

MORPHOLOGICAL, BIOCHEMICAL AND MOLECULAR CHARACTERIZATION OF AVOCADO CULTIVARS (*PERSEA AMERICANA* MILL.) IN CUBA

A-39

N.N. Rodríguez-Medina¹, W. Rohde², C. González-Arencia³, I. M. Ramírez-Pérez⁴, J. L. Fuentes-Lorenzo⁴, M.A. Román-Gutiérrez³, Xonia Xiqués-Martín³, D. Becker² y J.B. Velázquez-Palenzuela¹.

¹ Instituto de Investigaciones en Fruticultura Tropical. Ave 7^{ma} NO. 3005, e/ 30 y 32, Miramar, Playa, Ciudad de La Habana, Cuba. e-mail: iicif@ceniai.inf.cu.

² Max-Planck-Institut für Züchtungsforschung. Carl-von-Linné-Weg 10, D 50829, Köln, Germany. e. mail: rohde@mpiz-koeln.mpg.de

³ Facultad de Biología, Universidad de La Habana. Calle 25 e/ I y J, Vedado, Ciudad de La Habana, Cuba. e. mail: cglez@fbio.uh.cu.

⁴ Centro de Estudios Aplicados al Desarrollo Nuclear. Calle 30 No. 502 e/ 5^{ta} y 7^{ma}, Miramar, Playa, Ciudad de La Habana, Cuba. e. mail: fuentes@ceaden.edu.cu

A morphoagronomic, isoenzymatic and molecular characterization of the avocados (*Persea americana* Mill.) maintained in the collection of the Instituto de Investigaciones en Fruticultura Tropical in Cuba has been carried out. The analyses were, respectively, made according to the descriptors established by the International Plant Genetic Resources Institute, three enzyme systems (peroxidases, polyphenol oxidase and ascorbate oxidase) and the ISTR (Inverse Sequence-Tagged Repeat) technique. After the correlation matrix, the principal components analysis carried out with the variables 'color of lenticels of young twig'; 'anise smell in leaves'; 'peduncle length'; 'fruit skin surface'; 'fruit skin thickness'; 'pliability of fruit skin' and 'harvest time', allowed the grouping of the cultivars into two putative ecological groups. Those considered as Guatemalan x Antillean hybrids were included together with Guatemalan genotypes. Genetic analysis with the tree enzymatic systems were based on the variables 'total number of loci', 'total number of bands or alleles', 'total number of rare alleles', 'mean number of alleles per locus', 'percentage of polymorphic loci' and 'mean number of alleles per polymorphic loci'. A similarity matrix was constructed following the Zecanowski index. Cluster analysis resulted in five groups, with a high similarity in most of the Antillean cultivars and higher variability in Guatemalan cultivars and some hybrids. The ISTR technique was highly efficient to detect polymorphisms among the selected genotypes. Although cluster analysis did not allow an adequate grouping of the cultivars according to the ecological groups, probably due to the fact that just a single primer combination (F₃ + B₂B) was used, 100% of the bands obtained were polymorphic. Isozyme and DNA marker analyses produced specific band patterns that allowed the identification of the cultivars and the study of the genetic variability. These results might or might not coincide with the analyses based on morphoagronomic variables of antrropic selection that group the cultivars according to their ecological group.