

## Variable number of tandem repeat markers in the genome sequence of *Mycosphaerella fijiensis*, the causal agent of black leaf streak disease of banana (*Musa spp*)

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**ABSTRACT.** We searched the genome of *Mycosphaerella fijiensis* for molecular markers that would allow population genetics analysis of this plant pathogen. *M. fijiensis*, the causal agent of banana leaf streak disease, also known as black Sigatoka, is the most devastating pathogen attacking bananas (*Musa spp*). Recently, the entire genome sequence of *M. fijiensis* became available. We screened this database for VNTR markers. Forty-two primer pairs were selected for validation, based on repeat type and length and the number of repeat units. Five VNTR markers showing multiple alleles were validated with a reference set of isolates from different parts of the world and a population from a banana plantation in Costa Rica. Polymorphism information content values varied from 0.6414 to 0.7544 for the reference set and from 0.0400 and 0.7373 for the population set. Eighty percent of the polymorphism information content

values were above 0.60, indicating that the markers are highly informative. These markers allowed robust scoring of agarose gels and proved to be useful for variability and population genetics studies. In conclusion, the strategy we developed to identify and validate VNTR markers is an efficient means to incorporate markers that can be used for fungicide resistance management and to develop breeding strategies to control banana black leaf streak disease. This is the first report of VNTR-minisatellites from the *M. fijiensis* genome sequence.

**Key words:** Molecular markers; VNTRs; Genetic diversity; Population genetics; Black Sigatoka