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Genetic divergence of native jaboticaba fruit tree (*Plinia cauliflora*) based on fruit quality

Divergência genética de jaboticabeiras nativas (*Plinia cauliflora*) com base na qualidade dos frutos

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Abstract

Jaboticaba is a fruit specie widely known in Brazil, with wide commercial acceptance, however it is observed genetic erosion by anthropic action in their habitat. Thus, the objective of this study was to estimate the genetic divergence between native jaboticaba trees, based on physico-chemical characters, as a complementary tool to identify superior genotypes for selection as future cultivar or male parent. To this end, 15 variables were analyzed, linked to physical-chemical and biochemical characteristics of fruits that were harvested in two productive cycles. As a pre-selection, it was adopted the choose of 20% better genotypes that showed the highest frequency of superiority in evaluated characteristics and through genetic divergence select potential parents with their respective subsidiaries hybridizations. The characteristic that has contributed most to the genetic divergence was the equatorial diameter, explaining much of the total variation, thus being the most important component. There were differences among the populations grouped by Tocher method with those obtained with the dendrogram the nearest neighbor clustering method in relation to jaboticabeira plant groups. There was genetic variability among the analyzed jabuticabeira trees, and thus, it is recommended performing hybridization between genotypes 79 with 119 and 96 with 148.

Key words: Myrtaceae. Multivariate analysis. Genetical enhancement. Genetic diversity.

Resumo

A jaboticabeira é espécie frutífera nacionalmente conhecida e, com ampla aceitação comercial, contudo, o que se observa é ampla erosão genética ocorrida pela ação antrópica em seus habitats. Desta forma, o objetivo deste trabalho foi estimar a divergência genética entre plantas de jaboticabeiras nativas, com bases em características físicos e químicos dos frutos, como ferramenta complementar para identificar genótipos superiores para seleção como futuro cultivar ou genitor masculino. Para tal, foram analisadas 15 variáveis ligadas às características físico-químico e bioquímicas que os frutos colhidos apresentaram em dois ciclos produtivos. Como critério de pré-seleção foi adotada a escolha de 20% dos genótipos que apresentaram a maior frequência de superioridade nas características avaliadas e por meio da divergência

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genética selecionar possíveis genitores com suas respectivas hibridações controladas. A característica que mais contribuiu para a divergência genética foi o diâmetro equatorial explicando grande parte da variação total, sendo assim o componente de maior importância. Houve diferenças entre as populações agrupadas pelo método de Tocher com os obtidos com o dendograma pelo método de agrupamento do vizinho mais próximo em relação aos grupos de plantas de jaboticabeira. Existe variabilidade genética entre as plantas de jaboticabeira analisadas e, dessa forma recomenda-se a realização de hibridação entre os genótipos 79 e 119 e, 96 com 148.
Palavras-chave: Myrtaceae. Análise multivariada. Melhoramento genético. Diversidade genética.

Introduction

The Jaboticabeiras [*Plinia cauliflora* (Mart.) Kausel] occur generally in clusters that possibly were formed by related individuals, as already studied in the Southwest region of Paraná (DANNER, 2009; DANNER et al., 2010). However, due to the expansion of agricultural frontiers and forest fragmentation, occurrence sites of many species may have been lost, as they were previously found inside forests, with probable dispersal by animals (DANNER, 2009) and by Indians living in the region.

Forest fragmentation reduces the size of the reproductive population and the population density of plant species. Thus, the main consequences of population fragmentation and reduction are genetic drift, increased inbreeding and decreased gene flow (KAGEYAMA; GANDARA, 1998), and in the case of jaboticabeira, these conditions have been aggravated by the presence of polyembryony resulting from apomixis.

This phenomenon tends to decrease intrapopulation genetic diversity and increase interpopulation genetic diversity, compared to that of the original conditions. However, one should also consider the reproductive system of the species, which is not yet fully understood (DANNER, 2009; DANNER et al., 2011a), the pollen dispersal distance, which is dependent on the area of the reproductive neighborhood, the density and behavior of pollinators, and seed dispersal. These factors influence gene flow and are determinants for genetic diversity and structuring (SEBBENN, 2006).

As genetic diversity represents the potential of a population to produce different genotypes, it is critical for species survival, adaptation and evolution, especially under environmental changes and for selection in genetic breeding (ISAGI et al., 2007; CARVALHO, 2004), being primordial for the species in question.

It is important to emphasize that through the characterization of genetic diversity and its manner of distribution, it is possible to make rational and sustainable use of genetic resources, and contribute to prebreeding studies, in order to understand the available germplasm before introducing it in the breeding program (DANTAS et al., 2012).

In genetic breeding programs, information about genetic divergence within a species is fundamental to the rational use of genetic resources (LOARCE et al., 1996), as well as for the biological conservation of species and for studies of evolution and ecology of populations (DURAN et al., 2009).

Genetic divergence refers to the level of heterogeneity of a population or individuals of a particular species and can be assessed by means of predictive processes or multivariate techniques. The multivariate techniques are especially useful because they allow obtaining estimates of the general combining ability, in order to provide information on the concentration of predominantly additive genes in their effects, thereby aiding in the indication of parents used in intrapopulation breeding programs (CRUZ et al., 2012; MIRANDA et al., 2003). Among the multivariate statistical techniques, principal component analysis and clustering methods (CRUZ; REGAZZI, 1997) will be described.

The principal component analysis consists of retaining, in order of estimation, the maximum information in terms of total variation contained in the original data. The cluster analysis aims to use classification criteria to gather parental groupings in such a way that there is homogeneity within the group and heterogeneity between groups (CRUZ, 1990).

The study of genetic divergence also contributes to the evolution of the species with the identification of divergent genotypes, enabling inference about the specific capacity of combinations and heterosis (OLIVEIRA et al., 2003).

Studies involving native jaboticabeiras provide parameters for the identification of favorable parents to obtain segregating populations, for hybridization programs, in the selection of superior genotypes and, as a consequence, the result of obtaining genetically improved populations.

