**CURRICULUM VITAE**

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| **Personal Information** | | | | | F:\D\NAU\myself\lab\ID\章元明证件.bmp |
| Name | Yuan-Ming Zhang | Gender | Male | |
| Position Title | | Professor | | |
| Working Department | | Crop Genetics and Breeding | | |
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| Address | 1 Shizishan Rd., College of Plant Science and Technology, Huazhong Agricultural University, Wuhan 430070, China | | | |
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| **Research Interest** | | | | | |
| 1. Statistical Genetics and Genomics: Algorithms for genome-wide association studies, linkage analysis, genetic analysis in genetic mating design, and mixed major-genes plus polygenes inheritance;  2. Molecular evolution mechanism in the form of complex traits;  3. Genetics for quantitative traits in soybean. Our purpose is to validate the new algorithms. | | | | | |
| **Professional Memberships** | | | | | |
| ***BMC Genetics*** (SCI), Associate Editor  ***Canadian Journal of Plant Science*** (SCI), Associate Editor  ***Acta Agronomica Sinica***, Associate Editor  ***Frontiers in Genetics***, Review Editor  ***Journal of Genetics Study***, Associate Editor  ***Austin Biometrics and Biostatistics***,Associate Editor | | | | | |
| **Other Roles** | | | | | |
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| **Education & Working Experience** | | | | | |
| **Degree University Year**  Ph.D. Nanjing Agricultural University (NAU) 2000.03-2001.12.  M.Sc. NAU 1989.09-1992.07  B.Sc. Southwest Agricultural University 1982.09-1986.07  Postdoc University of California, Riverside 2003.01-2005.01  Visiting Scholar Southeast University (Mathematics) 1997.08-1998.01  Assistant, lecturer Southwest University at Rongchang campus 1986.07-1995.11  Associate Prof Southwest University at Rongchang campus 1995.12-1999.11  Associate Prof Nanjing Agricultural University 1999.11-2002.04  Professor Nanjing Agricultural University 2002.04-2014.07  Professor Huazhong Agricultural University 2014.07- | | | | | |
| **Publications** | | | | | |
| 1. Wen Jia, Zhao Xinwang, Wu Guorong, Xiang Dan, Liu Qing, Bu Su-Hong, Yi Can, Song Qijian, Jim M. Dunwell, Tu Jinxing, Zhang Tianzhen, Zhang Yuan-Ming\*. Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design. Scientific Reports, Accepted (2014 IF: 5.578) 2. Zhou Ling (#), Wang Shi-Bo (#), Jian Jianbo (#), Geng Qing-Chun, Wen Jia, Song Qijian, Wu Zhenzhen, Li Guang-Jun, Liu Yu-Qin, Jim M. Dunwell, Zhang Jin, Feng Jian-Ying Feng, Niu Yuan, Zhang Li, Ren Wen-Long & Zhang Yuan-Ming (\*). 2015. Identification of domestication-related loci associated with flowering time and seed size in soybean with the RAD-seq genotyping method. Scientific Reports 5: 9350 (DOI: 10.1038/srep09350) (2014 IF: 5.578) 3. Bu Su-Hong(#),Zhao Xinwang(#), Yi Can, Wen Jia, Tu Jinxing, Yuan-Ming Zhang\*. Interacted QTL mapping in partial NCII design provides evidences for breeding by design. PLoS ONE 10(3):e0121034. doi:10.1371/journal.pone.0121034 4. Xie F-T, Niu Y, Zhang J, Bu S-H, Zhang H-Z, Geng Q-C, Feng J-Y, Zhang Y-M\*. 