MARKER ASSISTED SELECTION FOR RENIFORM NEMATODE RESISTANCE USING SNP

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<u>Abstract</u>

The reniform nematode (RN), *Rotylenchulus reniformis* Linford & Oliveira, is an important pest of cotton and causes an estimated annual loss of \$100 million in United States alone. Discontinuation of nematicides such as TEMIK® had necessitated development of varieties with host RN resistance. RN resistance had been previously identified in diploid K-genome species *Gossypium longicalyx*, and in Inca GB713, a tetraploid wild Mexican race belonging to *G. barbadense* species. However, lack of commercial cotton cultivars with natural host resistance to reniform nematode is limiting cotton productivity. Previous efforts to identify QTL regions associated with RN resistance from the resistant sources were successful using Simple Sequence Repeat (SSR) markers (Gutiérrez et al., 2011). But single nucleotide polymorphisms (SNPs) are marker of choice for high throughput, automatable screening of large populations. Here we report SNP markers associated with RN resistance from Inca GB713 source. An interspecific mapping population was constructed by crossing an upland RN susceptible genotype with Inca GB713 and was used for phenotyping, genotyping and trait mapping purposes. Two QTLs, a major QTL on chromosome 18 were identified and had explained up to 37% of total phenotypic variation in RN resistance. These SNP markers would enable marker-assisted selection of resistant plants to expedite development of improved commercial cultivars through precision breeding.