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Phenotypic divergence of *Plinia* spp. genotypes based on plant growth behavior

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Abstract
Phenotypic divergence among population genotypes is useful to improve our knowledge about how to preserve the genetic resource available. The aim of this study was to evaluate the phenotypic divergence among jabuticaba genotype trees in relation to stem and primary shoot lenght analyzed in three consecutives productive cycles. The genotypes of jabuticaba trees were obtained from *Fruteiras Nativas* collection of Universidade Tecnológica Federal do Paraná (UTFPR – Campus Dois Vizinhos, Parana State, Brazil). The genotypes had their origin in forest fragments of the Southwest Region of Paraná and Minas Gerais State (Brazil). Phenotypic divergence was performed through analysis of variance (ANOVA), Mahalanobis distance, Tocher optimization cluster analysis and by the nearest neighbor method. The results obtained showed that the diversity among the genotypes were different according to the cycle analyzed since we obtained different groups for each year analyzed. Genotypes from Minas Gerais tended to remain in distinct groups, since it had low similarity with the others. The genotype 'Vitorino' had a high divergence among individuals from the same place.
Keywords: jabuticaba; Mahalanobis distance; Tocher clusterization.

Divergência fenotípica de *Plinia* spp. baseada no comportamento de crescimento das plantas

Resumo
A divergência fenotípica entre os genótipos de uma população é útil para que se tenha conhecimento sobre formas de conservação dos recursos genéticos disponíveis. O objetivo deste estudo foi avaliar a divergência fenotípica entre os genótipos de jabuticabeira em relação ao comprimento do caule e de brotações analisados em três ciclos produtivos consecutivos. Os genótipos de jabuticabeiras foram obtidos da coleção de Fruteiras Nativas da Universidade Tecnológica Federal do Paraná (UTFPR - Câmpus Dois Vizinhos, Paraná, Brasil). Os materiais são originários de fragmentos florestais da Região Sudoeste do Paraná e do Estado de Minas Gerais. A divergência fenotípica foi caracterizada por meio das análises de variância (ANOVA), distância de Mahalanobis, de análise de agrupamento de otimização de Tocher e pelo método do vizinho mais próximo. Os resultados obtidos demonstraram que a diversidade entre os genótipos foi diferente conforme o ciclo analisado, pois em cada ano houve a formação de grupos diferentes. Os genótipos provenientes de Minas Gerais tenderam a se manter em grupos distintos, já que possuíram baixa similaridade com os demais. O genótipo 'Vitorino' apresentou alta divergência entre indivíduos do mesmo local.
Palavras-chave: jabuticaba; distância Mahalanobis; clusterização de Tocher.

Introduction

The jabuticaba tree (*Plinia spp.*) belongs to the Myrtaceae family, and it is a native tree from Brazil mainly occurring in the Atlantic Forest Biome (tropical and humid subtropical climate) (MATTOS, 1983). It has an important economic potential, since it is the most widely native fruit specie cultivated in urban backyards and rural properties in the South and Southeast regions of Brazil (KINUPP *et al*., 2011).

It is possible to use the fruit for in natura consumption or by industrialization to obtain

jellies, vinegars, liqueurs and fermented beverages (DANNER *et al*., 2006), as well as to take advantage of nutraceutical characteristics for obtaining drugs or cosmetics (CITADIN *et al*., 2010).

Despite of these several agroindustrialization and commercialization possibilities, the number of commercial orchards of jabuticaba tree is still small. The main reasons are due to the long juvenile period when propagated through seeds and, by lack of technical information about plant growth management and genotypes superior selection (KINUPP *et al*., 2011).

In this way, studies focusing in the knowledge improvement of *Plinia* spp. species is necessary, specially in relation to the plant management system associated with the selection of the best genotype for each edaphoclimatic region.

The genetic diversity study and plant breeding program are capable to optimize genotype selection of individuals that show better adaptation responses for different regions and cultivation conditions (CRUZ; CARNEIRO, 2006).

Phenotypic characterization can help in the selection of jabuticaba tree genotypes and, if associated with statistical methods and models, may quantify the genetic divergence between among different environments for domestication. Methods and analysis for evaluating phenotypic divergence had already been used for the jabuticaba tree by means of the diversity of physico-chemical and biochemical characteristics of the fruit (WAGNER JÚNIOR *et al*., 2018; ZERBELLI *et al*., 2016). Similar studies were carried out with pinus (MISSIO *et al*., 2007), soybean (ALMEIDA *et al*., 2011), carrot (CARVALHO; SILVA, 2017), *Vigna unguiculata* (SANTOS *et al*., 2014), and yam (AZEVEDO *et al*., 2015).

