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SSR Marker(s) Associated with Root Knot Nematode Resistance Gene(s) in Cotton

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Root-knot nematode [*Meloidogyne incognita* (Kofoid and White) Chitwood] is a major pest on cotton (*Gossypium hirsutum* L.) across the U. S. Cotton Belt. DNA markers that enable marker-assisted selection for root-knot nematode resistance gene(s) will foster development of root-knot nematode-resistant cultivars. The objectives of this research were 1) to identify DNA markers associated with the resistance to root-knot nematodes in upland cotton, and 2) to determine the mode of inheritance of the root-knot nematode resistance gene(s). The moderately resistant line, Cleve wilt 6-1, and the susceptible cultivar, Stoneville 213, were crossed. The resulting F₁ and F₂ populations and both parents were genotyped using 120 simple sequence repeat (SSR) primer pairs, providing 16 polymorphic markers. Gall indices, which were the best measure of resistance, were used to determine that the population fit a 3:1 Mendelian segregation ratio (susceptible: resistant). Phenotypic and marker data indicate that Cleve wilt 6-1 was likely the source of the recessive gene for resistance to galling. The molecular marker BNL 1421 explained 8% of the variation in gall index in the segregating F₂ population. Mapmaker analysis indicated that BNL 1421 and BNL 1669 were linked with a distance of 15.4 cM. Both of these markers showed distorted segregation. The small effect of BNL 1421 on resistance could be due to the weak linkage of the marker with the root-knot nematode resistant trait or to false linkage, because they segregated abnormally.