

# 6<sup>th</sup> Global Summit on Plant Science

October 29-30, 2018 | Valencia, Spain

## Genome wide QTL mapping for resistance to *Verticillium* wilt, fiber quality and yield traits in cotton chromosome segment substitution lines

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The development of chromosome segment substitution lines (CSSLs) from *Gossypium barbadense* in *G. hirsutum* background provided ideal materials for further genome research and crop improvement through MAS. We had developed BC5F3:5 populations with the donor parent Hai1 and the recurrent parent CCRI36. In this study 300 CSSLs and their two parents were planted in a randomized complete block design with 2 replications in two ecological locations (Anyang and Xinjiang) in 2015 and 2016, respectively. *Verticillium* wilt resistance was collected at the time of July and August in the field. A total of 597 pairs simple sequence repeat (SSR) markers screened from 2292 pairs of markers in the high density map from a BC2F1 population of *G. hirsutum* × *G. barbadense* were used to identify the polymorphisms among the BC5F3:5 lines. A total of 56 quantitative trait locus (QTLs) for *Verticillium* wilt resistance were detected, 30 of them are stable, and 38 QTLs (68%) had negative additive effects, which indicate that the *G. barbadense* alleles increased *Verticillium* wilt resistance and decrease DI by about 2.64 to 13.23. By meta-analysis, 30 QTL hotspot regions for VW resistance were identified and 13 of them were new hotspot regions. 191 QTLs were detected for fiber yield and fiber quality, 98 for the fiber quality traits and 93 for the yield related traits, 54 of them are stable. Three chromosomes of Chr05, Chr10 and Chr20 contained more QTLs. 30 clusters with disease index and fiber related traits were identified on 16 chromosomes. Most of the fiber traits were clustered with the disease index stable QTLs. We found 6 clusters namely, C01-cluster-1, C05-cluster-4, C07-cluster-1, C19-cluster-2, C22-cluster-1 and C22-cluster-2, which had positive correlation between VW resistance and fiber quality traits. Two clusters, C10-cluster-1 and C25-cluster-1 had also positive correlation between VW resistance and yield related traits (boll weight and lint percentage). One cluster, C20-cluster-1 is important for VW resistance, fiber quality and fiber yield. So, these clusters and related QTLs are very important for breeding improvement of fiber quality and yield, VW disease resistance.



### Recent Publications

- Shi Y, Li W, Li A, Ge R, Zhang B, Li J, et al. (2015) Constructing a high-density linkage map for *Gossypium hirsutum* × *Gossypium barbadense* and identifying QTLs for lint percentage. Journal of Integrative Plant Biology 57(5):450-467.

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2. Shi Y, Zhan B, Liu A, et al. (2016) Quantitative trait loci analysis of *Verticillium* wilt resistance in interspecific back cross populations of *Gossypium hirsutum* × *Gossypium barbadense*. *BMC Genomics* 17(1):877.
3. Song W, Wang M, Su W, Lu Q, Xiao X, Cai J, et al. (2017) Genetic and phenotypic effects of chromosome segments introgressed from *Gossypium barbadense* into *Gossypium hirsutum*. *PLOS One* 12(9):e0184882.
4. Lu Q, Shi Y, Xiao X, Li P, Gong J, Gong W, et al. (2017) Transcriptome analysis suggests that chromosome introgression fragments from Sea Island cotton (*Gossypium barbadense*) increase fiber strength in upland cotton (*Gossypium hirsutum*). *G3: Genes, Genomes, Genetics* 7(10):3469-3479.
5. Li P, Wang M, Lu Q, Ge Qu, et al. (2017) Comparative transcriptome analysis of cotton fiber development of upland cotton (*Gossypium hirsutum*) and chromosome segment substitution lines from *G. hirsutum* × *G. barbadense*. *BMC Genomics* 18(1):705.

## Biography

Youlu Yuan has been involved in studies related to cotton hybrid vigor and molecular marker assisted selection about fiber quality; focus on cotton variety molecular design, especially on excellent fiber quality variety development. Since 2013 he worked as a Director of Bio-technology Research Department and PI of cotton variety molecular design unit.

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