Allele mining for abiotic stress tolerance.

We have contributed significantly in the areas of "Wheat and Seribotechnology". We are Internationally credited with establishing genetic transformation of Indian Wheat via *Agrobacterium*-mediated transformation. Wheat transgenics have also been generated in bread wheat, durum wheat and emmer wheat for herbicide tolerance, and for *pin2* gene in durum wheat. Our group was successful in accomplishing resistance against the Cereal Cyst Nematode in *T. durum* and therefore invited to the First International Cereal Cyst Nematodes Initiative in 2009, organized by CIMMYT at Antalya, Turkey. Double haploids have been used to create a homozygous population tolerant to drought and salinity stress.

Tolerance to heat stress is a major area in wheat and focus is on functional genomics of the sensitive and tolerant cultivars of wheat. Several Transcriptional Factors (TFs) and other heat stress-related genes have been functionally characterized and their genome-wide expression profiling undertaken in members of the Triticaceae.

We also have a keen interest in developmental biology and have contributed towards understanding the molecular basis of somatic embryogenesis. Analysis



of the genes encoding somatic embryogenesis receptor-like kinases (SERK) gene family has provided evidence for their role in other plant developmental processes.

Our lab has been a key player in the International efforts in the Genome Sequencing Programs at Delhi University. This effort was largely responsible for sequencing the long arm of chromosome 11 of rice genome in 2005. We have also sequenced the complete chloroplast genome of mulberry (*Morus indica*) in 2006, the first complete genome from India. Our group was also associated with the Tomato Genome Sequencing Initiative and have a keen interest in genoinformatics. At present, our group is involved in BAC-end sequencing of chromosome 2A of wheat under the IWGSC.



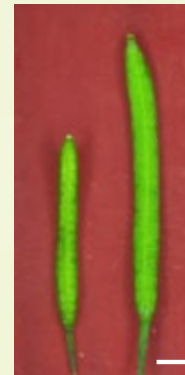
Fellowships & Awards

- Fellow, National Academy of Sciences, Allahabad, India, 2003.
- Fellow, Indian Academy of Sciences, Bangalore, India, 2010.
- Fellow, Indian National Science Academy, New Delhi, India, 2010.
- Fellow, National Academy of Agricultural Sciences, New Delhi, 2014.
- Fellow, The World Academy of Sciences, Trieste, Italy, 2016.
- Prof. J.C. Bose National Fellow for 2012-2017; 2017-2022, Department of Science & Technology, Government of India.
- Prof. Archana Sharma Memorial Award, Indian Science Congress Association, 2011-2012.
- Street Memorial Lecture Award for 2013-14 by the Plant Tissue Culture Association (India).
- Shri Ranjan Memorial Lecture Award (2014) by The National Academy of Sciences, India.
- Birbal Sahni Award Medal of the Indian Botanical Society for 2017.



Characterization of Wheat SERK gene Family

WT 35S:TaBRI1



TaBRI1 overexpression leads to Increased Seed Size and Weight



Select Publications

- 1 Singh, A., Khurana P., 2017. Ectopic expression of Triticum aestivum SERK genes (TaSERKs) control plant growth and development in Arabidopsis. Scientific Reports 7(1):12368.
- 2 Singh, A., Breja, P., Khurana JP, AND Khurana P., 2016. Wheat Brassinosteroid-Insensitive1 (TaBRI1) Interacts with Members of TaSERK Gene Family and cause Early Flowering and Seed Yield Enhancement in Arabidopsis. PLOS One (doi:10.1371/journal.pone.0153273).
- 3 Saeed, B., Baranwal VK., Khurana P. 2016. Comparative transcriptomics and comprehensive marker resource development in mulberry. BMC Genomics 17(1).
- 4 The Tomato Genome Consortium, 2012. The tomato genome sequence provides insights into fleshy fruit evolution. Nature 485 Number 7400 pp547-672.
- 5 Chauhan, H., Khurana, N., Nijhawan, A., Khurana, J.P., Khurana, P. 2012. The chloroplast small heat shock protein (sHSP26) is necessary for tolerance to heat stress and takes part from seed maturation to germination and imparts tolerance to heat stress. Plant, Cell & Environment 35: 1912-1931.
- 6 Chauhan, H., Khurana, P. 2011. Development of drought tolerant transgenic doubled haploid in wheat through Agrobacterium-mediated transformation. Plant Biotech. J. 9: 408-417.
- 7 Singhla, B., Tyagi, A.K., Khurana J.P., Khurana, P. 2007. Analysis of expression profile of selected genes expressed during auxin-induced somatic embryogenesis in leaf base system of wheat (Triticum aestivum) and their possible interactions. Plant Mol. Biology 65: 677-692.
- 8 RAVI, V., Khurana, J.P., Tyagi, A.K., Khurana, P. 2006. The chloroplast genome of mulberry (*Morus indica* cv. K2): complete nucleotide sequence, gene organization and comparative analysis. Tree Genetics & Genomes 3: 49-59.
- 9 INTERNATIONAL RICE GENOME SEQUENCING PROJECT, 2005. The map-based sequence of the rice genome. Nature 436: 793-800.
- 10 Patnaik, D., Khurana, P. 2003. Genetic transformation of Indian bread (T. aestivum) and pasta (T. durum) wheat by particle bombardment of mature embryo-derived calli. BMC Plant Biology 3: 5-16.

Prof. Anil Grover

Research Interests

We work on understanding how rice (*Oryza sativa* L.) plants respond to heat stress at the level of gene expression. Our transcriptome and proteome data suggest that overall the response of rice to heat stress involves signal perception and transduction, activation/synthesis of heat shock factors, genomic and proteomic alterations, ROS metabolism and a host of other proteins associated with biochemical, cellular and physiological processes and with 'unknown' functions. ClpATPases represent a class of molecular chaperones which help in preventing protein aggregation and disaggregating the toxic aggregates formed under stressful regimes. ClpB/Hsp100 proteins are strongly implicated in heat stress biology of diverse organisms. This activity of ClpB/Hsp100 proteins is reportedly mediated with the help of sHsps and Hsp70/Hsp40 proteins. ClpATPase gene family is constituted of 3 ClpB, 4 ClpC and 2 ClpD proteins in rice. Three ClpB of rice include a mitochondrial protein OsClpB-M, a chloroplastic protein OsClpB-P and a cytoplasmic protein OsClpB-C. OsClpB-C, OsClpB-P and OsClpB-M transcripts are strongly induced upon heat stress treatment. In Arabidopsis, we note that a bidirectional promoter is shared between two functionally dissimilar proteins that are involved in a common phenotype of heat tolerance: AtClpB-C which is a chaperone protein and AtCK2 which encodes for the choline kinase enzyme that has a role in plasma membrane synthesis. OsClpB-C,

