# Morphological Dissimilarity Among Assai Palm Trees Progenies from Anajás - PA

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## Abstract

The interest in assai fruits in different regions of the country necessitates genetic improvement of the species. With the aim of determining the dissimilarity of the assai palms trees grown in Tomé-Açu, Pará, the following characteristics were evaluated in 30 different progenies: average weight of the bunches (PMC), total fruit weight (PTF), average weight of empty bunches (PMCV), average length of the rachis/bunch (TMR), average weight of 100 fruits (PCF), total number of bunches (NTC), and total weight of the bunches (PTC). The experimental design utilized was randomized block, three replicates, and five plants per plot. The matrix of dispersion was obtained using multivariate methods, Unweighted Pair Group Method, with Arithmetic Mean (UPGMA). The average Euclidean distance was used as a dissimilarity measure. The results showed the presence of the G effect only in TMR and NTC and GxE interaction effect in all evaluated characteristics. PTC and PTF were responsible for 99.85% of the total diversity based on the mean Euclidean distance. With 50% of the dissimilarity limit, two large groups (A and B) were obtained, involving 70% of the progenies. With 70% of the dissimilarity limit, five groups ("a" to "e") were obtained with a majority group (a) containing 80% of the total progenies. The following conclusions were reached: there are pronounced effects of the different years on the characteristics PTF, NTC, and PTC and the progenies respond to environmental changes with significant G×E interaction; the most important characteristics for evaluation were PTC and PTF which are mainly responsible for the total divergence; the progenies are not classified sequentially in the dendrogram and there are divergences between access from close provenances for performing crosses.

**Keywords**: Euterpe oleracea, Euclidian distance, Choice of parents, Grouping analysis

## Introduction

The assai palm (*Euterpe oleracea*) known as the heart of palm is a producer fruit and a native specie of the Amazon region. A larger part of the fruit production comes from extrativism, with Pará state being the largest producer and main consumer. Plants are also established in dense and diversified natural populations in wetland areas. According to the latest estimate published by IBGE (2017), the national production of acai fruit was 1.334.517 tons of fruit with revenues of R$ 5.5 billion. It is interesting to note that Pará state was responsible for 95% while the Northern region was responsible for 99% of the national production.

Given the need to decrease seasonality and increase the supply of fruit, it is essential to introduce, improve or develop technologies that contribute effectively to increased productivity and improved quality with sustainability in the production systems. Genetic improvement research of *Euterpe oleracea* grown under irrigated conditions began at Embrapa Amazônia Oriental in 2003 with the establishment of a test of open-pollinated progenies (Farias Neto et al., 2005).

Firstly, the basic objective of a genetic improvement program is the selection and recommendation of genotypes that are more productive than the existing materials. This involves evaluation of genotype performance in different environments (year, location, and sowing time). This also includes obtaining detailed information about genotype behavior in intended locations, due to the possibility of G×E interaction that can result in inconsistency in the relative performance of the genotypes (Storck et al., 2014).

Information about the genetic divergence is also extremely important among groups of potential parents. This is because having as an objective the identification of hybrid combinations that may have a greater heterotic effect can guide the selection of superior genotypes to be used in crosses. In the case of the assai palm, information on genetic divergence serve as guidelines in choosing parents to obtain hybrid populations with high combining ability and to check the variability that is available in a germplasm bank. According to Cruz et al. (2012), among the quantitative methods, there exist predictive methods that are based on morphological differences (agronomic and molecular). These differences are quantified by some dissimilarity measure that expresses the degree of genetic diversity between the genotypes. The cluster analysis is an important statistical instrument and the classification criteria are used to arrange the parents in distinct groups. This results in homogeneity within the group and heterogeneity between the groups. By this means, it is possible to identify the genotypes that differ and have higher probability of success at crossings (Cargnelutti Filho et al., 2008).

