Embrapa Cerrados

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

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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 Roxa 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).

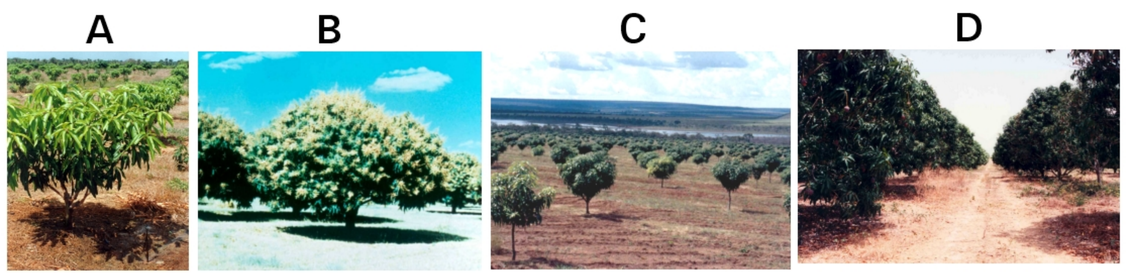

Figure 1. Mango genetic material cultivated in São Paulo (A and B) and in Savanna region (C and D).

MATERIAL AND METHODS

There were analyzed mango (*Mangifera indica* L.) genetic materials cultivated in different Brazilian regions: 'Keitt' cultivated in São Paulo (Keitt SP), 'Keitt' cultivated in Savanna region (Keitt SV), 'Palmer' cultivated in São Paulo (Palmer SP), 'Palmer' cultivated in Savanna region (Palmer SV), 'Joa', 'Bourbon' cultivated in São Paulo (Bourbon SP), 'Bourbon' cultivated in Savanna region (Bourbon SV), 'Tommy Atkins' cultivated in São Paulo (Tommy SP), 'Tommy Atkins' cultivated in Savanna region (Tommy SV), 'IAC-110' and 'Roxa'. A Fig. 1ilustra os materiais genéticos analisados neste trabalho.

Leaf samples of each genetic material were collected and the genomic DNA was extracted from each sample individually, by using the method of CTAB, with some modifications (Faleiro et al., 2003). DNA samples, from each genetic material, were amplified using the RAPD (*Random Amplified Polymorphic DNA*) technique. Amplification reactions were done in 13 uL total volume, containing Tris-HCl 10 mM (pH 8,3), KCl 50 mM, MgCl2 3 mM, 100 uM from each of the desoxiribonucleotídes (dATP, dTTP, dGTP e dCTP), 0,4 uM of a primer (Operon Technologies Inc., Alameda, CA, EUA), one unit of the *Taq* polimerase enzyme and, approximatelly , 15 ng of DNA. The decamer primers OPD-02, OPD-03, OPD-12, OPD-13, OPD-15, OPD-19, OPE-01, OPE-06, OPE-11, OPF-02, OPF-05, OPF-12, OPG-02, OPG-10, OPG-11, OPH-04, OPH-19 and OPH-20 were used to start the amplifications.

The obtained RAPD was transformed into a matrix of binary data, from which genetic similarity and distances based on the complement of the similarity coefficient of Nei and Li were calculated with the software Genes. The genetic distances were used to the cluster analysis by dendrogram using the UPGMA (Unweighted Pair-Group with Arithmetic Mean) method. The matrix of genetic distances was displayed in a biplot based on the multidimensional scaling, using the principal coordinates analysis method. The software SAS and Statistic were used for the analysis and plot construction.

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 (29.0%) 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 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 analysis. 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 misunderstandings 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 biplot based on the genetic distances (Fig. 4) is showed to supplement the results of the dendrogram and the similarity coefficient matrix. The biplot 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.

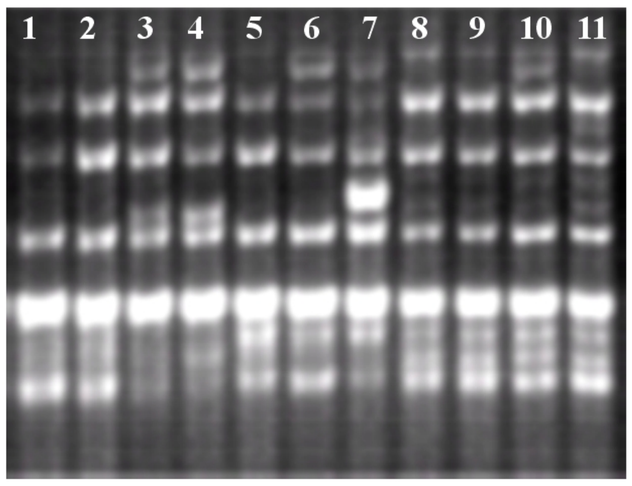

Figure 2. Amplification products of genomic DNA from 11 mango genetic material using the RAPD decamer primer OPH-19. The genetic material corresponding to each number is presented in the Table 1.

