MOLECULAR AND DISEASE CHARACTERIZATION OF *VERTICILLIUM DAHLIAE* ISOLATES FROM CHINA

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Abstract

Verticillium wilt is a serious disease of cotton in cooler cotton producing areas in the world. For effective management of the disease, it is imperative to know the underlying pathogen population. In 2015, we collected stem sections from wilted plants from seven counties of Southern and Northern Xinjiang regions in China. The stems were air-dried and shipped to USDA-ARS Cotton Pathology lab in College Station, TX. Stems were surface sterilized, cut in half, and placed on Komada medium. Eighty-five fungal isolates were obtained and found to be *Verticillium dahliae*. The isolates were divided into several genotypes based on PCR amplification with primers to VdD (defoliating), VdND (non-defoliating), Vd*Ave*1 (race 1) and race 2. All belonged to mating type MAT1-2, were positive for race 2, and negative for race 1 (Ave1). The isolates were separated based on VdD and VdND amplification and PHO sequence. 36% of the isolates were VdD, 55% were VdND, and 8% (or seven isolates) did not have either a VdD or a VdND PCR product. The PHO gene was sequenced for 83 isolates. The PHO types for defoliating strains are VCG1A and CHv1963. PHO types for non-defoliating strains are CHv1937 and CHv1966B. Disease assays using stem puncture inoculation of Acala 44 was used to differentiate and validate molecular genotyping of defoliating and non-defoliating isolates. For example, four of the isolates that did not have a VdD or VdND PCR band had a novel PHO sequence (CHv1963) and were confirmed to be the defoliating type by the disease assay. Overall, the disease assay confirmed pathotype predictions based on PCR and sequence analysis. However, a few isolates of these genotypes were found to be non-pathogenic.