IDENTIFICATION OF ROBUST MICROSATELLITE MARKERS FOR FIBER LENGTH IN *GOSSYPIUM* SPP.

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Abstract

Marker-assisted selection (MAS) is one molecular breeding method that promises to help breeders access unexploited genetic diversity and more efficiently pyramid quantitative trait loci (QTL) for fiber quality traits in Upland cotton (*Gossypium hirsutum*). Over the past 20 years, hundreds of quantitative trait loci for fiber quality traits have been reported in the literature. Yet, inconsistencies across studies regarding the effect and location of individual QTL have hindered the use of MAS for fiber quality traits. More recent advances in QTL mapping methods have enabled the identification of stable QTL. Identifying tightly linked markers to stable fiber quality QTL is important for the use and efficiency of MAS. The objectives of this research were to assess the effects of previously reported microsatellite markers (SSRs) for fiber length in three different genetic backgrounds, and ultimately identify robust SSRs applicable to MAS for fiber length within the Texas A&M University breeding program germplasm. Two Upland intra-specific $F_{2:3}$ populations (*G. hirsutum* /*G. hirsutum*) and one inter-specific $F_{2:3}$ population ((*G. tomentosum* /*G. mustelinum*) /*G. hirsutum*) were selected for the study based on pedigree and fiber quality. A subset of four SSRs predictive of fiber length across all three genetic backgrounds were identified in the $F_{2:3}$ progeny plants. There was a significant difference in mean fiber length of F_4 progeny rows based on genotype, and increasing the number of favorable alleles in the F_4 progeny rows from 0 to 4 resulted in a 4.70 mm increase in mean length. However, response to selection between the three populations was not uniform. Furthermore, within each population the identified SSRs explained only a minor proportion of the total variation in fiber length (2-11%). All four markers originated from three QTL mapping studies that utilized diverse sets of germplasm, including a random-mated recombinant inbred line population derived from 11 Upland parents, an exotic species cross, as well as a meta-analysis of fiber quality QTL. The results demonstrate that studies utilizing diverse germplasm are effective in mapping stable QTL for fiber quality.