

CURRICULUM VITAE

Personal Information					
Name	Jianwei ZHANG		Gender	Male	
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Research Interest					
Bioinformatics, Genomics					
Professional Memberships					
Editorial Board Member for the following journals: Associate Editor, BMC Genomics (2017.5 - present) Associate Editor, BMC Bioinformatics (2017.7 - present)					
Other Roles					
Education & Working Experience					
Education					
2006.06: Doctor of Science (Biochemistry & Molecular Biology with specialization in Bioinformatics), Huazhong Agricultural University, Wuhan, China					
2001.06: Bachelor of Science (Biotechnology), Huazhong Agricultural University, Wuhan, China					
Working					
Huazhong Agricultural University: National Key Laboratory of Crop Genetic Improvement, College of Life Science and Technology, and College of Informatics					
2019.11 - present: Professor					
2013.5 - 2019.10: Adjunct Research Fellow					

The University of Arizona: Department of Plant Sciences, and Arizona Genomics Institute
 2013.3 - 2019.5: Research Assistant Professor
 2011.5 - 2019.5: Leader of Bioinformatics Group
 2010.11 - 2013.2: Assistant Research Scientist
 2006.9 - 2010.10: Research Associate

Selected Publications

(Newest to oldest, #co-first authors, *corresponding authors, [full list of publications](#))

1. Sheng Y[#], Huang Y[#], Jin Z[#], Wang X, Liu C, Zhang J, Zhou Z, Chuang Ma, **Zhang J**^{*} and Chen M^{*}. Assembly of a high-quality reference genome and characterization of a chemical-mutagenized library of an elite soybean cultivar Tianlong 1. **Journal of Genetics and Genomics**, 2025, in press. DOI: 10.1016/j.jgg.2025.08.006
2. Gong C, Huang Y, Liu M, Zhou Y, Xu Y, Mohammed N, Qiao X, Zuccolo A, Xie W, Wing R^{*}, **Zhang J**^{*}, Zhou F^{*} and Lin Y^{*}. Continuous infiltration and evolutionary trajectory of nuclear organelle DNA in *Oryza*. **Genome Research**, 2025, 35:1349-1363. DOI: 10.1101/gr.279609.124
3. Liu X[#], Xia D[#], Luo J[#], Li M[#], Chen L, Chen Y, Huang J, Li Y, Xu H, Yuan Y, Cheng Y, Li Z, Li G, Wang S, Liu X, Liu W, Zhang F, Liu Z, Tong X, Hou Y, Wang Y, Ying J, Abdullaev M, Ergashev M, Zhang S, Yuan W, Xue D, **Zhang J**^{*} and Zhang J^{*}. Global protein interactome mapping in rice using barcode-indexed PCR coupled with HiFi long-read sequencing. **Advanced Science**, 2025, 12(11):2416243. DOI: 10.1002/advs.202416243
4. **Zhang J**^{#*}, Che J[#] and Ouyang Y^{*}. Engineering rice genomes towards green super rice. **Current Opinion in Plant Biology**, 2024, 82:102664. DOI: 10.1016/j.pbi.2024.102664
5. Huang Y, Wang Z, Schmidt M, Su H, Xiong L and **Zhang J**^{*}. DEGAP: Dynamic elongation of a genome assembly path. **Briefings in Bioinformatics**, 2024, 25(3):bbae194. DOI: 10.1093/bib/bbae194
6. Wang H[#], Fang T[#], Li X[#], Xie Y[#], Wang W, Hu T, Kudrna D, Amombo E, Yin Y, Fan S, Gong Z, Huang Y, Xia C, **Zhang J**^{*}, Wu Y^{*} and Fu J^{*}. Whole-genome sequencing of allotetraploid bermudagrass reveals the origin of *Cynodon* and candidate genes for salt tolerance. **The Plant Journal**, 2024, 118:2068-2084. DOI: 10.1111/tpj.16729
7. Huang Y, Koo D-H, Mao Y, Herman E, **Zhang J**^{*} and Schmidt M^{*}. A complete reference genome for the soybean cv. Jack. **Plant Communications**, 2024, 5(2):100765. DOI: 10.1016/j.xplc.2023.100765
8. Yu Z[#], Chen Y[#], Zhou Y[#], Zhang Y, Li M, Ouyang Y, Chebotarov D, Mauleon R, Zhao H, Xie W, McNally K, Wing R^{*}, Guo W^{*} and **Zhang J**^{*}. Rice Gene Index: a comprehensive pan-genome database for comparative and functional genomics of Asian rice. **Molecular Plant**, 2023, 16(5):798-801. DOI: 10.1016/j.molp.2023.03.012
9. Zhou Y[#], Yu Z[#], Chebotarov D[#], Chougule K[#], Lu Z, Rivera L, Kathiresan N, Al-Bader N, Mohammed N, Alsantely A, Mussurova S, Santos J, Thimma M, Troukhan M, Fornasiero A, Green C, Copetti D, Kudrna D, Llaca V, Lorieux M, Zuccolo A^{*}, Ware D^{*}, McNally K^{*}, **Zhang J**^{*} and Wing R^{*}. Pan-genome inversion index reveals evolutionary insights into the subpopulation structure of Asian rice. **Nature Communications**, 2023, 4:1567. DOI: 10.1038/s41467-023-37004-y
10. Yi X, Liu J, Chen S, Wu H, Liu M, Xu Q, Lei L, Lee S, Zhang B, Kudrna D, Fan W, Wing R, Wang X, Zhang M, **Zhang J**^{*}, Yang C^{*}, Chen N^{*}. Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. **G3**