The genetic divergence analysis among genotypes of jabuticaba population is a useful data to characterize the available genetic resources (DANNER, 2009), as well as to increase the efficiency of breeding programs (RODRIGUES *et al*., 2010; WAGNER JÚNIOR *et al*., 2011a; WAGNER JÚNIOR *et al*., 2011b).

The aim of this study was to evaluate the phenotypic divergence among jabuticaba genotypes trees in relation to stem and primary shoot lenght.

Material and Methods

It was evaluated 92 jabuticaba tree genotypes from a Native Fruit Collection. The genotypes were derived from seedlings from fruits collected come from the cities of Clevelândia, Vitorino, Chopinzinho, Coronel Vivida, Dois Vizinhos, Pato Branco and Imbituva. The genotypes from Minas Gerais were 'Silvestre', 'Sabará' and 'Açú'.

The collection was implanted in November 2009, with two-year-old seedlings from seeds. The climate of the region, according to Köppen classification is characterized as humid subtropical, Cfa type, without defined dry season whose average temperature of the hottest month is 22 °C and colder than 18 °C (ALVARES *et al*., 2013). The soil is classified as dystroferric red nitosoil (BHERING *et al*., 2008).

Growth analysis was carry out by monthly evaluations, obtaining stem lengths and primary shoots, beginning in July 2012 and ending in June 2015 (2012/2013, 2013/2014, 2014/2015), considering as three annual growth cycles.

The stem length was analyzed from the lap of the plant to the apex of the largest vertical bud. The length of the primary shoots (cm) was obtain from the point of its beginning in the main trunk until the apex of the same. The experimental design was completely randomized, with 92 genotypes and 12 replicates. Each treatment corresponded to one genotype and each replicate constituted each month of analysis for each annual cycle (12 months).

The variables were submited to analysis of variance (ANOVA) ($p \leq 0.05$). From the averages obtained the measures of dissimilarity by means of quantitative data, where it was calculated the matrix of distances of Mahalanobis (D^2) (MAHALANOBIS, 1936). After grouping was, obtain by the method of the nearest neighbor, where the distance between two groups had given by the smallest element of the set and the dendrogram creation represented these distances, having as criterion for defining the groups the line of 50% similarity. A cluster analysis was performed by the Tocher optimization method, which proceeds by dividing the set of genotypes into subgroups, by maximizing or minimizing some already established measures. All analyzes were processed in the GENES software (CRUZ, 2013).

Results and Discussion

Phenotypic differences were observed in

jabuticaba trees according to the different genotypes, for variables analyzed (stem and primary shoot length) in the cycles of 2012/2013, 2013/2014, 2014/2015.

Using the Tocher optimization method, based on the dissimilarity matrix through Mahalanobis distances, 14 groups were form in the first evaluation cycle (2012/2013) (Table 1) using the two variables evaluated. The group IV had a greater number of individuals (23), with 25% of them, all of them from Paraná. After that, group II appeared, with 20 genotypes mostly from Paraná, with only the 'Sabará 2-2' genotype from Minas Gerais, the genotype 'Dois Vizinhos' from Dois Vizinhos, but with parents from Paraguay also found in this group.

Table 1. Phenotypic divergence by the Tocher optimization grouping method for the 92 jabuticaba tree genotypes in the first, second and third evaluation cycles based on stem length.

Group	**Genotypes**
	First cycle
I	3 12 43 64 72 74 75 78 82 84 85 91 [(1)]
II	2 5 16 17 22 29 41 42 49 55 56 59 60 63 65 73 77 80 81 83
III	4 31 34 44 47 52 61
IV	7 8 9 10 11 13 18 19 21 23 24 32 33 35 40 45 46 48 50 51 54 66 79
V	15 28 39 57 62 86
VI	6 76 92
VII	1 36 38 70 71 87
VIII	14 25 69
IX	20 53 58
X	26 27 88
XI	37 90
XII	30 67
XIII	68
XIV	89
	Second cycle
I	2 5 8 9 10 11 14 16 17 18 19 21 22 23 24 25 32 33 35 41 42 49 50 51 54 55 56 60 63 65 73 77 79 80 83 [(1)]
II	4 7 20 31 34 40 44 45 46 47 48 52 53 59 61 76
III	6 13 66 89 90 92
IV	15 28 29 39 43 57 68 78 82 84 85 86 91
V	1 26 36 38 71 70 87 88
VI	12 37 64 74 75
VII	3 72
VIII	62 81
IX	30 67
X	69
XI	58
XII	27
	Third cycle
I	2 5 16 18 23 33 35 41 42 55 56 62 63 69 73 77 83[(1)]
II	9 10 11 13 17 19 21 22 24 25 49 50 51 54 79
III	4 20 31 34 48 44 53 58
IV	40 45 46 52 61 76
V	28 29 39 57 60 65 67 68 80 86 84
VI	3 12 37 43 72 74 75 82 85 91
VII	26 27
VIII	1 7 36 38 47 59 70 87

