GENETIC DIVERSITY ANALYSIS OF TAIWAN AVOCADO ACCESSIONS

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Forty-two avocado accessions maintained at the Chiayi Agricultural Experimental Station (Chiayi, Taiwan) were evaluated for genetic diversity using random amplified polymorphic DNA (RAPD) markers. A total of 107 polymorphic bands were detected for genetic diversity analysis upon polymerase chain reaction (PCR) amplification of 21 octamer primers, an average of five scorable bands per primer. These primers were considered highly informative because they amplified at least one polymorphic band that distinguished between accessions. Jaccard's coefficient was applied to calculate genetic similarity, and UPGMA cluster analysis to generate the dendrogram. The forty-two accessions were separated into three main groups by cluster analysis. They were first divided into two main groups, at 0.27 of Jaccard's coefficient similarity and the second main group was further separated into two subgroups, at 0.33. It suggested that there was high degree of genetic diversity between the first main groups of cultivated avocadoes as well as the two subgroups of the second main group. The first main group can be further divided into four subgroups. Cultivars assigned to the first two subgroups of the first main group are of either Guatemalan or West Indian origin. Except Nabel, a cultivar introduced from Guatemala, most cultivars of the third subgroup are hybrids between Mexican and Guatemalan varieties. The accessions of the first subgroup of the second main group are either hybrids of Mexican and Guatemalan varieties or Guatemalan cultivars. Mexican cultivars are assigned to the second subgroup of the second main group. The genetic diversity information revealed by this study provides a genetic basis for selection of parents to explore heterosis for avocado improvement.