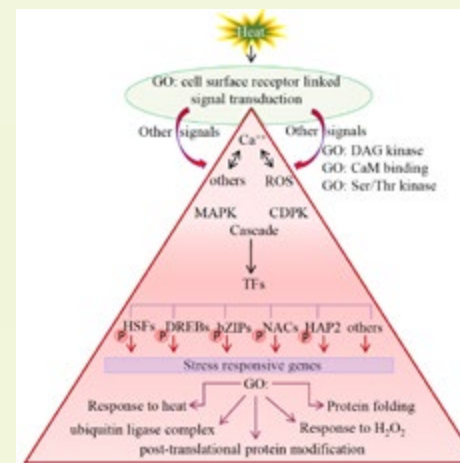
OsClpB-M and OsClpB-P confer partial tolerance to yeast Δ hsp104 mutant. OsClpB-C promoter is heat-regulated. 5'UTR of ClpB-C gene appears to have a role in translation process during heat stress. Rice has 23 sHsps genes which include 16 nucleocytoplasmic (C) sHsps (9 subfamilies), 3 mitochondrial (M) sHsps (2 subfamilies), 2 endoplasmic reticulum (ER)-localized sHsps, 1 plastidial (P) sHsp and 1 peroxisomal (Px) sHsp having 1 subfamily each. Most of these genes are heat-regulated. Rice Hsp70 superfamily genes are represented by 24 Hsp70 family and 8 Hsp110 family members. As against 22 DnaJ sequences noted in yeast, rice genome contains 104 J genes. From the complete genome sequence (Rice Annotation release 5), indications are that at least 25 genes constitute OsHsf gene family. From a near complete picture of TA potential of the OsHsf family comprising of 25 members emerging from our studies, it is concluded that the presence or absence of AHA motif is possibly not the only factor determining TA potential of OsHsfs. Our recent results show that heat stress regulated OsClpB-C gene expression is controlled by OsHsfA2c, OsHsfB4b and OsClpB-C regulon at the transcriptional level and by 5'UTR sequence at the translational level.



Fellowships & Awards

- Member, Board of Directors, International Society of Plant Molecular Biology (ISPMB) (2013- till date)
- Indo-Australia Visiting Fellowship, Indian National Science Academy award (2013)
- J.C. Bose Fellowship award, Department of Science and Technology, Government of India (2011-till date)
- Fellow, Indian Academy of Sciences (IASc), Bangalore (2007)
- Fellow, Indian National Science Academy (INSA), New Delhi (2007)
- Fellow, National Academy of Agricultural Sciences (NAAS), New Delhi (2003)
- Fellow, National Academy of Sciences (NASI), Allahabad (1999)
- National Bioscience Award, Department of Biotechnology (DBT), Government of India (2002)
- Editor, Special issue of "Current Science" on "Transgenic Crops" (2003)
- Indian National Science Academy Young Scientist Medal, New Delhi (1990)

OUR MODEL PRESENTING EVENTS OF HEAT STRESS RESPONSE



Sarkar NK, Kim Y-K and Grover A. 2014. Coexpression network analysis associated with call of rice seedlings for encountering heat stress. *Plant Molecular Biology* 84: 125-143.



The Team



Select Publications

- Lavania, D., Dhingra, A., and Grover, A. (2018). Analysis of transactivation potential of rice (*Oryza sativa* L.) heat shock factors. *Planta* (DOI: 10.1007/s00425-018-2865-2; in press).
- Mishra, R.C., and Grover, A. (2014). Intergenic sequence between Arabidopsis ClpB-C/Hsp100 and choline kinase genes functions as a heat inducible bidirectional promoter. *Plant Physiol* 166, 1646-1658.
- Sarkar, N.K., Kim, Y-K., and Grover, A. (2014). Coexpression network analysis associated with call of rice seedlings for encountering heat stress. *Plant Mol Biol*. 84, 125-143.
- Mittal, D., Madhyastha, D., and Grover, A. (2012). Genome-wide transcriptional profiles during temperature and oxidative stress reveal coordinated expression patterns and overlapping regulons in rice. *PLoS ONE* 7, 7. e40899. doi:10.1371/journal.pone.0040899.
- Singh, A., and Grover, A. (2010). Plant Hsp100/ClpB-like proteins: poorly-analyzed cousins of yeast ClpB machine. *Plant Mol Biol* 74, 395-404.
- Katiyar-Agarwal, S., Agarwal, M., and Grover, A. (2003). Heat tolerant basmati rice engineered by overexpression of hsp101 gene. *Plant Mol Biol* 51, 677-686.
- Agarwal, M., Sahi, C., Katiyar-Agarwal, S., Agarwal, S., Young, T., R Gallie, D., Sharma, V.M., Ganesan, K., and Grover, A. (2003). Molecular characterization of rice Hsp101: Complementation of yeast hsp104 mutation by disaggregation of protein granules and differential expression in indica and japonica rice types. *Plant Mol Biol*. 51, 543-553.
- Singla, S.L., Pareek, A., Kush, A.K., and Grover, A. (1998). Distribution patterns of the 104 kDa stress-associated protein in rice *Plant Mol Biol*. 37, 911-919.
- Pareek, A., Singla, S.L., and Grover, A. (1995). Immunological evidence for accumulation of two novel 104 and 90 kDa HSPs in response to diverse stresses in rice and in response to high temperature stress in diverse plant genera. *Plant Mol Biol*. 29, 293-301.
- Singla SL and A Grover. (1993). Antibodies raised against a yeast heat shock protein cross-react with a heat and abscisic acid-regulated polypeptide in rice. *Plant Mol Biol* 22, 1177-1180.

Prof. Indranil Dasgupta

Research Interests

Plant viruses have historically attracted the attention of researchers because of the diseases they cause in plants and the role they play in determining crop yields. More recently, plant viruses have emerged as models to understand intracellular trafficking and tools to develop gene expression and gene silencing platforms. Genes encoded by plant viruses often are masters of multi-tasking and their interactions with their host defense systems are broadening our understanding of their evolution. With these broad perspectives in mind, our group has been active in studying plant viruses.

Transgenic virus resistance: Our group has developed transgenic rice plants showing resistance against Indian isolates of Rice tungro bacilliform virus (RTBV) and Rice tungro spherical virus, using RNAi technology. Using a novel strategy based on trans-acting siRNAs, we have developed resistance in tomato against the highly infectious Tomato leaf curl New Delhi virus, a virus rapidly spreading to new regions of the World and to new plant hosts.

Viral variability: We have revealed new information on viruses infecting cassava, citrus, mentha, okra (bhendi) and rice focusing on their variability and genetic relationships. We have developed infectious clones of viruses infecting cassava and rice, which are being used to investigate the viral gene functions and interactions with the host plants. We have also looked at the role of whitefly vectors in transmission

of a cassava virus and the importance of amino acid residues of the viral coat protein in determining the symptoms.

Viral promoters: We found novel gene expression control elements embedded in the promoter of an Indian isolate of RTBV, which could be used to control heterologous gene expression in plants. This has been patented (US Patent no. 07728122, Eurasian patent no. 013229), awarded jointly to Department of Biotechnology, Government of India and University of Delhi and commercialized to a seed company. Subsequently, we have also shown the existence of negative control elements in the promoter, which has interesting applications in developing methods to detect viral movement.

Virus induced gene silencing (VIGS): We have developed a rice virus into a VIGS vector and demonstrated its effectiveness in silencing genes of rice, with a view to strengthen functional genomic initiatives for monocots. This has been awarded an Indian patent (No. 278167).

Plant-virus interactions: We are currently engaged in studying the interactions of plants such as rice and tobacco with viruses, focusing on the plant anti-viral defense and viral counter-defense.



