

**DEVELOPMENT OF VNTR MARKERS TO ASSESS GENETIC DIVERSITY OF
Mycosphaerella fijiensis, THE CAUSAL AGENT OF BLACK LEAF STREAK
DISEASE IN BANANAS (*Musa* spp.)**

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Mycosphaerella fijiensis, the causal agent of black leaf streak disease of banana, commonly known as Black Sigatoka, is one of the most devastating plant pathogens. Black leaf streak was first discovered in Fiji during the 1960s and the pathogen still actively colonizes new areas where bananas are grown. Using the genome sequence of *M. fijiensis* isolate CIRAD86 (<http://genome.jgi-psf.org/Mycfi1/Mycfi1.home.html>), we identified Variable Number of Tandem Repeat (VNTR) markers using a bioinformatics pipeline. The VNTR screening resulted in 1528 candidate VNTR loci of which many were imperfect repeats. Sixteen VNTR markers were selected based on repeat type, repeat length and the number of units of the repeat (6-15). Primers for these 16 VNTR markers were tested on a set of 12 reference isolates and five VNTR markers that showed multiple alleles were tested on *M. fijiensis* field isolates and on progeny of the cross between isolates CIRAD86 and CIRAD 139A. Numbers of alleles identified varied from 2 to 5 per locus. The markers allowed high throughput and robust scoring on 3% agarose gels and proved useful for genetic diversity and population genetic studies using basic molecular instrumentation. We envisage that this set will enable more detailed analyses of the large-scale migration pattern of this important pathogen as well as small-scale effects of fungicide treatments on the population diversity in banana plantations.