After presenting these aspects, based on the information cited above, this study was conducted to evaluate the dissimilarity in different progenies of the assai palm trees. The study also focuses on identifying the most divergent genotypes with the potential to generate superior genotypic combinations for intercrossings in the next stage of project conduction.

## Material and Methods

The study was conducted at the experimental base of Embrapa Amazonia Oriental located in the municipality of Tomé-Açu River in northeastern Pará, approximately between latitudes 01° 24' 46.14" and 01° 28' 4.11" South latitude and 48° 20' 4.60" and 48° 20' 31.84" West longitude from Greenwich. The area has a hot and humid climate, AMI climatic type, according to the Köppen classification. Although it is characterized as wet, there is a short dry season. Also, there is precipitation in two distinct periods, one being December to May (exceeding 150 mm per month) and another from June to November (mostly less than 100 mm per month). The average annual rainfall is around 2300 mm. The relative air humidity in the region presents little change throughout the year, ranging between 81% and 89% (average values per year). The air temperature has mean values of around 26 °C (Valente et al., 2014).

The seedlings were produced from seeds collected from native matrices of open pollination in the municipality of Anajás, PA in May 2004. The progenies test was planted in March 2005 using a randomized block experimental design involving 30 treatments (progenies), three replicates, and five plants per plot (plot area 6 m × 4 m), plus a side border in the experiment.

The characteristics that were evaluated during the period 2010 to 2012 included the following: average weight of the bunches (PMC, g), total fruit weight (PTF, g), average weight of empty bunches (PMCV, g), average length of the rachis/bunch (TMR, cm), average weight of 100 fruits (PCF, g), total number of bunches (NTC), and total weight of the bunches (PTC, g). The latter value was obtained by multiplying PMC and NTC.

Analysis of variance was performed based on the average values between plants in each plot to verify the presence or absence of statistically significant differences between the progenies in terms of characteristics. The statistical procedures adopted were those proposed by Cruz et al. (2012), where the statistical model used was:

$$Yij = m + Gi + Rj + eij$$

where Yij is the average phenotypic value middle of Y character measured in the genetic material i, in repetition j; m is the overall average from data in study; Gi is the effect of the i$^{th}$ genotype, random; Rj is the effect of the j$^{th}$ repetition; and eij is the average error associated with the observation Yij, random.

The effect of progeny or genotype was considered to be random because the behavior of these provided inferences about the population that gave rise to those used in this study.

The matrix of dispersion was obtained using multivariate methods. The progenies of assai palm were grouped using multivariate method of average link between groups (Unweighted Pair Group Method with Arithmetic Mean; UPGMA). The dendrogram was also created using the average Euclidean distance as a dissimilarity measure. The relative contribution of characteristics for the genetic divergence between the genotypes was quantified using the criterion of Singh (1981) as reported in Cruz et al. (2012). All procedures were performed using Genes statistical software (Cruz, 2013).

## Results and Discussion

Table 1 presents a summary of the analysis of variance with the mean squares and the significance determined using the F-test of the characteristics evaluated. Significant differences were observed between evaluated progenies (G) only for the characteristics TMR and NTC. This indicated the presence of genotypic variability and the possibility of existence of superior individuals. This is because Galate et al. (2014) did not observe differences for this second characteristic. The absence of variability may have been caused by the pre-selection performed at the collection time of the seeds to generate the plants installed in the experimental area, thereby standardizing them subjectively. For PTC, as cited by Galate et al. (2014), there was also no difference. This is in contrast to what was observed by Oliveira and Fernandes (2001) for PTC and PTF whose evaluated materials showed differences.

In the variation source denominated years (A), no significant differences were found. This means that in the experimental condition, the factors that were non-controllable were unable to generate possible differences in behavior between the progeny. This showed that there was environmental stability which is difficult to occur (Cruz et al., 2012).

Although there was a genotype effect only in the characteristics TMR and NTC, however, this did not affect the years. It can be observed in Table 1 that the G×E interaction was significant in all evaluated traits. This indicated that the genotypes interacted differently with the environmental conditions of each year.

