

# CURRICULUM VITAE

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Research Interest			
Bioinformatics, Genomics			
Professional Memberships			
Other Roles			
Education & Working Experience			
2006.6: Doctor of Science (Biochemistry & Molecular Biology with a specialization in Bioinformatics), Huazhong Agricultural University (HZAU)			
2001.6: Bachelor of Science (Biotechnology), HZAU			
Huazhong Agricultural University: National Key Laboratory of Crop Genetic Improvement			
2019.11 – present: Professor			
2013.5 – 2019.10: Adjunct Research Fellow			
University of Arizona: School of Plant Sciences & Arizona Genomics Institute			
2013.3 – 2019.5: Research Assistant Professor			



Photo

2010.11 – 2013.2: Assistant Research Scientist

2006.9 – 2010.10: Research Associat

## Publications

1. Song J-M, Lei Y, Shu C-C, Ding Y, Xing F, Liu H, Wang J, Xie W, Zhang J# and Chen L-L# (#corresponding authors). Rice Information GateWay (RIGW): A Comprehensive Bioinformatics Platform for Indica Rice Genomes. *Molecular Plant*, 2018, 11(3):505-507. DOI: 10.1016/j.molp.2017.10.003
2. Zhang J\*, Chen L\* (\*co-first authors), Sun S, Kudrna D, Copetti D, Li W, Mu T, Jiao W, Xing F, Lee S, Talag J, Song J, Du B, Xie W, Luo M, Maldonado C, Goicoechea J, Xiong L, Wu C, Xing Y, Zhou D, Yu S, Zhao Y, Wang G, Yu Y, Luo Y, Hurtado B, Danowitz A, Wing R and Zhang Q. Building two indica rice reference genomes with PacBio long read and Illumina paired-end sequencing data. *Scientific Data*, 2016, 3:160076. DOI: 10.1038/sdata.2016.76
3. Zhang J\*, Chen L\*, Xing F\* (\*co-first authors), Kudrna D, Yao W, Copetti D, Mu T, Li W, Song J, Xie W, Lee S, Talag J, Shao L, An Y, Zhang C, Ouyang Y, Sun S, Jiao W, Lv F, Du B, Luo M, Maldonado C, Goicoechea J, Xiong L, Wu C, Xing Y, Zhou D, Yu S, Zhao Y, Wang G, Yu Y, Luo Y, Zhou Z, Hurtado B, Danowitz A, Wing R and Zhang Q. Extensive sequence divergence between the reference genomes of two elite indica rice varieties Zhenshan 97 and Minghui 63. *Proceedings of the National Academy of Sciences of the United States of America*, 2016, 113(35):E5163-E5171. DOI: 10.1073/pnas.1611012113
4. Zhang J#, Kudrna D, Mu T, Li W, Copetti D, Yu Y, Goicoechea J, Lei Y and Wing R# (#corresponding authors). Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. *Bioinformatics*, 2016, 32(20):3058-3064. DOI: 10.1093/bioinformatics/btw370
5. Wei F\*, Zhang J\* (\*co-first authors), Zhou S, He R, Schaeffer M, Collura K, Kudrna D, Faga B, Wissotski M, Golser W, Rock S, Graves T, Fulton R, Coe E, Schnable P, Schwartz D, Ware D, Clifton S, Wilson R and Wing R. The Physical and Genetic Framework of the Maize B73 Genome. *PLoS Genetics*, 2009, 5(11):e1000715. DOI: 10.1371/journal.pgen.1000715
6. Zhang J, Li C, Wu C, Xiong L, Chen G, Zhang Q and Wang S. RMD: a rice mutant database

for functional analysis of the rice genome. *Nucleic Acids Research*, 2006, 34:D745-748.  
DOI: 10.1093/nar/gkj016

7. Zhang J, Feng Q, Jin C, Qiu D, Zhang L, Xie K, Yuan D, Han B, Zhang Q and Wang S. Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63. *The Plant Journal*, 2005, 42:772-780. DOI: 10.1111/j.1365-313X.2005.02408.
8. Full list of publications (<https://scholar.google.com/citations?user=LbvoiHoAAAAJ&hl=en>)