2014. Fine mapping of quantitative trait loci for seed size traits in soybean. Molecular Breeding 34:2165-2178 5. Meng Li, Xiaolei Liu, Peter Bradbury, Jianming Yu, Yuan-Ming Zhang\*, Rory J Todhunter, Edward S Buckler,Zhiwu Zhang\*. 2014. Enrichment of statistical power for genome-wide association studies. BMC Biology 12:73 (2013 IF: 7.43) 6. Xie Shang-Qian, Feng Jian-Ying, Zhang Y-M\*. 2014. Linkage group correction using epistatic distorted markers in F2 and backcross populations. Heredity 112: 479-488 7. Zhang W-J, Niu Y, Bu S-H, Li M, Feng J-Y, Zhang J, Yang S-X, Medrine Mmyi Odinga, Wei S-P, Liu X-F, Zhang Y-M\*. 2014. Epistatic association mapping for alkaline and salinity tolerance traits in the soybean germination stage. PLoS ONE 9(1): e84750 8. Li Qi-Gang, Zhang Li, Li Chun, Zhang Y-M\*. 2013. Comparative genomics suggests that an ancestral polyploidy event leads to enhanced root nodule symbiosis in the Papilionoideae. Molecular Biology and Evolution 30(12): 2602-2611 (2013 IF: 14.308) 9. Li Q-G, Zhang Y-M\*. 2013. The origin and functional transition of P34. Heredity 110(3): 259-266 10. Wen Jia, Can Van Toan, Zhang Y-M\*. 2013. Multi-QTL mapping for quantitative traits using distorted markers. Molecular Breeding 31(2): 395-404 11. Niu Yuan, Xu Yu, Liu Xiao-Feng, Yang Sheng-Xian, Wei Shi-Ping, Xie Fang-Teng, Zhang Y-M\*. 2013. Association mapping for seed size and shape traits in soybean cultivars. Molecular Breeding 31(4): 785-794 12. Xie Shang-Qian, Jia Wen, Zhang Y-M\*. 2013. Multi-QTL mapping for quantitative traits using epistatic distorted markers. PLoS ONE 8(7): e68510 13. Feng J-Y, Zhang J, Zhang W-J, Wang S-B, Han S-F, Zhang Y-M\*. 2013. An efficient hierarchical generalized linear mixed model for mapping QTL of ordinal traits in crop cultivars. PLoS ONE 8(4): e59541 14. Zhang T\*, Qian N, Zhu X, Chen H, Wang S, Mei H, Zhang Y. 2013. Variations and transmission of QTL alleles for yield and fiber qualities in upland cotton cultivars developed in China. PLoS ONE 8(2): e57220 15. Li C, Li Q-G, Jim M. Dunwell, Zhang Y-M\*. 2012. Divergent evolutionary pattern of starch biosynthetic pathway genes in grasses and dicots. Molecular Biology and Evolution 29(10): 3227- 3236 (2012 IF: 10.353) 16. Zhang J, Yue C, Zhang Y-M\*. 2012. Bias correction for estimated QTL effects using the penalized maximum likelihood method. Heredity 108: 396-402 17. Li C, Li M, Jim M. Dunwell, Zhang Y-M\*. 2012. Gene duplication and accelerated evolutionary rate contribute to the higher ability of protein synthesis in dicots. BMC Evolutionary Biology 12: 15 18. He Xiao-Hong, Hu Zhongli, Zhang Y-M\*. 2012. Genome-wide mapping of QTL associated with heterosis in the RIL-based NCIII design. Chin Sci Bull 57(21): 2655-2665 19. Liu R, Wang B, Guo W, Qin Y, Wang L, Zhang Y, Zhang T\*. 2012. Quantitative trait loci mapping for yield and its components by using two immortalized populations of a heterotic hybrid in *Gossypium hirsutum* L. Molecular Breeding 29(2): 297-311 20. Jiangbo Zhou, Yuan-Ming Zhang, Haiyan Lü, Aiqing You, Lili Zhu, Guangcun He\*. 2012. Transmission of important chromosomal regions under selection revealed in rice pedigree breeding programs. Molecular Breeding 30(2): 717-729 21. Chen X, Guo W, Liu B, Zhang Y, Song X, Zhang L, Zhang T\*. 