Given this information, it is known that the characterization of existing genetic resources serves as a strategy to mitigate damages already caused and to increase the exploitation of jaboticabeira in commercial crops (CITADIN et al., 2010), in agroforestry systems, and for use in permanent preservation areas and legal reserves (ZERBIELLI et al., 2016).

The genetic divergence between native jaboticabeiras plants, based on physical and chemical characteristics, was characterized in order to identify parents for use in future hybridizations, thereby seeking to broaden the genetic basis for these characteristics and making available information pertinent to the breeding program of this species.

Material and Methods

The study was carried out on a population of jaboticabeiras [*Plinia cauliflora*; (Mart.) Kausel] found in fragmented mixed ombrophilous forests or forests containing araucaria (DANNER et al., 2010). (26°26'17" S; 52°19'20" W; 963 m in altitude), located in the municipality of Clevelândia, in the Southwest region of Paraná. The study area has 12.3 hectares and 930 adult jaboticabeiras.

In 2013, 60 (sixty) fruits per plant were collected, and 80 were collected in 2014 (31/Oct/2013 and 29/Oct/2014), with 70 genotypes characterized in 2013 and 56 in 2014, of adult reproductive individuals, within the sampled plot.

Of the genotypes collected in 2013 (designated 54, 106, 169, and 212), the identifications were removed the next year; in numerically equivalent terms, in the 2014 survey, these genotypes received new codes: J7-01, J7-02, 345, and 347, respectively. Thus, it is possible that these renamed genotypes had also been evaluated in 2013, though there is no way to distinguish them.

The samples of ripe fruits were taken to the Laboratory of Vegetal Physiology, Universidade Tecnológica Federal do Paraná - Câmpus Dois Vizinhos, where the following assessments were performed.

The physicochemical characteristics were determined: polar diameter (PD, in mm) and equatorial fruit (ED, in mm); mass of the total fresh matter (g, gram); mass of the fresh matter of the bark (g); mass of the fresh seed matter (g); percentage of pulp (%, percentage); and content of total soluble solids (SST, ° Brix). The pulps were stored in a freezer (-18°C) for 15 days, and biochemical analyzes were then performed, including protein content [method of Bradford (1976)], total sugars [method of Dubois (1956)], anthocyanins and flavonoids [method of Lees; Francis (1972)], total phenols [method of Singleton et al. (1999)] and total titratable acidity (ATT) (INSTITUTO ADOLFO LUTZ, 2008). The ratio SST / ATT was estimated by the simple division of the means of the repetitions of SST by ATT.

To calculate the frequency, genotypes were ranked in terms of each of the 15 analyzed variables, from the 1st to the 70th or 56th genotype evaluated (in 2013 or 2014, respectively). Of these, 13

variables were classified by means of the variables in decreasing order, except for the variables "shell mass" and "total ATT", which were ranked in ascending order. The rank of each genotype in each of the variables was added, and applying the total value of the sum, the genotypes were then classified in ascending order. Genotypes ranked among the top 20% were selected (up to 14th in 2013 and up to 11th in 2014) (WAGNER JÚNIOR, 2007).

For the analysis of the genetic divergence, 33 genotypes were selected, with repeatability based on the characteristics of the main components. The cluster analysis was performed by the Tocher and nearest neighbor methods, using as a measure of dissimilarity the distance of Mahalanobis (CRUZ et al., 2012).

Results and Discussion

For each evaluation year, the genotypes ranked among the top 20% were selected (Table 1) (up to 14th in 2013 and up to 11th in 2014).

Table 1. Pre-selected genotypes among the top 20%, which showed the highest frequency of quality characteristics of jaboticaba tree fruits, collected in 2013 (70 genotypes) and 2014 (56 genotypes) in Clevelândia city, Paraná State, Brazil.

Genotypes of 2013	
Ranking	Genotype
1º	97
2º	91
3º	212
4º	54
5º	177
6º	169
7º	16
8º	43
9º	186
10º	194
11º	104
12º	157
13º	134
14º	154

Genotypes of 2014	
Ranking	Genotype
1º	J7-02
2º	194
3º	7
4º	J7-01
5º	118
6º	16
7º	42
8º	47
9º	153
10º	163
11º	105

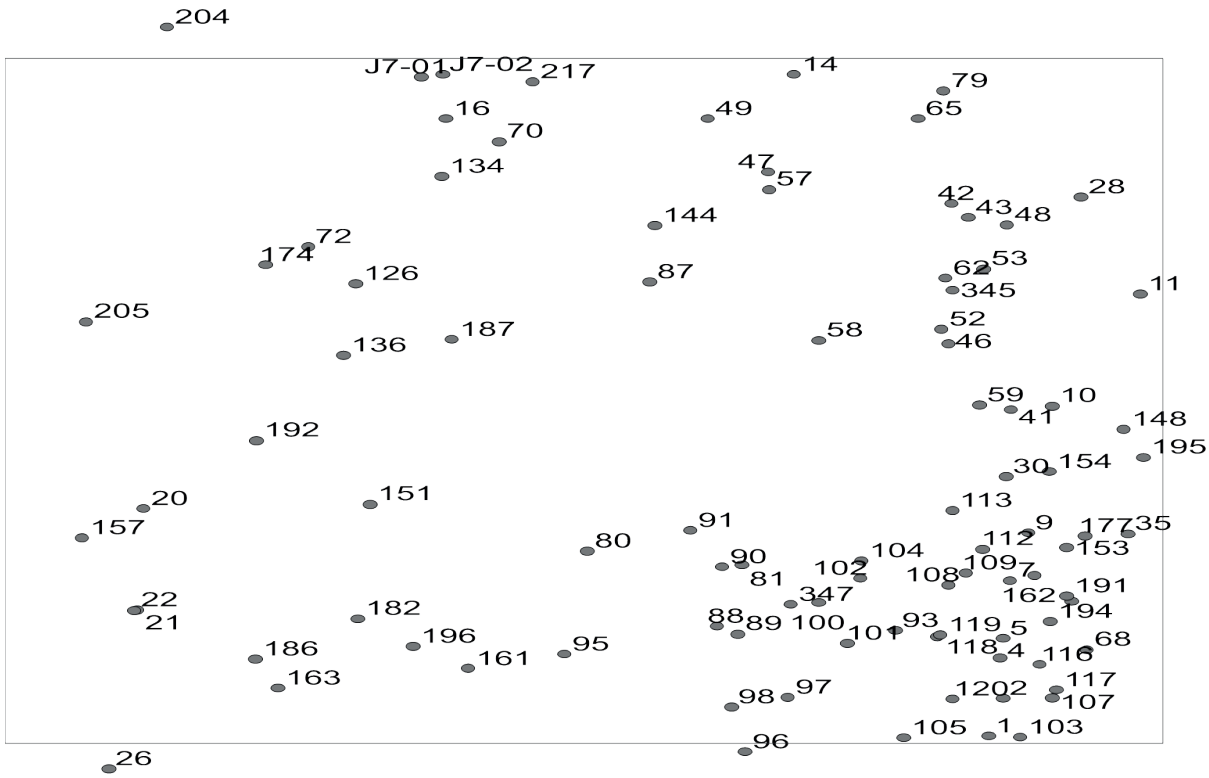
Genotypes 16 and 194 were highlighted in both selection indications, which allows them to be used as future cultivars and / or parents in order to obtain quality fruits, as based on physicochemical and nutraceutical variables.

