

I am pleased to be nominated as the chair of ICGI, If I am selected, I will contribute my best to work for this community, and spend my time to organize the activities of ICGI. The further development of the cotton genome and genomics and to use it for cotton research and genetic improvement should be the main task for the future work. The following is my brief introduction:

I am Xianlong Zhang, a professor of Huazhong Agricultural University, China. I took the vice president position from 2008 to 2018 at the HAU, and is the associate director of National Key Lab for Crop Genetic Improvement since 2002. I was continuously educated in Huazhong Agricultural University from 1980 to 1990 and earned my Ph.D. in 1990 from HAU and then I became a faculty member of HAU. I worked in plant genetics and improvement for thirty years, my research involves in cotton biotechnology, fiber development, cell differentiation, biotic and abiotic stress tolerance and cotton genomics. My Lab released the reference genomes of the two cultivated cotton species, *Gossypium hirsutum* and *G. barbadense*, and found the two subgenomes in cotton showed asymmetric selection (*Nature Genetics*, 2017; 2019). I am leading a cotton research group with high quality achievements. My group published 200 papers in cotton science in the international journals and released 15 varieties for commercial use. We are now developing mutant library by CRISPR, in which more than 1000 transcription factors have been knocked out, and the final goal is to find the key factors or regulation network controlling fiber development and other agronomic traits.

Selected publications:

1. Manghwar H, Li B, Ding X, Hussain A, Lindsey K, **Zhang X***, Jin S*. CRISPR/Cas Systems in Genome Editing: Methodologies and Tools for sgRNA Design, Off-Target Evaluation, and Strategies to Mitigate Off-Target Effects. **Advanced Science** (Weinh), 2020, 7(6):1902312
2. Shiming Liu, Xiaojun Zhang, Shenghua Xiao, Jun Ma, Weijun Shi, Tao Qin, Hui Xi, Xinhui Nie, Chunyuan You, Zheng Xu, Tianyi Wang, Yujing Wang, Zhennan Zhang, Jianying Li, Jie Kong, Alifu•Aierxi, Yu Yu, Keith Lindsey, Steven J. Klosterman, **Xianlong Zhang** and Longfu Zhu*, A single-nucleotide mutation in GLUTAMATE RECEPTOR-LIKE protein gene confers resistance to Fusarium wilt in *Gossypium hirsutum*, **Advanced Science** (accepted)
3. Wang M, Tu L, Yuan D, Zhu, Shen C, Li J, Liu F, Pei L, Wang P, Zhao G, Ye Z, Huang H, Yan F, Ma Y, Zhang L, Liu M, You J, Yang Y, Liu Z, Huang F, Li B, Qiu P, Zhang Q, Zhu L, Jin S, Yang X, Min L, Li G, Chen LL, Zheng H, Lindsey K*, Lin Z*, Udall JA*, **Zhang X***. Reference genome sequences of two cultivated allotetraploid cottons, *Gossypium hirsutum* and *Gossypium barbadense*. **Nature Genetics**, 2019, 51(2):224-229
4. Manghwar H, Lindsey K, **Zhang X***, Jin S*. CRISPR/Cas System: Recent Advances and Future Prospects for Genome Editing. **Trends in Plant Science**. 2019, 24(12):1102-1125
5. Ma Y, Min L*, Wang M, Wang C, Zhao Y, Li Y, Fang Q, Wu Y, Xie S, Ding Y, Su X, Hu Q, Zhang Q, Li X, **Zhang X***. Disrupted genome methylation in response to high temperature has distinct effects on microspore abortion and anther indehiscence. **Plant Cell**, 2018, 30(7):1387-1403

6. Wang M, Wang P, Lin M*, Ye Z, Li G, Tu L, Shen C, Li J, Yang Q*, **Zhang X***. Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. **Nature Plants**, 2018, 4(2):90-97
7. Wang M, Tu L, Lin M, Lin Z, Wang P, Yang Q, Ye Z, Shen C, Li J, Zhang L, Zhou X, Nie X, Li Z, Guo K, Ma Y, Huang C, Jin S, Zhu L, Yang X, Min L, Yuan D, Zhang Q, Lindsey K* , **Zhang X***. Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. **Nature Genetics**, 2017, 49(4):579-587
8. Wang M, Wang P, Tu L, Zhu S, Zhang L, Li Z, Zhang Q, Yuan D and **Zhang X***. Multi-omics maps of cotton fibre reveal epigenetic basis for staged single-cell differentiation. **Nucleic Acids Research**, 2016, 44(9):4067-4079
9. Sun L, Zhu L, Xu L, Yuan D, Min L, **Zhang X***. Cotton cytochrome P450 CYP82D regulates systemic cell death by modulating the octadecanoid pathway. **Nature Communications**, 2014, 5:5372
10. Wang PC, Zhang J, Sun L, Ma YZ, Xu J, Liang SJ, Deng JW, Tan JF, Zhang Q, Tu LL, Daniell Henry, Jin SX*, **Zhang XL***. High efficient multisites genome editing in allotetraploid cotton (*Gossypium hirsutum*) using CRISPR/Cas9 system. **Plant Biotechnology Journal**, 2018, 16(1):137-150