

**CHARACTERIZATION OF *FUSARIUM OXYSPORUM* GENOTYPES CAUSING
WILT IN GEORGIA COTTON**

A. A. Bell

**Southern Plains Agricultural Research Center, Agricultural Research Service, USDA
College Station, TX**

R. C. Kemerait

**Department of Plant Pathology, University of Georgia
Tifton, GA**

C. S. Ortiz

S. Prom

**Department of Plant Pathology and Microbiology, Texas A&M University
College Station, TX**

J. Quintana

**Southern Plains Agricultural Research Center, Agricultural Research Service, USDA
College Station, TX**

R. L. Nichols

**Cotton Incorporated
Cary, NC**

J. Liu

**Southern Plains Agricultural Research Center, Agricultural Research Service, USDA
College Station, TX**

Abstract

Since 2011, severe outbreaks of Fusarium wilt of cotton in Georgia have raised concerns about the genotypes of the causal pathogen, *Fusarium oxysporum* forma speciales *vasinfectum*. We recovered 492 *F. oxysporum* isolates from 107 wilted plants collected from 7 fields in 5 counties, and determined their relatedness utilizing vegetative complementation (VC) tests and DNA sequence analysis. Eight VCGs, VCG0111 (race 1), VCG0112 (race 2), VCG01117B, VCG01117C, VCG01118, VCG01119 (race 8), VCG01120 and VCG01121, were found and their phylogenetic relationships determined. VCG01121 has never before been reported, but was the most commonly isolated VCG in this collection. This VCG was especially prominent in Berrien County, the center of the outbreaks. Two pathogenicity tests that can distinguish vascular competent isolates from root-rot pathotype isolates were used to characterize the 8 VCGs. All 8 VCGs were the vascular competent pathotype and in our assays required root-knot nematode (*Meloidogyne incognita*) to cause wilt. Therefore, use of nematode resistance cultivars seems a viable approach to control this disease in Georgia when appropriate. Management of plant-parasitic nematodes to reduce the impact of Fusarium wilt can also be accomplished through use of nematicides.