MARKER ASSISTED SELECTION FOR NEMATODE RESISTANCE – PROGRESS

Ted P. Wallace
Peggy M. Thaxton
Jim Nichols
Mississippi State University
Mississippi State, MS
Brian E. Scheffler
USDA-ARS Genomics and Bioinformatics Research Unit
Stoneville, MS
Jodi A. Scheffler
USDA-ARS Crop Genetics Research Unit
Stoneville, MS

Abstract

Losses in yield attributed to nematodes have increased over recent years, especially in the southeastern states. Unfortunately, the entire species of upland cotton (*Gossypium hirsutum*) is considered susceptible to the reniform nematode. Although cotton is considered to be somewhat tolerant to root-knot nematodes, few varieties are considered resistant. A major development in the realm of nematode resistance came about when researchers at Texas A&M developed a reniform resistant upland breeding line via introgression from a wild species of cotton (*Gossypium longicalyx*). However, reports of stunting and other agronomic shortfalls associated with the original reniform resistant breeding line, designated "Lonren", have prevented the immediate use of resistance in commercial varieties. In 2007, a breeding program was initiated at Mississippi State University aimed at developing reniform resistant breeding lines adapted to Mississippi with desirable agronomic properties. Although an emphasis has been placed on developing reniform resistance breeding lines, combining resistance to both reniform and root-knot nematodes is also an important objective of the breeding program. Populations were developed from hybridization of reniform and root-knot nematode resistant breeding lines with elite public breeding lines and obsolete varieties. Following a seed increase in Tecoman, Mexico, F2 plants were subject to marker assisted selection (MAS). Previous selections (F2:F3) were planted as progeny rows and tested for homogeneity of resistance. Ninety F2 populations and 151 F2:F3 progeny rows were subject to MAS based upon markers for reniform (BNL3279) and root-knot (BNL3661 & CIR316ND) resistance. A total 5890 leaf samples were subject to marker analysis. Selection for root-knot resistance was ultimately based on the single marker CIR316ND due to unresolved difficulties encountered with the BNL3661 marker. Approximately 120 MAS F2 plants representing single species resistance, and 29 plants with genes for resistance to both species, were harvested for evaluation as progeny rows in 2012. The most important criteria for MAS of F2 resistant plants were absence of stunting and number of bolls produced. An unexpected amount of segregation was observed in F2:F3 progeny rows derived from homozygous resistant F2 plants. This observation raised questions concerning the ability to correctly tag and sample such a large volume of plants, and resulted in a decision to reduce the total number of samples (plants) for testing in 2012. Progeny rows with at least 80% of plants homozygous for resistance were subject to row selection, while remaining rows were subject to MAS of individual plants. As a result, 29 F2:F3 rows were selected and 100 individual F2:F3 plants were selected. Approximately half of the of the individual plants selected possessed genes for resistance to both nematode species. In addition to MAS for nematode resistance, 69 F4 and F5 breeding lines derived from reniform resistant plant selections, were evaluated in a replicated trial for yield and fiber quality traits. Lint yield varied from over 1300 lbs/a to less than 400 lbs/a. Top performing entries will be tested to confirm presence of marker (BNL3279) prior to multi-location yield testing in 2012. An evaluation for performance when grown in nematode infested soils, both in the greenhouse and in the field, will be carried out to confirm resistance.