IX	6 8 14 66
X	89 92
XI	15 30 78
XII	81
XIII	64
XIV	32
XV	71
XVI	88
XVII	90

(1)1 - Clevelândia 1-1; 2 - Clevelândia 1-2; 3 - Clevelândia 1-3; 4 - Clevelândia 1-4; 5 - Clevelândia 2-1; 6 - Clevelândia 2-2; 7 - Clevelândia 2-3; 8 - Clevelândia 3-1; 9 - Clevelândia 3-2; 10 - Clevelândia 6-1; 11 - Clevelândia 6-2; 12 - Clevelândia 7-1; 13 - Clevelândia 7-2; 14 - Clevelândia 7-3; 15 - Vitorino 1-1; 16 - Vitorino 1-2; 17 - Vitorino 1-3; 18 - Vitorino 2-1; 19 - Vitorino 2-2; 20 - Vitorino 2-3; 21 - Vitorino 2-4; 22 - Vitorino 2-5; 23 - Vitorino 3-1; 24 - Vitorino 3-2; 25 - Vitorino 3-3; 26 - Vitorino 4-1; 27 - Vitorino 4-2; 28 - Vitorino 4-3; 29 - Vitorino 4-4; 30 - Vitorino 4-5; 31 - Vitorino 5-1; 32 - Vitorino 5-2; 33 - Vitorino 5-3; 34 - Vitorino 5-4; 35 - Vitorino 6-1; 36 - Vitorino 6-2; 37 - Vitorino 6-3; 38 - Vitorino 6-4; 39 - Vitorino 7-1; 40 - Vitorino 7-2; 41 - Vitorino 7-3; 42 - Chopinzinho 1-1; 43 - Chopinzinho 1-2; 44 - Chopinzinho 2-1; 45 - Chopinzinho 2-2; 46 - Chopinzinho 2-3; 47 - Chopinzinho 4-1; 48 - Chopinzinho 4-2; 49 - Chopinzinho 4-3; 50 - Coronel Vivida 1-1; 51 - Coronel Vivida 1-2; 52- - Coronel Vivida 1-3; 53 - Coronel Vivida 2-1; 54 - Coronel Vivida 2-2; 55 - Coronel Vivida 2-3; 56 - Coronel Vivida 2-4; 57 - Coronel Vivida 2-5; 58 - Coronel Vivida 3-1; 59 - Coronel Vivida 3-2; 60 - Coronel Vivida 4-1; 61 - Coronel Vivida 4-2; 62 - Coronel Vivida 4-3; 63 - Coronel Vivida 4-4; 64 - Coronel Vivida 5-1; 65 - Coronel Vivida 5-2; 66 - Coronel Vivida 5-3; 67 - Sabará-1; 68 - Sabará-2; 69 - Sabará 1-1; 70 - Sabará 1-2; 71 - Sabará 2-1; 72 - Sabará 2-2; 73 - Sabará 2-3; 74 - Pato Branco 1-1; 75 - Pato Branco 1-2; 76 - Pato Branco 1-3; 77 - Pato Branco 4-1; 78 - Pato Branco 4-2; 79 - Pato Branco 4-3; 80 - Silvestre-1; 81 - Silvestre-2; 82 - Dois Vizinhos-1; 83 - Dois Vizinhos-2; 84 - Dois Vizinhos-3; 85 - Dois Vizinhos-4; 86 - Açú-1; 87 - Açú-2; 88 - Açú-3; 89 - Imbituva-1; 90 - Imbituva-2; 91 - Imbituva-3; 92 - Imbituva-4.