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11. Song J-M[#], Xie W-Z[#], Wang S[#], Guo Y-X, Koo D-H, Kudrna D, Gong C, Huang Y, Feng J-W, Zhang W, Zhou Y, Zuccolo A, Long E, Lee S, Talag J, Zhou R, Zhu X-T, Yuan D, Udall J, Xie W, Wing R, Zhang Q, Poland J*, **Zhang J*** and Chen L-L*. Two gap-free reference genomes and a global view of the centromere architecture in rice. **Molecular Plant**, 2021, 14(10):1757-1767. DOI: 10.1016/j.molp.2021.06.018
 12. Wu Z[#], Liu H[#], Zhan W[#], Yu Z, Qin E, Liu S, Yang T, Xiang N, Kudrna D, Chen Y, Lee S, Li G, Wing R, Liu J, Xiong H, Xia C, Xing Y, **Zhang J*** and Qin R*. The chromosome-scale reference genome of safflower (*Carthamus tinctorius*) provides insights into linoleic acid and flavonoid biosynthesis. **Plant Biotechnology Journal**, 2021, 19:1725-1742. DOI: 10.1111/pbi.13586
 13. Zhou Y[#], Chebotarov D[#], Kudrna D, Llaca V, Lee S, Rajasekar S, Mohammed N, Al-Bader N, Sobel-Sorenson C, Parakkal P, Arbelaez L, Franco N, Alexandrov N, Hamilton N, Leung H, Mauleon R, Lorieux M, Zuccolo A*, McNally K, **Zhang J*** and Wing R*. A platinum standard pan-genome resource that represents the population structure of Asian rice. **Scientific Data**, 2020, 7:113. DOI: 10.1038/s41597-020-0438-2
 14. Song J-M, Lei Y, Shu C-C, Ding Y, Xing F, Liu H, Wang J, Xie W, **Zhang J*** and Chen L-L*. Rice Information GateWay: A Comprehensive Bioinformatics Platform for *Indica* Rice Genomes. **Molecular Plant**, 2018, 11(3):505-507. DOI: 10.1016/j.molp.2017.10.003
 15. **Zhang J[#]**, Chen L[#], 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
 16. **Zhang J[#]**, Chen L[#], Xing F[#], 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
 17. **Zhang J***, Kudrna D, Mu T, Li W, Copetti D, Yu Y, Goicoechea J, Lei Y and Wing R*. 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
 18. Wei F[#], **Zhang J[#]**, 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
 19. **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
 20. **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.x