Association analysis of yield and fiber quality traits in *Gossypium barbadense* with SSRs and SRAPs

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ABSTRACT. Cotton is an important cash crop. Mining for quantitative trait loci related to yield and fiber quality traits using association analysis has many advantages for cotton research. In this study, 170 simple sequence repeats (SSRs) and 258 sequence-related amplified polymorphisms (SRAPs) were used to analyze the association of 3 yield component traits and 5 fiber quality traits of 55 *Gossypium barbadense* accessions in 2009 and 2010. Principal component analysis of SSRs and SRAPs showed 3 and 2 subgroups, respectively. The boundaries between the SRAP groups were much more defined than those of the SSRs. A mixed linear model was used to analyze association of yield and fiber quality traits with SSRs and SRAPs. A total of 72 loci were detected, including 28 loci of SSRs and 44 loci of SRAPs; 26 of these loci were related to yield component traits, and 46 of these loci were related to fiber quality traits. The mean phenotypic variations explained in the SSR and SRAP analysis were 8.89 and 8.61%, respectively. The locus with the highest phenotypic variation explained was NAU1164

(23.33%), which was related to fiber uniformity. The comparison of association results between the two datasets showed that mining quantitative trait loci using association analysis was more efficient with SRAPs than with SSRs.

Key words: *Gossypium barbadense*; Association analysis; SSR; SRAP