Genotypes 101, 103, 104 and 105, J7-01 and J7-02, and 153 and 154 have proximity within the sampled area (Figure 1). It was assumed that these genotypes could be clones from apomixis which, according to Danner et al. (2011b), can occur with jaboticabeira, as they are polyembryonic. In this case, there is a zygote embryo and one or more asexual embryos formed by apomixis, in which genome clones were generated by plants, with the intention of forming uniform orchards.

As for the assessment of divergence by the principal components method carried out in 2013, it was demonstrated that six variables [equatorial

(CP1) and polar (CP2) diameters and mass of fresh fruit (CP3), bark (CP4), seed (CP5) and pulp (CP6)] explain approximately 85% of the variation obtained by the 33 accessions studied.

Figure 1. Distribution of the jaboticaba tree genotypes from the forest fragment of Clevelândia city, Paraná State, Brazil, in the plot of 100 x 100 meters, whose fruits were harvested in at least one of the cycles 2013 and 2014, except for genotypes 54, 106, 169, 212 (harvested only in 2013).



The equatorial diameter explains 38.48% of the total variation, considering the component of greater relevance. The variables that contributed minimally to the study of genetic divergence among jaboticabeira genotypes were SST, ATT, proteins, total sugars, flavonoids, anthocyanins and total phenols, with a variation of less than 4%. In 2014, the same six main components were used, with these explaining 82.5% of the variation between the 33 accessions (Table 2). The importance of a variable being evaluated was related to the percentage of total variance that it explained (CRUZ et al., 2012).

The maximum heterotrophic effect in controlled crosses between the most divergent genotypes can be observed in Figures 2 A, B, C, D and E, with the formation of seven, six, five, five and four groups, respectively. In all the main components, it was always observed that jaboticabeiras 148 and 16 were each in isolated groups due to the divergence of these with the others in the characteristics analyzed. It is known that the use of parental genotypes with greater divergence increases the heterosis manifested in the hybrids, with probability of occurrence of superior segregants in advanced generations, and must be used to recommend crosses, avoiding those genotypes within the same group (DESTRO, 1991).

It was verified that the largest group comprised jaboticabeiras 204, 120, 118, 100, 107, 11, 104, 105, 108, 79, 117, 49, 88, 119, 47, 10, 42, 194, 163 and 80 (Figure 2-A). The second largest group occurred

with genotypes 35, 101, 98 and 65, along with 57, 177, 96 and 162, both groups being followed by the formation of 166 with 102. Genotype 41, as well as those already cited (16 and 148), appeared in clusters formed by an individual.