The group I, grouped 12 individuals, with varied origin and in general, with the smallest lengths of stem. The group X was form by individuals with greater stem length (‘Vitorino 4-2’, ‘Vitorino 4-1’ e ‘Açú-3’). In groups XIII and XIV, only one individual was group, being these 'Sabará-2' and 'Imbituva-1', respectively (Table 1).

In the group XII, the genotypes with the longest shoot length, corresponding to 'Sabará 1' and 'Vitorino 4-5' were arrange. The group VII grouped genotypes with averages close to the upper ones, which makes them individuals with growth potential. The group V was composed of genotypes that have smaller averages for stem length and sprouting.

The group VI, grouped genotypes with intermediate means for stem length and with the lowest averages for shoots, it being constitute by the genotypes 'Imbituva 4', 'Clevelândia 2-2' and 'Pato Branco 1-3'. Genotypes that generally present low stem length, but with bud size close to upper were grouped in-group VIII ('Vitorino 3-3', 'Clevelândia 7-3' and 'Sabará 1-1').

In groups IX and X, the genotypes presented mean stem growth and sprouts among the lowest found or in intermediate bands for group IX and with the lowest averages for the first cycle in-group XI.

The genotype 'Sabará 1’ remained distant from the others in the first and second cycle and both accompanied by the 'Vitorino 4-5' genotype. However, in the third cycle these were separate into very distant groups and grouped with, other 10 and 2 individuals, respectively (Table 1).

In the second growth cycle (Table 1), a smaller number of groups were form. Of the analyzed genotypes, 36.96% belong to group I, with: ‘Clevelândia 2-3’, ‘Vitorino 3-1’, ‘Vitorino 6-1’, ‘Vitorino 5-3’, ‘Vitorino 2-2’, ‘Clevelândia 7-3’, ‘Clevelândia 6-2’, ‘Coronel Vivida 1-2’, ‘Vitorino 1-2’, ‘Vitorino 3-2’, ‘Clevelândia 3-2’, ‘Clevelândia 3-1’, ‘Pato Branco 4-3’, ‘Coronel Vivida 2-3’, ‘Chopinzinho 4-3’, ‘Chopinzinho 1-1’, ‘Coronel Vivida 1-1’, ‘Clevelândia 6-1’, ‘Vitorino 3-3’, ‘Vitorino 2-1’, ‘Coronel Vivida 2-2’, ‘Vitorino 2-5’, ‘Vitorino 5-2’, ‘Vitorino 2-4’, ‘Sabará 2-3’, ‘Dois Vizinhos-2’, ‘Clevelândia 1-2’, ‘Clevelândia 2-1’, ‘Pato Branco 4-1’, ‘Silvestre-1’, ‘Coronel Vivida 5-2’, ‘Vitorino 7-3’, ‘Coronel Vivida 2-4’, ‘Coronel Vivida 4-1’, ‘Coronel Vivida 4-4’, with only two genotypes from Minas Gerais‘Sabará 2-3’ e ‘Silvestre 1’. Group II, ‘Vitorino 7-2’, ‘Chopinzinho 2-2’, ‘Chopinzinho 2-3’, ‘Chopinzinho 4-2’, ‘Pato Branco 1-3’, ‘Coronel Vivida 3-2’, ‘Coronel Vivida 4-2’, ‘Coronel Vivida 1-3’, ‘Clevelândia 1-4’, ‘Chopinzinho 2-1’, ‘Clevelândia 2-3’, ‘Vitorino 5-4’,

‘Chopinzinho 4-1’, ‘Vitorino 5-1’, ‘Vitorino 2-3’, ‘Coronel Vivida 2-1’. In this, there were no genotypes from Minas Gerais, as well as in the group VI, which it was also the group of genotypes with the smallest stem size. In group V formed by 'Sabará 1-2', 'Açú-2', 'Clevelândia 1-1', Açú-3 ',' Vitorino 6-4', ' Vitorino 4-1', ' Vitorino 6-2', 'Sabará 2-1' presents genotypes with good stem size, with values close to the upper ones.

The Group XII, the genotype 'Vitorino 4-2' presented a longer length of the primary shoots, as well as the groups XI and X, represented by 'Vitorino 4-5' and 'Sabará-1' and 'Sabará 1-1', respectively (Table 1).