The coefficient of variation (CV) was low to the characteristics PCF and TMR; medium for PMC and PMCV; and high for PTF, NTC, and PTC.

In this latter group, the values showed that there was high variability between the different progenies. This was characterized by high interaction with environmental factors and thus indicating less experimental precision. As the assai palm has not yet been domesticated, there was no selection and this maintains the natural variability of the specie.

**Table 1.** Summary of analysis of variance for average weight of the bunches (PMC, in grams), total fruit weight (PTF, in grams), average weight of empty bunches (PMCV, in grams), average length of the rachis/bunch (TMR, in cm), average weight of 100 fruits (PCF, in grams), total number of bunches (NTC), and total weight of the bunches (PTC, in grams) obtained by multiplying PMC and NTC in 30 progenies of assai palm over a four-year period. Anajás, PA.

| FV | GL | PMC | PTF | PMCV | TMR | PCF | NTC | PTC |
|---|---|---|---|---|---|---|---|---|
| Repetition | 2 | 858467.43 | 110310102.29 | 191630.12 | 184.27 | 111.20 | 32.15 | 360447629.99 |
| Genotypes (G) | 29 | 329237.02$^{ns}$ | 75162813.75$^{ns}$ | 24859.16$^{ns}$ | 39.24** | 553.55$^{ns}$ | 12.76** | 153418709.32$^{ns}$ |
| Years (A) | 3 | 52994283.19$^{ns}$ | 5134789466.24$^{ns}$ | 976134.49$^{ns}$ | 18097.77$^{ns}$ | 1753.91$^{ns}$ | 653.83$^{ns}$ | 7784830599.94$^{ns}$ |
| G × E | 87 | 89243.76** | 20666719.53** | 2707.34** | 39.50** | 18.69** | 4.23** | 44090616.17** |
| Error | 238 | 137491.02 | 29198481.92 | 6814.75 | 42.09 | 93.08 | 6.40 | 54287392.32 |
| Total | 359 | | | | | | | |
| Mean | | 2811.70 | 21751.63 | 651.46 | 65.74 | 140.15 | 10.19 | 28378.74 |
| CV% | | 13.19 | 24.84 | 12.67 | 9.87 | 6.88 | 24.83 | 25.96 |

ns: not significant; * and **: significance at 5% and 1% probability, respectively, using the F-test.

Two characteristics, the main one being PTC followed by PTF, were responsible for 99.85% of the total diversity based on average Euclidean distance and the criterion of Singh (1981) shown in Table 2. Other characteristics can be considered as component parts of these two.

The characteristics PMC and PMCV made small and insignificant contributions to the diversity, while TMR, PCF, and NTC did not contribute to the diversity of 30 progenies. This means that with this set of genotypes and in these experimental conditions, these five characteristics did not contribute to the presence of diversity. On the other hand, PTF and PTC had very high participation. However, this behavior may be different when used with another set of genotypes and in other environmental conditions.

Despite this finding, a large number of characteristics to be evaluated causes less efficiency gains and higher costs and requires more time to perform the measurements in a genetic improvement program. Therefore, some should be discarded in the field evaluations and specifically the characteristics to be PMC, PMCV, TMR, PCF, and NTC.

**Table 2.** Relative contribution of average weight of the bunches (PMC, in grams), total fruit weight (PTF, in grams), average weight of empty bunches (PMCV, in grams), average length of the rachis/bunch (TMR, in cm), average weight of 100 fruits (PCF, in grams), total number of bunches (NTC), and total weight of the bunches (PTC, in grams) obtained by multiplying PMC and NTC to the divergence in 30 progenies of assai palm based on average Euclidean distance and criterion of Singh (1981). Anajás, PA.

| Characteristic | S.j | S.j (%) |
|---|---:|---:|
| PMC | 23,869,683.79 | 0.1438 |
| PTF | 5,449,303,996.66 | 32.8313 |
| PMCV | 1,802,288.86 | 0.0109 |
| TMR | 2,845.07 | 0.0000 |
| PCF | 40,132.31 | 0.0002 |
| NTC | 925.39 | 0.0000 |
| PTC | 11,122,856,425.37 | 67.0137 |

S.j: measure of the relative importance of the variable j for the study of genetic diversity; S.j%: measure of the relative importance of the variable j for the study of genetic diversity, expressed as percentage.

