**CURRICULUM VITAE**

|  |  |
| --- | --- |
| **Personal Information**  | http://cpst.hzau.edu.cn/szdw/jsml/js/201705/W020170524410192951656.png |
| Name | Yan Jianbing | Gender | Male |
| Position Title | Professor |
| Working Department | College of Plant Sciences&Technology |
| Email |  yjianbing@mail.hzau.edu.cn |
| Address | College of Plant Sciences&Technology, Huazhong Agricultural University, Shizishan Street, Hongshan, 430070, Wuhan, China |
| Tel | 027-87280110 | Fax  |  |
| **Research Interest**  |
| Details could be found in www.maizego.org* Genetic basis of quantitative traits in maize
* Association mapping and QTL cloning
* Maize genomics and molecular breeding
 |
| **Professional Memberships** |
| * 2010.09-now, Professor, College of Plant Sciences & Technology/ College of Life Sciences & Technology/ National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University
* 2009.09-2011.03 Scientist, International Maize and Wheat Improvement Center.
* 2008.10-2009.08 Associate scientist, International Maize and Wheat Improvement Center
* 2006.10-2008.09 Post-doctoral associate, International Maize and Wheat Improvement Center.
* 2007.01-07; 10-12 Visiting Scientist, Institute Genomic Diversity, Cornell University
* 2005.10-2009.07 Associate professor, College of Agronomy and biotechnology, China Agricultural University.
* 2003.12-2005.09 Assistant professor, College of Agronomy and biotechnology, China Agricultural University.
 |
| **Other Roles** |
| Director, College of Plant Sciences & Technology |
| **Education & Working Experience** |
| * Ph.D. Plant Genetics, Huazhong Agricultural University,China,1998/9-2003/6
* B.S. Biotechnology, Huazhong Agricultural University,China,1995/9-1999/6
 |
| **Publications** |
| 1. Liu H, Luo X, Niu L, Xiao Y, Chen L, Liu J, Wang X, Jin M, Li W, Zhang Q,Yan J\*(2016) Distant eQTLs and non-coding sequences play critical roles in regulating gene expression and quantitative trait variation in maize. Mol Plant, DOI:10.1016/j.molp.2016.06.0162. Pan Q, Li L, Yang X, Tong H, Xu S, Li Z, Li W, Muehlbauer G, Li J, Yan J\* (2016) Genome-wide recombination dynamics are associated with phenotypic variation in maize. New Phytol, 210: 1083-10943. Xiao Y, Tong H, Yang X, Xu S, Pan Q, Qiao F, Raihan M, Luo Y, Liu H, Zhang X, Yang N, Wang X, Deng M, Jin M, Zhao L, Luo X, Zhou Y, Li X, Liu J, Zhan W, Liu N, Wang H, Chen G, Cai Y, Xu G, Wang W, Zheng D, Yan J\* (2016) Genome-wide dissection of the maize ear genetic architecture by using multiple populations. New Phytol, 210: 1095-11064. Jin M, Liu H, He C, Fu J\*, Xiao Y, Wang Y, Xie W, Wang G, Yan J\*(2016) Maize pan-transcriptome provides novel insights into genome complexity and quantitative trait variation. Sci Rep, 6:189365. Li X, Li L, Yan J\* (2015) Dissecting meiotic recombination based ontetrad analysis by single microspore sequencing in maize. Nat Commun, 6: 66486. Wen W, Li K, Alseekh S, Omranian N, Zhao L, Zhou Y, Xiao Y, Jin M, Yang N, Liu H, Florian A, Li W, Pan Q, Nikoloski Z, Yan J\*, Fernie A\* (2015) Genetic determinants of the network of primary metabolism and their relationships to plant performance in a maize recombinant inbred line population. the Plant Cell, 27: 1839–18567. Liu H, Wang X, Warburton M, Wen W, Jin M, Deng M, Liu J, Tong H, Pan Q, Yang X, Yan J\*(2015) Genomic, transcriptomic and phenomic variation reveals the complex adaptation of modern maize breeding. Mol Plant, 8(6): 871-8848. Liu J, Deng M, Guo H, Raihan D, Luo J, Xu Y, Dong X, Yan J\* (2015) Maize orthologs of rice GS5 and their