GENOTYPIC EVALUATION OF CURRENT FIELD POPULATIONS OF *FUSARIUM OXYSPORUM* F. SP. *VASINFECTUM* ISOLATES FROM CALIFORNIA

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Abstract

Fusarium wilt caused by *Fusarium oxysporum* f. sp. *vasinfectum* (FOV) race 4 has been a recurring and expanding threat to cotton in California. It was first identified in the United States in the San Joaquin Valley of California in 2001. More recently FOV race 4 was reported in the Upper Rio Grande Valley in El Paso and Hudspeth counties in Texas in 2017 and in Las Cruces and Berino, New Mexico in 2019. It was previously thought that FOV race 4 was a clonal population in California based on DNA sequencing of the translation elongation factor (EF-1α), phosphate permease (PHO), and beta-tubulin genes, and RFLP analysis. However, our results confirm there are two common genotypes present in California cotton fields. *Fusarium* isolates were collected from symptomatic cotton plants in 13 commercial fields in the San Joaquin Valley during the 2017 to 2019 growing seasons. Isolates were identified to species using DNA sequencing of the EF-1α gene. Based on the EF-1α gene, there were a total 179 isolates of *F. oxysporum* and two isolates of *F. solani*. For *F. oxysporum* isolates, FOV race 4 specific primers identified 171 isolates as FOV race 4. Further genotyping of the FOV race 4 isolates was assessed using primers that identified the absence (N genotype) or presence (T genotype) of the insertion of the transposable element *Tfo1* in the PHO gene unique to some FOV race 4 isolates. Our results identified 112 FOV race 4 isolates as the T genotype and 59 isolates as the N genotype. These results confirm previous findings where a selection of historical isolates from California from 2001 to 2014 were genotyped using the same set of primers. The majority of the historical isolates tested were the T genotype, while one isolate from Merced county was identified as the N genotype. In this study, both the N and T genotypes were commonly isolated from symptomatic cotton collected from fields in Merced county. Although at a lower frequency than the T genotype, the N genotype was also isolated from symptomatic cotton from fields in Kern, Kings, and Tulare counties where it has not previously been reported. Currently, studies are being conducted to determine if the two FOV race 4 genotypes common in California cotton fields respond similarly to Pima and Upland germplasm with high to moderate levels of tolerance.