

Identification of Quantitative Trait Loci Controlling Seed Physical and Nutrient Traits in Cotton

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Cotton (*Gossypium* spp.) is the leading fiber crop, and an important source of the important edible oil and protein meals in the world. Complex genetics and strong environmental effects hinder much progress in seed quality trait breeding in cotton. The use of molecular markers will improve our understanding of the genetic factors conferring seed quality traits, and it is expected to assist in selection of superior genotypes. This study was conducted to identify QTLs associated with seed physical traits and seed nutrient traits in cotton. To achieve this objective, a population of 140 BC₁S₁ lines developed from a cross between TM-1 and Hai 7124 was evaluated at Nanjing, China in 2003 and 2004. A linkage map consisting of 918 markers from this population was used to identify QTLs using QTLNetwork-2.0 software. Eleven single QTL were identified for kernel percentage, kernel oil percentage, kernel protein percentage, and seven amino acids (Asp, Ser, Gly, Ile, Leu, Phe, and Arg). Phenotypic variation explained by an individual QTL ranged from 10.89% to 46.28%. Two epistatic QTL for Cys and Leu were detected, explaining 9.55% and 4.43% of phenotypic variation. QTL detected for seed quality traits in cotton in this experiment are expected to be useful for further breeding programs targeting development of cotton with improved nutrient quality.