2012. Molecular mechanisms of fiber differential development between G. barbadense and G. hirsutum revealed by genetical genomics. PLoS ONE 7(1): e30056 22. Guo H-L, Li Y, Xuan J-P, Liu J-X\*, Zhang Y-M, Zheng Yi-Qi. 2012. Association of molecular markers with cold tolerance and green period in Zoysiagrass (*Zoysia Willd*.). Breeding Science 62: 320-327 23. Li C, Zhang Y-M\*. 2011. Molecular evolution of glycinin and β-conglycinin gene families in soybean (Glycine max L. Merr.). Heredity 106: 633-641 24. Xu Y, Li H-N, Li G, Wang X, Cheng L, Zhang Y-M\*. 2011. Mapping quantitative trait loci for seed size traits in soybean (Glycine max L. Merr.). Theor Appl Genet, 122: 581-594 25. He X-H, Qin H, Hu Z, Zhang T, Zhang Y-M\*. 2011. Mapping of epistatic quantitative trait loci in four-way crosses. Theor Appl Genet 122: 33-48 32 Lü H-Y, Liu X-F, Wei S-P, Zhang Y-M\*. 2011. Epistatic association mapping in homozygous crop cultivars. PLoS ONE 6(3): e17773 26. He X-H, Zhang Y-M\*. 2011. A complete solution for dissecting pure main and epistatic effects of QTL in triple testcross design. PLoS ONE 6(9): e24575 27. Kuang F-L, Wang X, Zhou L, Zhang Y-M\*. 2011. Linkage graph analysis: A linkage-group-based QTL synthesis analysis approach. China Sci Bull 56: 1092-1099 28. Zhu X, Ai N, Zhang Y, Guo W, Zhang T-Z\*. 2011. Relationships between differential gene expression and heterosis in cotton hybrids developed from the foundation parent CRI-12 and its pedigree-derived lines. Plant Science 180: 221-227 29. Dou BD\*, Hou BW, Wang F, Yang JB, Ni ZF, Sun QX, Zhang Y-M\*. 2010. Further mapping of quantitative trait loci for female sterility in wheat. Genetics Research 92(1): 63-70 30. Liu G, Li M, Wen J, Du Y, Zhang Y-M\*. 2010. Functional mapping of quantitative trait loci associated with rice tillering. Molecular Genetics and Genomics 284: 263-271 31. Li G-J, LI H-N, Cheng L-G, Zhang Y-M\*. 2010. QTL Analysis for Dynamic Expression of Chlorophyll Content in Soybean (Glycine max L. Merr.) Acta Agronomica Sinica 36(2): 242-248 32. Lü H-Y, Li M, Yao L-L, Li G-J, Lin F, Zhang Y-M\*. 2009. Multi-loci in silico mapping in inbred lines. Heredity 103: 346-354 33. Zhang Y-M\*, Gai JY. 2009. Methodologies for segregation analysis and QTL mapping in plant. The third International Conference on Quantitative Genetics. Genetica 136: 311-318 34. He X-H, Zhang Y-M\*. 2008. Mapping epistatic quantitative trait loci underlying endosperm traits using all markers on the entire genome in random hybridization design. Heredity 101:39-47 35. Zhang Y-M\*, Lü H-Y, Yao L-L. 2008. Multiple quantitative trait loci Haseman-Elston regression using all markers on the entire genome. Theor Appl Genet 117: 683-690 36. Zhu C, Zhang Y-M\*, Guo Z. 2008. Mapping quantitative trait loci for binary trait in the F2:3 design. Journal of Genetics 87(3): 201-207 37. Qin H, Guo W, Zhang Y-M, Zhang TZ\*. 2008. QTL mapping of yield and fiber traits based on a four-way cross population in Gossypium hirsutum L. Theor Appl Genet 117: 883-894 38. Zhu C, Wang C, Zhang Y-M\*. 