Sumeet Mankar, Ph.D.

Plant Breeding and Genetics | Genomics | Bioinformatics | Computational Biology

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EDUCATION

Doctor of Philosophy (Ph.D.) | Plant Breeding **2021**
Texas A&M University, USA | Advisor: Dr. Endang Septiningsih

Master of Philosophy (M.Phil.) | Biological Science **2017**
University of Cambridge, UK | Advisor: Late Dr. Ian Mackay

Master of Science (M.Sc.) | Biotechnology **2011**
Tamil Nadu Agricultural University, India | Advisor: Dr. R. Chandra Babu

Bachelor of Science (B.Sc.) | Agricultural Biotechnology **2009**
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, India

PROFESSIONAL EXPERIENCE

Research Scientist & Postdoctoral Research Associate **July 2021 – Present**

Donald Danforth Plant Science Center, USA

- Genome-wide association mapping (MashR) of 80 3D root and panicle architecture traits in the Sorghum Association Panel.
- 4D root phenotyping, and GWAS of 150 weedy rice accessions using multi-trait, multi-locus (MSTEP) models to reveal structural variants underlying the evolution of weedy rice.
- Comparative genomics of root system architecture across 50 industrial hemp lines; identified 72 candidate genes conserved among maize, sorghum, and rice.

Graduate Research Assistant **Aug 2017 - May 2021**

Soil and Crop Science Department, Texas A&M University, USA

- GWAS of 300 rice accessions under dry direct-seeded (DDSR) conditions to identify loci for nutrient uptake, early vigor, and root traits; integrated RNA-seq analysis to uncover nutrient-related candidate genes.
- Designed a bioinformatics pipeline for functional analysis of seed shattering genes in ryegrass (*Lolium perenne*).
- Performed GWAS for 21 cold-stress traits, discovering 77 QTLs (31 novel) and three tolerant genotypes, providing new targets for breeding climate-resilient rice.
- Identified genetic loci associated with salinity tolerance in 278 rice accessions using GWAS and 7K SNP chip data, informing stress-resilient breeding programs.

Research Scholar **Jan 2018 - Dec 2018**

International Rice Research Institute, Philippines

- Evaluated rice diversity panel using association mapping under dry direct-seeded rice conditions.

Graduate Research Scholar **Oct 2015 - April 2017**

University of Cambridge, United Kingdom

- Conducted high-throughput phenotyping for trait dissection in the NIAB MAGIC wheat population using RGB *LemnaTec* Smart-House imaging.

Visiting Scholar **Jan 2015 - May 2015**

International Rice Research Institute, Philippines

- Evaluation of the rice MAGIC population for salinity stress tolerance

Research Scholar **Aug 2012 - Sept 2014**

Seoul National University, South Korea

- Abiotic stress breeding in rice and Arabidopsis, and phytohormone signaling and regulation.

Research Trainee - Assistant Wheat Breeder **Nov 2011 - July 2012**

Pragati Agro Ent. Pvt Ltd, India

- Genetic improvement of wheat for abiotic and biotic stress tolerance

Graduate Research Assistant **Aug 2009 - Oct 2011**

Tamil Nadu Agriculture University, India

- Association Mapping of Drought Resistance Traits in Rice (*Oryza sativa* L). Planned and evaluated four populations for drought resistance in rice and functionally analyzed the linkage disequilibrium and genetic diversity in rice.