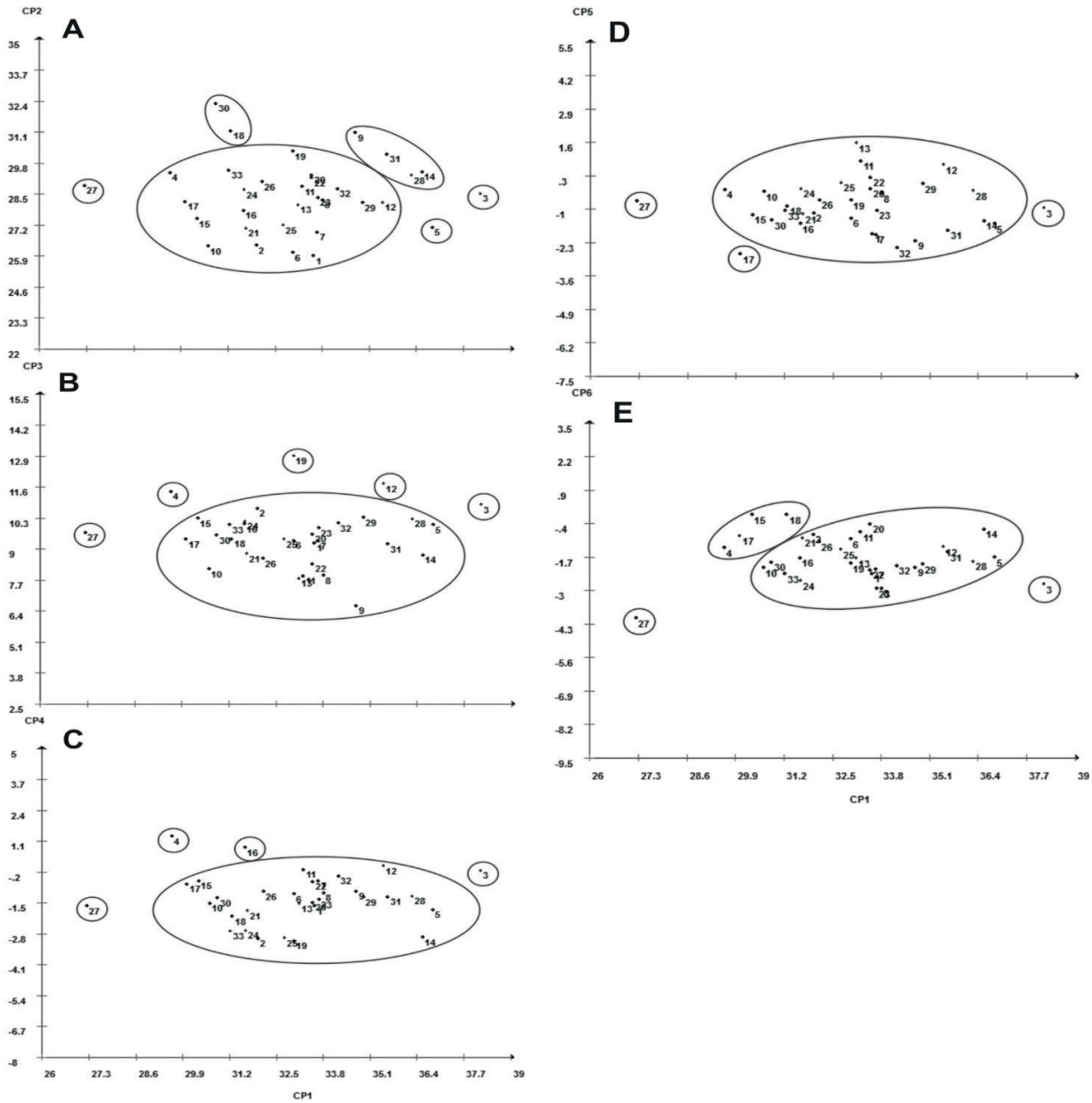
Table 2. Estimates of the eigenvalues and the proportion of variance explained by the principles components analysis obtained by fruits characteristic evaluated in 2013 and 2014 with 33 jaboticaba trees genotypes from the forest fragment of Clevelândia city, Paraná State, Brazil.

Components	Eigenvalue	% da variance	% acumulate
		2013	
Equatorial Diameter	5,3875497	38,4824976	38,48
Polar Diameter	2,2379513	15,9853665	54,47
fresh fruit matter	1,5225999	10,8757139	65,34
fresh peel matter	1,1223848	8,0170343	73,36
fresh seed matter	0,9465739	6,7612421	80,12
fresh pulp matter	0,7811195	5,5794249	85,70
Pulp yield	0,7384209	5,2744350	90,98
Soluble solids	0,507384	3,6241713	94,60
Titratable Total Acidity	0,3621061	2,5864725	97,19
Pulp proteins	0,2239283	1,5994878	98,79
Total pulp sugars	0,1284602	0,9175731	99,70
Pulp Flavonoids	0,037314	0,2665284	99,97
Pulp anthocyanins	0,003004	0,0214568	99,99
Total pulp phenols	0,0012034	0,0085959	100,00
		2014	
Equatorial Diameter	4,2688859	30,4920421	30,49
Polar Diameter	2,3253252	16,6094660	47,10
fresh fruit matter	1,7662900	12,6163569	59,72
fresh peel matter	1,3407375	9,5766966	69,30
fresh seed matter	1,0177024	7,2693029	76,56
fresh pulp matter	0,836846	5,9774711	82,54
Pulp yield	0,7351068	5,2507629	87,79
Soluble solids	0,5364897	3,8320694	91,62
Titratable Total Acidity	0,4809676	3,4354826	95,06
Pulp proteins	0,4384833	3,1320234	98,19
Total pulp sugars	0,2429041	1,7350296	99,93
Pulp Flavonoids	0,0077438	0,0553127	99,98
Pulp anthocyanins	0,0025043	0,0178881	100,00
Total pulp phenols	0,0000134	0,0000957	100,00

The jaboticabeiras were framed together in a single group including 10, 11, 41, 42, 47, 49, 57, 65, 79, 88, 96, 98, 100, 101, 102, 105, 107, 108, 117, 118, 119, 120, 162, 163, 166, 177, 194, and 204; and the rest were isolated, forming five groups with a single genotype in each, these being formed by 148, 35, 104, 80 and 16 (Figure 2-B).

A similar grouping can be observed in Figure 2C, differing only by the presence of five groups and replacing of genotype 104 by genotype 100. In this way, the groups were constituted by 148 (I), 35 (II), 100 (III), 16 (IV), and 10, 11, 41, 42, 47, 49, 57, 65, 79, 80, 88, 96, 98, 101, 102, 104, 105, 107, 108, 117, 118, 119, 120, 162, 163, 166, 177, 194, and 204 (V).

Figure 2. Distribution of the 33 jaboticaba tree genotypes from the Clevelândia city, Paraná State forest fragment, in relation to the principles components analysis of fruits collected in 2013: equatorial diameter (CP1) and polar diameter (CP2) "A" CP1 and fresh matter mass fruit (CP3) "B"; CP1 and fresh matter mass of the peel (CP4) "C" CP1 and mass of fresh seed matter (CP5) "D"; CP1 and fresh matter of the seed (CP5) "**E**". Legend genotypes: 1: 10; 2: 11; 3: 16; 4: 35; 5: 41; 6: 42; 7: 47; 8: 49; 9: 57; 10: 65; 11: 79; 12: 80; 13: 88; 14: 96; 15: 98; 16: 100; 17: 101; 18: 102; 19: 104; 20: 105; 21: 107; 22: 108; 23: 117; 24: 118; 25: 119; 26: 120; 27: 148; 28: 162; 29: 163; 30: 166; 31: 177; 32: 194; 33: 204.



