



Evaluation of microsatellite loci from libraries derived from the wild diploid ‘Calcutta 4’ and ‘Ouro’ banana cultivars

P.R.O. Silva¹, O.N.J. Jesus², S. Creste³, A. Figueira⁴, E.P. Amorim² and C.F. Ferreira²

¹Núcleo de Biotecnologia, Universidade Federal do Recôncavo da Bahia, Cruz das Almas, BA, Brasil

²Núcleo de Biologia Avançada, Embrapa Mandioca e Fruticultura, Cruz das Almas, BA, Brasil

³Instituto Agrômico de Campinas, Campinas, SP, Brasil

⁴Centro de Energia Nuclear na Agricultura, Universidade de São Paulo, Piracicaba, SP, Brasil

Corresponding author: C.F. Ferreira
E-mail: claudia.ferreira@embrapa.br

Genet. Mol. Res. 14 (3): 11410-11428 (2015)

Received January 14, 2015

Accepted May 15, 2015

Published September 25, 2015

DOI <http://dx.doi.org/10.4238/2015.September.25.9>

ABSTRACT. Microsatellite markers have been widely used in the quantification of genetic variability and for genetic breeding in *Musa* spp. The objective of the present study was to evaluate the discriminatory power of microsatellite markers derived from ‘Calcutta 4’ and ‘Ouro’ genomic libraries, and to analyze the genetic variability among 30 banana accessions. Thirty-eight markers were used: 15 from the ‘Ouro’ library and 23 from the ‘Calcutta 4’ library. Genetic diversity was evaluated by considering SSR markers as both dominant markers because of the presence of triploid accessions, and co-dominant markers. For the dominant analysis, polymorphism information content (PIC) values for 44 polymorphic markers ranged from 0.063 to 0.533, with a mean value of 0.24. A dendrogram analysis separated the BGB-Banana accessions into 4 groups: the ‘Ouro’

and 'Muísa Tia' accessions were the most dissimilar (93% dissimilarity), while the most similar accessions were 'Pacovan' and 'Walha'. The mean genetic distance between samples was 0.74. For the analysis considering SSR markers as co-dominants, using only diploid accessions, two groups were separated based on their genome contents (A and B). The PIC values for the markers from the 'Calcutta 4' library varied from 0.4836 to 0.7886, whereas those from the 'Ouro' library ranged from 0.3800 to 0.7521. Given the high PIC values, the markers from both the libraries showed high discriminatory power, and can therefore be widely applied for analysis of genetic diversity, population structures, and linkage mapping in *Musa* spp.

Key words: Genetic variability; Molecular characterization; *Musa* spp; Microsatellites