PUBLICATIONS

Published

- Morales, EY., Griffiths, M., **Mankar, S.,** Bagnall, G., John McKay, J., and Topp, C.N. (2026). Diversity of root system architecture and root-to-shoot biomass distribution in industrial hemp (*Cannabis sativa* L.). *PloS one*
- Wagh, S.G., Patil, A.M., Patil, G.B., **Mankar, S.P.**, Rastogi, K., and Nishiguchi, M., 2025. Small RNA and Epigenetic Control of Plant Immunity. *DNA*, 5(4), P.47.
- Wagh, S., Patil, A., **Mankar, S.P.,** Patil, G. (2025). Current progress on CRISPR/Cas9 applications in plants. In (eds) Plant Genome Editing Series, Vol. 3. Interdisciplinary Biotechnological Advances. Springer, Singapore.
- Rastogi, K., **Mankar, S.P.,** *et al* Septiningsih, E.M. (2025). CRISPR/Cas9 multiplex genome editing to enhance grain lysine concentration in a US rice cultivar. *Current Plant Biology,* 42, 100490.
- Maity, A., **Mankar, S.P.,** Rastogi, K., *et al.,* and Bagavathiannan, M. (2025). GWAS for identifying the gene(s) controlling regrowth rate, seed shattering, and tiller production in Italian Ryegrass. *Weed Science* (Accepted - Oct 2025)
- Rastogi, K.*, **Mankar, S. P.*,** and Septiningsih, E. M. (2025). Genome-wide association study for traits related to cold tolerance and recovery during the seedling stage in rice. *Crop Science,* 65, e70003.
- Wagh, S., Shelake, R., Patil, A., Mankar, S., Cerveny, J. (2024). Microbes Enhance Climate-Ready Crops for Sustainable Agriculture. Rhizospheric Interactions for Abiotic Stress Mitigation. Cambridge Scholars Publishing: ISBN: 978-1-0364-1512-9, Pages: 100-122. (Book Chapter)
- Rastogi, K., **Mankar, S.,** and Septiningsih, E.M. (2024). Genome-wide association study for traits related to cold & recovery during the seedling stage in rice. *Genome, 23, 4 (Pre-print).*
- Deshmukh, V., **Mankar, S. P.,** *et al.,* & Babu, R. C. (2018). Genome-wide consistent molecular markers associated with phenology, plant production, and root traits in diverse rice (*Oryza sativa* L.) accessions under drought in rainfed environment. *Current Science*, *114*(2), 329.
- Wade, L. J., Bartolome, V., Mauleon, R., Vasant, V. D., **Prabhakar, S. M.,** Chelliah, M., *et al.,* & Patil, K. G. (2015). Environmental response and genomic regions correlated with rice root growth and yield under drought in the *OryzaSNP* panel across multiple study systems. *PloS one*, 10(4), e0124127.
- Suji, K. K., Prince, K. S. J., **Mankar, P. S.,** Kanagaraj, P., Poornima, R., Amutha, K., *et al.,* & Babu, R. C. (2012). Evaluation of rice (Oryza sativa L.) near-isogenic lines with root QTLs for plant production and root traits in rainfed target populations of the environment. *Field Crops Research*, 137, 89-96.
- Suji, K.K., *et al.,* **Mankar, S.,** and Babu, R. C. (2012). Mapping QTLs for plant phenology and production traits using indica rice (*Oryza sativa* L.) lines adapted to a rainfed environment. *Molecular Biotechnology*, 52(2), 151-160.
- Pradeepa, N., *et al.,* **Prabhakar, M. S.,** & Babu, R. C. (2012). *In silico* analysis of a consensus QTL for drought resistance in rice. *Online Journal of Bioinformatics*, 13, 1-13.

FELLOWSHIPS, RECOGNITIONS, and AWARDS (Selected)

- Travel Grant to attend AI Genomic Prediction | CSTM | 2024
- Travel Grant PAG30 | CSTM | 2023
- Encompass Scholar | Tri-society and Bayer Crop Sciences, USA | 2021 - 2022
- Bayer-Monsanto Beachell-Borlaug International Scholarship (Ph.D.) | Bayer Crop Sciences, USA | 2017 - 2021
- Graduate Research Assistantship | Texas A&M University, USA | 2017 - 2021

- Monsanto Beachell-Borlaug International Scholarship (M.Phil.) | Bayer Crop Sciences, USA | 2015 - 2017
- Brain Korea 21 Plus Research Fellowship | Seoul National University, South Korea | 2013 - 2014
- Graduate Scholarship for Excellent Foreign Students | Seoul National University, South Korea | 2012 - 2014

CONFERENCES PRESENTATION (Selected)

- A comprehensive phenomics study of above- and below-ground traits in a maize diversity panel under nitrogen limitation. *Oral presentation at the Maize Genetics Conference in Saint Louis, MO, USA, in May 2025.*
- Genome-wide association mapping of 3D panicle architecture traits using Sorghum. *Oral presentation at ASA, CSSA, SSSA International Annual Meeting in Saint Louis, MO, USA in November 2023.*
- Deciphering the genetic determinants of 3D panicle architecture traits using Sorghum. *Oral presentation at Plant and Animal Genome XXVII Conference (January 12-16, 2019) in January 2023, San Diego, USA.*
- Phenotypic Comparison of Root System Architecture in Weedy and Cultivated Rice. *Oral presentation at ASA, CSSA, SSSA International Annual Meeting in Baltimore, MD, USA in November 2022.*
- High-Resolution Genome-Wide Association Study of Yield-Related Traits for Direct-Seeded Rice. *Oral presentation at ASA, CSSA, and SSSA International Annual Meetings, San Antonio, TX, in November 2019.*
- Genome-Wide Association Mapping on Nutrient Uptake and Other Related Traits under Direct-Seeded Cultivation using a Subset of the 3K Rice Diversity Panel. *Plant and Animal Genome XXVII Conference (January 12-16, 2019).*
- Genome-wide Association Mapping for Nutrient Uptake under DDSR Rice Conditions. *Oral presentation at the 5th International Rice Congress, Singapore 2018.*
- Development, Evaluation, and Validation of Wild Rice MAGIC Populations for Improved Agronomic Traits and Multi-environment Stress Tolerance. *Oral presentation at the Monsanto Ankeny facility, IA, USA, in October 2016 - 2017.*

SERVICES

Leadership

Postdoc representative, Maize Genetics Membership Committee	2023 - 2025
Seminar Coordinator, Committee for Scientific Training and Mentoring	2021 - 2022
Departmental Mentor, Indian Graduate Student Organization	2017 - 2019
International Student Representative, University of Cambridge	2015 - 2017