Group IV ('Vitorino 7-1', 'Sabará -2', 'Vitorino 4-4', 'Vitorino 4-3', 'Pato Branco 4-2', ‘Dois Vizinhos - 3 ',' Dois Vizinhos -1', ' Chopinzinho 1-2', ' Vitorino 1-1 ',' Imbituva-3, Açú-1') presented genotypes with stem lengths between the smallest and shoot lengths between (Clevelândia 2-2, 'Imbituva-1', 'Clevelândia 7-2', 'Colonel Vivida 5-3', 'Imbituva' and ' -2 ',' Imbituva -4 '). In the group IV, three of the four genotypes of ‘Dois Vizinhos’ were this group and the other group I.

The same occurred for the divergence between the genotypes in the third cycle (Table 1). However, this it was obtained the largest number of groups, reaching 17. Six groups with only one genotype were form in each ('Silvestre - 2', 'Coronel Vivida 5-1', 'Vitorino 5-2', 'Sabará 2-1', 'Açú -3' and 'Imbituva'). The genotype with the highest stem mean was the Imbituva and the one with the highest sprout in this cycle the 'Sabará 2-1'. The other 93.48% were group in 11 groups, which shows low diversity among the genotypes.

The group I was compose of genotypes with distinct characteristics, as there was genotypes with higher averages for shoot length (‘Chopinzinho 1-1’, ‘Coronel Vivida 2-4’, ‘Coronel Vivida 4-3’, ‘Sabará 2-3’, ‘Vitorino 7-3’, ‘Dois Vizinhos-2’, ‘Coronel Vivida 4-4’, ‘Clevelândia 2-1’, ‘Vitorino 6-1’, ‘Pato Branco 4-1’, ‘Sabará 1-1’, ‘Coronel Vivida 2-3’, ‘Vitorino 5-3’, ‘Vitorino 2-1’, ‘Clevelândia 1-2’, ‘Vitorino 3-1’) and genotypes of origin in Minas Gerais (‘Sabará 1-1’, ‘Sabará 2-3’). The group II, also presents this characteristic, it being form by ‘Vitorino 2-2’, ‘Coronel Vivida 1-2’, ‘Chopinzinho 4-3’, ‘Vitorino 1-3’, ‘Clevelândia 6-2’, ‘Coronel Vivida 2-2’, ‘Vitorino 3-3’, ‘Clevelândia 6-1’, ‘Vitorino 2-5’, ‘Vitorino 2-4’, ‘Clevelândia 3-2’, ‘Vitorino 3-2’, ‘Coronel Vivida 1-1’, ‘Pato Branco 4-3’, ‘Clevelândia 7-2’.

The group III was formed by genotypes ‘Clevelândia 1-4’, ‘Vitorino 5-1’, ‘Jaboticabal 4-2’, ‘Chopinzinho 2-1’, ‘Vitorino 5-4’, ‘Vitorino 2-3’, ‘Coronel Vivida 2-1’, ‘Coronel Vivida 3-1’ and in the group IV by ‘Vitorino 7-2’, ‘Chopinzinho 2-2’, ‘Coronel Vivida 4-2’, ‘Chopinzinho 2-3’, ‘Pato Branco 1-3’, ‘Coronel Vivida 1-3’.

The groups V and VI were formed by genotypes ‘Silvestre-1’, ‘Açú-1’, ‘Dois Vizinhos-3’, ‘Coronel Vivida 4-1’, ‘Sabará-2’, ‘Coronel Vivida 5-2’, ‘Sabará-1’, ‘Coronel Vivida 2-5’, ‘Vitorino 7-1’, ‘Vitorino 4-3’, ‘Vitorino 4-4’ and ‘Clevelândia 7-1’, ‘Vitorino 6-3’, ‘Sabará 2-2’, ‘Pato Branco 1-1’, ‘Chopinzinho 1-2’, ‘Clevelândia 1-3’, ‘Pato Branco 1-2’, ‘Dois Vizinhos-1’, ‘Imbituva-3’, ‘Dois Vizinhos-4’. The group VII presented two genotypes, both of which have low averages for stem length.

The groups VIII and IX had genotypes with intermediate means for both variables. In-group X, only the 'Imbituva' ('1 and 3') genotypes, which have stem lengths and shoots with the lowest averages, was present. The group XI represents stem-length and shoot-length genotypes with intermediate values ('Vitorino 1-1' and 'Pato Branco 4-2'). However, it grouped the genotype that had one of the smallest measures of stem and the largest of shoots ('Vitorino 4-5').