2007. Modeling segregation distortion for viability selection I. Reconstruction of linkage maps with distorted markers. Theor Appl Genet 114: 295-305 39. Zhu C, Zhang Y-M\*. 2007. An EM algorithm for mapping segregation distortion loci. BMC Genetics 8: 82 40. Zhu C, Huang J, Zhang Y-M\*. 2007. Mapping binary trait loci in the F2:3 design. Journal of Heredity 98:337-344 41. Geng J, Zhu C, Zhang X, Cheng Y, Zhang Y-M\*, Hou X\*. 2007. A genetic linkage map of nonheading chinese cabbage. Journal of American Society for Horticultural Science 132: 816-823 42. Zhu C, Wang F, Wang J，Li G，Zhang H\*, Zhang Y-M\*. 2007. Reconstruction of linkage maps in the segregation populations of backcross, double haploid and recombinant inbred line. Chin Sci Bull 52: 1648-1653 43. Wang X, Hu Z, Wang W, Li Y, Zhang Y-M, Xu C\*. 2007. A mixture model approach to the mapping of QTL controlling endosperm traits with bulked samples Status. Genetica 132: 59-70 44. Zhang Y-M\*. 2006. Advances on methods for mapping QTL in plants. China Sci Bull 51: 2223-2231 45. Zhang Y-M\*. 2006. Shrinkage estimation method for mapping multiple quantitative trait loci. Acta Genetica Sinica 33(10): 861-869 46. Xue Y, Wan J\*, Jiang L, Wang C, Liu L, Zhang Y-M, Zhai H. 2006. Identification of quantitative trait loci associated with aluminum tolerance in rice (*Oryza sativa* L.). Euphytica 150: 37-45 47. Zhang Y-M, Mao Y, Xie C, Smith H, Luo L, Xu S\*. 2005. Mapping quantitative trait loci using naturally occurring genetic variance among commercial inbred lines of maize (*Zea mays* L.). Genetics 169: 2267-2275 48. Wang H, Zhang Y-M, Li X, Masinde GL, Mohan S, Baylink DJ, Xu S\*. 2005. Bayesian shrinkage estimation of quantitative trait loci parameters. Genetics 170: 465-480 (Comment: Nat Rev Genet 2006, 7: 229-237) 49. Zhang Y-M, Xu S\*. 2005. A penalized maximum likelihood method for estimating epistatic effects of QTL. Heredity 95: 96-104 50. Luo L, Zhang Y-M, Xu S\*. 2005. A quantitative genetics model for viability selection. Heredity 94: 347-355 (Editor Comment: Heredity 2005 94: 273-274) 51. Xu C, Zhang Y-M, Xu S\*. 2005. An EM algorithm for mapping quantitative resistance loci. Heredity 94: 119-128 52. Zhang Y-M, Xu S\*. 2005. Advanced statistical methods for detecting multiple quantitative trait loci. Recent Research Developments in Genetics and Breeding 2: 1-23 (Invited Review) 53. Hansen C, Yi N, Zhang Y-M, Xu S, Gavora J, Cheng HH\*. 2005. Identification of QTL for  production traits in chickens. Animal Biotechnology 16: 67-79 2004 3 Zhang Y-M, Xu S\*. 2004. Mapping quantitative trait loci in F2 incorporating phenotypes of F3 progeny. Genetics 166: 1981-1993 54. Zhang Y-M\*, Gai JY, Yang Y-H. 2003. The EIM algorithm in the joint segregation analysis of quantitative traits. Genetics Research 81: 157-163 55. Tao A, Zeng H, Zhang Y-M，Xie G-S, Qin F-L, Zheng Y-L, Zhang D-P\*. 2003. Genetic analysis of the low critical sterility temperature point in photoperiod-thermo sensitive genic male sterile rice. Acta Genetica Sinica 30(1): 40-48 | | | | | |
| **Additional Information** | | | | | |
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