

## Genomic Differentiation Between *Gossypium barbadense* and *G. hirsutum*

ZHANG Tian-zhen<sup>1,2</sup>

(1. Cotton Research Institute, Nanjing Agricultural University, Nanjing 210095, China; 2. National Key Laboratory of Crop Genetics and Germplasm Enhancement, Hybrid Cotton R&D Engineering Center/MOE, China)

Sea Island cotton (*Gossypium barbadense* L.) has superior fiber quality properties, while Upland cotton (*G. hirsutum* L.) is characterized by its high yield. Although these two species are easily crossed, it is difficult to integrate their superior genes. It will be very helpful to molecular breeding and evolution study in *Gossypium* to reveal genomic differentiation between *G. barbadense* and *G. hirsutum*. An enhanced genetic map consisting of 2247 loci and covering 3514.6 cM, with an average inter-marker distance of 1.5 cM has been developed. Two distorted intervals were found in the A7 and D7 homoeologous chromosome pairs. There were 17 consecutive loci spanning 15.4 cM in A7 and 16 loci spanning 13.2 cM in D7. They were skewed towards the heterozygotes, which indicated that Hai 7124 alleles were preferentially transmitted in these intervals. Based on this map, we tagged more than 10 QTLs and/or genes influencing depression, and male and female sterility. Two novel Dobzhansky-Muller type genes interacting to cause hybrid lethality between *G. hirsutum* and *G. barbadense* have been identified. Hybrid lethality is a major mechanism of isolation, which plays an important role in the process of speciation. The lethal symptom was controlled by two dominant complementary genes, one from *G. hirsutum* and another from *G. barbadense* cv. Coastland R4-4. We could anchor one gene on chromosome D8 and another on chromosome D11 by the molecular tagging. In order to associate differentially expressed genes with super fiber qualities in *G. barbadense*, 68 additional QTLs, 31 in A-subgenome, and 37 in D-subgenome chromosomes, and 125 epistatic QTLs were tagged. The numbers and genetic effects of epistatic QTL are much more than those of the tagged additional QTL. Using microarray technology, we discovered many novel genes and identified a large number of genes differentially expressed during fiber cell elongation and in second wall deposits between *G. hirsutum* and *G. barbadense*. More than 20000 fiber-derived ESTs in *G. barbadense* were sequenced, their EST unigenes identified, and the unigene SNPs will be developed by comparing with those in *G. hirsutum* and further mapped in tetraploid cotton. We developed one set of chromosome segment substitution lines (CSSL) lines consisting of 330 different lines in which 1~4 different lines had the same or overlapped substituted segments using *G. hirsutum* acc. TM-1 as the recipient parent and *G. barbadense* cv. Hai 7124 as the donor parent by molecular assisted-selection in BC5S<sub>1,3</sub>. The genetic length of the substituted segments covered 5271.9 cM in total with an average distance of segment by 10.9 cM, 1.5 times of total genetic length of Upland cotton. It is an ideal material for genome differentiation between *G. barbadense* and *G. hirsutum* and especially for QTL mapping. Our above research provided a platform to co-map fiber QTL, fiber-derived EST unigenes, and fiber-derived EST unigene eQTL.