The limit of the establishment of the groups in the dendrogram according to Cruz et al. (2012) was performed to obtain the average dissimilarity measures (50%) for composition of different groups. This is based on changes in levels and also on the fact that there had been genetic selection process in the progenies evaluated. It has also been adopted for formation of groups within a limit with 70% of dissimilarity.

The grouping method between the genetic materials used was the UPGMA (Unweighted Pair Group Method with Arithmetic Mean). The criterion used for the composition of groups is based on average distance between all pairs of items that make up each group. In terms of genetic improvement, Gonçalves et al. (2008) refers to the UPGMA method as superior to the single linkage method and the complete linkage method.

In Figure 1, based on the 50% criterion of the dissimilarity between groups and the seven evaluated characteristics, there was the formation of a greater group, denominated group A, containing 16 progenies (from 4 to 26, not in sequential order) which was subdivided into subgroups. The second great group, denominated group B, was composed of five progenies (from 16 to 28, not in sequential order). The A and B groups involving 21 of 30 progenies were evaluated, i.e. 70% of the material was evaluated.

The smaller groups, identified by the letters C to H, were composed of only one or two progenies. Thus, this composed of six more groups of dissimilarity. In contrast, Yokomizo et al. (2012) obtained groups with similar amount of genotypes with no major groups. A large number of dissimilarity groups are important because it shows that there is variability available for genetic improvement.

Additionally, the dissimilarity presence and the formation of groups was due to the collection performed in the native population with crossfertilization adding variations among progenies and also involving genetic material without any effective selection process carried out. The collection process, of course, managed to capture genetic variability which can be made available and exploited in genetic improvement programs for the species.

The differences that allowed formation of groups from the progenies makes them highly promising for obtaining genetic combinations, especially if intercrossings between individuals of different groups are considered and avoiding crossings within groups which possibly contain similar progenies.

With this information, it is possible to guide future crosses involving plants from groups A and B as parents on one side and the progenies of other groups on the other. Therefore, the existing variability will be explored more efficiently.

The adoption of the 70% to dissimilarity limit (i.e. in relation to the previous limit of 50%) supposes a greater difference between each group. This allows for the grouping of the progenies in five groups (“a” to “e”), with the largest group, in this case "a", containing 24 progenies of 30 evaluated. This means that 80% of the genetic material were similar in the seven evaluated characteristics simultaneously. The groups "b" to "e" were formed by one or two progenies only. This was different to that observed by Oliveira et al. (2007) whose groups contained a greater number of progenies (two to five). However, the formation of a larger group with about 80% of evaluated genetic material and other sub-smaller groups was similar to that reported by Galate et al. (2012).

These results demonstrate the existence of variability among the genotypes collected by using the limit of 70% of the progeny which are grouped together to form the group identified as "a". Consequently, the progenies belonging to this group was used for crosses directed with progenies of the other groups and avoiding the intersection within the groups in order to reduce the efforts of workforce, physical space, and time.

There was no numerical sequence arrangement of progenies in the dendrogram which was similar to that cited by Oliveira et al. (2007). This demonstrated that despite the genotypes numeration that keep the sequence of the collection process in the locality of Anajás, there was no concordance in the dispersion of the dissimilarity groups. This behavior can be further explained by the GxE interaction of the evaluated genotypes. The different GxE interaction may have generated distinct phenotypes making it impossible to observe a continuous distribution. However, this is in contrast to that obtained by Galate et al. (2012) with low genetic variability in the genotypes which was evaluated in their work.

