Sumeet Mankar, Ph.D.

Plant Breeding and Genetics | Comparative Genomics | Bioinformatics | Computational Biology
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SUMMARY

Motivated and collaborative plant genomics researcher with 3+ years of experience in forward and reverse genetics, QTL mapping, and multi-location field trials using rice, sorghum, maize, soybean, and cover crops. Led multi-disciplinary, multi-institutional research projects. Skilled in integrating high-throughput genotypic and phenotypic data to uncover genetic determinants of complex traits to accelerate crop improvement pipelines. Proven ability to design and analyze large-scale experiments using advanced statistical genetics tools, delivering key insights into trait architecture for breeding decisions.

AREAS OF EXPERTISE

Bioinformatics: Pangenome Development, WGS analysis, Synteny analysis, RNA-seq, genome assembly/alignment, variant calling (GATK), transcriptomics, metagenomics.

Plant Breeding: Development of biparental, MAGIC, and diversity panels; breeding simulations (e.g., AlphaSimR), Heritability, GxE, BLUPs, population structure (PCA, LD), GWAS (TASSEL, Plink, GAPIT, mrMLM, MashR), QTL mapping (QTL Cartographer, R/qtl), Genomic prediction (G-BLUP, Bayesian models, ridge regression, cross-validation).

Field Experimentation: Multi-location trial design, field operations, phenotypic selection, and data collection.

Phenomics: X-ray computed tomography, UAV (FieldImageR), Image analysis (PlantCV), ImageJ.

Data Science & Visualization: Exploratory data analysis, machine learning, predictive modeling, FieldBook, BreedingView, Adobe Illustrator, ggplot2, Matplotlib, Seaborn, and Inkscape for data visualization and presentation.

Programming & Tools: R, Python, bash, Linux, AWS, high-performance computing.

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: 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 of 3D root and panicle architecture traits in SAP. Led GWAS genome-wide association mapping (**MashR**) using 80 3D root and panicle architecture traits. Identified 14 significant genomic regions and six genes contributing to root and panicle architecture traits. Characterized two significant root genes for rooting angle and nodal root in sorghum. <u>Leading Pan-genomics project in sorghum and collards to identify structural variation for root system architecture related genes.</u>
- Developed a genomics and data analysis pipeline for root and agronomic traits using the Buckler-Goodman maize diversity association panel. Led the development of a large-scale data analysis pipeline to understand plant root responses to nutrient and water limitations and identified beneficial haplotypes that enhance yield under stress. Analyzed 261 traits related to leaf and kernel ionomics, root, and agronomic traits from 272 inbred lines, approximately 4000 plants per two field seasons, yielding 1255 MTAs (BigsnpR).
- High-throughput phenotyping and genotyping for root system architecture traits in weedy rice. Evaluated a diversity panel of 180 rice accessions using a 4D root imaging system. Designed and executed - GWAS study using multi-trait,

multi-locus stepwise (**MSTEP**) model for root traits. Identifying the structural variation through pangenome analysis. Studying the evolution of weedy rice compared to wild and domesticated rice.

- Evaluated a GWAS panel for root system architecture and root: shoot biomass distribution in industrial hemp. Investigated the evolutionary dynamics of root system architecture genes across 150 hemp lines. Identified seven root architecture genes using a comparative genomics approach across maize, sorghum, and rice.
- Navigated project timelines, data confidentiality, and cross-functional communication in a fast-paced R&D environment, ensuring alignment with organizational and compliance standards.

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

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

- Genome-wide association study (GWAS) for dry direct-seeded rice (DDSR) traits. Designed and executed - GWAS for nutrient uptake, early vigour, root, and agronomic traits using 300 rice accessions in DDSR conditions. Performed *RNA-seq* analysis to identify differentially expressed genes for nutrient uptake in rice.
- Validated anthocyanin genes underlying purple leaf color in purple rice using CRISPR/Cas9 multiplex genome editing.
- Designed bioinformatics and data analysis pipeline for "Functional analysis and identification of genes controlling the seed shattering in ryegrass (*Lolium perenne*)".