The genotypes 'Açú 3', 'Imbituva 1' and 'Imbituva 2' were group into groups with two or one, individuals in the first and third cycle, respectively (Table 1). The genotype 'Silvestre 2', remained with another genotype in the second cycle and unique in the third. These genotypes presented a more homogeneous behavior, due to the formation of distinct groups with the passing of the cycles, which might be relate to their origin. The genotypes of Minas Gerais were present in groups with two or one individual.

Danner (2009) in his work that gave rise to these genotypes was obtain based on the evaluated characters, homogeneity in the formation of the groups for the original Tocher method. For the author, 90% of the accessions evaluated were group according to the site of occurrence, which it may had occurred because the species did not present a generalized dispersion prior to the colonization of the Southwest Region of Paraná and that the geographic isolation allowed the evolution of these materials, with the formation of families sharing the same gene pool.

Martins (2013), carried out work of genetic characterization through the leaves of jabuticaba tree through molecular markers of the

plants present in the collection of Native Fruit of UTFPR - Campus Dois Vizinhos, and obtaining by the grouping method of Tocher the formation of eight groups of genotypes, of which, of 110 accessions 89 formed a single group, with and of these no individuals from Minas Gerais. The second group was form with 11 accesses, except one that had origin in Minas Gerais. This demonstrated that the groups formed had low diversity among individuals. However, as there were accesses from different sites, it was observed that, in general, the existence of a diversity level with 10% of individuals represented alone, values greater than 50% of all allelic diversity, which generates disproportionate to the gene pool.

Guedes (2009), when evaluating the genetic divergence based on the fruits of Jabuticaba Sabará, observed that the 25 accessions used formed only 3 groups. The group I was composed by 23 individuals. Through the dissimilarity obtained by the Tocher method, from the mean Euclidean distances, estimated from 11 descriptors, it was possible to verify low genetic variability among such jabuticaba trees. However, the 'Sabará' genotypes evaluated for stem length and primary shoots showed divergence from one access to another and tended to form small or distinct groups.

Through the generalized distance of Mahalanobis, it was observed in the dendrogram by the nearest neighbor method, that there was for the first cycle (Figure 1) the formation of 7 groups, with the genotypes' Vitorino 4-5 'and' Sabará 1 ', which before formed a group, they were separate, forming one group each. The genotype 'Vitorino 4-2' also formed a group with only one individual. The group that goes from the genotype 'Vitorino 4-1' to 'Vitorino 2-3', by the grouping of Tocher formed 3 distinct groups, not staying in this analysis. The group formed from 'Vitorino 6-3' to 'Imbituva 2' was the same as occurred using Tocher. These small groups were form by individuals with the same place of origin described as 'Vitorino'. The other individuals were from Minas Gerais.

The group III formed by Tocher also repeated the same genotypes by the dendrogram, it being practically represent by individuals coming from the Southwest Region of Paraná. The last group formed had 75% of the genotypes, and in this, there was representative of Minas Gerais ('Sabará 2') and 'Imbituva 1', which had formed a distinct group by the Tocher method.

In the second cycle (Figure 2), two groups were form. One group existed only one genotype ('Vitorino 4-5'), the other genotypes (98.91%), remained in the large group. This represented, unlike the others, uniformity in the divergence between the genotypes. For the third cycle (Figure 3), four groups were formed, the first by the genotypes 'Vitorino 4-1' and 'Vitorino 4-2'. The 'Imbituva 2' genotype formed the second group. The third group consisted of all individuals who had formed groups III, IV, VIII and X by the Tocher method. The other genotypes were grouped in-group IV.

In the first year of analysis, the accesses that showed the greatest phenotypic divergence were Vitorino 4-2 and Vitorino 4-5 (Figure 1), and in the following years, it was repeat with the Vitorino 4-2 access. However, with this difference being more distant from Sabará 2-2 (Figure 2) and Clevelândia 7-1 (Figure 3).

Wagner Júnior *et al*. (2018), observed that there was phenotypic divergence among jabuticaba fruits characteristics (polar and equatorial diameter; mass of the total fresh matter; mass of the fresh matter of the bark; mass of the fresh seed matter; percentage of pulp; and content of total soluble solids and biochemical analyzes including protein content total sugars, anthocyanins and flavonoids, total phenols and total titratable acidity) of 33 genotypes from same occurrence area. For these authors, six groups were formed regarding the divergence based on the Tocher method and three groups when using the Mahalanobis method. This difference between the methods was also observed in this study.

