EXPERIENCES IN BREEDING FOR FOV4 RESISTANCE/TOLERANCE IN UPLAND AND MOLECULAR BREEDING OPPORTUNITIES

Mauricio Ulloa
USDA-ARS, PA, CSRL, Plant Stress and Germplasm Development
Lubbock, TX
Robert B. Hutmacher
Tari Lee Frigulti
West Side Research and Extension Center
University of California
Five Points, CA
Margaret L. Ellis
Department of Plant Science
California State University
Fresno, CA
Robert L. Nichols
Cotton Incorporated
Cary, NC
Sukumar Saha
USDA-ARS, SA, CSRL, Genetics and Sustainable Agriculture Research.
Mississippi State, MS
David M. Stelly
Texas A & M University
College Station, TX
Philip A. Roberts
University of California Riverside
Riverside, CA

Abstract

Fusarium oxysporum f. sp. *vasinfectum* (*Fov*) race 4 (FOV4) has been a threat to cotton production in the San Joaquin Valley of California for over 15 years, and recently this pathogen has been identified in the El Paso, TX area. Isolates of FOV4 that were not previously known in North America and that are extraordinarily pathogenic on cotton have been found in the U.S. The disease is a continuing problem, contaminating soils and causing cotton yield losses when susceptible varieties are grown. Symptoms of FOV4 in cotton (*Gossypium* spp.) differ between Pima (*G. barbadense*) and Upland (*G. hirsutum*) types. Early season (1st to 8th leaf) mortality is an important phenotypic trait for identifying tolerance/resistance in both Upland and Pima germplasm. In some infected Upland lines early, foliar symptoms are not evident. The most diagnostic symptom of FOV4 in Upland cotton is basal vascular staining. Staining can be limited to the hypocotyl, upper tap root, and lateral roots. Host-plant resistance and planting tolerant/resistant cultivars is an effective strategy to manage FOV4 damage and limit losses in cotton. Progress has been made in identifying and developing resistant/tolerant Pimas. A high level of tolerance to FOV4 was identified in a commercial Pima cotton (*G. barbadense* L.), Phytogen 800®. The source of the tolerance is believed to have originated in Pima S-6 germplasm. So far, high resistance/tolerance has not been reported among U.S. released Upland cotton cultivars or lines. USDA-ARS and Univ. of California, with the support of Cotton Inc, CA Cotton Alliance and CA Cotton Growers Association, have conducted research and identified potential good Upland FOV4-tolerant germplasm for future germplasm releases. Additional research on FOV4 phenotypic disease response-evaluations, and genetic and QTL mapping analyses on germplasm, progeny, mapping populations, and cotton chromosome substitution lines, identified molecular markers such as SSRs and SNPs (using the SNP63K cotton array), and specific chromosomal regions associated with FOV4 resistance/tolerance. Resistant/tolerant cultivars or germplasm may not express similar modes of inheritance of resistance when they are derived from different genetic backgrounds or are challenged by different *Fov* races of different geographic origin. The postulated pathogenicity mechanisms and the inheritance of *Fov* resistance significantly differ among *Fov* races for cotton genotypes. Previous reports indicated FOV4 resistance is associated with a complex allelic-recombination and duplicated marker-loci between chromosomes 14 and 17. Genomic islands or regions on chromosomes 3, 6, 8, 11, and 25 have also been reported to be associated with allelic dosage for FOV4 tolerance. Additional QTL analyses revealed that cotton genotypes and progeny share quantitative resistance genes for plant defense against *Fov* races (1, 4, and 7). With the recent identification of FOV4 in Texas and the proximity of this pathogen to the largest Upland cotton producing region underscore the urgent need to expeditiously elevate FOV4-tolerance/resistance levels of the elite U.S. Upland gene pool to reduce vulnerability in the cotton industry.