

## ACADEMIC CREDENTIALS:

- DST National Post-Doctoral Fellow, Institute of TransDisciplinary Health Science and Technology, Bangalore, India
- Ph.D, Department of Genetics & Plant Breeding, University of Agriculture Sciences, Bangalore, India
- M.Sc, Department of Genetics & Plant Breeding, University of Agriculture Sciences, Bangalore, India
- B. Sc, (Agriculture), University of Agriculture Sciences, Bangalore, India

## RESEARCH AREA:

My research focuses on integrating genomics, transcriptomics, proteomics, gene editing, speed-breeding and bioinformatics in understanding agronomically important traits in rice and finger millet to develop high yielding and consumer demand-driven trait-specific varieties. We generated huge amount of sequence data and made available to the public in NCBI database. We sequenced and annotated first *indica* rice cultivar (HR-12) from India. Complete genomes of Fingermillet, Indian Sandalwood, Horsegram and *Sarocladium oryzae* (rice sheath rot causing pathogen) were sequenced, assembled, annotated first time in the world and published in highly reputed scientific journals (Refer to Publication list).

**Key words:** genome sequencing, rice neck blast, glycemic index, phytic acid, nutrigenomics, gene editing, marker assisted selection

## PROFESSIONAL EXPERIENCE:

1. **Harvard University-** Completed a short course on “**CRISPR: Gene-editing Applications**” from Harvard’s Office of the Vice Provost for Advances in Learning (VPAL), in association with HarvardX, USA.
2. **Centre for Cellular and Molecular Platforms (C-CAMP), NCBS, Bangalore -** Took lead in genome sequencing, functional annotation and other NGS analyses of rice, neem, Sandalwood, *Magnaporthe* and *Sarocladium oryzae* from 2011 to 2015.
3. **The Ohio State University, Columbus, USA -** Took lead in sequencing of rice landraces and NGS data analyses at Plant Disease Resistance and Functional Genomics Lab, Department of Plant Pathology, College of Food, Agricultural, and Environmental Sciences, Ohio State University, Ohio, USA.
4. **Beachell-Borlaug Scholars Leadership Development Training, USA-** Got training on presentation skills, time management through goal setting, global proficiency and

professional image, team building, business etiquette, dining tutorial, self-awareness, intercultural competence, held at Tero Learning Centre, Des Moines, Iowa state, USA.

5. **Monsanto Research Centre, Bangalore-** Involved in Marker Assisted Breeding, Pre-selection and haplotype estimation in Corn Breeding. I was part of Corn SNP genotyping team from Monsanto, India with Monsanto, St. Louis and Ankeny (Headquarters, USA).
6. **Monsanto Inc., Philippines-** Ten days training on Marker Assisted Backcross Breeding in Corn and Barcoding of corn breeding nurseries at Monsanto Inc., General Santos City, Philippines.

### AWARDS AND RECOGNITION:

- Jawaharlal Nehru Award for Outstanding Doctoral Thesis Research under Crop Science, ICAR, New Delhi
- Monsanto's Beachell-Borlaug International Fellowship Award (Received a grant of \$1,44,239), Texas A&M, USA.
- Biotechnology Ignition Grant Award, BIRAC, DBT, Government of India.
- Rapid Recognition Award, Monsanto, Bangalore.
- Monsanto Emerging Star Award, Monsanto, Bangalore.

### RESEARCH PAPERS

1. Banakar, S.N., PrasannaKumar, M., **Mahesh, H B.**, Parivallal, P.B., Puneeth, M., Gautam, C., et al. (2022). Red-seaweed biostimulants differentially alleviate the impact of fungicidal stress in rice (*Oryza sativa* L.). *Scientific reports* 12(1), 1-12.
2. Chandrashekar, B., PrasannaKumar, M., Parivallal, P.B., Pramesh, D., Banakar, S.N., Patil, S.S., et al. (2022). Host range and virulence diversity of *Pectobacterium carotovorum* subsp. *brasiliense* strain RDKLR infecting radish in India, and development of a LAMP-based diagnostics. *Journal of Applied Microbiology*.
3. Sahana, B.N., PrasannaKumar, M., **Mahesh, H B.**, Buella Parivallal, P., Puneeth, M., Gautam, C., et al. (2022). Biostimulants derived from red seaweed stimulate the plant defence mechanism in rice against *Magnaporthe oryzae*. *Journal of Applied Phycology* 34(1), 659-665.
4. **Mahesh, H B.**, Prasannakumar, M., Manasa, K., Perumal, S., Khedikar, Y., Kagale, S., et al. (2021). Genome, Transcriptome, and Germplasm Sequencing Uncovers Functional Variation in the Warm-Season Grain Legume Horsegram *Macrotyloma uniflorum* (Lam.) Verdc. *Frontiers in plant science* 12.
5. **Mahesh, H B.**, Shirke, M.D., Wang, G.-L., and Gowda, M. (2021). In planta transcriptome analysis reveals tissue-specific expression of pathogenicity genes and microRNAs during rice-*Magnaporthe* interactions. *Genomics* 113(1), 265-275.

