

DISTRIBUTION, DETECTION, EVOLUTIONARY RELATIONSHIP, AND PATHOGENICITY OF THE FOUR SUB-GENOTYPES OF RACE 4 (VCG0114) OF FUSARIUM WILT PATHOGEN OF COTTON

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Abstract

A highly virulent cotton wilt pathogen, *Fusarium oxysporum* f. sp. *vasinfectum* VCG0114 (race 4) was found in West Texas in 2017, after being known in California since 2001. From wilted plants, we isolated 66 race 4 and 19 putative race 7 isolates from West Texas in 2017 and from China in 2015, respectively. Pathogenicity tests on three cotton hosts, DNA sequence analyses, and VCG analyses of these isolates compared to that of California isolates showed that race 4 and 7 were not different. Texas isolates were significantly more virulent than China and California isolates on Pima S-7. Virulence of China and California isolates was similar. All isolates belonged to the nematode-independent pathotype and VCG0114. Four sub-genotypes within VCG0114 were identified based on transposable element (*TfoI*, *MULE*, and *MITE*) insertion patterns within the PHO gene and their evolutionary relationship was established. Texas isolates were comprised of two sub-genotypes of which one was the major sub-genotype of California and the other the minor sub-genotype of China. Simple PCR methods were developed to specifically determine and detect the VCG0114 genotype as well as the four sub-genotypes. This will greatly facilitate monitoring and tracing the movement of these sub-genotypes of VCG0114 and will aid in breeding for resistance.

We have identified a highly resistant line of *Gossypium arboreum* (Acc. No. 190) for race 4. This race 4 resistance was introgressed via a triple-species hybrid into Barbren 713-32 lines that are highly resistant to both root-knot and reniform nematodes but susceptible to race 4. Soil inoculation pathogenicity assays of advanced introgressed lines showed that they are highly resistant to race 4.