CURRICULUM VITAE

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Research Interest

In the era of increasing food demand along with global population surge and the looming global climate crisis, how plants adapt to future environmental changes is a fundamental question for world agriculture. Our group are focusing on studying crop environmental adaptation, especially maize abiotic stress biology. We use genetic, molecular and bioinformatics approaches to reveal the genetic basis and/or molecular mechanisms of maize abiotic stress responses/tolerance. Our goals are to identify genetic loci and/or favorable alleles for genetic engineering and to develop molecular makers for stress-tolerant maize breeding.

Professional Memberships

Other Roles

Education & Working Experience

2013.4-present Professor. Huazhong Agricultural University, Wuhan, HB 430070, China

2012.6-2013.3 Associate Research Scientist in MCDB, Yale University, New Haven, CT 06520-8104 USA. Research: Hormone signaling and plant developmental.

2009.7-2012.6 Postdoctoral researcher with Dr. Haiyang Wang and Dr. Xing Wang Deng at MCDB, Yale University, New Haven, CT USA. Research: Hormones, Phosphatases and plant developmental.

2007.6-2009.7 Postdoctoral researcher with Dr. Haiyang Wang at the Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, NY USA. Research: light signaling and plant developmental.

2000.9-2007.3 College of life science and technology, Huazhong Agricultrural University. Wuhan, China. Major: Biochemistry and molecular biology. Research: Hormones, transcription factors and plant developmental.

1996.9-2000.7 B.S, College of Fisheries, Huazhong Agricultrural University. Wuhan, China. Major: Fishery

Publications

1. Sun X, Xiang Y, Dou N, Zhang H, Pei S, Franco AV, Menon M, Monier B, Ferebee T, Liu T, Liu S, Gao Y, Wang J, Terzaghi W, Yan J, Hearne S, Li L[#], Li F[#], Dai M[#]. The role of transposon inverted repeats in balancing drought tolerance and yield-related traits in maize. Nat Biotechnol. 2022. doi: 10.1038/s41587-022-01470-4.
2. Liang X, Xu X, Wang Z, He L, Zhang K, Liang B, Ye J, Shi J, Wu X, Dai M, Yang W[#]. StomataScorer: a portable and high-throughput leaf stomata trait scorer combined with deep learning and an improved CV model. Plant Biotechnol J. 2022. 20(3):577-591.
3. Zhang P, Dai M[#]. CircRNA: a rising star in plant biology. J Genet Genomics. 2022. S1673-8527(22)00155-2.
4. Zhang F, Wu J, Sade N, Wu S, Egbaria A, Fernie AR, Yan J, Qin F, Chen W[#], Brotman Y[#], Dai M[#]. Genomic basis underlying the metabolome-mediated drought adaptation of maize. Genome Biol. 2021. 22(1):260.
5. Wu X, Feng H, Wu D, Yan S, Zhang P, Wang W, Zhang J, Ye J, Dai G, Fan Y, Li W, Song B, Geng Z, Yang W, Chen G, Qin F, Terzaghi W, Stitzer M, Li L, Xiong L, Yan J, Buckler E, Yang W[#], Dai M[#]. Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. Genome Biol. 2021. 22(1):185.
6. Zhang H, Sun X, Dai M[#]. Improving crop drought resistance with plant growth regulators and rhizobacteria: Mechanisms, applications, and perspectives. Plant Commun. 2021. 3(1):100228.
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8. Zhang H, Xiang Y, He N, Liu X, Liu H, Fang L, Zhang F, Sun X, Zhang D, Li X, Terzaghi W, Yan J, Dai M[#]. Enhanced Vitamin C Production Mediated by an ABA-Induced PTP-Like Nucleotidase Improves Drought Tolerance of Arabidopsis and Maize. Mol Plant. 2020. pii: S1674-2052(20) 30035-6.
9. Yu X, Dong J, Deng Z, Jiang Y, Wu C, Qin X, Terzaghi W, Chen H, Dai M[#] and Deng XW[#]. (2019). Arabidopsis PP6 phosphatases dephosphorylate PIF proteins to repress photomorphogenesis. PNAS. 116(40):20218-20225
10. He Z, Wu J, Sun X, Dai M[#]. (2019). The maize clade A PP2C phosphatases play critical roles in multiple stress responses. Int J Mol Sci 20(14). pii: E3573
11. Zhang P, Fan Y, Sun X, Chen L, Terzaghi W, Bucher E, Li L, Dai M[#]. (2019). A large-scale circular RNA profiling reveals universal molecular mechanisms responsive to drought stress in maize and Arabidopsis. Plant J. 98(4):697-713.
12. Luo X, Wang B, Gao S, Zhang F, Terzaghi W, Dai M[#]. (2019). Genome-wide association study dissects the genetic bases of salt tolerance in maize seedlings. J Integr Plant Biol. 61(6):658-674.
13. He Z, Zhong J, Sun X, Wang B, Terzaghi W, Dai M[#]. (2018). The maize ABA receptors ZmPYL8, 9 and 12 facilitate plant drought resistance. Front Plant Sci. 9:422.
14. Chen L, Zhang P, Fan Y, Lu Q, Li Q, Yan J, Muehlbauer GJ, Schnable PS, Dai M, Li L[#]. (2018). Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. New Phytol. 217:1292-1306.
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16. Xiang Y, Sun X, Gao S, Qin F, Dai M[#]. (2017). Deletion of an endoplasmic reticulum stress response element in a ZmPP2C-A gene facilitates drought tolerance of maize seedlings. Mol Plant. 10:456-469.

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