Analyzing Figure 2D, which involves the relationship of the components, equatorial diameter × mass of the fresh seed matter, jaboticabeiras 10, 11, 35, 42, 47, 49, 57, 65, 79, 88, 98, 100, 102, 104, 105, 107, 108, 117, 118, 119, 120, 148, 166, 194 and 204 compose one group, which is followed by the group constituted by genotypes 163, 80, 162, 96, 41 and 177 as the second major grouping, and finally, three isolates are represented by jaboticabeiras 148, 101 and 16.

In Figure 2-E, the number of groups was reduced in relation to that of the other main components present (Figure 2A, B, C, and D); however, the largest group involved 27 of the 33 jaboticabeira described, separating this from genotypes 35, 101, 98, and 102, which constituted a group, and from 148 and 16, which formed two other isolates.

Figure 3-A, B, C, D and E reveals the formation of seven, six, nine, nine and seven groups, respectively. The results show greater divergence between the main components in 2014 compared to that in 2013. As seen in Figure 3A, there were two groups with one genotype (35 and 105), others with three (102, 117, and 119; 16, 104, and 88), four (57, 47, 49, and 42), and seven (204, 162, 80, 194, 118, 108, and 101), and the largest with fourteen (107, 96, 100, 163, 41, 177, 11, 79, 65, 148, 120, 10, 98, and 166).

In Figure 3B, six groups were formed, but in five of these, there were few accesses [57 (group I), 88 (group II), 105 (group III), 47 and 49 (group IV), 108, 117 and 119 (group V), and in the largest group, 25 accesses, 10, 11, 16, 35, 41, 42, 65, 79, 80, 96, 98, 100, 101, 102, 104, 107, 118, 120, 148, 162, 163, 166, 177, 194 and 204 (group VI)].

In relation to Figures 3C and 3D, both formed nine genotype groups; however, the groups with the lowest number of genotypes did not have similarity, the only exception being 105, which appeared isolated in both figures. This genotype was also isolated in the other analyzed components (Figures 3A, 3B, and 3E), indicating such divergence in relation to the others.

In the analysis demonstrated by Figure 3, the other eight groups were formed by isolated genotypes 119, 108 and 16, along with two groups of two genotypes each (104 and 88; 42 and 100). In addition, two groups each consisted of six genotypes, with 57, 117, 107, 102, 49 and 47 in one group and 194, 98, 166, 101, 35, and 118 in the other. The group with the highest number of genotypes was formed by 10, 11, 41, 65, 79, 80, 96, 120, 163, 177 and 204.

When comparing Figures 3-C and 3D, a larger number of jaboticabeiras was observed in a single group, with both figures revealing that nine groups were formed: the groups formed by an individual involved genotypes 57, 49, 162, 194 and 105; one group of two genotypes with 42 and 107; one group of four with 102, 47, 117 and 119; one group of nine consisting of 11, 41, 79, 80, 96, 100, 163, 177 and 204; and a group with thirteen genotypes including 10, 148, 166, 101, 35, 65, 120, 98, 118, 108, 3, 104 and 88.

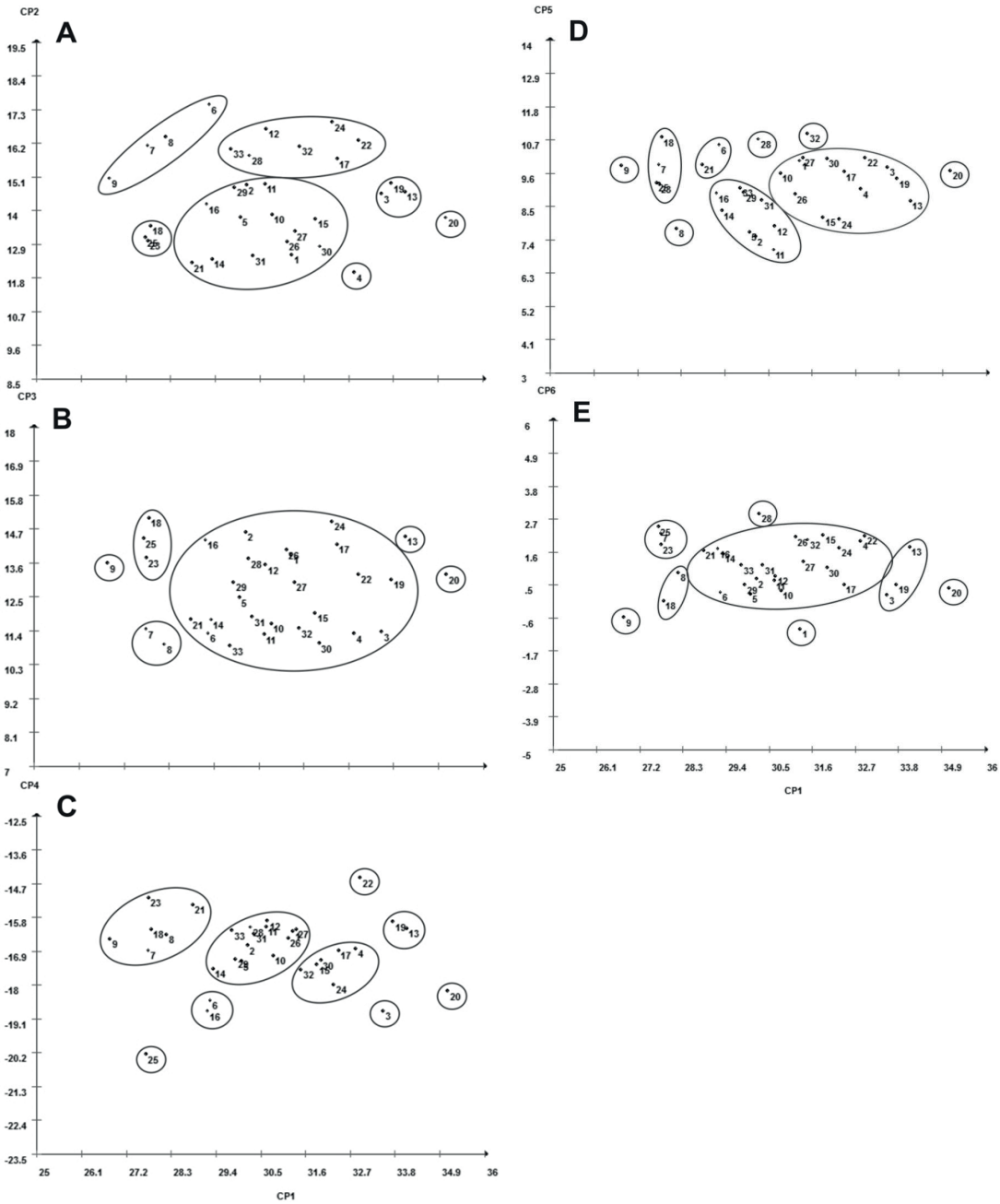
One group in figure 3-E is the largest, containing 22 of the 33 genotypes analyzed, these being 11, 35, 41, 42, 65, 79, 80, 96, 98, 100, 101, 107, 108, 118, 120, 148, 162, 163, 166, 177, 194 and 204. The other groups had three (119, 117 and 47; 88, 104 and 16), two (102 and 49), and one genotype each (57, 10 and 105).

