

QTL Mapping of Genes Resistant to *Verticillium* Wilt in Cotton

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Abstract: A genetic linkage map was constructed using 136 F₂ individuals developed by a cross of *Gossypium hirsutum* cv. Handan208 × *G. barbadense* cv. Pima90. The linkage map comprised 99 loci mapped to 17 linkage groups with an average distance of 18.61 cM between markers, covering 1842.8cM, or approximately 36.8% of

the total cotton genome. This map was used to map the lesion length of vascular bundle, which is a factor associate with *Verticillium* wilt, by both one-factor analysis and composite interval methods. Three QTLs were detected on two linkage groups, and explained 15.39%, 54.11% and 57.18% of the phenotypic variance, respectively, which might mean that the resistance of V. wilt is controlled by two major QTLs and one minor QTL.

Key word: cotton; *Verticillium* wilt; molecular markers linkage map; QTL mapping