Constructing Molecular Marker Linkage Maps of Chromosome 14Sh and 22Sh and QTL Mapping for Major Traits by Use of Substitution Lines of *Gossypium hirsutum* L.

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CSB14Sh, which is isogenic for its recurrent parent TM-1 except for chromosome 14 short arm, was crossed with TM-1, and the F_2 population was produced. A total of 3800 SSR primer pairs covering the whole genome were used to screen polymorphism among two parents, TM-1 and CSB14Sh, and their F_1 progeny, which resulted in 15 polymorphic primer pairs. The 15 polymorphic primer pairs amplified 23 marker loci. Linkage test indicated that 21 of 23 loci could be mapped to one linkage group, and it covered a distance of 65.3 cM. Compared with the map constructed previously, the linkage group was mapped to chromosome 14. Twenty-two QTLs for main traits were mapped in the F_2 and $F_{2,3}$ generations in three environments, among which 8 QTLs were measured in two environments (generations). So they are characterized stable QTLs. Five QTL regions were determined. The additive contribution rate of those QTLs measured above is more than 15%. There may be two reasons: first, they do contribute greatly to the genetic effects; second, the result may be caused by large experiment error due to the small population size (only 63 plants). Thus, single segment substitution lines of short arm of chromosome 14 are being constructed to verify the above results. A high density molecular genetic map of short arm of chromosome 22 was constructed from an F_2 TM-1 × CSB22Sh population. A total of 4800 SSR primer pairs were used to screen polymorphism among the two parents, TM-1 and CSB22Sh, and their F_1 progeny. The 51 polymorphic primer pairs were screened, and 65 polymorphic markers were amplified in the F_2 population. Linkage test indicated that 63 markers are anchored in one linkage group, covering a total genetic distance of 89 cM. Thirty-three QTLs for main traits were mapped in the F_2 and $F_{2,3}$ generations in three environments. Thirteen of the 33 QTLs were measured in two environments, and therefore they were considered stable QTLs. Thirty-six epistasis QTLs were identified, among which 4 QTLs were stable. Eight condense regions were found. These results provide important information for utilizing the short arm of chromosome 22 in the MAS.