In general, when comparing the results of the main components in both years of analysis (Figures 2-A, B, C; D, and E, and Figures 3-A, B, C, D, and E) it was verified that, even when using the same variables, most of the groups formed did not have the same formation with the exception of some joined accesses.

This fact was related to the variation in the values of the averages obtained from one year to the next in the analyzed variables; similar behavior was previously described by Citadin et al. (2005). This relationship also reflects the fact that such plants are found in nature, without any kind of management,

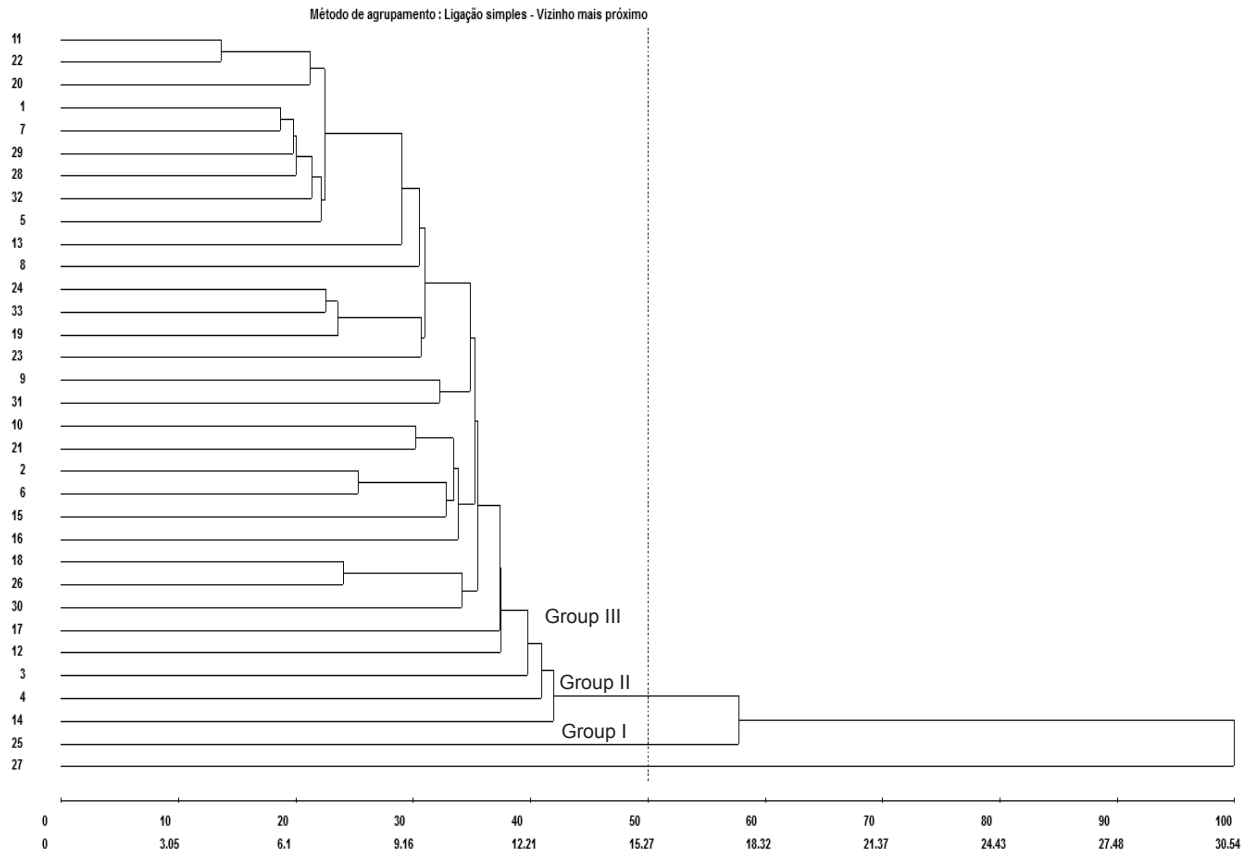
which allows such behavior from one year to the next. It is important to perform such evaluations in additional cycles because in this way, we can apply repeatability and stability analyses based on such hypotheses described above.

Figure 3. Distribution of the 33 jaboticaba tree genotypes from the Clevelândia cty, Paraná State forest fragment, in relation to the principles components, analysis of fruits collected in 2014: equatorial diameter (CP1) and polar diameter (CP2) "A" and CP1 and fresh matter mass of the fruit (CP3) "B"; CP1 and fresh matter mass of the peel (CP4) "C"; CP1 and fresh seed mass (CP5) "D"; CP1 and fresh matter of the seed (CP5) "**E**". Legend genotypes: 1: 10; 2: 11; 3: 16; 4: 35; 5: 41; 6: 42; 7: 47; 8: 49; 9: 57; 10: 65; 11: 79; 12: 80; 13: 88; 14: 96; 15: 98; 16: 100; 17: 101; 18: 102; 19: 104; 20: 105; 21: 107; 22: 108; 23: 117; 24: 118; 25: 119; 26: 120; 27: 148; 28: 162; 29: 163; 30: 166; 31: 177; 32: 194; 33: 204.



