MAPPING OF SSR MARKERS ASSOCIATED WITH RENIFORM NEMATODE RESISTANCE IN AN INTERSPECIFIC CROSS OF *GOSSYPIUM*

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Abstract

The reniform nematode (RN), *Rotylenchulus reniformis* Linford & Oliveria, is an important pathogen of Upland cotton (*Gossypium hirsutum* L.) in the Southern US. The discovery of molecular markers closely associated with RN resistance gene (s) in the *G. barbadense* L. accession GB713 would be very helpful in cotton breeding programs. In the present study, our objectives were to: (i) discover simple sequence repeat (SSR) markers linked with GB713 RN resistance Quantitative Trait Loci (QTLs), and (ii) map associated SSR markers to specific chromosomes. We scored 300 F_2 plants from the cross of GB713 × Acala Nem-X for RN reproduction which was expressed as the percentage of the reproduction on Acala Nem-X, nematodes per gram soil (RN g^{-1}soil), and $\log_{10}(X+1)$ nematodes per gram soil (log RN g^{-1}soil). This interspecific F_2 population was fingerprinted with SSR markers that covered most of the chromosomes of cotton. Results indicated one QTL on chromosome 21 was at map position 168.6 (LOD 28.0) flanked by SSR markers BNL 1551_162 at position 154.2 and GH 132_199 at position 177.3. A second QTL on chromosome 21 at map position182.7 (LOD 24.6) was flanked by SSR markers BNL 4022_199 at position 180.6 and BNL 3279_106 at position 184.5. A third QTL with relatively small genetic effects was localized on chromosome 18 at map position 39.6 (LOD 4.0) flanked by SSR markers BNL 1721_178 at position 27.6 and BNL 569_131 at position 42.9. These SSR alleles should help in the selection of plants with high levels of RN resistance in segregating populations. Following the previously established notation used for naming *G. longicalyx* and *G. aridum* sources of resistance, we suggest the use of Ren^{barb1}, Ren^{barb2}, and Ren^{barb3} to designate these QTLs on the chromosome 21 and chromosome 18, respectively.