## Dissection of Genetic Bases of Fiber Quality in Gossypium hirsutum with Molecular Markers

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Abstract: An intraspecific F<sub>2</sub> population consisted of 119 plants, developed from the cross between Gossypium hirsutum, cv. Jimian 5 and Acala 3080, was genotyped with SSR, RAPD and SRAP markers, which showed that only 46 (pairs of) primers from 1120 could amplify polymorphic bands and revealed 54 polymorphic loci (34 SSRs, 15 RAPDs and 5 SRAPs). The data were subsequentially analyzed using Mapmaker 3.0. Among the 54 loci, 34 loci were arranged into 10 linkage groups and 20 loci were unlinked with any other loci. Fiber quality measurements were conducted by harvesting fiber from individ-

ual  $F_{\scriptscriptstyle 2}$  plants and  $F_{\scriptscriptstyle 2}\text{-derived}$   $F_{\scriptscriptstyle 3}$  families which were trailed with two replications arranged in complete randomized plots. Based on those polymorphic loci and fiber quality data from F2 plants and F<sub>2:3</sub> families, single marker analysis and One-way ANOVA were conducted and found that five markers were significantly related to fiber length, one marker to uniformity, three markers to fiber strength, six markers to fiber elongation, four markers to micronaire value. Of those significant markers, BNL1521 was simultaneously related to fiber length, elongation and micronaire value, BNL1694 simultaneously to fiber length and strength. Two-way ANOVA was conducted for digenic interactions of co-dominant markers and one significant interaction was detected for fiber strength and micronaire, respectively.

Key words: cotton; molecular marker; single marker analysis; fiber quality