6. Prasanna, S., Prasannakumar, M., **Mahesh, H B.**, Babu, G.V., Kirnaymayee, P., Puneeth, M., et al. (2021). Diversity and biopotential of *Bacillus velezensis* strains A6 and P42 against rice blast and bacterial blight of pomegranate. *Archives of Microbiology* 203(7), 4189-4199.
7. Prasannakumar, M., Netravathi, L., **Mahesh, H B.**, Parivallal, P.B., Puneeth, M., Sathish, A., et al. (2021). Comparative metagenomic analysis of rice soil samples revealed the diverse microbial population and biocontrol organisms against plant pathogenic fungus *Magnaporthe oryzae*. *3 Biotech* 11(5), 1-11.
8. Prasannakumar, M., Parivallal, B.P., Manjunatha, C., Pramesh, D., Narayan, K.S., Venkatesh, G., et al. (2021). Rapid genotyping of bacterial leaf blight resistant genes of rice using loop-mediated isothermal amplification assay. *Molecular Biology Reports* 48(1), 467-474.
9. Prasannakumar, M., Parivallal, P.B., Pramesh, D., **Mahesh, H B.**, and Raj, E. (2021). LAMP-based foldable microdevice platform for the rapid detection of *Magnaporthe oryzae* and *Sarocladium oryzae* in rice seed. *Scientific reports* 11(1), 1-10.
10. Saha, P., Sarker, A., Sabnam, N., Shirke, M.D., **Mahesh, H B.**, Nikhil, A., et al. (2021). Comparative analysis of secondary metabolite gene clusters in different strains of *Magnaporthe oryzae*. *FEMS Microbiology Letters* 368(1), fnaa216.
11. Prasannakumar, M., Buella Parivallal, P., Manjunatha, C., **Mahesh, H B.**, Pramesh, D., Narayan, K.S., et al. (2020). Loop-mediated isothermal amplification assay for pre-symptomatic stage detection of *Xanthomonas axonopodis* pv. *punicae* infection in pomegranate. *Australasian Plant Pathology* 49(4), 467-473.
12. Prasannakumar, M., **Mahesh, H B.**, Desai, R.U., Kunduru, B., Narayan, K.S., Teli, K., et al. (2020). Metagenome sequencing of finger millet-associated microbial consortia provides insights into structural and functional diversity of endophytes. *3 Biotech* 10(1), 1-17.
13. Krishna, P., Prasanna Kumar, M., Channappa, M., Devanna, P., Singh, K., Eeregowda, P.M., et al. (2020). Antibiotic resilience in *Xanthomonas axonopodis* pv. *punicae* causing bacterial blight of pomegranate. *Current Science (00113891)* 119(9).
14. Pramesh, D., Prasannakumar, M.K., Muniraju, K.M., **Mahesh, H B.**, Pushpa, H., Manjunatha, C., et al. (2020). Comparative genomics of rice false smut fungi *Ustilaginoidea virens* Uv-Gvt strain from India reveals genetic diversity and phylogenetic divergence. *3 Biotech* 10(8), 1-14.
15. Amruta, N., Prasanna Kumar, M., Kandikattu, H.K., Sarika, G., Puneeth, M., Ranjitha, H., et al. (2019). Bio-priming of rice seeds with novel bacterial strains, for management of seedborne *Magnaporthe oryzae* L. *Plant Physiology Reports* 24(4), 507-520.
16. Chandrashekar, B., Prasannakumar, M., Puneeth, M., Teli, K., Priyanka, K., **Mahesh, H B.**, et al. (2018). First report of bacterial soft rot of carrot caused by *Klebsiella variicola* in India. *New Disease Reports* 37(1), 21.

