

DR. SHIKHA MITTAL

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Educational Qualification (Qualified ICAR-NET)

Degree	Institute	Year	Subject
Ph.D	Sam Higginbottom University of Agriculture, Technology and sciences, Allahabad (Workplace: IARI, New Delhi)	2019	Bioinformatics
M.Sc	Banasthali Vidyapith University, Jaipur	2012	Bioinformatics
B.Sc	SBSPGI, Dehradun (HNB Garhwal University)	2010	Biotechnology

Work experience (9 years)

Position	Brief description	Institute	Year
Project Scientist-I	NGS data analysis, Genome-wide association studies, genomic selection, SNP/SSR identification, Primer designing, genome annotation, comparative genomics	ICAR-National Bureau of Plant Genetic Resources	2020-2022
Post-doctoral Fellow	Role of TLRs in Nucleic acid recognition, microarray data analysis, NGS data analysis	Jawaharlal Nehru University	2019-2020
Research Associate	Whole genome and transcriptomic data analysis, GBS data analysis, Statistical data analysis using SAS, SNP/SSR identification, Genome annotation, Primer designing, R language	ICAR-Indian Agricultural Statistics Research Institute	2017-2019
Senior Research Fellow	GWAS, Genomic Selection, RNA-Seq data analysis, microarray data analysis using R, KEGG pathway analysis, genomics, SNP and SSR identification	ICAR-Indian Agricultural Research Institute	2014-2017
Lecturer	Teaching undergraduate students, practical	DAV(PG) college, Muzaffarnagar	2012-2014

Technical Knowledge

- **Working Expertise:** NGS data analysis (Whole genome and transcriptome), Microarray Data Analysis, Genomics, transcriptomics and Proteomics, gene annotation, gene networking, genomic selection, genome-wide association mapping and mirna-mra identification.
- **NGS analysis tools:** BWA, Bowtie, SAMtools, GATK pipeline, freebayes, Trinity, SOAP-denovo, SPAdes, Velvet, AbySS, MIRA, BED tools, FASTQC, TopHat, cufflinks, CLC Genomics workbench, STAR, Velvet, MAKER pipeline.

- **Software Packages:** CLC-Bio, Discovery studio, BLAST2Go, Cytoscape, Circos, IGB, IGV, MISA, SnpEff, STRING, MEME suite, Transfac, DAVID, AgriGO, WEGO, iTOL, DnaSP, PlantCARE, PLACE, MEGA, iTOL, FigTree, MUSCLE, CLUSTALW, BLAST, FASTA, AUGUSTUS, PrimerQuest, TSSP softberry, STRUCTURE and TASSEL.
- **Databases:** NCBI, Ensemble, Phytozome, MaizeGDB, Gramene, TAIR, miRBase, PlantGDB.
- **Scripting languages:** R, Perl.
- **Operating systems:** Unix, Linux and Windows.
- **Important Courses Studied:** Molecular Computational biology, Functional and Comparative genomics, Biodiversity and bioinformatics, Disease related Computational biology, Database management system, Evolutionary computing, Pharmacogenomics and Computer aided drug designing, Proteomics, Structural biology, statistical techniques.

