MAPPING AND QTL IDENTIFICATION OF SSR MARKERS ASSOCIATED WITH ROOT KNOT NEMATODE RESISTANCE IN THREE RIL POPULATIONS OF UPLAND COTTON

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Abstract

The root-knot nematode (RKN) is a serious pathogen of cotton growing regions of the U.S. The use of resistant varieties potentially would be the most economical and environmentally safe method to control RKN; however, information regarding markers linked to resistance is still limited. The objectives of this study were: 1) to detect SSR markers linked with RKN genes in three RIL populations segregating for RKN resistance; 2) to map these markers to specific chromosomes to facilitate marker assisted selection. The test included three recombinant inbred line (RIL) populations developed from the crosses of resistant parent M240, moderate resistant Clevewilt 6-1 and susceptible parent ST213 (Clevewilt 6-1 x M240, Clevewilt 6-1 x ST213 and M240 x ST213). These populations were grown in greenhouse conditions, inoculated with RKN eggs, and scored for gall index and number of eggs per plant. DNA samples were taken from plants of all populations and genotyped with simple sequence repeat (SSR) markers. Results indicated that a minimum of two major genes are involved in the Auburn source of RKN resistance (i.e. M240). One gene is located on chromosome 11 and linked to the marker CIR 316-202. This CIR 316-202 allele is present in Clevewilt 6-1, which is one of the parents of Auburn 623RNR, and in all RKN resistance sources with the exception of M155. Another gene is on chromosome 14 and is linked to the markers BNL 3545-118, BNL3644-195, and BNL3661-185. These three alleles are present in Mexico Wild, which is the other parent of Auburn 623RNR, and in all of the RKN resistance sources with the exception of M120. The SSRs identified in this study could be used to select plants with higher levels of RKN resistance in segregating populations. A project to test this recommendation is currently under progress.