



Genetic identification of *Theobroma cacao* L. trees with high Criollo ancestry in Soconusco, Chiapas, Mexico

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Genet. Mol. Res. 13 (4): 10404-10414 (2014)

Received October 11, 2013

Accepted July 7, 2014

Published December 12, 2014

DOI <http://dx.doi.org/10.4238/2014.December.12.2>

ABSTRACT. Criollo-type cacao trees are an important pool of genes with potential to be used in cacao breeding and selection programs. For that reason, we assessed the diversity and population structure of Criollo-type trees (108 cultivars with Criollo phenotypic characteristics and 10 Criollo references) using 12 simple sequence repeat (SSR) markers. Cultivars were selected from 7 demes in the Soconusco region of southern Mexico. SSRs amplified 74 alleles with an average of 3.6 alleles per population. The overall populations showed an average observed heterozygosity of 0.28, indicating heterozygote deficiency (average fixation index $F = 0.50$). However, moderate allelic diversity was found within populations

(Shannon index for all populations $I = 0.97$). Bayesian method analysis determined 2 genetic clusters ($K = 2$) within individuals. In concordance, an assignment test grouped 37 multilocus genotypes (including 10 references) into a first cluster (Criollo), 54 into a second (presumably Amelonado), and 27 admixed individuals unassigned at the 90% threshold likely corresponding to the Trinitario genotype. This classification was supported by the principal coordinate analysis and analysis of molecular variance, which showed 12% of variation among populations ($F_{ST} = 0.123$, $P < 0.0001$). Sampled demes sites (1-7) in the Soconusco region did not show any evidence of clustering by geographic location, and this was supported by the Mantel test ($R_{xy} = 0.54$, $P = 0.120$). Individuals with high Criollo lineage planted in Soconusco farms could be an important reservoir of genes for future breeding programs searching for fine, taste, flavor, and aroma cocoa.

Key words: Population structure; Genetic diversity; Genetic resources; Fine flavor cocoa; Simple sequence repeat markers