

CURRICULUM VITAE

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Research Interest			
<p>Rice is the most important crops in the world. Crown root (adventitious roots) are important components of rice root system and play essential roles in water and nutrients absorption. Our lab is interested in understanding the basic mechanisms controlling crown roots initiation, emergence and elongation and translating that knowledge into solutions for agriculture.</p>			
Professional Memberships			
Other Roles			
Education & Working Experience			
Education:			
Ph.D. 09/2004-06/2009: Huazhong Agriculture University, 1 Shizishan Street, Wuhan, Hubei 430070, China			
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M.S. 09/1997-07/2000: Northwest Agriculture & Forestry University (former Northwestern Agricultural University), Yangling, Shaanxi 712100, China			

Major: Botany

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Major: Biology Education

Professional Experiences:

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Publications

1. Lu Y, Zhou DX, Zhao Y* (2020). Understanding epigenomics based on the rice model. *Theor Appl Genet.* 2020 Jan 2. doi: 10.1007/s00122-019-03518-7.
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3. Zhou S, Jiang W, Zhao Y, Zhou DX. (2019). Single-cell three-dimensional genome structures of rice gametes and unicellular zygotes. *Nat Plants.* 2019. 5(8):795-800.
4. Cheng S, Tan F, Lu Y, Liu X, Li T, Yuan W, Zhao Y*, Zhou DX*(2018). WOX11 recruits a histone H3K27me3 demethylase to promote gene expression during shoot development in rice. *Nucleic Acids Research.* 46(5):2356-2369 (co- correspondence)
5. Lu Y, Xu Q, Liu Y, Yu Y, Cheng ZY, Zhao Y, Zhou D-X*(2018): Dynamics and

- functional interplay of histone lysine butyrylation, crotonylation, and acetylation in rice under starvation and submergence. *Genome Biology*, 19:144.
6. Tan F, Lu Y, Jiang W, Wu T, Zhang R, Zhao Y, Zhou D-X*(2018): DDM1 Represses Noncoding RNA Expression and RNA-Directed DNA Methylation in Heterochromatin. *Plant Physiology*, 177:1187-1197.
 7. Zhou C, Wang C, Liu H, Zhou Q, Liu Q, Guo Y, Peng T, Song J, Zhang J, Chen L, Zhao Y, Zeng Z*, Zhou D-X*(2018): Identification and analysis of adenine N(6)-methylation sites in the rice genome. *Nature Plants* 2018, 4:554-563.
 8. Zhang H, Zhao Y, Zhou D-X*(2017): Rice NAD⁺-dependent histone deacetylase OsSRT1 represses glycolysis and regulates the moonlighting function of GAPDH as a transcriptional activator of glycolytic genes. *Nucleic Acids Research*, 45:12241-12255
 9. Zhou S, Jiang W, Long F, Cheng S, Yang W, Zhao Y*, Zhou DX*(2017). Rice homeodomain protein WOX11 recruits a histone acetyltransferase complex to establish programs of cell proliferation of crown root meristem. *The Plant Cell*, 29(5):1088-1104 (co- correspondence)
 10. Jiang W, Zhou S, Zhang Q, Song H, Zhou DX, Zhao Y* (2017). Transcriptional regulatory network of WOX11 involved in the control of crown root development, cytokinin signals, and redox in rice. *Journal of Experimental Botany*, 68(11):2787-2798
 11. Cheng S, Zhou D-X, Zhao Y* (2016). WUSCHEL-related homeobox gene WOX11 increases rice drought resistance by controlling root hair formation and root system development. *Plant Signal & Behavior*, 11(2):e1130198
 12. Tan F, Zhou C, Zhou Q, Zhou S, Yang W, Zhao Y, Li G, Zhou D-X* (2016). Analysis of DDM1 and DRM2 orthologs reveals specific features of rice DNA methylation pathways. *Plant Physiology*. 171(3):2041-54
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14. Zhang H, Lu Y, Zhao Y, Zhou Dao-Xiu (2016). OsSRT1 is involved in rice seed development through regulation of starch metabolism gene expression. *Plant Science*. 248:28-36
15. Zhao Y*, Cheng S, Song Y, Huang Y, Zhou S, Liu X, Zhou D-X (2015). The interaction between rice ERF3 and WOX11 promotes crown root development by regulating gene expression involved in cytokinin signaling. *The Plant Cell*, 27(9): 2469-83
16. Li J, Zhao Y*, Chu H, Wang L, Fu Y, Liu P, Upadhyaya N, Chen C, Mou T, Feng Y, Kumar P, and Xu J* (2015). SHOEBOX modulates root meristem size in rice through dose-dependent effects of gibberellins on cell elongation and proliferation *PLoS Genetics*, 11(8):e 1005464
17. Chen X, Liu X, Zhao Y, Zhou D-X* (2015). Histone H3K4me3 and H3K27ME3 regulatory genes control stable transmission of an epimutation in rice. *Scientific Report*, 5:13251.
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20. Zhang J, Tang W, Huang Y, Niu X, Zhao Y, Han Yi*, Liu Y* (2015). Down-regulation of a LBD-like gene, OsIG1, leads to occurrence of unusual double ovule and developmental abnormalities of various floral organs and megagametophyte in rice. *Journal of Experiment Botany*. 66(1):99-112.
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22. Liu X, Zhou C, Zhao Y, Zhou S, Wang W and Zhou D-X*(2014). The rice enhancer of

- zeste[E(z)] genes SDG711 and SDG718 are respectively involved in long day and short day signaling to mediate the accurate photoperiod control of flowering time. *Frontiers in Plant Science*, 5:591
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 24. Zhong X, Zhang H, Zhao Y, Sun Q, Hu Y, Peng H, Zhou D-X* (2013). The rice NAD⁺-dependent histone deacetylase OsSRT1 targets preferentially to stress and metabolism-related genes and transposable elements. *PLoS ONE*. 8(6):e66807
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