

LIV Reunião Anual da ISTH / LIV Reunión Anual de la ISTH / LIV Annual Meeting of the ISTH
P.007 - MOLECULAR CHARACTERIZATION OF MANGO (*Mangifera indica* L.) BY RAPD MARKERS

Isis Gomes de Brito Souza¹, Fábio Mendonça Diniz², Valdomiro Aurélio Barbosa de Souza², Sérgio Emílio dos Santos Valente¹, Fábio Barros Britto² e Paulo Sarmanho da Costa Lima²

1. Departamento de Biologia (UFPI), Campus Universitário Ministro Petrônio Portella - Bairro Ininga – Teresina, PIAUÍ. CEP: 64.049-550;
2. Pesquisadores da Embrapa Meio-Norte, Av. Duque de Caxias, 5650 – Teresina, PIAUÍ, Brazil. CEP: 64006-220.

The use of molecular data for improving plant crops is only possible after determining the genetic variability that is present within a species. This variability could be estimated by molecular markers, such as RAPD (Random Amplified Polymorphic DNA), which shows several advantages such as simplicity, low cost and the possibility of assessing numerous loci in the genome. Thus, the present work was carried out to determine the genetic variability of *Mangifera indica* L. by RAPD markers. Forty-two genotypes of different mango varieties, growing at Embrapa Mid-North, were used for the analysis. The DNA was extracted and purified using the PUREGEN™ DNA Purification Kit. DNA was amplified by the Polymerase Chain Reaction (PCR) and PCR products were resolved by electrophoresis in 1,4% agarose gel and stained with ethidium bromide. The gels were then scored according to the presence (1) or absence (0) of bands. This information was used to construct a binary matrix and estimate the genetic distance among specimens. Fifty-five DNA loci were amplified by six primers, being all of them polymorphic. According to the Jaccard index, five distinguishable groups were identified. The most similar genotypes were 'Rosa 41' and 'Rosa 48' (94%). On the other hand the less genetically related genotypes were 'CPAC-44' (10%) and, 'Edward' and 'Maça' (10%). These data have shown that the analyzed genotypes presented high variability, and this information could be used for management and genetic improvement purposes. Apoio : Banco do Nordeste.