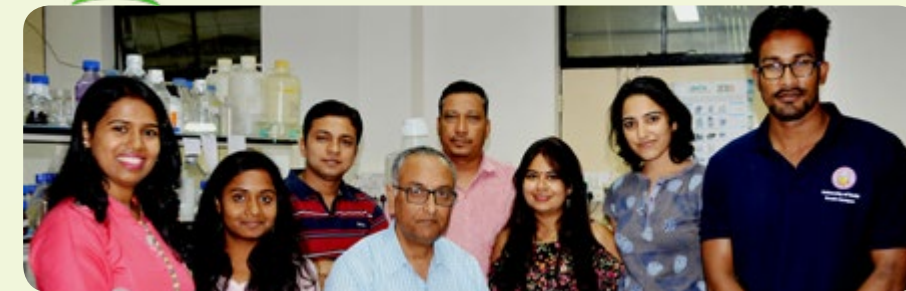
Fellowships & Awards

- Fellow, Indian National Science Academy, New Delhi
- Fellow, Indian Academy of Sciences, Bangalore
- Fellow, National Academy of Sciences India, Allahabad
- Member, Editorial Board, Journal of Biosciences
- Member, Editorial Board, Virus Disease
- Visiting Professorship, Northwest University of Agriculture and Forestry, China
- J. C. Bose Fellowship.

Select Publications

- 1 Kant R. and Dasgupta I. (2017). Phenotyping of VIGS-mediated gene silencing in rice using a vector derived from a DNA virus. *Plant Cell Reports* 36: 1159-1170.
- 2 Borah B.K., Zarreen F., Baruah G. and Dasgupta I. (2016). Insights into the control of geminiviral promoters. *Virology* 495: 101-111.
- 3 Valarmathi P., Kumar G., Robin S., Manonmani S., Dasgupta I. and Rabindran R. (2016). Evaluation of virus resistance and agronomic performance of rice cultivar ASD 16 after transfer of transgene against Rice tungro bacilliform virus by backcross breeding. *Virus Genes* 52: 521-529.
- 4 Singh A., Taneja J., Dasgupta I. and Mukherjee S.K. (2014). Development of plants resistant to tomato geminiviruses using artificial trans-acting small interfering RNA. *Molecular Plant Pathology* 16: 725-734.
- 5 Borah B.K., Sharma S., Kant R., Johnson A.M.A., Saigopal D.V.R. and Dasgupta I. (2013). Bacilliform DNA-containing plant viruses in the tropics: commonalities within a genetically diverse group. *Molecular Plant Pathology* 14: 759-771.
- 6 Purkayastha A., Sharma S. and Dasgupta I. (2010). A negative element in the downstream region of the Rice tungro bacilliform virus promoter is orientation- and position independent and is active with heterologous promoters. *Virus Research* 153: 166-171.
- 7 Purkayastha A., Mathur S., Verma V., Sharma S. and Dasgupta I. (2010). Virus-induced gene silencing in rice using a vector derived from a DNA virus. *Planta* 232: 1531-1540.
- 8 Mittal D., Borah, B.K. and Dasgupta I. (2008). Agroinfection of cloned Sri Lankan cassava

The Team



mosaic virus DNA to Arabidopsis thaliana, Nicotiana tabacum and cassava. *Archives of Virology* 153: 2149-2155.

- 9 Tyagi H., Rajasubramaniam S., Rajam M.V. and Dasgupta I. (2008). RNA-interference in rice against Rice tungro bacilliform virus results in its decreased accumulation in inoculated rice plants. *Transgenic Research* 17:897-904

- 10 Mathur S. and Dasgupta I. (2007). Downstream promoter sequence of an Indian isolate of Rice tungro bacilliform virus alters tissue-specific expression in host rice and acts differentially in heterologous systems. *Plant Molecular Biology* 65: 259-275.



Prof. Sanjay Kapoor

Research Interests

Molecular events that follow the establishment of floral organ primordia, ultimately culminate into development of male (pollen) and female (embryo sac) gametophytes in specialized sex organs known as the androecium and gynoecium. The gametes thus formed undergo fertilization and develop into seeds. Understanding the underlying gene regulatory networks that control the development of reproductive floral organs, and the male and female gametophytes therein, involves: (a) Identification of the genetic components involved, and (b) Their classification into pair wise protein-protein and protein-DNA interactomes, followed by construction of biologically realistic gene regulatory networks.

Our lab aims to unravel these networks to understand developmental mechanisms in terms of mechanistic models and, thus, pave the way for translating genetic interactions into phenotypic traits. In this regard, we have carried out whole genome microarray-based transcriptome analysis of about 30 tissues/stages of rice vegetative and reproductive development, which has helped in the identification of several co-expressed groups of genes. These groups either show similar up-regulation profiles or express in a tissue or developmental

stage specific manner, and thus, constitute putative interactomes. The transcriptomic analysis has been refined to include subtractive logic in order to shortlist genes that express specifically in individual tissues/stages of development for validation of function and/or promoter activities. For gene function validation RNAi/miRNA based silencing and ectopic expression strategies in transgenic rice and/or Arabidopsis are being followed. Whereas, promoter activities are being determined by driving expression of GUS and/or GFP like reporter gene in transgenic systems.

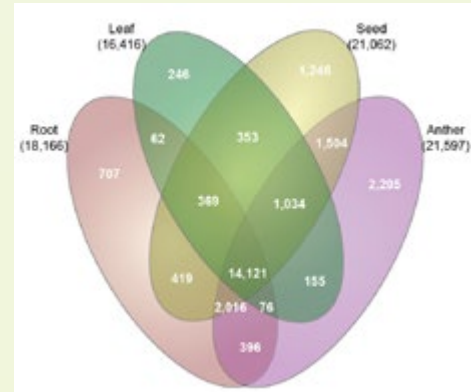
Our group has also worked extensively on the role of MADS box transcription factors and components of RNAi machinery. One of the MADS gene, *OsMADS29*, has been found to play important role in grain filling during seed development in a cereal-specific manner by controlling plant hormone homeostasis and starch metabolism. *MADS29* has been found to interact with 19 other seed-expressed MADS-box protein which may provide specificity as well as diversity to its targets. Our recent experimental data suggest that *MADS29* seems to regulate plastid biogenesis and differentiation of proplastids into amyloplast by affecting hormone homeostasis in the target cells. It seems that *MADS29* may have evolved in monocots,



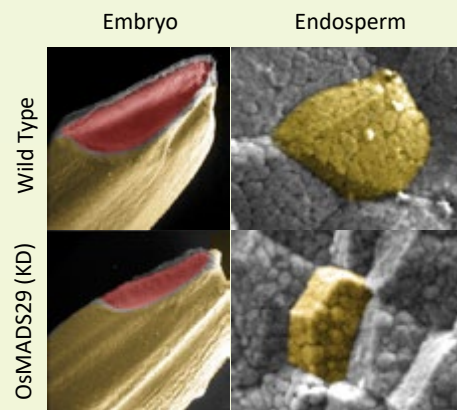
especially cereals, contributing to the development of starchy endosperm during seed development. Currently, we are working on using this knowledge to transform non-seed cells into sink cells, so that, one day we might be able to synthesize starch without growing cereals crops for it.

Awards and Distinctions

- Fellow of the National Academy of Sciences, India (December 7, 2013)
- Associate editor, Journal of Plant Biochemistry and Biotechnology (2016 -)
- 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).



