QTL MAPPING OF RESISTANCE TO ROOT-KNOT NEMATODES IN THE WILD COTTON GERMPLASM LINE M-495 RNR

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Abstract

Root-knot nematode (RKN) has the potential to cause significant economic loss in upland cotton (Gossypium hirsutum L.). The development and use of cultivars with resistance to RKN offers the best management tool for RKN. However, the progress in developing RKN resistant cultivars is hampered by the current screening process for identifying resistance genotypes that is tedious, time consuming and destructive. Our long-term goal is to develop a ‘breeder friendly’ selection tool to allow effective manipulation of RKN resistance in breeding programs. In this study, our objective is to identify quantitative trait loci (QTLs) for nematode resistance in cotton. A genetic linkage map was constructed by the F2 segregation population derived from a cross between M495, a RKN resistant cotton line, and Pima S6, a RKN susceptible line. We identified 346 polymorphic loci with 275 pairs of SSR primers. The genetic map with 288 loci was constructed, which had a whole length of 1984.8 cM and covered 39% of the whole cotton genome. Moreover, the galling index of the F2 plants were analyzed by composite interval mapping (CIM) and 2 putative QTLs were detected for galling index on Chromosome 11 and 20, respectively. These QTLs explained their corresponding phenotypic variations with 23.38% and 9.20%, respectively. These results provide references for screening nematode resistant progenies in the breeding population.