Research Highlights

- Worked on SNP chip array development of wheat using 50 accessions including different varieties and landraces of approximately 20 countries.
- Done comparative transcriptome analysis of Ricebean contrasting accessions.
- Performed reference based assembly of wheat genotype i.e., KRL3-4 under sodicity stress.
- Performed Whole genome assembly and metassembly of *Brassica fruticulosa*, a wild species of Brassicaceae family.
- Compared mitochondrial genomes of different species of Apis.
- Done assembly of chloroplast genomes of *Brassica juncea*, *Brassica nigra*, and *Brassica rapa*.
- Performed Genomic selection and GWAS in maize.
- Compared accuracies of seven genomic selection models (Parametric, non-parametric and semi parametric) for drought tolerance in maize.
- Comprehensively identified and characterized 15 drought responsive transcription factors and studied how these transcription factors interact with each other under drought stress in maize.
- Characterized CDPK gene family under drought stress in different species including, Arabidopsis, Maize, rice and Sorghum and also predicted 3D structure of CDPK proteins.
- Identified drought responsive candidate miRNAs and their targets in two contrasting genotypes of maize.
- Conducted transcriptomic analysis in maize under water-logging stress to identify, SSRs, SNPs.
- Studied genome-wide expression and function interaction of genes under drought stress in maize.
- In maize hybrids, identified candidate genes controlling drought related traits.
- Identified co-regulated genes under abiotic stress in *Cicer arietinum*.
- Did nucleotide diversity analysis and synonymous and non-synonymous substitution analysis in *Francisellatularensis*.
- Characterized and compared different transporters including YSL, OPT, ZIP and NRAMP in *Zea mays*, *Brachypodium distachyon*, *Oryza sativa*, *Arabidopsis thaliana* and *Setaria italica*.
- Transcriptomic data analysis and identification of SSR markers in Clusterbean.
- Transcriptomic analysis of different species of Brassica.

Published Papers (Total IF: 67.2)

1. **Shikha Mittal**, Geeta Prasad, Arvind Kumar, Divya Chauhan, Tanmaya Kumar Sahu, Sundeep Kumar, Rakesh Singh, Mahesh C. Yadav, Amit Kumar Singh (2021). Transcriptome analysis of bread wheat genotype KRL3-4 provides a new insight into regulatory mechanisms associated with sodicity (high pH) tolerance. *Frontiers in genetics* (IF: 4.599).
2. **Shikha Mittal**, Sachin Kumar Verma, Gayacharan C., Dhammaprakash Wankhede, Swarup Kumar Parida, Debasis Chattopadhyay, Geeta Prasad, Dwijesh Chandra Mishra, Dinesh Chandra Joshi, Mohar Singh and Kuldeep Singh, Amit Kumar Singh (2021). Transcriptome analysis reveals key pathways and candidate genes controlling seed development and size in ricebean (*Vigna umbellata*). *Frontiers in genetics* (IF: 4.599).
3. **Shikha, M.**, Kanika, A., Rao, A. R., Mallikarjuna, M. G., Gupta, H. S., & Nepolean, T. (2017). Genomic selection for drought tolerance using genome-wide SNPs in maize. *Frontiers in plant science*, 8, 550 (IF: 5.753).
4. **Mittal, S.**, Banduni, P., Mallikarjuna, M. G., Rao, A. R., Jain, P. A., Dash, P. K., & Thirunavukkarasu, N. (2018). Structural, Functional, and Evolutionary Characterization of Major Drought Transcription Factors Families in Maize. *Frontiers in chemistry*, 6 (IF: 5.221).
5. **Mittal, S.**, Mallikarjuna, M. G., Rao, A. R., Jain, P. A., Dash, P. K., & Thirunavukkarasu, N. (2017). Comparative Analysis of CDPK Family in Maize, Arabidopsis, Rice, and Sorghum Revealed Potential Targets for Drought Tolerance Improvement. *Frontiers in chemistry*, 5, 115 (IF: 5.221).
6. Pradhan AK, Kumar S, Singh AK, Budhlakoti N, Mishra DC, Chauhan D, **Mittal S**, Grover M, Kumar S, Gangwar OP, Kumar S, Gupta A, Bhardwaj SC, Rai A and Singh K (2020) Identification of QTLs/Defense Genes Effective at Seedling Stage Against Prevailing Races of Wheat Stripe Rust in India. *Front. Genet.* 11:572975. doi: 10.3389/fgene.2020.572975 (IF: 4.599).
7. Nepolean, T., Kaul, J., Mukri, G., & **Mittal, S.** (2018). Genomics-enabled next-generation breeding approaches for developing system-specific drought tolerant hybrids in maize. *Frontiers in plant science*, 9, 361 (IF: 5.753).
8. Arora, K., Panda, K. K., **Mittal, S.**, Mallikarjuna, M. G., Rao, A. R., Dash, P. K., & Thirunavukkarasu, N. (2017). RNAseq revealed the important gene pathways controlling adaptive mechanisms under waterlogged stress in maize. *Scientific reports*, 7(1), 10950 (IF: 5.133).
9. Aravind, J., Rinku, S., Pooja, B., **Shikha, M.**, Kaliyugam, S., Mallikarjuna, M. G., ...& Nepolean, T. (2017). Identification, characterization, and functional validation of drought responsive microRNAs in subtropical maize inbreds. *Frontiers in plant science*, 8, 941 (IF: 5.753).
10. Van Gioi, H., Mallikarjuna, M. G., **Shikha, M.**, Pooja, B., Jha, S. K., Dash, P. K., ...& Nepolean, T. (2017). Variable level of dominance of candidate genes controlling drought functional traits in maize hybrids. *Frontiers in plant science*, 8, 940 (IF: 5.753).
11. Arora, K., Panda, K. K., **Mittal, S.**, Mallikarjuna, M. G., & Thirunavukkarasu, N. (2017). In Silico Characterization and Functional Validation of Cell Wall Modification Genes Imparting Waterlogging Tolerance in Maize. *Bioinformatics and biology insights*, 11, 1177932217747277 (IF: 2.063).
12. Upadhyay, U., Thirunavukkarasu, N., **Mittal, S.**, & Singh, P. In silico analysis of drought tolerant Micro-RNAs in Maize.
13. Thirunavukkarasu, N., Sharma, R., Singh, N., Shiriga, K., Mohan, S., **Mittal, S.**, ...& Hossain, F. (2017). Genomewide expression and functional interactions of genes under drought stress in maize. *International journal of genomics*, 2017 (IF: 2.326).

