

**TRACKING ASPERGILLUS FLAVUS INFECTION IN COTTONSEED TO PREVENT PREHARVEST
AFLATOXIN CONTAMINATION****K. Rajasekaran****J. W. Cary****D. Bhatnagar****T. E. Cleveland****USDA-ARS, SRRC****New Orleans, LA****Abstract**

An understanding of the pathogenic diversity present in a population of a given disease organism is necessary for the effective development and deployment of host-plant resistance. The need for rapid and accurate diagnostic tools for identifying races or genotypes of the Fusarium wilt pathogen, *Fusarium oxysporum* f. sp. *vasinfectum*, has increased since it was shown that populations in the United States are no longer limited to races 1 and 2. Multi-gene phylogenies have revealed the presence of races 3, 4, and 8, as well as four novel genotypes in the U.S. A DNA-based macroarray using the translation elongation factor gene was developed to rapidly and accurately identify races 1, 3, 4, 8, and Australian biotypes. A broad understanding of the genetic diversity of this fungus is a first step toward characterizing its pathogenic diversity.