

Dissection of Genetic Effects of Quantitative Trait Loci (QTL) in Transgenic Cotton

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When alien DNA inserts into cotton genome in multi-copy manner, several QTL in cotton genome are disrupted, which are called dQTL in this study. Transgenic mutant line is near-isogenic to its recipient which is divergent for the dQTL from remaining QTL. So, a set of data from a transgenic QTL mutant line produced by *Agrobacterium*-mediated transformation, 30074, its recipient, their F₁ hybrids between them, and three elite lines were analyzed under a modified additive-dominance model with genotype by environment interactions in three different environments to dissect the genetic effects due to dQTL from the whole genome based genetic effects. Our result showed the dQTL had significant additive effects on lint percentage, boll weight, and boll number per square meter, while it had little genetic association with fiber traits, seed cotton yield, and lint yield. The dQTL in 30074 could significantly increase lint percentage and boll number, while significantly decreasing boll weight, had little effect on fiber traits, and those from recipient and three elite lines had significant genetic effects on lint percentage. In addition, the remaining QTL, other than the dQTL, had significant additive effects on seed cotton yield, fruiting branch number, uniformity index, Micronaire and short fiber index, and significant dominance effects on seed cotton yield, lint yield, and boll number per square meter. The additive effects and dominance effects in homozygous and heterozygous condition for each line were predicted also in the study.