

**PROGRESS REPORT ON INTROGRESSION OF RENIFORM NEMATODE
RESISTANCE FROM *G. LONGICALYX* INTO UPLAND COTTON**

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Abstract Only

In a long-term cotton improvement project being conducted jointly by USDA-ARS and Texas A&M University at College Station, TX, resistance to the reniform nematode is being introgressed into Upland cotton from *Gossypium longicalyx*. The objective is a package of breeding lines and genetic markers that will allow the cotton seed industry to quickly incorporate a high level of resistance to the reniform nematode in contemporary cultivars. To achieve introgression, two triple species hybrids are being used as bridges between *G. hirsutum* and nematode-immune *G. longicalyx*. The resistance trait in our material is inherited like a single dominant gene and we are introgressing it by backcrossing onto *G. hirsutum* repeatedly, selecting for resistance at each generation. The project integrates interactive components focused on breeding, resistance evaluation, cytogenetic analysis, field evaluation, and marker development to maximize speed and likelihood of success. During the last 2 years since our last progress report on the breeding component of the project at the Beltwide Conferences, we have conducted hundreds of crosses and evaluated more than 1,700 progeny for resistance. We are carrying forward 28 progeny lines, each of which was generated from a single resistant plant produced by crossing *G. hirsutum* onto one of the two male-sterile hybrids mentioned above. As of this date, we have advanced and recovered resistance in two progeny lines through the third, 18 through the fourth, six through the fifth, one through the sixth and one through the seventh backcross generation. Heterozygous resistant plants in the eight families advanced to the fifth and greater backcross generations, are virtually immune to the reniform nematode, cytogenetically normal, and morphologically indistinguishable from agronomic cotton under greenhouse conditions. We are in the process of self-pollinating advanced resistant plants in several families, and conducting test crosses of the progeny produced, in order to generate and identify plants homozygous for the resistance gene(s). We also have made considerable initial progress toward the development of AFLP markers co-segregating with resistance.