## PHYLOGENETIC ANALYSIS BASED ON THE PKS GENE INVOLVED IN FUSARIC ACID BIOSYNTHESIS REVEALS CLOSE RELATIONSHIP BETWEEN US RACE 1 LINEAGE ISOLATES AND AUSTRALIAN BIOTYPE ISOLATES OF *FUSARIUM OXYSPORUM* F. SP. *VASINFECTUM*

J. Liu A. A. Bell R. D. Stipanovic L. S. Puckhaber USDA-ARS-SPARC College Station, TX

## <u>Abstract</u>

Isolates of Fusarium oxysporum f. sp. vasinfectum, the causal agent of fusarium wilt of cotton, vary significantly in their virulence. Isolates have been further subcategorized into pathogenic races based on their differential interaction with host genotypes. Phylogenetic analysis based on three nuclear genes revealed several lineages consisting of race 1 (includes race 2 and 6), race 3 (includes race 5), race 4 (includes race 7), race 8, and Australian biotype lineages. The Australian lineage is the most distantly related among the lineages. Because the pathogenicity of a pathogen is primarily dependent on its virulence factors, using virulence factor related genes for the phylogenetic analysis may reveal better relationships of various pathotypes in terms of host specificity and disease mechanism. We have previously identified and cloned a PKS gene involved in fusaric acid biosynthesis and confirmed that fusaric acid, a potent phytotoxin of cotton, plays an important role in the pathogenicity of the Australian biotype isolate. The objective of this research was to test whether the phylogenetic analysis based on partial sequences of this PKS gene can provide disease mechanism based relationships among existing races and biotypes. Our results with PKS gene genealogy revealed close relationship among US race 1 lineage isolates, the Australian biotype lineage isolates, and the Australian Seed isolate that had similar host ranges and pathogenicity. Therefore, phylogenetic analysis based on partial sequences of the PKS gene involved in the biosynthesis of a virulence factor fusaric acid can provide disease mechanism based relationships among existing races and biotypes and reveals better correlation with isolates' pathogenicity and host ranges.