17. **Mahesh, H B.**, Subba, P., Advani, J., Shirke, M.D., Loganathan, R.M., Chandana, S., et al. (2018). Multi-omics driven assembly and annotation of the sandalwood (*Santalum album*) genome. *Plant Physiology*, pp. 01764.02017.
18. Hittalmani, S., **Mahesh, H B.**, Shirke, M.D., Biradar, H., Uday, G., Aruna, Y., et al. (2017). Genome and transcriptome sequence of finger millet (*Eleusine coracana* (L.) Gaertn.) provides insights into drought tolerance and nutraceutical properties. *BMC genomics* 18(1), 1-16.
19. **Mahesh, H B.**, Meghana, S., Shailaja, H., Prasannakumar, M., Mahadevu, P., Channabyregowda, M., et al. (2016). Acquisition of the grasshopper retro transposon by rice Magnaporthe isolates indicates a dynamic gene flow between rice and non-rice Magnaporthe population. *J Pathol Microbiol* 1(2), 1011.
20. **Mahesh, H B.**, Shirke, M.D., Singh, S., Rajamani, A., Hittalmani, S., Wang, G.-L., et al. (2016). Indica rice genome assembly, annotation and mining of blast disease resistance genes. *BMC genomics* 17(1), 1-12.
21. Shirke, M.D., **Mahesh, H B.**, and Gowda, M. (2016). Genome-wide comparison of Magnaporthe species reveals a host-specific pattern of secretory proteins and transposable elements. *PloS one* 11(9), e0162458.
22. Hittalmani, S., **Mahesh, H B.**, Mahadevaiah, C., and Prasannakumar, M.K. (2016). De novo genome assembly and annotation of rice sheath rot fungus *Sarocladium oryzae* reveals genes involved in Helvolic acid and Cerulenin biosynthesis pathways. *BMC genomics* 17(1), 1-13.
23. Gowda, M., Shirke, M.D., **Mahesh, H B.**, Chandarana, P., Rajamani, A., and Chattoo, B.B. (2015). Genome analysis of rice-blast fungus *Magnaporthe oryzae* field isolates from southern India. *Genomics data* 5, 284-291.
24. Kuravadi, N.A., Yenagi, V., Rangiah, K., **Mahesh, H B.**, Rajamani, A., Shirke, M.D., et al. (2015). Comprehensive analyses of genomes, transcriptomes and metabolites of neem tree. *PeerJ* 3, e1066.

## BOOK CHAPTERS:

1. **Mahesh, H B.**, and Gowda, M. (2022). "Sandalwood: The King of Aroma in Plant Kingdom," in *The Sandalwood Genome*. Springer, 1-5.
2. **Mahesh, H B.**, Shirke, M.D., Manasa, K., and Gowda, M. (2022e). "Whole Genome Sequence of Sandalwood and Its Comparative Study," in *The Sandalwood Genome*. Springer, 47-55.
3. **Mahesh, H B.**, Manasa, K., Shirke, M.D., and Raghavendra, N. (2022c). "Mining of SSRs and SNPs in Sandalwood Genome," in *The Sandalwood Genome*. Springer, 57-64.

4. **Mahesh, H B.**, Manasa, K., Prasannakumar, M., Shirke, M.D., Kole, C., and Gowda, M. (2022a). "Future Prospects of Sandalwood Research," in *The Sandalwood Genome*. Springer, 99-103.
5. **Raghavendra, N.**, and **Mahesh, H.** (2022). "Sandalwood Essential Oil and Its Phyto-Chemistry," in *The Sandalwood Genome*. Springer, 83-88.
6. **Mahesh, H B.**, Manasa, K., Raghavendra, N., Shirke, M.D., and Hittalmani, S. (2022b). "The Complete Genome Sequence of Finger Millet," in *The Finger Millet Genome*. Springer, 101-111.
7. **Mahesh, H B.**, Shirke, M.D., Ghodke, I., and Raghavendra, N. (2022d). "Role of Inducible Promoters and Transcription Factors in Conferring Abiotic Stress-Tolerance in Small Millets," in *Omics of Climate Resilient Small Millets*. Springer, 69-86.
8. Annegowda, D.C., Prasannakumar, M.K., **Mahesh, H.B.**, Siddabasappa, C.B., Devanna, P., Banakar, S.N., et al. (2021). "Rice Blast Disease in India: Present Status and Future Challenges," in *Rice*. IntechOpen).