trans-regulator are associated with kernel development. J Integr Plant Biol, 57(11):943-9539. Ding J, Ali F, Chen G, Li H, Mahuku G, Yang N, Narro L, Magorokosho C, Makumbi D, Yan J\*(2015) Genome-wide association mapping reveals novel sources of resistance to northern corn leaf blight in maize. BMC Plant Biol, 15:20610. Guo T, Yang N, Tong H, Pang Q, Yang X, Tang J, Wang J, Li J, Yan J\* (2014) Genetic basis of grain yield heterosis in an “immortalized F2s” maize population. Theor Appl Genet,127: 2149-215811. Wen W, Li D, Li X, Gao Y, Li W, Li H, Liu J, Liu H, Chen W, Luo J\*, Yan J\* (2014) Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. Nat Commun, 5:343812. Yang N, Lu Y, Yang X, Huang J, Zhou Y, Ali F, Wen W, Liu J, Li J, Yan J\*(2014) Genome wide association studies using a new nonparametric model reveal the genetic architecture of 17 agronomic traits in an enlarged maize association panel. PLoS Genet, 10(9): e100457313. Li H, Peng Z, Yang X, Wang W, Fu J, Wang J, Han Y, Chai Y, Guo T, Yang N, Liu J, Warburton ML, Cheng Y, Hao X, Zhang P, Zhao J, Liu Y, Wang G\*, Li J\*, Yan J\* (2013) Genome-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels. Nat Genet, 45: 43-5014. Fu J, Cheng Y, Linghu J, Yang X, Kang L, Zhang Z, Zhang J, He C, Du X, Peng Z, Wang B, Zhai L, Dai C, Xu J, Wang W, Li X, Zheng J, Chen L, Luo L, Liu J, Qian X, Yan J\*, Wang J\*, Wang G\* (2013) RNA sequencing reveals the complex regulatory network in the maize kernel. Nat Commun, 4:283215. Yang Q, Li Z, Li W, Ku L, Ye J, Li K, Yang N, Li Y, Zhong T, Li J, Chen Y\*, Yan J\*, Yang X\*, Xu M\* (2013) CACTA-like transposable element in ZmCCT attenuated photoperiod sensitivity and accelerated the postdomestication spread of maize. Proc Natl Acad Sci USA, 110(42): 16969-1697416. Xue Y, Warburton ML, Sawkins M, Zhang X, Setter T, Xu Y, Grudloyma P, Gethi J, Ribaut JM, Li W, Zhang X, Zheng Y, Yan J\* (2013) Genome-wide association analysis for nine agronomic traits in maize under well-watered and water-stressed conditions. Theor Appl Genet, 126(10): 2587-259617. Fu Z, Chai Y, Zhou Y, Yang X, Warburton ML, Xu S, Cai Y, Zhang D, Li J, Yan J\* (2013) Natural variation in the sequence of PSY1 and frequency of favorable polymorphisms among tropical and temperate maize germplasm. Theor Appl Genet, 126(4): 923-3518. Xu S, Zhang D, Cai Y, Zhou Y, Shah T, Ali F, Li Q, Li Z, Wang W, Li J, Yang X, Yan J\* (2012) Dissecting tocopherols content in maize (Zea mays L.), using two segregating populations and high-density single nucleotide polymorphism markers. BMC Plant Biol, 12:20119. Yang X, Gao S, Xu S, Zhang Z, Prasanna BM, Li L, Li J, Yan J\* (2011) Characterization of a global germplasm collection and its potential utilization for analysis of complex quantitative traits in maize. Mol Breeding, 28 (4): 511-52620.Yan J#, Kandianis C#, Harjes C, Bai L, Kim E, Yang X, Skinner D, Fu Z, Mitchell S, Li Q, Fernandez M, Zaharieva M, Babu R, Fu Y, Palacios N, Li J, Dellapenna D, Brutnell T, Buckler ES, Warburton ML\*, Rocheford T\* (2010) Rare genetic variation at Zea mays crtRB1 increases β-carotene in maize grain. Nat Genet, 42 (4): 322-327 (# co-first author) |
| **Additional Information**  |
| **Honors*** Japan International Award for Yong Agricultural Researchers 2010
* Dupont Young Professor Award 2011
* Hubei Chutian Scholar Professor 2011
* New Century Excellent Talents in University 2011
* Natural Science Foundation for Excellent Youth 2012

**Services in editorial boards*** Theoretical and Applied Genetics
* Frontiers in Plant Genetics and Genomics
 |