translational changes during the *Musa*-pathogen interaction, representing a link between genotypic and phenotypic information. Proteomic analysis, in overlap with the transcriptome information generated by NGS pyrosequencing, will contribute to genetic improvement of *Musa*.
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Characterization of EST-Derived SSR Markers in *Musa acuminata*

V.O. Cruz[1], V.C.R. Azevedo[2], A.Y. Ciampi[2], E.P. Amorim[3], C.C.F. Ferreira[3] and R.N.G. Miller[1]

[1]Universidade de Brasília, Departamento de Biologia Celular, Brasília, DF, Brazil; [2]EMBRAPA Recursos Genéticos e Biotecnologia, Brasilia, DF, Brazil; [3]EMBRAPA Mandioca e Fruticultura Tropical, Cruz das Almas, BA, Brazil

Banana (*Musa* spp.) is one of the world's most important monocotyledonous crops. Many cultivars are susceptible to fungal diseases such as black leaf streak and Sigatoka leaf spot, which attack leaf tissues and can cause production losses of up to 100%. Genetic breeding programs have been based upon selection of resistant individuals. The objectives of this study were to characterize 303 SSR markers derived from cDNA libraries prepared from *Musa acuminata* leaf materials contrasting in resistance, and *in vitro* infected with *Mycosphaerella fijiensis* (the causal agent of black leaf streak), and to identify potential association with Sigatoka resistance. A total of 170 primer pairs were designed from the Cavendish subgroup, cultivar 'Grande Naine' (AAA) (susceptible), together with 133 pairs in *Musa accuminata* ssp. *burmannicoides* 'Calcutta 4' (resistant). Marker polymorphism was initially examined using four DNA bulks obtained from 20 A-genome diploid individuals contrasting in resistance to black leaf streak and Sigatoka leaf spot. Primer annealing temperatures were optimized between 50-60°C and polymorphism examined on 4% polyacrylamide gels with silver staining. Currently, 25% of the loci display polymorphism, 25% display monomorphism, 34% show problems in amplification and the other 16% are in the process of characterization. Polymorphic markers were tested against individualized bulks in order to determine if members displayed common alleles. Data were analysed using the software Powermaker 3.25. A total of between two and seven alleles per locus were observed, with an average of four. From an expected heterozygosity (*He*) of 0.55, an observed heterozygosity (*Ho*) of 0.48 was observed, with a PIC value of 0.50. Polymorphic markers will be important in genotyping and in genetic map construction for *Musa* segregating populations.