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Genetic Linkage Map and QTL Analysis of Agronomic and Fiber Quality Traits in an Intraspecific Population

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Molecular markers may enhance breeding for quantitatively inherited traits. We developed a restriction fragment length polymorphism (RFLP) genetic linkage map of cotton (*Gossypium hirsutum* L.) from 119 F_{2,3} progeny from the cross MD5678ne × Prema, and used it for quantitative trait loci (QTL) analysis for agronomic and fiber quality traits. The linkage map comprises 81 loci mapped to 17 linkage groups with an average distance between markers of 8.7 centiMorgans (cM), covering 700.7 cM, or approximately 15% of the recombinational length of the cotton genome. Lint percentage and fiber strength were negatively correlated ($r = -0.41$), as were fiber strength and fiber perimeter ($r = -0.38$). In addition, fiber strength was positively correlated with 50% fiber span length ($r = 0.36$) and 2.5% span length ($r = 0.31$). Twenty-six QTLs were detected on nine linkage groups, and explained from 3.4 to 44.6% of the trait variation. Two QTLs were detected for lint yield and three for lint percentage, explaining from 5 to 20% of the variation in each trait. Three QTLs for fiber strength and two QTLs for fiber 2.5% span length were detected. A QTL near locus A42B1b explained 4.8% of the phenotypic variation in lint percentage, 24.6% of the variation in fiber strength, 11.5% of the variation in 2.5% span length, and 11.3% of the variation in perimeter. As expected, the Prema parent contributed QTLs for low yield of fibers that were long, strong, and fine while QTLs from MD5678ne imparted high yield of short, coarse, and weak fibers. The QTL positions on the linkage groups suggest that genes conferring fiber quality may cluster on the same cotton chromosome(s).