

**RESISTANCE TO RENIFORM NEMATODE FROM *G. HIRSUTUM* AND
G. LONGICALYX SOURCES: A COMPARISON**

Çiğdem Sürmelioglu

Roelof Sikkens

Rachel Sharpe

Department of Agronomy and Soils, Auburn University

Auburn, AL

Scott Moore

Department of Entomology and Plant Pathology, Auburn University

Auburn, AL

Edzard Van Santen

Department of Agronomy and Soils, Auburn University

Auburn, AL

Kathy Lawrence

Department of Entomology and Plant Pathology, Auburn University

Auburn, AL

David Weaver

Department of Agronomy and Soils, Auburn University

Auburn, AL

Cotton, *Gossypium* spp., is a significant fiber crop which is harvested in almost every tropical country as well as in many parts of the subtropical world. It is the fourth most important row crop in the U.S. and the most important industrial crop, with a farm-value of more than \$5.6 billion in 2007. Its diversity of use in different areas such as textile, food, feed, and chemical industries makes it a miracle crop and cotton will continue to be a major agricultural commodity in the upcoming years. Besides several pests affecting cotton, nematodes are of major concern. Reniform nematode, *Rotylenchulus reniformis* is the number one nematode pest of cotton in the U.S. *Gossypium longicalyx*, *G. herbaceum*, *G. arboreum* are the wild cotton accessions that are highly resistant to reniform nematode. The sedentary semi-endoparasitic parasite affects cotton through reductions in yield, boll size, and lint percentage.

The reniform nematode was first reported in upland cotton in Georgia and Louisiana and has been increasing as a pest problem of cotton in the U.S. especially in Alabama, Louisiana, and Mississippi. Adapted upland cotton cultivars lack genetic resistance, so only nematicides and crop rotation have been used as management options. Unfortunately, these options may not be good from an economic standpoint and so are not preferred by producers. Consequently, genetic resistance would be a very attractive management option for both breeders and producers. Because the nematode causes a \$400 million loss annually in cotton production, a reniform nematode resistant upland cotton germplasm would be beneficial to the cotton industry.

Recently, molecular approaches have been applied in the development of reniform nematode resistance in upland cotton, particularly in the area of searching for and incorporating resistance from resistant related species. *G. hirsutum*, being an allotetraploid, makes introgression from related species difficult since other cotton species are mostly diploids. Recent studies have mostly focused on the use of simple sequence repeats (SSR) that are between 1-6 base pairs as molecular markers for reniform nematode resistance.

In a previous study by our research group, several upland cotton accessions were found to be moderately resistant to reniform nematode. Two of those accessions, TX 245 and TX 1419, had very low nematode numbers in comparison to control PM 1218, an adapted cultivar. TX 245 and TX 1419 were then used as parents to incorporate resistance into adapted germplasm. Major objectives of our study were to evaluate resistance to reniform nematode from *G. hirsutum* and *G. longicalyx* sources and to determine the inheritance of resistance to reniform nematode within F_{2,3} progenies of resistant parent LONREN1 (*G. longicalyx* source), moderately resistant TX 245 and TX 1419 (*G. hirsutum* source), adapted PM 1218, and FM 966. Reniform nematode screening was conducted on F_{2,3} progenies of TX245 × PM1218 and TX1419 × PM1218 crosses including TX 245, TX 1419, PM1218, and LONREN1 as the control group in one of the experiments. In the second experiment, F_{2,3} progenies of LONREN1 × FM 966 were evaluated and PM1218 (adapted cultivar), LONREN1, LONREN1m, and LONREN2 (highly resistant) were the control group. Seeds were planted in the greenhouse and plants were inoculated with 1000 nematode juveniles one week after the planting. Nematode extractions were done via Baerman funnel technique sixty days after inoculation

and nematodes were counted under a light microscope to determine nematode reproduction. Reniform nematode numbers per gram of plant root were analyzed via SAS. Entries in both of the experiments were evaluated in sets (10 reps/ set). Progenies of TX lines were evaluated in 6 sets (23 entries, including controls/set) whereas LONREN progenies were evaluated in 5 sets (25 entries, including controls/set).

In the first experiment, neither the progenies nor the parents (PM 1218 and TX 245) showed resistance to reniform nematode in comparison to the highly resistant LONREN1. Results were similar for TX 1419 and its progenies. Results from the previous study could not be repeated. However, there were 21 promising progenies within the distribution among 100 progenies of LONREN1 \times FM 966 cross in the second experiment. Those promising progenies had very low nematode numbers similar to the highly resistant parent LONREN1.

In conclusion, results from the previous studies regarding resistance of *G. hirsutum* accessions could not be repeated. No resistance was found within TX lines; *G. hirsutum* is still lacking in resistance. However, *G. longicalyx* source LONREN1 is much superior to *G. hirsutum* in resistance to reniform nematode. Also, 21% of F_{2:3} progenies of LONREN1 \times FM 966 had low nematode numbers similar to resistant LONREN1.