Analysis of rice anther transcriptome



Effect of *OsMADS29* Silencing on embryo and endosperm Development

Select Publications

- 1 Chawla M, Verma V, Kapoor M, Kapoor S (2016) A novel application of periodic acid–Schiff (PAS) staining and fluorescence imaging for analysing tapetum and microspore development. *Histochemistry and Cell Biology* 1–8.
- 2 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* 65:5339–5350.
- 3 Nayar, S., Sharma, R., Tyagi, A.K. and 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. Cover Page Article.
- 4 Baranwal V, Mikkilineni V, Zehr-Barwale U, Tyagi AK and Kapoor S (2012) Heterosis: Emerging ideas about hybrid vigour. *Journal of Experimental Botany* 63(18):6309-6314. Opinion Article.
- 5 Sharma R, Agarwal P, Ray S, Deveshwar P, Sharma P, Sharma N, Nijhawan A, Jain M, Singh AK, Singh VP, Tyagi AK and 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.
- 6 Deveshwar, P., Bovill, W.D., Sharma, R., Able, J.A., and Kapoor, S. (2011). Analysis of anther transcriptomes to identify genes contributing to meiosis and male gametophyte development in rice. *BMC Plant Biology* 11:78.
- 7 Arora, R., Agarwal, P., Ray, S., Singh, A.K., Singh, V.P., Tyagi, A.K., and Kapoor, S. (2007). MADS-box gene family in rice: Genome-wide identification, organization and expression profiling during reproductive development and stress. *BMC Genomics* 8.

The Team



Vibha Verma
CSIR SRF



Neelima Boora
UGC JRF



Ridhi Khurana
JRF



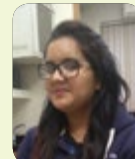
Gautam Gawande
UGC-BSR JRF



Sanchi Bhimrajka
Inspire Fellow



Komal Chaprana
CSIR JRF



Utkrishta Hira
JRF



Haney Gupta
Technical Assistant



Sudhir Kumar
Growth room

- 8 Kapoor, S., Kobayashi, A., and Takatsuji, H. (2002). Silencing of the tapetum-specific zinc finger gene TAZ1 causes premature degeneration of tapetum and pollen abortion in *Petunia*. *Plant Cell* 14, 2353-2367.
- 9 Kapoor, S., and 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. *Plant Cell* 11, 1799-1810.

Prof. Arun Kumar Sharma

Research Interests

Structural and functional genomics of tomato: I contributed to "Indian initiative on Tomato Genome Sequencing" where part of chromosome 5 of tomato has been sequenced by BAC by BAC approach. In order to study gene regulation during ripening of tomato fruits 110 ripening-related genes of tomato have been cloned. Expression of these genes at different stages of fruit ripening has been analyzed. One of the gene which codes for a MADS box containing factor, LeMAD-RIN has been studied further. Transgenic tomato plants showing RNAi for this gene have been produced. The plants mutant for this gene have been utilized to differentiate ethylene regulated fruit ripening-related genes from ethylene regulated genes which are not related to fruit ripening, using microarray analysis. Two other genes *LeEIL1* and *LeEIL3*, involved in ethylene signal transduction have been silenced by RNAi to produce plants with delayed ripening phenotypes. Genes encoding Ethylene Response Factors (ERFs) are being used to alter their expression by genetic engineering approaches to achieve better quality of tomato fruits.

Genetic manipulation of tomato for cold resistance: Attempt has been made to engineer cold resistance in tomato using *OSISAP1* gene of rice. A complete gene family of homologs of this rice gene has been characterized from tomato. Further, subtraction libraries have been made and sequenced for analysis

of cold regulated genes of tomato. Several important genes with potential for improving cold tolerance have been identified. Transgenic plants over-expressing genes encoding for mitogen activated protein kinase 3 and alternative oxidase 1 have been produced. These plants are showing improved tolerance to various abiotic stresses.

Role of DNA methylation: A study has been carried out to understand the role of methylated DNA binding proteins of *Arabidopsis* in gene silencing. Genes for most of the 13 methylated DNA binding proteins of *Arabidopsis* have been cloned. Role of genes is being investigated by their silencing and over-expression. Using an experimental system involving silencing of *gus* reporter gene, it has been demonstrated for the first time that AtMBD6 has a role in miRNA-mediated silencing of genes and gene silencing and AtMBD5, 9 and 13 have role in siRNA-mediated gene silencing. Alteration of some of the tomato homologs of these genes encoding these proteins is being used to alter expression of ripening related genes in tomato by epigenetic approaches.

Awards and Distinctions

- National Academy of Sciences, Allahabad, India, 2012.



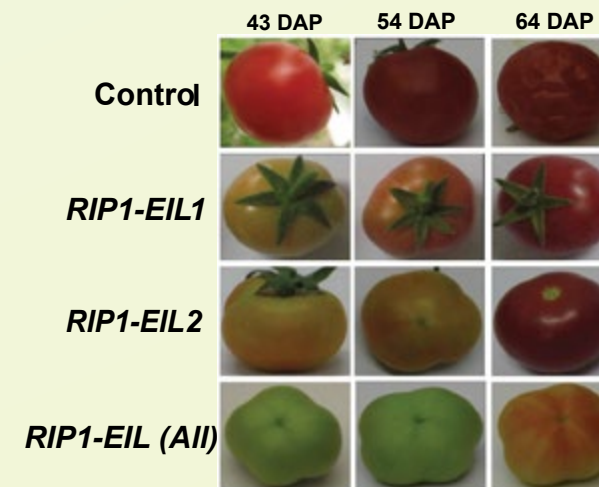
Select Publications

- Parida, A.P., Sharma, A. and Sharma, A.K. (2017) AtMBD6, a methyl CpG binding domain protein, maintains gene silencing in Arabidopsis by interacting with RNA binding proteins. *J. Biosci.* 42:57-68.
- Agarwal, P., Kumar, R. Pareek, A. and Sharma, A.K. (2017) Fruit preferential activity of tomato RIP1 gene promoter in transgenic tomato and Arabidopsis. *Mol. Gen. Genomics* 292:145-156.
- Kumar, R., Jiwani, G., Pareek, A., SravanKumar, T., Khurana, A. and Sharma, A.K. 2016. Evolutionary profiling of group II PLP-dependent decarboxylase gene family suggests expansion and functional diversification of histidine decarboxylases in tomato. *The Plant Genome.* 9:1-15.
- Kumar R., Agarwal P., Pareek A., Tyagi A.K. and Sharma A.K. (2015). Genomic Survey, Gene Expression, and Interaction Analysis Suggest

Diverse Roles of ARF and Aux/IAA Proteins in Solanaceae. *Plant Mol. Biol. Rep.* 33:1552-1572.

- Kumar, R. and Sharma, A. K. (2014) Ethylene perception and signaling in ripening fruit. In: Nath, P., Bouzayen, M., Mattoo, A. K. and Pech, J. C. (Eds.), *Fruit ripening: Physiology, Signalling and Genomics*. Publisher: CABI, Oxfordshire, U K, pp 193-201.
- Sharma A.K. and Sharma M.K. (2014). Plants as host for recombinant DNA. In: Das, H.K. (Ed.), *Gene and its Engineering*. Wiley India Pvt. Ltd. New Delhi, India, pp. 410-433.
- Kumar R, Khurana, A and Sharma A.K. (2014). Role of plant hormones and their interplay in development and ripening of fleshy fruits. *J. Exp. Bot.* 65:4561-4575.
- Kumar R, Khurana A and Sharma A.K. (2013). Molecular regulators of fruit ripening. *Stewart Postharvest Review*. Published online December 2013, doi: 10.2212/spr.2013.4.6
- Tomato Genome Consortium (2012) The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*, 485:635-641.
- Kumar, R., Agarwal, P, Tyagi, A.K. and Sharma, A.K. (2012) Genome-wide investigation and expression analysis suggest diverse roles of auxin-responsive GH3 genes during development and response to different stimuli in tomato (*Solanum lycopersicum*). *Mol Gen. Genomics.* 287:221-235.

