

**DNA MARKERS DIAGNOSTIC OF GENETIC  
FACTORS CONTROLLING LEAF PUBESCENCE  
IN COTTON**

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Upland cotton (*Gossypium hirsutum* L.) genotypes have varying densities of trichomes on the leaves of mature plants, hence their species name. Most modern cultivars are "smooth", with few if any trichomes. The use of pubescence in pest management has been proposed as one alternative to heavy reliance on pesticides. A detailed RFLP map was used to map genes affecting density of leaf trichomes. Based on quantitative measures of young and mature leaves, four QTLs were mapped. A QTL on an A-subgenome chromosome that imparts dense leaf pubescence is inferred to be the  $H_1$  locus. A second QTL at the homoeologous location of a D-subgenome chromosome fits the description of the  $Sm_1$  locus. Two additional QTLs explained significant phenotypic variation in leaf pubescence. Some QTLs appeared to be specific to particular developmental stages; for example, A-2 reduced hairiness only in young leaves while A-3 increased hairiness in mature leaves. A widely used qualitative classification system may partly confound leaf pubescence, and was not sensitive enough to detect alleles such as  $Sm_1$  that had small phenotypic effect.