

QTL Analysis in Tetraploid Cotton

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QTL analyses were performed in tetraploid cotton. An interspecific F_2 population consisting of 69 plants, which was developed from the cross between *Gossypium hirsutum* L., cv. Handan 208 (characterized as high fiber yield) and *G. barbadense* L., cv. Pima 90 (characterized as excellent fiber quality), was genotyped with SSR, RAPD, SRAP, and REMAP markers. A 1029-locus linkage map was constructed covering 5472.3 cM with an average distance of 5.32 cM between two markers. The genetic linkage map was used to identify the QTLs affecting fiber yield and quality traits in 69 $F_{2:3}$ family lines, and a total of 52 QTLs were identified. QTL analysis was also conducted using the advanced-generation population from this cross. One-way ANOVA revealed that 6 markers were significant for fiber length, 8 markers for uniformity, 4 markers for micronaire, 19 markers for strength, and 10 markers for elongation. Association mapping revealed that 12 markers showed marker-trait association with fiber length, 10 markers with uniformity, 5 markers with micronaire, 45 markers with strength, and 32 markers with elongation. Two different analyses detected similarity of five markers, which were significant for several traits. Xinluzao 1 (XLZ1), a susceptible *G. hirsutum* cultivar, and Hai 7124 (H7124), a resistant *G. barbadense* line, and their $F_{2:3}$ families were used to map and study the disease index induced by *Verticillium* wilt. A total of 430 SSR loci were mapped into 41 linkage groups; the map spanned 3745.9 cM, and the average distance between adjacent loci was 8.71 cM. Four and five QTLs were detected based on the disease index investigated on July 22 and August 24 in 2004, respectively. These nine QTLs explained 10.63% to 28.83% of the phenotypic variance, six of them located on D sub-genome. A genetic linkage map was constructed based on an F_2 population derived from the intraspecific cross of DH962 (an accession from an advanced generation of Jimian 6 *G. thurberi*) and Jimian 5. A total of 506 loci were obtained and 472 loci were assigned to 50 linkage groups. The map covered 3129.5 cM with a mean density of 6.2 cM per locus. A total of 6 QTLs associated to yield-related traits were detected. The 6 QTLs were distributed in 3 groups and explained 11.28% to 20.99% of the trait variation. Four QTLs were detected for fiber-related traits. They were distributed in 4 groups and explained 10.87% to 43.88% of the trait variation. The present QTL analyses gave us a comprehensive understanding of the genetics of economic traits in cotton, and may provide a useful tool for breeders to apply them in cotton breeding.