The Team



Delay of tomato fruit-ripening by silencing of LeEIL genes

Prof. Girdhar Kumar Pandey

Research Interests

Evolutionarily plants have adopted a sessile habit to sustain in an environment. This immobile nature has made plants to evolve an intricate sensing and signaling network in response to both favorable and unfavorable conditions. The adaptive and defense machinery of plants consists of a plethora of networks or pathways, which enable in activating and responding against these stresses. Calcium acts as a ubiquitous player in many of the signaling pathways in all eukaryotes, be it physiological or developmental processes. One of the most important phenomenon calcium regulate is the signal transduction network for sensing and responding to environmental stimuli. In the calcium mediated signaling network, a change in calcium concentration is designated as "calcium signature" upon sensing a stimuli, which is being sensed by a plethora of calcium sensors such as Calmodulin, CDPK, and CBL-CIPK networks in plants. My group is studying the role of several downstream components in calcium signaling, which might be working with calcium sensors/relay, and ultimately acting on effectors molecules in modulating a response either by change in gene expression or direct physiological regulation. At present, we are extensively investigating some of the key players such as calcium sensors, kinases, phosphatases, transcription factors and transporters/ channels to understand the stress signaling mechanism in plants. In near future, we wanted to investigate the detailed

mechanistic interplay and cross talk of different signaling cascades with calcium signaling network in Arabidopsis and rice model systems under different stress conditions. The interaction of several pathways to converge and diverge at some points will be investigated by using the advanced tools of genetic and functional genomics where several networks can be mapped collectively. With the extensive knowledge of complex interplay of stress signaling networks, molecular and genetic manipulation of key/master regulators will be targeted, which will be useful for agricultural biotechnology sector. And hence, desired traits can be imparted in the crop plants to adapt to a higher degree of stresses, without losing crop yield and productivity.



Awards and Distinctions

- Fellow, National Agricultural Academy of Sciences (NAAS), New Delhi
- Fellow, National Academy of Sciences, India (NASI)
- National Bioscience Award, 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
- Editorial Board member, Scientific Reports
- Academic Editor, PLoS One

The Team



Select Publications

- 1 Shankar, A., Fernandes, J.L., Kaur, K., Sharma, M., Kundu, S., and Pandey, G.K. (2017) Rice Phytoglobin regulate responses under low mineral nutrients and abiotic stresses in Arabidopsis thaliana. *Plant Cell Environ.* 41: 215-230.
- 2 Sanyal, S.K., Kanwar, P.K., Samtani, S., Kaur, K., Jha, S.K. and Pandey, G.K. (2017) Alternative splicing of CIPK3 results in distinct target selection to propagate ABA signaling in Arabidopsis. *Front. Plant Sci.* 8:1924.
- 3 Sanyal, S.K., Kanwar, P., Yadav, A.K., Sharma, C., Kumar, A., and Pandey, G.K. (2017) Arabidopsis CBL interacting protein kinase 3 interacts with ABR1, an APETALA2 domain transcription factor, to regulate ABA responses. *Plant Sci.* 254: 48-59.
- 4 Yadav, A.K., Shankar, A., Jha, S.K., Kanwar, P., Pandey, A. and Pandey, G.K. (2015) A rice tonoplasmic calcium exchanger, OsCCX2 mediates Ca²⁺/cation transport in yeast. *Sci. Rep.* 26:17117.
- 5 Pandey, G.K., Kanwar, P., Singh, A., Steinhorst, L., Pandey, A., Yadav, A.K., Tokas, I., Sanyal, S., Kim, B.G., Lee, S.C., Cheong, Y.H., Kudla, J., Luan, S. (2015) CBL-interacting protein kinase, CIPK21, regulates osmotic and salt stress responses in Arabidopsis. *Plant Physiol.* 169:780-92.
- 6 Shankar, A., Srivastava, A.K., Yadav, A.K., Sharma, M., Pandey, A., Raut, V.V., Das, M.K., Suprasanna, P., and Pandey, G.K. (2014) Whole genome transcriptome analysis of rice seedling reveals alterations in Ca²⁺ ion signaling and homeostasis in response to Ca²⁺ deficiency. *Cell Calcium* 255:155-65.
- 7 Pandey, G.K., Grant, J.G., Cheong, Y.H., Kim, B.G., Li, L., and Luan, S. (2007) Calcineurin-B-Like Protein CBL9 Interacts with Target Kinase CIPK3 in the Regulation of ABA Response in Seed Germination. *Mol. Plant.* 1: 238-248.
- 8 Pandey, G.K., Cheong, Y.H., Kim, B.G., Grant, J.G., Li, L. and Luan, S. (2007) CIPK9: a calcium sensor-interacting protein kinase required for low-potassium tolerance in Arabidopsis. *Cell Res.* 17: 411-421.
- 9 Pandey, G.K., Grant, J.G., Cheong, Y.H., Kim, B.G., Li, L. and Luan, S. (2005) ABR1, an AP2-Domain Transcription Factor that Functions as a Repressor of ABA Response in Arabidopsis. *Plant Physiol.* 139: 1185-1193.
- 10 Pandey, G.K., Kim, K.N., Cheong, Y.H., Grant, J.G., Li, L., Hung, W., D'Angelo, C., Weini, S., Kudla, J. and Luan, S. (2004) The calcium sensor CBL9 modulates ABA sensitivity and biosynthesis in Arabidopsis. *Plant Cell.* 16: 1912-1924.

Dr. Saurabh Raghuvanshi

Research Interests

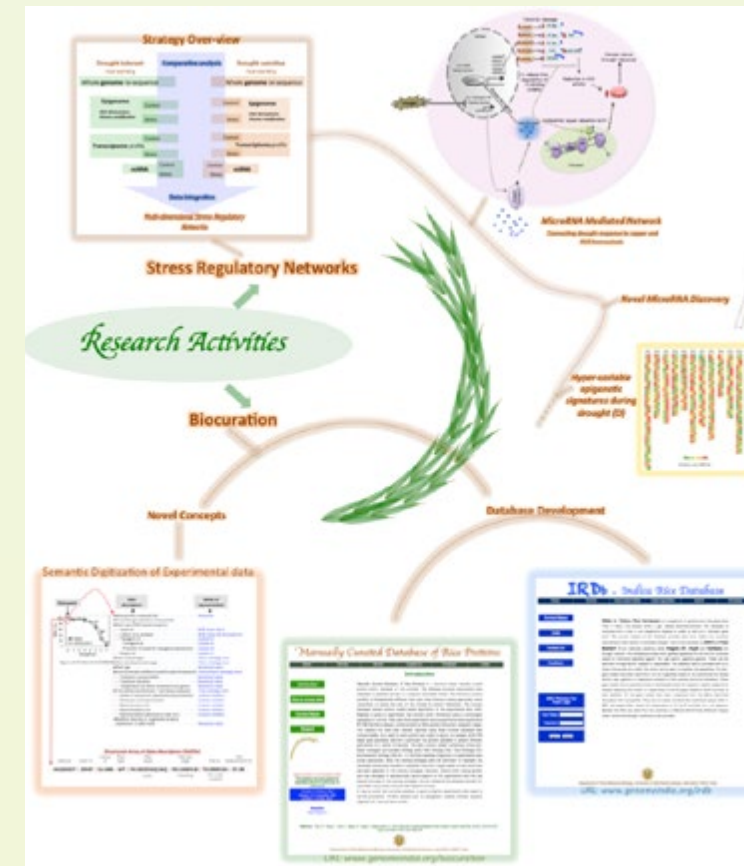
Our group is working on an integrated approach of comparative genomics on different dimensions of genome, epigenome (DNA methylation & histone modification) and transcriptome (including miRNome) to understand the evolution of drought tolerance response in *indica* rice cultivars. We are especially interested in miRNA mediated regulatory networks in rice. We 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.

