EVALATION AND GENETIC ANALYSIS OF VERTICILLIUM WILT RESISTANCE IN THE US

UPLAND COTTON Abdelraheem Abdelraheem Soum Sanogo Jinfa Zhang New Mexico State University Las Cruces, NM V. Kuraparthy North Carolina State University Raleigh, NC Amanda Hulse-Kemp Texas A & M University **College Station, TX David Stelly** Texas A & M University **College Station, TX** Lori Hinze **Crop Germplasm Research College Station, TX Don Jones Cotton Incorporated** Cary, NC

<u>Abstract</u>

Verticillium wilt (VW) is one of the major problems in Upland cotton production in the US and worldwide. VW is caused by Verticillium dahliae (Kleb.), which is a soil borne fungal pathogen with a broad range of hosts. Severe infections with VW can cause leaf necrosis, stem discoloration, plant wilting, defoliation and plant death, resulting in yield loss and reduction on fiber quality. The most effective method of controlling VW is to develop resistant cotton cultivars; however, resistance sources of VW in Upland cotton are lacking and the genetic basis of VW resistance is currently poor understood. In breeding for other traits under non-VW field conditions, desirable genes or alleles for VW resistance are randomly fixed. Therefore, a genome-wide association study (GWAS) can be used to identify molecular markers associated with cotton cultivars and breeding lines with VW resistance. In this study, an association mapping panel comparing of 376 Upland cotton accessions collected from 14 different cotton production states was used to assess VW based on four replicated tests in the greenhouse. The genotypes were arranged in a randomized complete block design with two replicates and to perform a GWAS to identify associated markers for VW resistance using a 63K SNP Array. Inoculations were made when seedlings were at 2-3 true leaf stage with V. dahliae followed by screening for VW resistance 30 and 52 days after inoculation. A disease severity rating for each plant was determined based on scale from 0-5 rating scale, where 0 for no symptoms and 5 for a full plant defoliation and/or plant death. The number of total leaves, infected leaves and defoliated leaves were counted for each plant to calculate percentages of infected leaves and defoliated leaves. Statistical significant differences were detected for genotype, tests and their interactions for all parameters expect for percentage of infected plants, indicating that a uniform inoculum was made with minimal escapes. The results showed that germplasm developed in the southwest region had the lowest VW disease severity ratings, indicating that they carry more resistance genes and/or alleles against VW. Although VW resistance QTL (quantitative trait loci) detected were distributed on the entire tetraploid genome based on general linear and mixed linear models, the majority of the markers associated with VW resistance were on chromosomes 5, 7, 16, 19, 2, and 24. Furthermore, chromosome 23 had the highest number of marker associated with VW resistance and these markers were clustered at 10 and 30-35 Mb regions. The results will facilitate the understanding of the molecular genetic basis of VW resistance and marker-assisted selection for VW resistant cultivars in Upland cotton.