These results led to similar conclusions to those obtained by Oliveira et al. (2007), who cites the evidence of wide divergence among accessions, even from nearby provenances, indicating that crosses made between the most divergent can provide an increase in the variability and allow the selection of superior individuals.

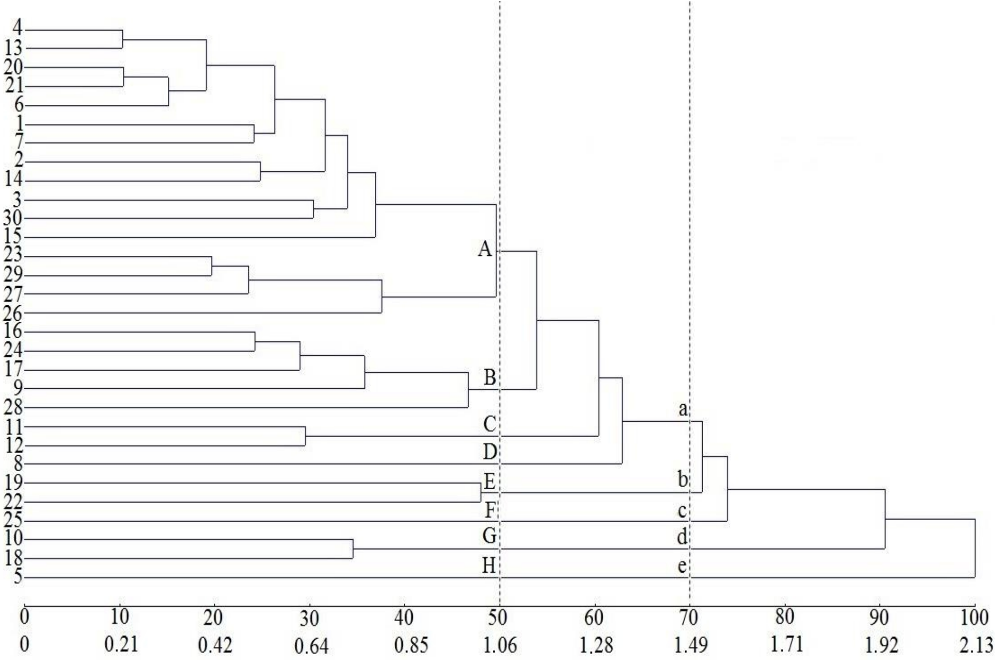

**Figure 1.** Dissimilarity phenogram obtained using the UPGMA clustering method, based on the average Euclidean distance in average weight of the bunches (PMC, in grams), total fruit weight (PTF, in grams), average weight of empty bunches (PMCV, in grams), average length of the rachis/bunch (TMR, in cm), average weight of 100 fruits (PCF, in grams), total number of bunches (NTC), and total weight of the bunches (PTC, in grams) obtained by multiplying PMC and NTC of 30 progenies of assai palms. Anajás, PA.

The main results obtained were of that the characteristics PTC and PTF which were responsible for 99.85% of the total diversity based on average Euclidean distance and the Singh criterion. In the dendrogram, the two larger groups involved 70% of the progenies when using the limit of 50% of dissimilarity and a larger group comprised 80% of the progenies when the limit was 70% of dissimilarity.

## Conclusion

The CVs experiment indicated that the characteristics PTF, NTC, and PTC have uncertain behavior and are dependent on the local conditions. This is in contrast to the characteristics with greater genetic influence, namely PCF and TMR.

The progenies respond to environmental changes because there was a significant G×E interaction in all characteristics.

However, there is an indication to dispose PMC, PMCV, TMR, PCF, and NTC and maintain PTC and PTF because they are responsible for total divergence.

The progeny does not classify sequentially in the dendrogram based on the average Euclidean distance. Nevertheless, we observe the existence of divergence among accessions of close provenance which allows one to choose the most divergent for the achievement of the crossing.

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