Research Scholar **Jan 2018 - Dec 2018**

International Rice Research Institute, Philippines

- Evaluated rice diversity panel using association mapping under dry direct-seeded rice conditions. Designed and implemented genomic selection strategies for drought-resistant DDSR rice. Conducted phenotypic and genomic analyses for rice adaptation under abiotic stress conditions.
- Computed quantitative genetic parameters using R, SAS, and Python.

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

University of Cambridge, United Kingdom

- High-throughput phenotyping for trait dissection in the NIAB MAGIC wheat population. Conducted High-throughput phenotyping in wheat using RGB *LemnaTec* Smart-House imaging. Simulated population crossing for wild rice MAGIC population development.

Research Scholar **Aug 2012 - Sept 2014**

Seoul National University, South Korea

- Abiotic stress breeding in rice and Arabidopsis, and phytohormone signaling and regulation.
- Performed cloning, transformation, and functional studies in Rice, Arabidopsis, *Setaria viridis.*
- Characterized P450 genes for herbicide and pesticide resistance.

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. Functionally analyzed the linkage disequilibrium and genetic diversity in rice.
- Development and validation of molecular markers for marker-assisted selection.

PUBLICATIONS

Published

- **Rastogi, K**., Mankar, S.P., … 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., … and Bagavathiannan, M. (2025). GWAS for identifying the gene(s) controlling regrowth rate, seed shattering, and tiller production in Italian Ryegrass. *Weed Science* (Accepted - July 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.,** ... & 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 target populations of the environment. *Current Science*, *114*(2), 329.
- Wade, L. J., Bartolome, V., Mauleon, R., Vasant, V. D., **Prabhakar, S. M.,** Chelliah, M., ... & 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., ... & 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., ….., **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., …, **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.

In-Review, Submitted, and In Preparation

- **Mankar, S**., Shao, R., Cho, M., Li, M., Eveland, A., Kellogg, T., Topp, C.N. (2025). Genome-wide association mapping of 3D root and panicle architecture traits using Sorghum Association Panel. *The Plant Cell*
- Wagh, S., Patil, A., Pawar, B., **Mankar, S.,** Cerveny, J., Shelake, R. (2025). Current Progress on CRISPR/Cas9 Applications in Plants. Plant Genome Editing Development and Technologies Volume 1. *Springer Nature Book Series*.
- Morales, EY., Griffiths, M., **Mankar, S.,** Bagnall, G., John McKay, J., and Topp, C.N. (2025). Diversity of root system architecture and root-to-shoot biomass distribution in industrial hemp (*Cannabis sativa* L.) lines. Plant Phenomics.
- **Mankar, S**., Griffiths, M., Kosola, E., Wedger, M.J., Olsen, K., Topp, C.N. (2025). Deciphering the genetic determinants of root system architecture traits using the Weedy Rice Association Panel. *New Phytologists*.
- Wagh, S., Patil, A., Patil, G., Mankar, S., Rastogi, K., Nishiguchi, M. (2025). Epigenetic and Small RNA Control of Plant Immunity. *DNA MDPI*. (Submitted: June 2025)
- Luebbert, C., **Mankar, S**., Rajurkar, A., Topp, C., Baxter, I., Leakey, A. (2025). A comprehensive phenomics study of above and belowground traits in a maize diversity panel under nitrogen limitation. *Plant Cell.*
- **Mankar, S**., Kosola, E., .. Olsen, K., Topp, C.N. (2025). Dissecting the gene regulatory network of seed architecture and morphology traits using Weedy Rice Association Panel and Biparental mapping populations. *Plant Phenomics*.
- **Mankar, S**., Sandhu, N., Cruz, T., Kumar, A., Septiningsih, E.M. (2025). Dissecting the genetic determinants of ionomics traits improving nutrient uptake under DDSR cultivation. *Frontier in Genetics* (Submitted May 2025 - In Review).
- **Mankar, S**., Sandhu, N., … A., Septiningsih, E.M. (2025). *RNA-seq* analysis reveals differentially expressed genes in rice shoots promoting nutrient uptake under DDSR conditions. *Frontier in Plant Sciences* (In Review).
- **Mankar, S**., Sandhu, N., Cruz, T., Rastogi, K., Kumar, A., Septiningsih, E.M. (2025). Dissecting the genetic determinants of early seedling and root vigor under direct-seeded rice cultivation. *Nature Scientific Reports.*
- Rastogi, K.*, **Mankar, S.***, and Septiningsih, E.M. (2025). Dissecting salt tolerance mechanism at the seedling stage using an association mapping study in USDA mini-core rice germplasm. (In Preparation).
- **Rastogi, K.**, Lopez, M., Prior, M.J., **Mankar, S.,** ... and Septiningsih, E. M. Functional Analysis of *qSub8.1*: A Novel QTL for Submergence Tolerance in Rice (In Preparation).