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 through 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.

Our data models completely digitize the experimental data such that one can access even a single data point (e.g. a bar of a bar-graph) from a collection of hundreds of publications. The efficacy of these models has been demonstrated by developing an international literature-based database of rice proteins entitled MCDRP or 'Manually Curated Database of Rice Proteins (www.genomeindia.org/biocuration)" which currently has data for over 2000 rice proteins from over 500 research articles. We have also developed another database entitled 'Indica Rice Database' (www.genomeindia.org/irdb) based on the molecular data from various indica rice cultivars.

Awards

NASI-Young Scientist Platinum Jubilee Award in Plant Sciences, 2006. **Citation:** For outstanding contribution in the field of Genomics and Bioinformatics



Select Publications

- 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.
- 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.
- 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.
- International Rice Genome Sequencing Project (2005). The map-based sequence of the rice genome. *Nature* 436: 793–800.
- Itoh, T. et al. (2007). Curated genome annotation of *Oryza sativa* ssp. *japonica* and comparative genome analysis with *Arabidopsis thaliana*. *Genome Res.*: 175–183.
- 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.
- 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.
- 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.
- 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.
- Tanaka, T. et al. (2007). The Rice Annotation Project Database (RAP-DB): 2008 update. *Nucleic Acids Res.* 36: D1028–D1033.

Dr. Surekha Katiyar-Agarwal

Research Interests

Molecular Basis of Stress Responses in Plants: Plants respond to harsh environmental conditions by undergoing changes at molecular, biochemical and physiological level. **Small RNAs** have emerged as crucial regulators of development and stress responses in plants. Genome-wide discovery of small RNAs in economically important crops such as wheat, mustard, potato, chickpea and rice has been carried out by our research group. We also work on elucidating the molecular and physiological function of stress-associated gene families such as **tetraspanins (TETs)** and **HSFs** (heat shock transcription factors). Tetraspanins are transmembrane proteins which act as dynamic 'facilitators' in organizing 'microdomain web' at cell surface, thereby modulating signalling cascades. HSFs are regulators of several stress-responsive genes. We found that the tetraspanin genes are differentially expressed in different tissues and diverse abiotic stresses in rice. Modulation of expression of TET5 and HSFC1 in rice results in altered response to salinity/drought stress. Efforts are being made to identify the interacting partners and probable targets of these proteins, which would provide insights into their biological function in stress response pathway.

Molecular Basis of Leaf Senescence in Plants: Leaf senescence is a complex, yet highly orchestrated, stage of plant development, involving age-dependent degeneration ultimately leading to

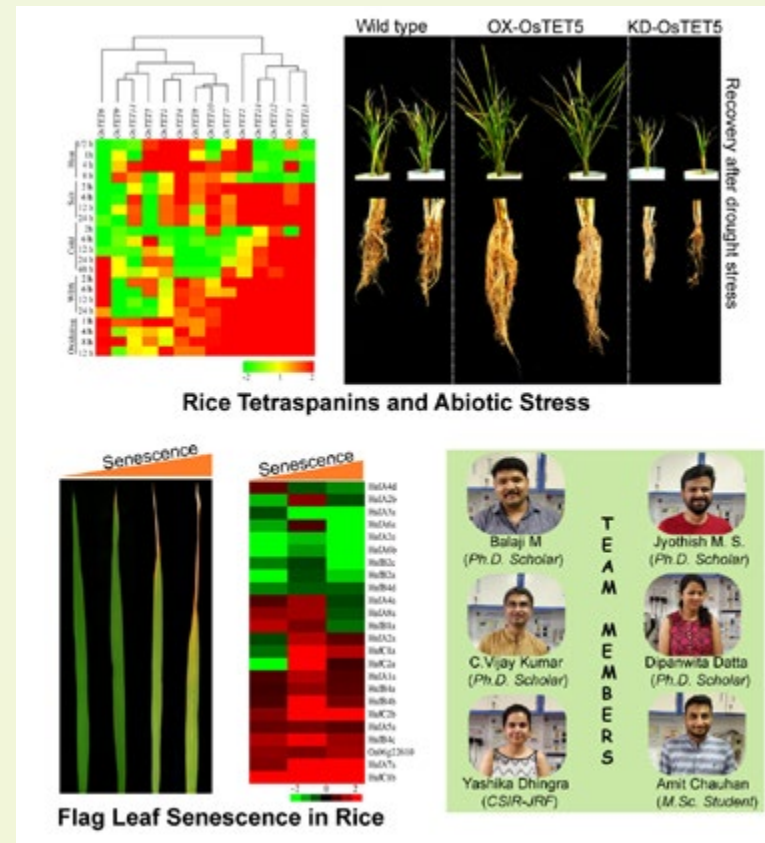
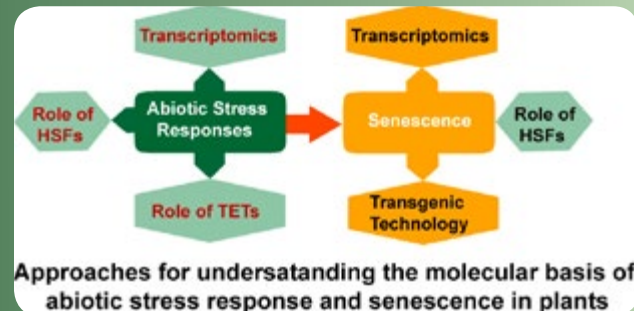
death. In agricultural aspects, leaf senescence is thought to limit the yield in crops and it is a major cause of post-harvest spoilage of vegetable crops. Moreover, abiotic stresses accelerate senescence in plants leading to enormous negative agro-economic impact. Our group is involved in unravelling 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 with respect to their role in regulating leaf senescence.

Our results would provide an insight into the mechanism of stress tolerance and senescence in plants. It would be worthwhile to explore the overlap in the two pathways and the components associated with them. The information generated would be useful in engineering 'designer plants' by transgenic technology with enhanced tolerance to different abiotic stresses and altered senescence.



