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for sustainable resource management”

Genetic Diversity of Native Guatemalan Avocado Using SSR Molecular Markers

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Abstract

Avocado is one of the most widely consumed crops worldwide and originated in the Sierra Nevada region in California eight to five million years ago. In Guatemala, a high genetic diversity has been reported by morphological characterisations, but due the cross-pollination and interracial hybridisations, these characterisations present complications and it is not possible to detail the total genetic richness. Molecular markers are a useful tool for this type of studies because they are free of environmental effects and focus on differences at the DNA level. The main objective of this study was to analyse the genetic diversity of 189 materials of native Guatemalan avocado collected in seven populations located in eight departments of the country, using 11 SSR molecular marker. A total number of 262 polymorphic alleles were detected with a mean number of 10.701 per population. Among population, the expected heterozygosity varied from 0.738 to 0.837. The analysis of molecular variance (AMOVA) showed that only 2% genetic variation existed among population, while 65% existed within individuals and 33% existed among individuals. Moderate differentiations among the analysed populations were indicated by F_{st} index 0.018. Structure analysis suggested two and four cluster for the whole avocado materials. The lack of population structure is attributed to the process of selection, the system of cross-pollination, the exchange of seeds and the process of domestication to which the avocado is still subject. We therefore suggest the protection of the phylogenetic resource, as well as a complementary agromorphological characterisation, to establish an adequate strategy of exploitation through plant breeding programs.

Keywords: Avocado, genetic diversity, Guatemala, SSR