For the formation of the dendrogram using the nearest neighbor method, regarding the analyses of 2013, the largest distance was considered to be the value between 84 and 40 (obtained by D2), which was set as 100%. The greatest divergence observed among populations was between accesses 96 and 148, belonging to groups I and IV, by the Tocher method (Table 3) and/or groups II and I by the nearest neighbor method (Figure 4), thus demonstrating the greater heterotic potential of these two combinations.

Figure 4. Dendrogram of genetic dissimilarities among 33 genotypes of jaboticaba trees from a forest fragment of Clevelândia city, Paraná State, obtained by the "nearest neighbor" method based on data from the 2013 analyzes of fruit quality variables (equatorial and polar diameters; fruits, peel, seed and pulp, pulp yield, soluble solids, titratable total acidity, pulp proteins, total pulp sugars, pulp flavonoids, pulp anthocyanins and total pulp phenols) in 2013, using the generalized distance of Mahalanobis. In the X axis were represented the percentages of the distances between the populations and in the Y axis the 33 genotypes were represented. Legend genotypes: 1: 10; 2: 11; 3: 16; 4: 35; 5: 41; 6: 42; 7: 47; 8: 49; 9: 57; 10: 65; 11: 79; 12: 80; 13: 88; 14: 96; 15: 98; 16: 100; 17: 101; 18: 102; 19: 104; 20: 105; 21: 107; 22: 108; 23: 117; 24: 118; 25: 119; 26: 120; 27: 148; 28: 162; 29: 163; 30: 166; 31: 177; 32: 194; 33: 204.



The smallest divergence occurred between jaboticabeiras 79 and 108, both belonging to the same group in both analyses (Table 3 and Figure 4). Thus, the use of these individuals in controlled hybridizations is not recommended, since endogamy can lead to inbreeding depression, causing loss of vigor by the homozygosis of deleterious genes (MIRANDA FILHO, 2001; FALCÃO et al., 2001).

These results emphasize divergence, as the physical location between accesses 79 and 108 (72 m) within the sampled area, although presenting a smaller divergence, was more distant than were accesses 96 and 148 (57 m), which were among the most distant in relation to the others (Figure 4). It was assumed that these factors might be related to some seed disperser that geographically spread the accesses of lower divergence (79 and 108).

Table 3. Grouping resulting from the Tocher method based on the Mahalanobis distance between the 33 jaboticaba tree genotypes, sampled in 2013, from the forest fragment of Clevelândia city, Paraná State, Brazil.

Group	Genotype
I	10; 11; 16; 41; 42; 47; 49; 57; 65; 79; 80; 88; 96; 98; 100; 101; 102; 104; 105; 107; 108; 117; 118; 119; 120; 162; 163; 177; 194; 204
II	166
III	35
IV	148

The seed dispersers of this species are rodents, birds and monkeys (GRESSLER et al., 2006), which can be found in such fragmented forests. In addition, it is possible to suggest the presence of common kinship, a fact that remarkably illustrates how the local ecosystem originally involved the existence of a contiguous Araucaria Forest in this region before anthropic exploration, which facilitated gene flow between individuals.

In Figure 4, three groups were identified, two with a single individual (148 and 119) and the other with one. In the dendrogram formed based on the analyses of 2014, by the nearest neighbor method, it was considered to be greater distance than that characterized by the values of 230 and 31. This greater divergence was between jaboticabeiras 79 and 119, with less divergence between 96 and 98.

The most divergent genotypes were categorized in groups I and IV by the Tocher method (Table 3), and in groups I and V by the nearest neighbor method (Figure 5), verifying among groups a greater heterotic potential in these two combinations as well.

The distance of the most divergent genotypes (148 and 119) was 79 m within the area, with those of smaller value (96 and 98) being 6.6 m. In the latter, it may have been influenced by inbreeding or even by material of the same genetic constitution, since in jaboticabeira polyembryony is common, as results from apomixis.

By the Tocher method, it was observed in Table 4 that there were six groups, consisting of the following: one genotype in groups VI (119), V (118), IV (57), two in group III (16 and 42), five in group II (47, 204, 49, 162 and 194), and the other 21 jaboticabeiras in group I.

Genetic variability is of fundamental importance for species evolution. It is also in populations with genetic variability that the selection of genotypes yielding phenotypes with characteristics of agronomic interest, such as larger and tastier fruits and resistance to diseases and pests, can be accomplished.

It was verified in this study that there were some differences between the populations grouped by the Tocher method versus those obtained with the dendrogram using the closest neighbor grouping method (Table 4 and Figure 5, respectively).

However, what was visualized is that accesses 47, 204, 49 and 162 exhibited union within the same group in both analyses (Table 4 and Figure 5), both

