# USING SSR MARKERS TO SELECT FOR ROOT-KNOT NEMATODE RESISTANCE IN A COTTON BREEDING PROGRAM

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## Abstract

The root-knot nematode (*Meloidogyne incognita* (Kofoid and White) Chitwood) [RKN] is a serious cotton (*Gossypium hirsutum* L.) pest causing substantial yield loss throughout the United States. Common methods of managing RKN infestations include crop rotation, nematicides and resistant cultivars. Although developing RKN resistant cultivars through traditional breeding methods is a time consuming and often difficult process, it is arguably the most effective and cheapest option available. Breeding for RKN resistance traditionally involves scoring the number of galls found on the roots of plants grown in RKN infected soils, either in a greenhouse or in a field situation. These methods are time consuming, expensive and can be inaccurate. Development of effective marker assisted selection (MAS) techniques using methods such as simple sequence repeat (SSR) primers could potentially have a large impact on a breeder's ability to effectively develop RKN resistant cultivars and sidestep some of the problems of traditional breeding methods. Two populations were developed through crosses using M240 and LA887, two RKN resistant lines, along with a common parent LA1110147, a suspected susceptible line. Correlation analysis revealed that SSR marker BNL1231 may be useful in screening plants derived from M240 for RKN resistance. Analysis also showed that SSR marker BNL1231 may be useful in screening populations derived from LA887 although the correlation was not as strong. We suggest that the usefulness of this marker may vary depending on the pedigree of the parents used to create the population. Our data indicate that SSR marker CIR316 may be of limited value for selecting for resistance in our populations. Most of the published research shows an excellent correlation between CIR316 and RKN resistance. This has been done primarily in interspecific crosses between *Gossypium hirsutum* L. and *Gossypium barbadense* L. It is possible that CIR316 may not be polymorphic enough in intraspecific populations, or that our electrophoresis method is not of high enough resolution, to make useful distinctions between resistant and susceptible plants in intraspecific *G. hirsutum* L. x *G. hirsutum* L. crosses such as in our study.