

Professor Yuan-Ming Zhang leads the Group of the statistical genomics at College of Plant Science and Technology of Huazhong Agricultural University, Wuhan 430070, China. He has developed a series of new methodologies in mining genes for quantitative traits in crops and led his students to investigate genetic relationship between genomic variation and specific trait formation in crops. Current research interests include GWAS, QTL mapping, bulked segregation analyses, macro-evolutionary biology, and applications of these methods to the genetic dissection of quantitative traits in crops.

Ph D	Nanjing Agricultural University	2000.09-2001.12
MS	Nanjing Agricultural University	1989.09-1992.07
BS	Southwest Agricultural University	1982.09-1986.07
Postdoc	University of California, Riverside (Statistical Genetics and Genomics with Prof Shizhong Xu)	2003.01-2005.01

2014.7 ~ Present    Huazhong Agricultural University; Professor (2014.06)

1999.11 ~ 2014.6    Nanjing Agricultural University  
Professor (2002-04), Associate Professor (1999.11)

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Associate Professor (1995.12); Lecturer (1992.12)

### Selected Papers (\*: corresponding authors)

1. Li# Hong-Fu, Wang# Jing-Tian, Zhao Qiong, **Zhang Yuan-Ming\***. BLUPmrMLM: A fast mrMLM algorithm in genome-wide association studies. *Genomics Proteomics Bioinformatics* 2024, qzae020, doi: 10.1093/gpbjnl/qzae020
2. Wang Jing-Tian, Chang Xiao-Yu, Zhao Qiong, **Zhang Yuan-Ming\***. FastBiCmrMLM: a fast and powerful compressed variance component mixed logistic model for big genomic case-control genome-wide association study. *Briefings in Bioinformatics* 2024, 25(4), bbae290
3. Jiang Guo-Liang\*, Istvan Rajcan, **Zhang Yuan-Ming**, Han Tianfu, Rouf Mian. Editorial: soybean molecular breeding and genetics. *Front Plant Sci* 2023,14:1157632
4. Zhao Qiong, Shi Xiao-Shi, Wang Tian, Chen Ying, Yang Rui, Mi Jiaming\*, Zhang Ya-Wen\*, **Zhang Yuan-Ming**. Identification of QTNs, QTN-by-environment interactions, and their candidate genes for grain size traits in main crop and ratoon rice. *Front Plant Sci* 2023; 14: 1119218
5. Wang Xiaoyu, Zhang Xiaowei, Fan Daoran, Gong Juwu, Li Shaoqi, Gao Yujie, Liu Aiyong, Liu Linjie, Deng Xiaoying, Shi Yuzhen, Shang Haihong, **Zhang Yuanming\***, Youlu Yuan\*.

