FINGERPRINTING ANALYSIS OF MANGO (Mangifera indica L.) CULTIVARS INTRODUCED OR DEVELOPED IN BRAZIL USING RAPD MARKERS

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Cerrados
EmbRAPA

INTRODUCTION

The enlargement of the actual genetic base of Brazilian cultivars is a relevant strategy to assure the sustainability and the improvement of this important agricultural activity. In that way, some Brazilian cultivars, such as IAC-110, Bourbon and Reva and other introduced cultivars, such as Keitt, Palmer and Joa have been evaluated to substitute ‘Tommy Atkins’ (Pinto et al., 2002a).

These cultivars mentioned above, have been cultivated in different regions with some phenotypic variations. These variations can be from genetic or environmental origin, which can be determined through DNA molecular markers. This tool has been useful in several steps of breeding programs.

OBJECTIVE

The objective of this work was to evaluate the genetic similarities of 11 mango genetic materials using RAPD markers besides inferring about the genetic or environmental origin of the phenotypic variations observed in these cultivars grown in different Brazilian regions (Fig. 1).

RESULTS

A total of 186 RAPD bands were generated with the 18 decamer primers (a mean of 10.3 bands per primer). Among the 186 bands, 132 (71.0%) were polymorphic and 54 (28.9%) monomorphic. The products of amplification of the DNA for the 11 mango genetic materials obtained by the primer OPD-02 are shown in Fig. 2. The mean of bands per primer and the number of polymorphic bands obtained in this study were similar to the one obtained by Ravishankar et al. (2000).

The genetic similarities among the 11 mango genetic materials ranged from 0.728 to 0.985 (Table 1). It is possible to assume that there is no genetic variation between ‘Tommy Atkins’ cultivated in São Paulo and Savanna region, considering that 2 to 3% of the RAPD bands could be resulted from wrong amplification. The same result was detected for Keitt and Palmer cultivars. ‘Bourbon’ cultivated in São Paulo was genetically different from ‘Bourbon’ cultivated in Savanna region, with similarity coefficient of 0.830 between them. In some Brazilian regions, the cultivar Bourbon is wrongly named ‘Espada’ (Pinto et al., 2002b), and this misinterpretations or this synonym error can explain this high genetic distance observed in this study. ‘Joa’ was less genetically related to any other cultivar analyzed (Fig 2). ‘Palmer’ was the cultivar more genetically related to ‘Joa’ with similarity coefficient of 0.796. According to Pinto et al. (2002b), ‘Joa’ was originated from seedlings of ‘Palmer’. Brazilian cultivar ‘Roxa’ also showed low similarity coefficient to other analyzed cultivars, except to ‘Tommy Atkins’.

The cluster analysis, based on the genetic distances, shows that the Brazilian cultivars, ‘Roxa’ and ‘IAC-110’ showed the shortest genetic distances to ‘Tommy Atkins’ (Fig 3), which can be explained through the genetic origin of Brazilian cultivars. The dendrogram also showed that ‘Joa’ was less genetically related to other analyzed cultivars. The dispersion of the cultivars in a bipart based on the genetic distances (Fig 4) is showed to supplement the results of the dendrogram and the similarity coefficient matrix. The bipart shows the genetic difference between ‘Bourbon’ cultivated in São Paulo and in Savanna region. It can be observed that ‘Roxa’ and ‘Joa’ are at extreme positions in the dispersion plot.

LITERATURE CITED

