A PCR-BASED METHOD FOR THE IDENTIFICATION OF HIGHLY PATHOGENIC CALIFORNIA RACE 4 ISOLATES OF *FUSARIUM OXYSPORUM* F. SP. *VASINFECTUM*

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Abstract

Reliable detection methods for the early identification of pathogen infested fields and seeds lots are imperative to decrease crop loss and pathogen movement. A highly virulent California race 4 (Cal race 4) isolate of *Fusarium oxysporum* f. sp. *vasinfectum* (Fov) was first identified in 2001 in California cotton fields. The pathogen can cause severe wilt of cotton even in the absence of nematodes. Available detection methods for this pathogen have been previously developed, but false positive results have been observed with non-target race 3 and 7 isolates. We have developed a new, PCR based, identification method based on a genomic-transposon junction region unique to Cal race 4 isolates. A three-primer multiplex PCR system has been designed where amplicon size differentials discern between Cal race 4 isolates and isolates belonging to other Fov races, including the race 4 reference strain. Ninety four Fov isolates, one isolate each from 10 other *F. oxysporum* formae speciales, and a *F. verticillioides* isolate were tested and delivered the expected results. Additionally, 12 cotton-associated fungal species of diverse genera were analyzed and failed to produce an amplicon of either size. The developed multiplex PCR assay was reliable in detecting Cal race 4 isolates with no cross reactivity found to date; providing a tool for the specific detection of the highly pathogenic Fov Cal race 4 isolates.