- (2022) AAQSP increases mapping resolution of stable QTLs through applying NGS-BSA in multiple genetic backgrounds. *Theor Appl Genet* 135: 3223-3235
6. Han Xu, Zhang Ya-Wen, Liu Jin-Yang, Zuo Jian-Fang, Zhang Ze-Chang, Guo Liang, **Zhang Yuan-Ming\***. (2022) 4D genetic networks reveal the genetic basis of metabolites and seed oil-related traits in 398 soybean RILs. *Biotechnology for Biofuels and Bioproducts* 15: 92
  7. Li Mei, Zhang Ya-Wen, Xiang Yu, Liu Ming-Hui, **Zhang Yuan-Ming\***. (2022) IIIVmrMLM: the R and C++ tools associated with 3VmrMLM, a comprehensive GWAS method for dissecting quantitative traits. *Mol Plant* 15(8): 1251-1253
  8. Zuo Jian-Fang, Muhammad Ikram, Liu Jin-Yang, Han Chun-Yu, Niu Yuan, Jim M. Dunwell, **Zhang Yuan-Ming\***. (2022) Domestication and improvement genes reveal the differences of seed size- and oil-related traits in soybean domestication and improvement. *Computational and Structural Biotechnology Journal* 20: 2951–2964
  9. Li Pei, Wei Liu-Qiong, Pan Yi-Fan, **Zhang Yuan-Ming\***. (2022) dQTG.seq: A comprehensive R tool for detecting all types of QTLs using extreme phenotype individuals in bi-parental segregation populations. *Computational and Structural Biotechnology Journal* 20: 2332-2337
  10. Li Pei, Li Guo, Zhang Ya-Wen, Zuo Jian-Fang, Liu Jin-Yang, **Zhang Yuan-Ming\***. (2022) A combinatorial strategy to identify various types of QTLs for quantitative traits using extreme phenotype individuals in F<sub>2</sub>. *Plant Communications* 3(3): 100319
  11. Li Mei<sup>#</sup>, Zhang Ya-Wen<sup>#</sup>, Zhang Ze-Chang, Xiang Yu, Liu Ming-Hui, Zhou Ya-Hui, Zuo Jian-Fang, Zhang Han-Qing, Chen Ying, **Zhang Yuan-Ming\***. (2022) A compressed variance component mixed model for detecting QTNs, and QTN-by-environment and QTN-by-QTN interactions in genome-wide association studies. *Molecular Plant* 15(4): 630-650
  12. Zhou Ya-Hui, Li Guo, **Zhang Yuan-Ming\***. (2022) A compressed variance component mixed model framework for detecting small and linked QTL-by-environment interactions. *Briefings in Bioinformatics* 23(2): bbab596
  13. Liu Lü-Meng<sup>#</sup>, Zhang Han-Qing<sup>#</sup>, Cheng Kun, **Zhang Yuan-Ming\***. (2021) Integrated bioinformatics analyses of *PINI*, *CKX*, and yield-related genes reveals the molecular mechanisms for the difference of seed number per pod between soybean and cowpea. *Frontiers in Plant Science* 12: 749902
  14. Cheng Kun, Pan Yi-Fan, Liu Lü-Meng, Zhang Han-Qing, **Zhang Yuan-Ming\***. (2021) Integrated transcriptomic and bioinformatics analyses reveal the molecular mechanisms for the differences in seed oil and starch content between *Glycine max* and *Cicer arietinum*. *Frontiers in Plant Science* 12: 743680
  15. Han Xu, Xu Zhuo-Ran, Zhou Ling, Han Chun-Yu, **Zhang Yuan-Ming\***. (2021) Identification of QTNs and their candidate genes for flowering time and plant height in soybean using multi-locus genome-wide association studies. *Molecular Breeding* 41: 39
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17. Bu Suhong, Wu Weiren\*, **Zhang Yuan-Ming\***. (2021) A multi-locus association model framework for nested association mapping with discriminating QTL effects in various subpopulations. *Frontiers in Genetics* 11: 590012
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  24. Zuo Jian-Fang, Niu Yuan, Cheng Peng, Feng Jian-Ying, Han Shi-Feng, Zhang Ying-Hao, Shu Guoping, Wang Yibo, **Zhang Yuan-Ming\***. (2019) Effect of marker segregation distortion on high density linkage map construction and QTL mapping in soybean (*Glycine max* L.). *Heredity* 123(5): 579-592
  25. Zhang Hongwei#, Wang Xi#, Pan Qingchun#, Li Pei#, Liu Yunjun, Lu Xiaoduo, Zhong Wanshun, Li Minqi, Han Linqian, Juan Li, Wang Pingxi, Li Dongdong, Liu Yan, Li Qing, Yang Fang, **Zhang Yuan-Ming\***, Wang Guoying\*, Li Lin\*. (2019) QTG-seq accelerates QTL fine mapping through QTL partitioning and whole-genome sequencing on bulked segregant samples. *Molecular Plant* 12(3): 426-437
  26. **Zhang Yuan-Ming\***, Jia Zhenyu, Jim M. Dunwell. (2019) Editorial: The applications of new multi-locus GWAS methodologies in the genetic dissection of complex traits. *Frontiers in Plant Science* 10: 100
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#### **Editorial Board Member/Associate Editor**

Heredity; BMC Genomics; Frontiers in Genetics; Frontiers in Plant Science (Guest)