SCREENING MICROBIAL RESISTANCE TO FUSARIC ACID, AN ANTIBIOTIC AND PHYTOTOXIN PRODUCED BY FUSARIUM WILT PATHOGENS F. K. Crutcher Southern Plains Agricultural Research Center, Agricultural Research Service, USDA **College Station, TX** and Eastern Agricultural Research Center, Montana State University Sidney, MT L. S. Puckhaber R. D. Stipanovic A. A. Bell Southern Plains Agricultural Research Center, Agricultural Research Service, USDA **College Station, TX** R. L. Nichols **Cotton Incorporated** Carv, NC K. S. Lawrence Department of Entomology and Plant Pathology, Auburn University Auburn, AL J. Liu Southern Plains Agricultural Research Center, Agricultural Research Service, USDA **College Station**, TX

<u>Abstract</u>

Fusaric acid (FA), produced by fungal pathogen Fusarium oxysporum f. sp. vasinfectum (FOV), is likely a key intermediate in development of Fusarium Wilt of cotton (Gossypium spp.) and may also function as a defense against other soil microbes. Several microbes we tested appear to have evolved unique detoxification mechanisms of FA. We screened bacteria and fungi from soils infested with FOV and from laboratory sources to evaluate their ability to grow in the presence of FA and to alter the structure of FA into less toxic compounds. Bacterial strains failed to chemically modify FA. However certain Gram-negative bacteria, mainly in the genus of Pseudomonas, were found to be highly resistant. The FA resistance was positively correlated with the number of genes predicted to be FA efflux pumps in the genome of the bacteria. Phylogenetic analysis revealed that fusaric acid resistant protein family (FUSC) efflux pump proteins having high sequence identities with the functionally characterized FA resistance proteins FusC or Fdt might be the major contributors of FA resistance. Most fungi, on the other hand, converted FA to less toxic compounds regardless of the level of FA resistance they exhibited. Five conversion products were detected. The detoxification of FA involved either oxidation of the butyl side chain or reduction of the carboxylic acid group. Production of structurally related derivatives from widely different phyla indicates that resistance to FA by altering its structure is highly conserved. A few FA resistant saprophytic or potential biocontrol strains of fungi failed to alter FA, which suggested possible involvement of efflux transporters. FOV also utilized major facilitator superfamily transporter to pump out FA. Deployment of efflux and/or derivatization mechanisms may be a common feature of fungal FA resistance.