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
- Geostadt Pvt. Ltd. Need-Based Scholarship | University of Cambridge, UK | 2018 - 2019
- 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 San Diego, USA in January 2023.*
- 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.*
- Genome-Wide Association Studies for Grain Yield Traits in DDSR Rice Conditions. *Oral presentation at the Plant Breeding Symposium, Texas A&M, USA, in 2020.*
- 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 in 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 and 2017.*

CERTIFICATION

- Multi-Omic Integration for AI Genomic Prediction Breeding | University of Florida | July 2024
- Next Generation Sequencing and Whole Genome Sequencing | Nyberman | Mar 2024
- Intermediate Python | DataCamp | June 2020
- Introduction to Data Science in Python | DataCamp | May 2020
- Introduction to Linux, HPRC | Texas A&M University | Jan 2019
- Introduction to RNA-seq and ChIP-seq data analysis | University of Cambridge | Nov 2016
- Data Analysis and Visualization in R | University of Cambridge | May 2016
- Statistical Analysis using R | University of Cambridge | Apr 2016
- An Introduction to Using Ensembl Genome Browser | University of Cambridge | Mar 2016
- Unix: Building, Installing and Running Software | University of Cambridge | Nov 2015

SERVICES

Leadership

Postdoc representative, Maize Genetics Membership Committee	2023 - Present
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
Indian Student Association, Seoul National University, South Korea	2012 - 2014
Batch Representative, Tamil Nadu Agricultural University	2010 - 2011

Mentoring

Mentoring 6 interns, and 4 lab technicians, Topp Root Genetics Lab, DDSPC	2021 – 2024
Mentoring Student Workers, Crop Genome Editing Lab, TAMU	2019 – 2021
Mentoring Graduate Students, Rice Genetics lab, TAMU	2017 – 2019
Mentored 2 undergraduate students for a six-month project, Rice Molecular Breeding Lab	2010 – 2011
Teaching Assistant, Plant Molecular Breeding, TNAU	2009 – 2010

PROFESSIONAL MEMBERSHIP

Maize Genetics Membership Committee	Mar 2023 – Present
American Society of Agronomy (ASA)	May 2017 – Present
Crop Science Society of America (CSSA)	May 2017 – Present
Soil Science Society of America (SSSA)	May 2017 – Present
Association of Agricultural Scientists of Indian Origin (AASIO)	May 2017 – Present
Soil and Crop Sciences Graduate Students Organization (SCGO), TAMU	Aug 2017 – May 2021
Indian Graduate Student Association (IGSA), TAMU	Aug 2017 – May 2021

REFERENCES

Principal Investigator
Dr Christopher Topp
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Donald Danforth Plant Science Center,
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Dissertation Advisor
Dr. Endang M. Septiningsih
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Department of Soil and Crop Science
Texas A&M University, USA
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