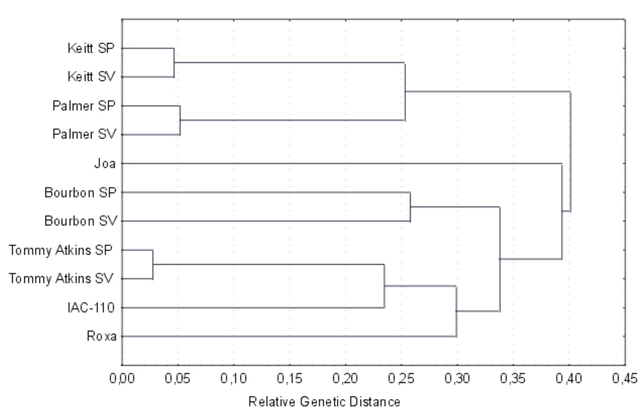

Figure 2. Cluster analysis of 11 mango genetic materials using the genetic distances among them calculated with 186 RAPD markers. The UPGMA method was used as agglomeration criteria. SP = cultivated in São Paulo; SV = cultivated in Savanna region.

Table 1. Genetic similarity among 11 mango genetic materials calculated by Nei and Li similarity coefficient, using 186 RAPD markers.

Cultivars	1	2	3	4	5	6	7	8	9	10	11
1 Keitt SP	1										
2 Keitt SV	**0,978**	1									
3 Palmer SP	0,862	0,882	1								
4 Palmer SV	0,860	0,868	**0,984**	1							
5 Joa	0,775	0,772	0,787	0,796	1						
6 Bourbon SP	0,748	0,762	0,757	0,764	0,798	1					
7 Bourbon SV	0,752	0,775	0,780	0,785	0,749	**0,830**	1				
8 Tommy Atkins SP	0,806	0,808	0,807	0,833	0,761	0,831	0,814	1			
9 Tommy Atkins SV	0,809	0,810	0,809	0,835	0,767	0,822	0,826	**0,985**	1		
10 IAC-110	0,818	0,819	0,791	0,802	0,768	0,762	0,794	0,867	0,869	1	
11 Roxa	0,787	0,788	0,739	0,759	0,728	0,745	0,804	0,834	0,831	0,829	1

SP – cultivated in São Paulo
SV – cultivated in Savanna region

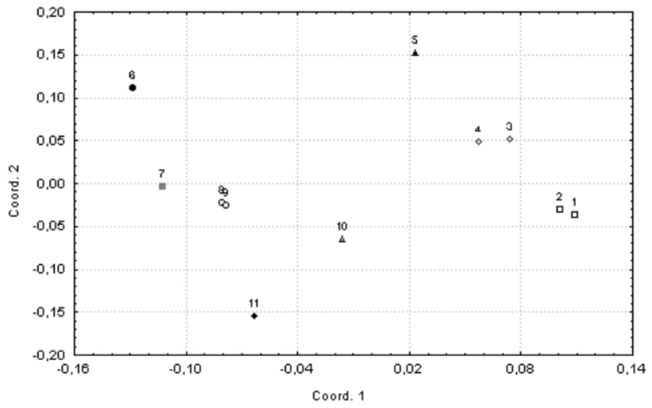

Figure 4. Dispersion analysis of 11 mango genetic materials using the genetic distances among them calculated with 186 RAPD markers. The variety corresponding to each number is presented in the Table 1.

CONCLUSIONS

The results of this work show the utility of the molecular markers to study the genetic relationships among mango cultivars. The phenotypic differences observed in 'Tommy Atkins', 'Keitt' and 'Palmer' cultivated in São Paulo and Savanna region are not related to genetic origin. 'Bourbon' cultivated in São Paulo was genetically different from that cultivated in Savanna region, which means that the same synonym used in São Paulo and Savanna regions is merely due to similarity of fruit morphology. The Brazilian cultivars, 'Roxa' and 'IAC-110' are important alternatives to enlarge the genetic base of the cultivars commercially grown in Brazil.

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