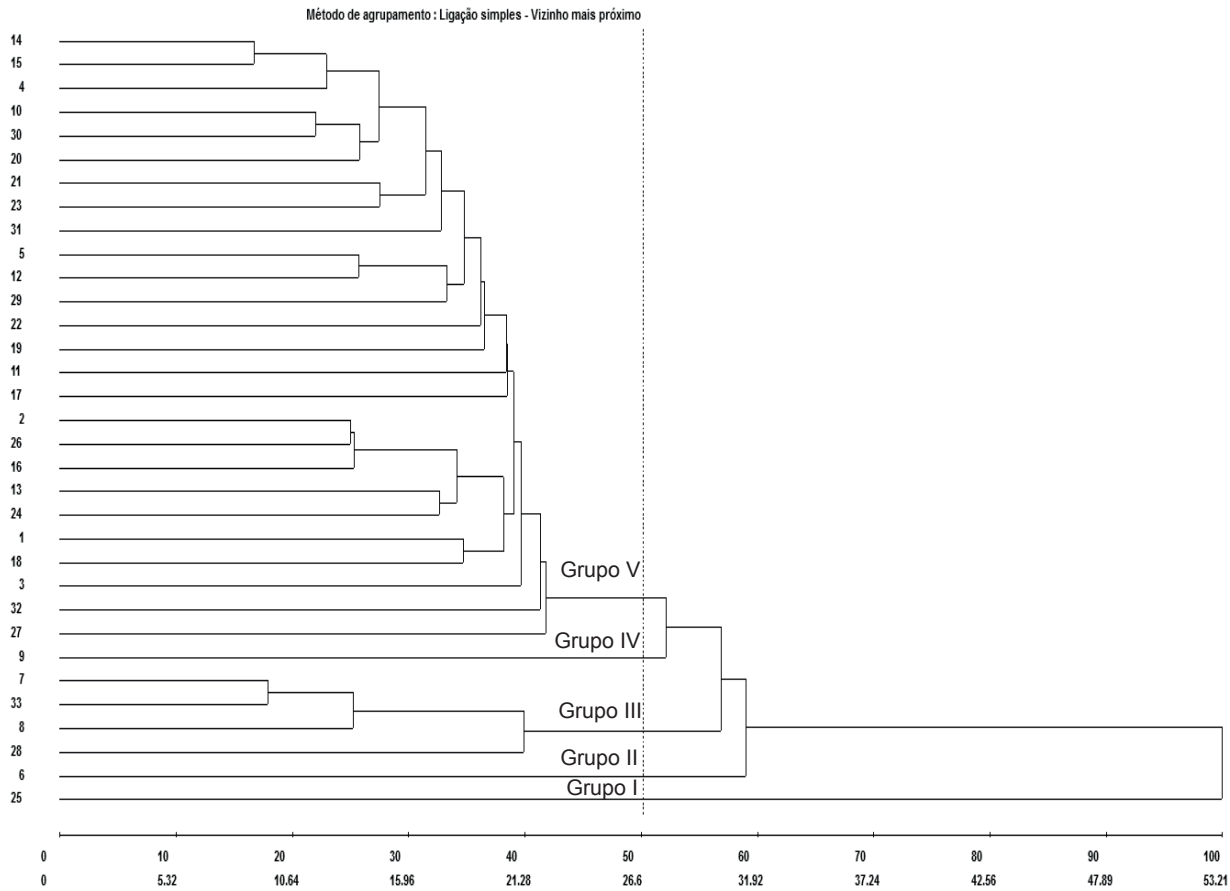
119 and 57 were present as isolates, and the largest group was formed by 10 (1), 11 (2), 35 (4), 41 (5), 65 (10), 79 (11), 80 (12), 88 (13), 96 (14), 98 (15), 100 (16), 101 (17), 102 (18), 104 (19), 105 (20), 107 (21), 108 (22), 117 (23), 120 (26), 148 (27), 163 (29), 166 (30), and 177 (31).

Table 4. Grouping resulting from the Tocher method based on the Mahalanobis distance between the 33 jaboticaba tree genotype, sampled in 2014, from the forest fragment of Clevelândia city, Paraná State, Brazil.

Group	Genotypes
I	10; 11; 35; 41; 65; 79; 80; 88; 96; 98; 100; 101; 102; 104; 105; 107; 108; 117; 120; 148; 163; 166; 177
II	47; 204; 49; 162; 194
III	16; 42
IV	57
V	118
VI	119

According to Figure 5, five groups were formed: group I by jaboticabeira 119 (25), group II with 42 (6), group III having 162 (28), 49 (8), 204 (33), and 47 (7), group IV by 57 (9) and group V by the others [10 (1), 11 (2), 16 (3), 35 (4), 41 (5), 65 (10), 79 (11), 80 (12), 88 (13), 96 (14), 98 (15), 100 (16), 101 (17), 102 (18), 104 (19), 105 (20), 107 (21), 108 (22), 117 (23), 118 (24), 120 (26), 148 (27), 163 (29), 166 (30), 177 (31), and 194 (32)].

Figure 5. Dendrogram of genetic dissimilarities among 33 jaboticaba trees genotypes from a forest fragment of Clevelândia city, Paraná State, obtained by the "nearest neighbor" method based on data from the 2014 analyzes of fruit quality variables (equatorial and polar diameters; fruits, peel, seed and pulp, yield of pulp, soluble solids, titratable total acidity, pulp proteins, total pulp sugars, pulp flavonoids, pulp anthocyanins and total pulp phenols) in 2014, using the generalized distance of Mahalanobis. In the X axis were represented the percentages of the distances between the populations and in the Y axis the 33 genotypes were represented. Legend genotypes: 1: 10; 2: 11; 3: 16; 4: 35; 5: 41; 6: 42; 7: 47; 8: 49; 9: 57; 10: 65; 11: 79; 12: 80; 13: 88; 14: 96; 15: 98; 16: 100; 17: 101; 18: 102; 19: 104; 20: 105; 21: 107; 22: 108; 23: 117; 24: 118; 25: 119; 26: 120; 27: 148; 28: 162; 29: 163; 30: 166; 31: 177; 32: 194; 33: 204.



Carpentieri-Pípolo et al. (2000) recommend the use of parental genotypes; however, these have the greatest possible divergence to maximize heterosis in hybrids, increasing the probability of occurrence of higher segregants in advanced generations and broadening the genetic base. This factor must be taken into account in the choice of which jaboticabeiras will be used as mothers.

Conclusion

There are differences between the populations of jaboticabeira plants grouped by the Tocher method versus those obtained with the dendrogram by the nearest neighbor grouping method.

There is genetic variability between the jaboticabeira plants analyzed, and therefore, it is recommended to perform hybridization between genotypes 79 with 119 and 96 with 148.

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