FITOGENÉTICOS

VII Simposio de Recursos Genéticos para América Latina y el Caribe

GENETIC SIMILARITIES AMONG *Oenocarpus mapora* ACCESSIONS USING RAPD MARKERS

Elisa FERREIRA MOURA[1], Maria do Socorro PADILHA DE OLIVEIRA[2]

Embrapa Amazônia Oriental, Belém, Pará, Brazil [1]elisa@cpatu.embrapa.br , [2]spadilha@cpatu.embrapa.br

ABSTRACT

Oenocarpus mapora is an Amazonian species commonly used by the native populations. Analysis of genetic variability contained in a germplasm bank was done using RAPD markers. Seventy-six individuals were sampled from 25 accessions originated from nine cities of Brazilian states. It was evaluated 104 polymorphic bands, amplified by 12 primers. The level of polymorphism was high, since similarities varied form 0.97 to 0.36. Two groups were generated on the dendrogram, similar at 0.52, which indicates high genetic differentiation among the sampled genotypes.

INTRODUCTION

The species *Oenocarpus mapora*, commonly known as bacaby, bacaba or bacabinha can generate a lot of products. Since it is plant with so many uses, the utilization of *O. mapora* can be stimulated in communities living close to areas with high densities of this species. Besides commercialization of products generated by the palm, the consumption of fruits in its natural form can be used as nutritional complement. The possibility for keeping a small part of *O. mapora* genetic variability on germplasm Banks reduces the risk of losses caused by environmental degradation. Embrapa Eastern Amazon has established a germplasm bank of species of the genus *Oenocarpus*, which includes *O. mapora*. The genetic characterization of this bank is necessary to verify its level of variability, aiming the support for genetic breeding programs.

The aim of this paper was to characterize genetically the germplasm bank of *O. mapora* using RAPD molecular markers (*Random Amplified Polymorphic* DNA).

MATERIAL AND METHOD

It was sampled folioles of young leaves from adult palms that belong to the Germplasm Bank of Oenocarpus/*Jessenia* complex from Embrapa Eastern Amazon. Folioles were sampled from 76 plants, which belong to 25 accessions from nine different places (Cruzeiro do Sul, Rio Branco and Sena Madureira, State of Acre; Itacoatiara and Parintins; State of Amazonas; Abaetetuba, Colares, Coqueiro and Santo Antonio do Tauá, State of Pará). DNA was extracted according to Doyle and Doyle protocol (1990) with modifications. After quantification on agarose gel at 1%, DNA was diluted to10 ng.ml^{-1}. The PCR reactions were prepared to a final volume of 15 ml, according to protocol cited by Oliveira et al. (2008), using primers previously selected, and were done in a thermocycler following program described by Oliveira et al. (2008). The reaction products were applied to agarose gel at 1% and separated by electrophoresis, in a horizontal cube under constant 100 V voltage for two hours. The gels were visualized in an ultraviolet light transiluminator and the images were digitally captured.

The binary matrix was used to obtain the genetic similarities between plants, using the Dice coefficient in the NTSYS-pc 2.1 program (Rohlf, 2000). This coefficient was used due to the possible presence of hybrids in the analysis. The dendrogram was generated using the SAHN procedure of the NTSYS-pc 2.1 program (Rohlf, 2000) by the UPGMA method.

RESULT AND DISCUSSION

The number of polymorphic bands evaluated was 104, obtained from 102 primers. There was 100% of polymorphism, which means that all amplified bands were polymorphic. The genetic similarities among plants varied from 0.969 (between two individuals from Santo Antonio do Tauá, PA) to 0.166 (between an individual of Sena Madureira, AC and one from Abaetetuba, PA), with average of 0.6432. However, as it can be seen on the dendrogram (Figure 1), this individual from Sena Madureira did not group with the others, which can possibly be a plant identification failure on the germplasm bank. Thus, when this accession was removed from the analysis, the genetic similarities varied from 0.969 to 0.355 (between an individual from Cruzeiro do Sul, AC and one from Itacoatiara, AM), amplitude that is still high, with 0.654 of average. The dendrogram showed the formation of two groups (Figure 1). In the first group, there are only

individuals from the Acre province, while in the second group, there are the individuals from Pará and Amazonas. The distinct differentiation of genotypes from Acre may be an indicative of small gene flow between this area and the region of Pará and Amazonas. In *Bactris gasipaes*, species that contains determined landraces, the analysis with AFLP markers separated two landraces and the similarity among them was 0.795, by the Jaccard coefficient (Clement et al., 2002). In this study with *O. mapora*, the two groups visualized in the dendrogram are separated by a similarity of approximately 0.52. Even though different coefficient (Dice) was used, the similarity among the two groups of *O. mapora* can be considered much smaller than the one among *B. gasipaes* landraces. Thus, it can be inferred that there is considerable variability in the germplasm bank of O. *mapora*, with occurrence of distinct differentiation among some material from different places.

