



Mapping QTLs for drought tolerance in an $F_{2:3}$ population from an inter-specific cross between *Gossypium tomentosum* and *Gossypium hirsutum*

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ABSTRACT. Cotton is one of the most important natural fiber crops in the world. Its growth and yield is greatly limited by drought. A quantitative trait locus (QTL) analysis was therefore conducted to investigate the genetic basis of drought tolerance in cotton (*Gossypium* spp) using 188 $F_{2:3}$ lines developed from an inter-specific cross between a wild cotton species, *G. tomentosum*, and an upland cotton, *G.*

hirsutum (CRI-12). A genetic map was constructed using 1295 simple sequence repeat markers, which amplified 1342 loci, distributed on 26 chromosomes, covering 3328.24 cM. A field experiment was conducted in two consecutive years (2014 and 2015) and 11 morphological and physiological traits were recorded under water-limited (W1)/well-watered (W2) regimes at three growth stages (bud, flowering, and full boll). The traits measured included chlorophyll content, plant height, leaf area, leaf number, leaf fresh weight, leaf dry weight, boll weight, number of bolls per plant, and the number of fruiting branches. Sixty-seven and 35 QTLs were found under the W1 and W2 conditions, respectively. Of these, the majority exhibited partial dominance or over-dominance genetic effects for increasing the trait values. Four consistent QTLs were found under the W1 treatment on chromosomes 5, 8, 9, and 16, whereas no consistent QTL was found in W2. Thirteen QTL clusters were also identified on nine chromosomes (2, 3, 5, 6, 9, 14, 15, 16, and 21). These results will help to elucidate the genetic basis of drought tolerance in cotton.

Key words: *Gossypium*; Genetic map; Drought tolerance; Simple sequence repeat markers; Quantitative trait loci