14. Mallikarjuna, M. G., Nepolean, T., **Mittal, S.**, Hossain, F., Bhat, J. S., Manjaiah, K. M., & Gupta, H. S. (2016). In-silico characterisation and comparative mapping of yellow stripe like transporters in five grass species. *Indian J. Agric. Sci*, 86, 621-7 (**IF: 0.28**).
15. Mishra, D. C., **Mittal, S.**, Singh, I., Kumar, S., & Rai, A. (2016, March). Identification of coregulated genes of chick pea under abiotic stress. In 2016 International Conference on Bioinformatics and Systems Biology (BSB) (pp. 1-4). IEEE.
16. S.S. Chauhan, **Shikha Mittal**, PragatiMisra (2016). Comparative analysis of Heat shock transcription factor in *Solanum tuberosum* and *Solanum lycopersicum*. *International Journal of Scientific Research*.
17. S.S. Chauhan, **Shikha Mittal**, PragatiMisra (2018). Genome-wide identification and comparative analysis of HSF genes among Solanaceae members. *Journal of Pharmacognosy and Phytochemistry*

Published Book chapters

1. Singh N., **Mittal S.**, Thirunavukkarasu N. (2019) Effect of Drought Stress and Utility of Transcriptomics in Identification of Drought Tolerance Mechanisms in Maize. In: Rajpal V., Sehgal D., Kumar A., Raina S. (eds) *Genetic Enhancement of Crops for Tolerance to Abiotic Stress: Mechanisms and Approaches*, Vol. I. Sustainable Development and Biodiversity, vol 20. Springer, Cham. https://doi.org/10.1007/978-3-319-91956-0_4.
2. Mishra P., Maurya R., Avashthi H., **Mittal S.**, Chandra m., Ramteke WR (2021). Genome assembly and annotation. In: *Bioinformatics: Methods and applications*, Elsevier (<https://doi.org/10.1016/B978-0-323-89775-4.00013-4>).

Awards and Honours:

- **Qualified ICAR-NET** examination in biotechnology subject in December 2015.
- **Best poster award** in “Interdrought-V” conference organized by ICRISAT, Hyderabad.
- **GYAN scholarship award** in the NGBT 2018 conference organized by SGRF.