Zerbielli *et al*. (2016) evaluated twelve physicochemical characters of 40 jabuticaba tree (*Plinia cauliflora*) genotypes in a naturally occurring site by the UPGMA clustering method, using average Euclidean distance and observed that even though the jabuticaba tree occur in the same location, they present significant differences between their individuals. This variability can be used as traits of interest in species breeding.

This analysis becomes important when trying to obtain heterosis, thus it being recommended possible future crosses between such accesses.

Figure 1. Dendrogram obtained by the nearest neighbor method, from the distance of Mahalanobis to the 92 genotypes of jabuticaba tree of the UTFPR Native Fruit Trees Collection, Campus Dois Vizinhos in the first genotype growth cycle 1 - Clevelândia 1-1; 2 - Clevelândia 1-2; 3 - Clevelândia 1-3; 4 - Clevelândia 1-4; 5 - Clevelândia 2-1; 6 - Clevelândia 2-2; 7 - Clevelândia 2-3; 8 - Clevelândia 3-1; 9 - Clevelândia 3-2; 10 - Clevelândia 6-1; 11 - Clevelândia 6-2; 12 - Clevelândia 7-1; 13 - Clevelândia 7-2; 14 - Clevelândia 7-3; 15 - Vitorino 1-1; 16 - Vitorino 1-2; 17 - Vitorino 1-3; 18 - Vitorino 2-1; 19 - Vitorino 2-2; 20 - Vitorino 2-3; 21 - Vitorino 2-4; 22 - Vitorino 2-5; 23 - Vitorino 3-1; 24 - Vitorino 3-2; 25 - Vitorino 3-3; 26 - Vitorino 4-1; 27 - Vitorino 4-2; 28 - Vitorino 4-3; 29 - Vitorino 4-4; 30 - Vitorino 4-5; 31 - Vitorino 5-1; 32 - Vitorino 5-2; 33 - Vitorino 5-3; 34 - Vitorino 5-4; 35 - Vitorino 6-1; 36 - Vitorino 6-2; 37 - Vitorino 6-3; 38 - Vitorino 6-4; 39 - Vitorino 7-1; 40 - Vitorino 7-2; 41 - Vitorino 7-3; 42 - Chopinzinho 1-1; 43 - Chopinzinho 1-2; 44 - Chopinzinho 2-1; 45 - Chopinzinho 2-2; 46 - Chopinzinho 2-3; 47 - Chopinzinho 4-1; 48 - Chopinzinho 4-2; 49 - Chopinzinho 4-3; 50 - Coronel Vivida 1-1; 51 - Coronel Vivida 1-2; 52- - Coronel Vivida 1-3; 53 - Coronel Vivida 2-1; 54 - Coronel Vivida 2-2; 55 - Coronel Vivida 2-3; 56 - Coronel Vivida 2-4; 57 - Coronel Vivida 2-5; 58 - Coronel Vivida 3-1; 59 - Coronel Vivida 3-2; 60 - Coronel Vivida 4-1; 61 - Coronel Vivida 4-2; 62 - Coronel Vivida 4-3; 63 - Coronel Vivida 4-4; 64 - Coronel Vivida 5-1; 65 - Coronel Vivida 5-2; 66 - Coronel Vivida 5-3; 67 - Sabará-1; 68 - Sabará-2; 69 - Sabará 1-1; 70 - Sabará 1-2; 71 - Sabará 2-1; 72 - Sabará 2-2; 73 - Sabará 2-3; 74 - Pato Branco 1-1; 75 - Pato Branco 1-2; 76 - Pato Branco 1-3; 77 - Pato Branco 4-1; 78 - Pato Branco 4-2; 79 - Pato Branco 4-3; 80 - Silvestre-1; 81 - Silvestre-2; 82 - Dois Vizinhos-1; 83 - Dois Vizinhos-2; 84 - Dois Vizinhos-3; 85 - Dois Vizinhos-4; 86 - Açú-1; 87 - Açú-2; 88 - Açú-3; 89 - Imbituva-1; 90 - Imbituva-2; 91 - Imbituva-3; 92 - Imbituva-4.

