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Quantitative Trait Loci Associated with Agronomic and Fiber Traits of Upland Cotton

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Identification of quantitative trait loci (QTLs) for agronomic and fiber traits in upland cotton (*Gossypium hirsutum* L.) and their allelic association with molecular markers would be useful in cotton breeding. We used the mixed model approach of Zhu and Weir (1998) to analyze for QTLs associated with 19 agronomic and fiber traits across 96 F_2 -derived families from the cross of two cotton lines, MARCABUCAG8US-1-88 x 'HS46' (female parent). In the mixed model, molecular markers are random variables and QTLs are fixed variables. Thus, with the mixed model analysis, the QTLs are not dependent upon a particular fixed set of markers being in the model. The model also provides estimates of additive and dominance genetic effects as well as the direction of the effects of alleles from both parents. The fiber and agronomic traits, except seed index and bloom rate, were measured in F_2 -derived F_5 families. We mapped 100 QTLs to 60 maximum likelihood positions in 24 linkage groups. Several QTLs influence more than one trait. The most frequent association of QTLs with multiple traits was for fiber traits related to maturity and fineness. A positive correlation among traits would be beneficial for marker-assisted selection in plant breeding as well as for cloning genes for transformation. For example, in linkage group 14 near markers C117C5RI and F26ERI, a QTL is located that affects micronaire, arealometer high pressure reading, weight fineness, and wall thickness. In linkage group 19, four closely linked QTLs, located in an 8 cM region near marker C80F1RV, influence strength, fineness, and maturity of fiber. Maximum likelihood locations such as those obtained in this study do not necessarily represent physical distances, thus, a physical map of linkage groups is also needed.