FIELD SURVEY, DETECTION AND CHARACTERIZATION OF FUSARIUM WILT RACE 4 IN COTTON IN NEW MEXICO

Jinfa Zhang
Yi Zhu
Abdelraheem Abdelraheem
Philip Lujan
John Idowu
New Mexico State University
Las Cruces, NM
Robert Nicholas
Tom Wedegaertner
Cotton Incorporated
Cary, NC

Abstract

In this study, 588 cotton fields in three counties of South New Mexico including Dona Ana (468 fields), Luna (107 fields) and Sierra (13 fields) were surveyed between June 12 and 20, 2019. The occurrence of the symptomatic plants was sporadic with a disease incidence ranging from 1% to 5% in infected areas, mostly in Pima cotton fields. A total of 113 cotton plant samples from 113 cotton fields with apparent symptoms including wilting, necrosis, chlorosis or dead seedlings were collected. More than 600 root tissues (5-6 sections per plant sample) from the 113 plant samples were plated on APDA for isolation. Out of the 1275 colonies obtained from the cotton roots, 772 colonies were identified as *Fusarium* spp. based on their cultural and morphological characteristics. Of a total of 158 *Fusarium* spp. isolates, 84 isolates were identified as *F. oxysporum* (FOV), 35 isolates as *F. solani*, 24 isolates as *F. fujikuroi* and 15 isolates as *F. proliferatum*. Portions of translation elongation factor (EF-1α), phosphate permease (PHO) and β-tubulin (BT) genes were PCR amplified and sequenced using previously reported primers. The amplification of the EF-1α, PHO and BT genes each yielded a single PCR product with an approximate length of 1800 bp, 1900 bp and 1900 bp, respectively, as expected. Sequence analyses of all the isolates showed that sequences for 40 isolates from nine Pima cotton fields were identical to those of the reference FOV race 4 (FOV4) isolates, confirming the existence of FOV4 in New Mexico. The sub-genotypes of the FOV4 isolates were further determined by a multiplex PCR using four pairs of specific primers as previously reported. The result showed that four FOV4 isolates from four fields belonged to the MT genotype (with a PCR product of 583 bp in size). The other five FOV4 isolates belonged to the Null genotype (396 bp).