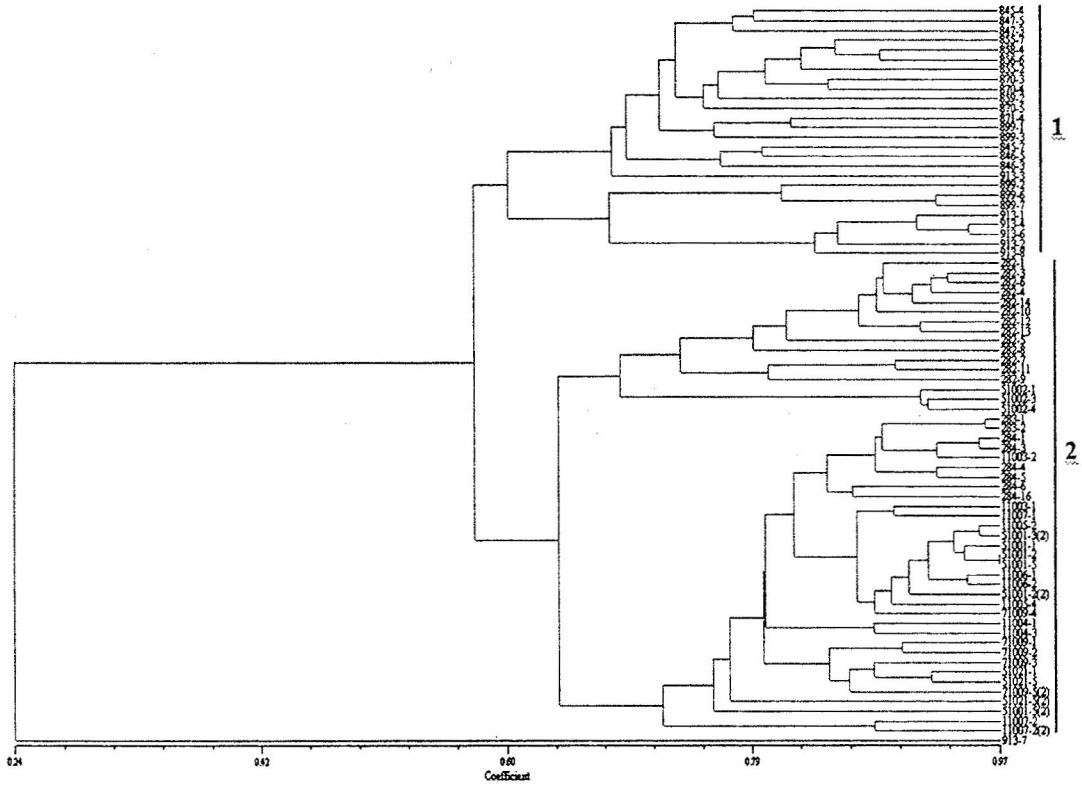

Figure 1. Dendrogram obtained from Dice genetic similarities generated from RAPD data among 76 genotypes contained in the bank germplasm of *Oenocarpus mapora*.

BIBLIOGRAPHIC REFERENCES

DOYLE, J.J. and DOYLE, J.L. 1990. Isolation of plant DNA from fresh tissue. *Focus* 12, 13-15.

CLEMENT, Charles R.; SOUSA, Nelcimar Reis; Rodrigues, Doriane Picanço; Astolfi-Filho, Spártaco; Moreno, Yolanda Nuñéz; Pascual, Vicente Torres and Rodríguez, Franscisco Javier Gallego 2002. Use of AFLP to distinguish landraces of pejibaye (*Bactris gasipaes*) in Brazilian Amazonia. *Scientia Agricola* 4, 749-753.

OLIVEIRA, Maria do Socorro Padilha de; SILVA, Kaesel Jackson Damasceno 2008. Diferenciação genética entre procedências de açaizeiro por marcadores RAPD e SSR. *Revista Brasileira de Fruticultura* 30, 438-443.

ROHLF F.J. 2000. Numerical taxonomy and multivariate analysis system. New York: Exeter Software 38 p. (version 2.1).