

CURRICULUM VITAE

Personal Information			
Name	Zhongxu Lin	Gender	Male
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Research Interest			
<p>Development of molecular markers in cotton: We firstly applied SRAP markers and applied them in cotton; we have developed nearly 4000 EST-SSRs, which account for about 1/4 of total SSRs in the world. In recent years, we focus on developing functional markers for fiber development genes, miRNAs and their targets and resistance gene homologs in cotton. Now, we are developing SNP/Indel by high-throughput sequencing technologies.</p> <p>Genetic linkage map construction and QTL mapping: A high-density interspecific genetic map was constructed (> 5000 loci). This map has been effectively applied in genomic structure explanation, QTL mapping, and introgression lines development by MAS. An intraspecific linkage map of upland cotton with 1013 loci was also constructed to map QTLs for yield and fiber related traits.</p> <p>Germplasm development: Benefited from our high-density genetic map, we developed nearly 10000 introgression lines by backcrossing upland cotton with other tetraploid cottons and marker assisted selection. These introgression lines are fundamental materials to study the quantitative genetics and to clone functional genes in cotton.</p> <p>QTL cloning: We are now cloning yield-related QTL, morphological traits genes using introgression lines to reveal their functions in cotton.</p>			
Professional Memberships			
Editorial member of Journal of Plant Studies and Advances in Agriculture			
Other Roles			
Education & Working Experience			
B. A.: College of Agronomy, Huazhong Agricultural University, Wuhan, Hubei, 1996-2000. Major: Crop Genetics and Breeding			

Ph D: College of Plant Science & Technology, Huazhong Agricultural University, Wuhan, Hubei, 2000-2005.

Major: Crop Genetics and Breeding

2005.07-2007.12: Lecturer, College of Plant Science & Technology, Huazhong Agricultural University, Wuhan, Hubei

2008.01-2012.12: Associated professor, College of Plant Science & Technology, Huazhong Agricultural University, Wuhan, Hubei

2009.12.29—2010.8.31: Visiting scholar, New Mexico State University, USA

2013.01-Now: Professor, College of Plant Science & Technology, Huazhong Agricultural University, Wuhan, Hubei

Publications

1. Nie X, Tu J, Wang B, Zhou X*, **Lin Z***. A BIL population derived from *G. hirsutum* and *G. barbadense* provides a resource for cotton genetics and breeding. PLoS One. 2015, 10(10):e0141064.
2. Chen X, Jin X, Li X, **Lin Z***. Genetic mapping and comparative expression analysis of transcription factors in cotton. PLoS One, 2015, 10(5): e0126150.
3. Hantao Wang, Xin Jin, Beibei Zhang, Chao Shen and **Zhongxu Lin***. Enrichment of an intraspecific genetic map of upland cotton by developing markers using parental RAD sequencing. DNA Research, 2015, 22(2), 147–160
4. Ximei Li, Wenhui Gao, Huanle Guo, Xianlong Zhang, David D Fang and **Zhongxu Lin***. Development of EST-based SNP and InDel markers and their utilization in tetraploid cotton genetic mapping. BMC Genomics 2014, 15: 1046
5. Gaofeng Ren, Ximei Li, **Zhongxu Lin***. Mining, genetic mapping and expression analysis of EST-derived resistance gene homologs (RGHs) in cotton. BMC Plant Biology, 2014, 14: 203
6. Hantao Wang, Ximei Li, Wenhui Gao, Xin Jin, Xianlong Zhang, **Zhongxu Lin***. Comparison and development of EST–SSRs from two 454 sequencing libraries of *Gossypium barbadense*. Euphytica, 2014, 198:277–288.
7. Li X, Yuan D, Zhang J, **Lin Z***, Zhang X. Genetic mapping and characteristics of genes specifically or preferentially expressed during fiber development in cotton. PLoS ONE, 2013, 8(1): e54444.
8. Xuemei Chen, Wenhui Gao, Jinfang Zhang, Xianlong Zhang and **Zhongxu Lin***. Linkage mapping and expression analysis of miRNAs and their target genes during fiber development in cotton. BMC Genomics 2013, 14:706.
9. Bin Wang, Yichun Nie, **Zhongxu Lin***, Xianlong Zhang, Junjie Liu and Jing Bai.

Molecular diversity, genomic constitution, and QTL mapping of fiber quality by mapped SSRs in introgression lines derived from *Gossypium hirsutum* × *G. darwinii* Watt. *Theor Appl Genet*, 2012, 125:1263-1274.

10. Xiaqing Wang, Gaofeng Ren, Ximei Li, Jianli Tu, **Zhongxu Lin*** and Xianlong Zhang. Development and evaluation of Intron and Insertion–Deletion markers for *Gossypium barbadense*. *Plant Mol Biol Rep*, 2012, 30 (3), 605-613.
11. Yu Y, Yuan DJ, Liang SG, Li XM, Wang XQ, **Lin ZX***, Zhang XL. Genome structure of cotton revealed by a genome-wide SSR genetic map constructed from a BC₁ population between *Gossypium hirsutum* and *G. barbadense*. *BMC Genomics*, 2011, 12:15

Additional Information