

Characterization and genetic distance analysis of isolates of *Peronosclerospora sorghi* using AFLP fingerprinting

Abstract

Sorghum downy mildew, caused by the obligate oomycete *Peronosclerospora sorghi*, has been controlled through the use of resistant cultivars and seed treatment with metalaxyl. A recent outbreak in fields planted with treated seed revealed the presence of a metalaxyl-resistant variant. Here, PCR-based methods including amplification from RAPD primers and two systems of automated AFLP analysis have been used to detect DNA-level genetic variation among 14 isolates including metalaxyl-resistant and susceptible isolates, as well as representatives of common pathotypes 1 and 3 and a new pathotype. In total, 1708 bands were detected after amplification of EcoRI/MseI fragments with 16 primer combinations. Nearly as many amplified products were observed using eight primer pairs with three-base extensions (LI-COR) as with two-base extensions (ABI-Prism genetic capillary system). Approximately 25 % of the bands were polymorphic across the 14 isolates, with the majority of differences specific to the pathotype P1 isolate. The AFLP banding patterns are consistent with metalaxyl resistance and the new pathotype having evolved from pathotype 3.