Awards and Distinctions

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



Select Publications

- McLoughlin, F., Basha, E., Fowler, M.E., Kim, M., Bordowitz J., Katiyar-Agarwal, S., Vierling, E. (2016). Class I and II small heat-shock proteins protect protein translation factors during heat stress. *Plant Physiol.* 172:1221-1236.
- Mani, B., Agarwal, M., Katiyar-Agarwal, S. (2015). Comprehensive expression profiling of rice tetraspanin genes reveals diverse roles during development and abiotic stress. *Front. Plant Sci.* 6:1088.
- Bhardwaj, A.R., Joshi, G., Pandey, R., Goel, S., Jagannath, A., Kumar, A., Katiyar-Agarwal, S., Agarwal, M. (2014). A genome-wide perspective of miRNAome in response to high temperature, salinity and drought stresses in Brassica juncea (Czern) L. *PLoS ONE* 9:e92456.
- Pandey, R., Joshi, G., Bhardwaj, A.R., Agarwal, M., Katiyar-Agarwal, S. (2014). A comprehensive genome-wide study on tissue-specific and abiotic stress-specific miRNAs in Triticum aestivum. *PLoS ONE* 9:e95800.
- Zhang, X., Zhao, H., Gao, S., Wang, W.C., Katiyar-Agarwal, S., Huang, H.D., Raikhel, N., Jin, H. (2011). Arabidopsis Argonaute 2 regulates innate immunity via miRNA393(l)-mediated silencing of a golgi-localized SNARE gene, MEMB12. *Molecular Cell* 42:356-66.
- Katiyar-Agarwal, S., Jin, H. (2010). Role of small RNAs in host-microbe interactions. *Annu. Rev. Phytopathol.* 48:225-246.
- Katiyar-Agarwal, S., Gao, S., Vivian-Smith, A., Jin, H. (2007). A novel class of bacteria-induced small RNAs in Arabidopsis. *Genes and Dev.* 21:3123-3134.
- 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* 103:1802-1807.
- Katiyar-Agarwal, S., Zhu, J., Kim, K., Agarwal, M., Fu, X., Huang, A., Zhu, J-K. (2006). The plasma membrane Na⁺/H⁺ antiporter SOS1 interacts with RCD1 and functions in oxidative stress tolerance in Arabidopsis. *Proc. Natl. Acad. Sci. USA* 103:18816-21.
- Verslues, P.E., Agarwal, M., Katiyar-Agarwal, S., Zhu, J., Zhu, J-K. (2006). Methods and concepts in quantifying resistance to drought, salt and freezing, abiotic stresses that affect plant water status. *Plant J.* 45: 523-539.

Administrative Structure of the Department

Head of the Department :

Prof. Paramjit Khurana

Teaching Faculty :

Prof. Akhilesh Kumar Tyagi

Prof. Jitendra P. Khurana

Prof. Anil Grover

Prof. Indranil Dasgupta

Prof. Sanjay Kapoor

Prof. Arun Kumar Sharma

Prof. Girdhar Kumar Pandey

Assoc. Prof. Saurabh Raghuvanshi

Asstt. Prof. Surekha Katiyar-Agarwal

Non-teaching Staff :

Technical Staff

Mr Ramesh Chandra - Technical Officer

Mr Prakash Chandra - Senior Technical Assistant

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

No. of Seats: 12

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: a written entrance examination, followed by an interview. Candidates are called for the interview based on performance in written examination and the final selection is based on the combined performance in written exam and the interview. A total of 12 students are selected from general and reserved categories (as per University rules).

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

Doctor of Philosophy in

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 area offered are: Functional Genomics, Epigenomics, Gene Regulatory Networks, Molecular Basis of Plant Reproduction and Yield, Post-harvest Biotechnology, Abiotic Stress Biology (Heat & Osmotic Stress, Role of Small RNAs, Signal Transduction during stress), 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.	Scholar	Supervisor	Research Topic	Regn #	Date of Registration	Tentative Date of completion	Funding Agency of
1	Aishwarye Sharma	J.P. Khurana & Paramjit Khurana	Functional Analysis of some rice bZIP Transcription Factors for their role in Abiotic Stress Response and Plant Development	SF-1/Ph.D./2017/1180	2017-09-06	2022-09-05	UGC
2	Akanksha Bhatnagar	J.P. Khurana	Functional characterization of genes involved in regulating the development and abiotic stress response in rice	SF-1/Ph.D./2013/925	2013-04-16	2018-04-15	CSIR
3	Amrapali	Arun Sharma	Study of mechanism of action of Methyl CpG binding-domain proteins AtMBD1 and AtMBD13 in gene regulation in <i>Arabidopsis</i>	SF-1/Ph.D./2012/904	2012-08-23	2018-08-22	UGC
4	Ankita Prusty	Akhilesh K. Tyagi	Functional analysis of genes involved in seed development in rice	SF-1/Ph.D./2016/1114	2016-08-16	2021-08-15	DST
5	Balaji M.	Surekha Katiyar-Agarwal	Molecular characterization of stress associated proteins in plants	SDC-12/12	2012-07-12	2017-07-11	UGC Non-Net
6	Barkha Ravi	Girdhar K. Pandey	Elucidation of potassium sensing and signaling machinery in <i>Arabidopsis</i> and Rice	SF-1/Ph.D./2017/1181	2017-08-25	2022-08-24	UGC Non-Net
7	Bhoomika Sharma	Arun Sharma	Regulation of ripening in tomato by genetic manipulation of the epigenome	SF-1/Ph.D./2016/1115	2016-08-16	2021-08-15	DBT
8	Chanderkant Chowdhary	Paramjit Khurana	Wheat chromosom 2A BAC end sequencing and functional characterization of genes associated with stress tolerance	SF-1/Ph.D./2012/960	2012-07-12	2017-07-11	DBT
9	Cheeni Vijayakumar	Surekha Katiyar-Agarwal	Functional characterization of Arabidopsis Hsfs	SF-1/Ph.D./2013/926	2013-04-16	2018-07-12	UGC
10	Deepika Sharma	Saurabh Raghuvanshi	Analysis of drought responsive regulatory network in plants	SF-1/Ph.D./2015/1055	2015-10-29	2020-10-28	UGC

Ph.D. Scholars

Sl. No.	Scholar	Supervisor	Research Topic	Regn #	Date of Registration	Tentative Date of completion	Funding Agency of Fellowship
11	Dipanwita Datta	Surekha Katiyar-Agarwal	Understanding the molecular basis of development and stress tolerance	SF-1/Ph.D./2018/1238	2018-03-27	2023-03-26	UGC Non-Net
12	Eshan Sharma	J.P. Khurana	Functional characterization of some stress response genes in rice	SF-1/Ph.D./2012/908	2012-11-16	2017-11-15	CSIR
13	Garima Singh	Anil Grover	Regulation of heat stress genes in rice and <i>Arabidopsis</i>	SF-1/Ph.D./2013/939	2013-07-22	2018-07-21	UGC
14	Gaurav Kumar	Indranil Dasgupta	Molecular analysis of stress response dynamics in rice (<i>Oryza sativa</i> L.) against rice tungro viruses and assessment of RNAi mediated viral resistance in transgenic and backcrossed rice varieties	SF-1/Ph.D./2011/849	2011-11-11	2017-11-10	UGC
15	Gautam Gawande	Sanjay Kapoor	Identification and functional characterization of gene regulatory networks involved in plant reproductive development	SF-1/Ph.D./2015/1056	2015-10-29	2020-10-28	UGC-BSR
16	Harsha Samtani	Paramjit Khurana	Comparative Genomics for Thermal Stress Tolerance in Members of the Triticeae	SF-1/Ph.D./2017/1182	2017-09-06	2022-09-05	UGC
17	Jyothish M.S.	Surekha Katiyar-Agarwal	Molecular studies on gene regulation during stress and development in plants	SF-1/Ph.D./2012/899	2012-07-12	2018-07-11	UGC
18	Kamlesh Kumari	Indranil Dasgupta	Studies on interaction of rice with its viruses	SF-1/Ph.D./2015/1059	2015-10-29	2021-10-28	UGC
19	Kanika Gupta	Indranil Dasgupta	Functional studies on viral promoters	SF-1/Ph.D./2015/1057	2015-10-29	2021-10-28	DST
20	Kanwaljeet Kaur	Girdhar K. Pandey	Interplay between kinases and phosphatases	SF-1/Ph.D./2015/1039	2015-06-15	2020-06-14	DBT

