



Genetic diversity of *Mycosphaerella fijiensis* in Brazil analyzed using an ERIC-PCR marker

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ABSTRACT. The Enterobacterial repetitive intergenic consensus (ERIC) marker was used to analyze the genetic variability of *Mycosphaerella fijiensis*, the causative agent of Black Sigatoka disease in banana plants. A total of 123 isolates were used, which were divided into populations based on their original hosts and collection sites in Brazil. A total of 9 loci were amplified, 77.8% of which were found to be polymorphic. The genetic diversity found in the population was 0.20. Analysis of molecular variance (AMOVA) demonstrated that the highest level of genetic variation is within populations. Cluster analysis revealed three main groups in Brazil, with no correlation between geographic and genetic distance.

Key words: Black Sigatoka; *Pseudocercospora fijiensis*; Banana plant; *Musa* spp; Genetic variability