Research Experience

- **Bachelor’s thesis** - Micropropagation in *Bacopamonneri* (August 2009-May 2010).
- **Master’s thesis**
 - ❖ Nucleotide diversity analysis in *Francisellatularensis* (July-Dec, 2011)
 - ❖ Study of co-regulated genes during abiotic stress in *Cicer arietinum* (Jan-June, 2012).
- **Ph.D thesis** – Identification and networking of stress responsive genes in maize (Jan 2015-2019).

Published Abstracts in Conferences

- **Shikha Mittal**, A.R. Rao, S.S. Banga (2018). “Identification of functional elements on de novo assembled genome of *Brassica fruticulosa*, a wild crucifer resistant to *Lipaphiserysimi*”, in **NGBT 2018**, Jaipur.
- **Shikha Mittal**, M.G. Mallikarjuna, Nepolean T (2017). “Genome-wide identification, characterization and validation of drought-responsive CDPK gene family in *Arabidopsis*, maize, rice and sorghum” in **IIT, Delhi**.

- Nepolean T, **Shikha Mittal**, T. Mohapatra et al. (2016). “Genomic Selection for drought tolerance in maize” in BSC-2016 organized by KrishiSanskriti, **JNU, New Delhi**.
- M.G. Mallikarjuna, Nepolean T, **Shikha Mittal**, Firoz Hossain, et al. (2015). “Genome – wide expression of transcriptomes under iron and zinc stresses revealed candidate genes for kernel iron and zinc accumulation in maize” in 3rd IPPC, **JNU, New Delhi**.
- Nepolean T, Rinku Sharma, **Shikha Mittal**, et al (2016). “Co-expression Pattern and Functional Interaction of Drought – responsive Transcription Factors and Genes in Wheat, Rice and Maize” in BSC-2016 organized by KrishiSanskriti, **JNU, New Delhi**.
- **Shikha Mittal**, Prashant Ankur Jain (2015). “Revealing importance of differentially expressed genes towards biotic and abiotic stresses” in NCBPAH, **SHIATS, Allahabad**.

Training, Seminars and Conferences

- Presented poster in “**XIV Agricultural Science Congress on Innovations for Agricultural Transformation**” held at National agricultural Science Complex, New Delhi during 20-23 February, 2019.
- Presented poster on Identification of functional elements on de novo assembled genome of Brassica fruticulosa, a wild crucifer resistant to Lipaphiserysimi”, in **NGBT 2018**, Jaipur.
- Participated Workshop-cum-Training on “**Statistical and Computational analysis of phenotypic and genomic data of mustard germplasm**” organized by IASRI, New Delhi.
- Presented poster on the topic Genome-wide identification, characterization and validation of drought-responsive CDPK gene family in Arabidopsis, maize, rice and sorghum in “**Supercomputing facility for Bioinformatics & Computational biology**” organized by IIT, Delhi.
- Received Best poster presentation award on “**Comparison of genomic selection models under drought stress in subtropical maize**” in Interdrought-V conference organized by ICRISAT, Hyderabad.
- Short term course on “**Genomics for crop improvement**” (SFC-GCI) organized by Department of Biotechnology, MNNIT, Allahabad.
- Participated in DBT sponsored National workshop on “**Biological Databases and Data mining**” organized by Centre for Bioinformatics, Department of Bioscience and Biotechnology, Banasthali University, Rajasthan.
- Participated in national seminar organized by “**Commemorating 150 years of Mendel’s laws of inheritance**” organized by ICAR-Indian Agricultural research Institute, New Delhi.
- Presented paper in seminar on “**Modern Approaches in Biosciences**” organized by Department of Biosciences, DAV college, Muzaffarnagar.
- Attended workshop on “**Intellectual Property Rights**” organized by Directorate of Innovation, Projects and consultancy.
- Participated in Awareness Program on “**Take it to the Breeders & Researchers – The Plant breeders & Researchers Right through awareness**” organized by SHIATS university.