Ph.D. Scholars

Sl. No.	Scholar	Supervisor	Research Topic	Regn #	Date of Registration	Tentative Date of completion	Funding Agency of Fellowship
21	Komal	Sanjay Kapoor	Functional characterization of regulatory components involved in reproductive development in rice	SF-1/Ph.D./2017/1157	2018-03-15	2023-03-14	CSIR-UGC-NET
22	Lalit Dev Tiwari	Anil Grover	Functional relevance of heat shock genes in Arabidopsis and rice	SF-1/Ph.D./2013/927	2013-04-16	2018-04-15	UGC
23	Lisha Khungar	Anil Grover	Analysis of the Protein Quality Control Mechanisms Underlying Adaptations of Plants to Heat Stress	SF-1/Ph.D./2017/1183	2017-09-06	2022-09-05	DST Inspire
24	Madhvi Naresh	Indranil Dasgupta	Plant gene silencing induced by virus injection	SF-1/Ph.D./2014/987	2014-04-15	2019-04-14	UGC
25	N. Pavithran	Girdhar K. Pandey	Functional analysis of calcium and potassium nutrient signaling in plants	SF-1/Ph.D./2018/1236	2018-03-15	2023-03-14	UGC Non-Net
26	Neelima Boora	Sanjay Kapoor	Identification and nutrient functional characterization of components involved in reproductive development in rice.	SF-1/Ph.D./2015/1060	2015-10-29	2020-10-28	CSIR-JRF
27	Nikita Sharma	Paramjit Khurana	Molecular regulation of plant somatic embryogenesis	SF-1/Ph.D./2017/1158	2017-01-19	2021-01-18	UGC
28	Nisha Negi	Paramjit Khurana	Genetic manipulation of M. indica variety V.	SF-1/Ph.D./2013/966	2013-10-23	2018-10-22	DST
29	Pratibha Gour	Saurabh Raghuvanshi	Somatic digitization and characterization of molecular networks in rice	SF-1/Ph.D./2015/1016	2015-10-29	2020-10-28	UGC
30	Priya Gambhir	Arun Sharma	Characterization of roles of ethylene response factor during tomato fruit ripening	SF-1/Ph.D./2015/1062	2015-10-29	2020-10-28	DBT

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Ph.D. Scholars

Sl. No.	Scholar	Supervisor	Research Topic	Regn #	Date of Registration	Tentative Date of completion	Funding Agency of Fellowship
31	Richa Babbar	Anil Grover	Analysis of heat stress response in rice and Arabidopsis	SF-1/Ph.D./2013/933	2013-07-22	2018-07-21	DST
32	Ridhi Khurana	Sanjay Kapoor	Functional characterization of regulators of seed development in rice	SF-1/Ph.D./2017/1157	2017-01-19	2022-01-18	DBT Project Fellow
33	Rinchuila Shimpurai	Anil Grover	Heat stress biology in plants	SF-1/Ph.D./2016/1117	2016-09-14	2021-09-13	UGC
34	Ringyao Jajo	Saurabh Raghuvanshi	Analysis of Stress Responsive Transcription Factors in Rice	SF-1/Ph.D./2017/1185	2017-08-25	2022-08-24	CSIR
35	Ritesh Kumar	Anil Grover	Studies on the gene expression under stress condition in rice	SF-1/Ph.D./2013/941	2013-07-22	2018-07-21	UGC
36	Sanchi Bhimrakja	Sanjay Kapoor	Understanding and Optimization of Gene Regulatory Networks Involved in Reproductive Development in Cereals	SF-1/Ph.D./2017/1186	2017-08-25	2022-08-24	UGC Non-Net
37	Sanskriti Ravi	Arun Sharma	Study on effect of alteration of genomic DNA methylation on ripening of tomato	SF-1/Ph.D./2018/	2018-03-15	2023-03-14	CSIR
38	Santosh Kumar	Saurabh Raghuvanshi	Study of epigenetic regulatory mechanisms in rice	SF-1/Ph.D./2012/897	2012-07-12	2017-07-11	DBT
39	Saroj Kumar Jha	Girdhar K. Pandey	Functions of Ca ²⁺ transporters	SF-1/Ph.D./2014/975	2014-01-06	2019-01-05	DST
40	Satyam Vergish	J.P. Khurana	Role of F-box proteins in light signalling and biological clock in rice.	SF-1/Ph.D./2013/940	2013-07-22	2018-07-21	ICMR

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Ph.D. Scholars

Sl. No.	Scholar	Supervisor	Research Topic	Regn #	Date of Registration	Tentative Date of completion	Funding Agency of Fellowship
41	Shaloo Meena	Paramjit Khurana	Comparative and functional genomics of the thermal stress response in wheat	SF-1/Ph.D./2015/1040	2015-05-22	2020-05-21	DBT
42	Shipra Singh	J.P. Khurana	Functional analysis of genes involved in light and hormone signalling in rice and <i>Arabidopsis</i>	SF-1/Ph.D./2016/1116	2016-08-16	2021-08-15	CSIR
43	Shivam Sharma	Akhilesh K. Tyagi	Functional characterization of selected differentially expressed genes (OsCDPK29 and OsTFII13) in rice development	SF-1/Ph.D./2018/1240	2018-03-15	2023-03-14	CSIR
44	Sibaji K. Sanyal	Girdhar K. Pandey	Plant Ca ²⁺ signaling	SF-1/Ph.D./2014/1024	2014-12-17	2019-12-16	DBT
45	Utkarsh Raghuvanshi	Arun Sharma	Transcriptome analysis and genetic manipulation for improving tomato fruit quality	SF-1/Ph.D./2014/999	2014-08-12	2019-08-11	DBT
46	Vaishali	Saurabh Raghuvanshi	To study miRNA expression and regulation in rice	SF-1/Ph.D./2016/1118	2016-08-26	2021-08-25	UGC Non-Net
47	Vibha Verma	Sanjay Kapoor	Functional delineation of regulatory components involved in the process of starch biosynthesis	SF-1/Ph.D./2013/929	2013-04-16	2018-04-15	CSIR-JRF Project Fellow
48	Vijendra Singh	Arun Sharma	Characterization of the role of proteins interacting with <i>Arabidopsis</i> DNA binding domain proteins	SF-1/Ph.D./2015/1065	2015-10-29	2020-10-28	UGC
49	Vishal	Akhilesh K. Tyagi	Investigations on the mechanism of action of stress-associated protein (SAP) genes of rice	SF-1/Ph.D./2018/1241	2018-03-15	2023-03-14	CSIR



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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 contents were proofread by Dr. Surekha Katiyar-Agarwal. The royalty free images, which were subsequently modified, used to develop the cover were obtained from <https://pngtree.com>.

Notes



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