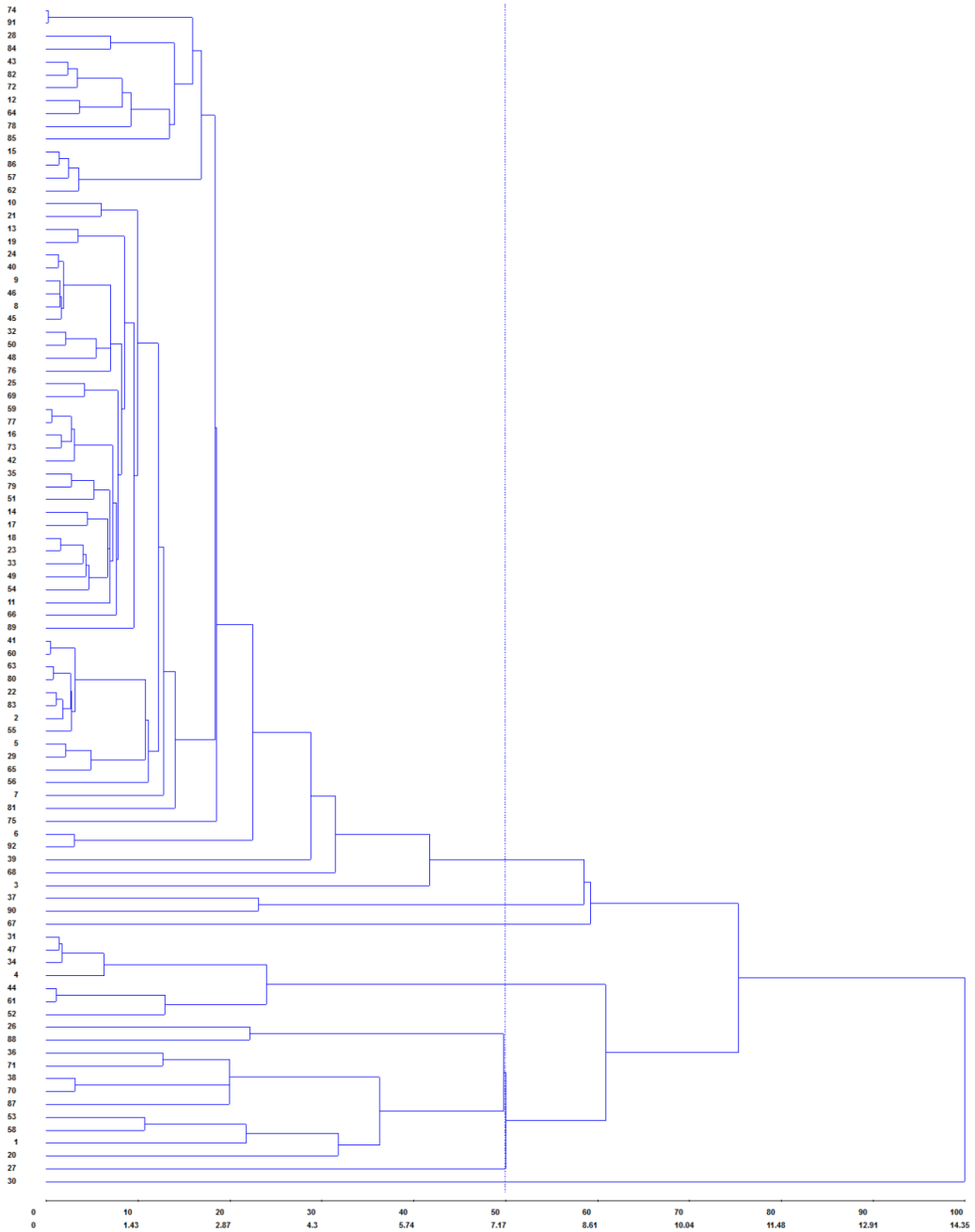


Figure 2. Dendrogram obtained by the nearest neighbor method, from the distance of Mahalanobis to the 92 genotypes of jabuticaba tree of the UTFPR Native Fruit Trees collection, Campus Dois Vizinhos in the second genotype growth cycle. 1 - Clevelândia 1-1; 2 - Clevelândia 1-2; 3 - Clevelândia 1-3; 4 - Clevelândia 1-4; 5 - Clevelândia 2-1; 6 - Clevelândia 2-2; 7 - Clevelândia 2-3; 8 - Clevelândia 3-1; 9 - Clevelândia 3-2; 10 - Clevelândia 6-1; 11 - Clevelândia 6-2; 12 - Clevelândia 7-1; 13 - Clevelândia 7-2; 14 - Clevelândia 7-3; 15 - Vitorino 1-1; 16 - Vitorino 1-2; 17 - Vitorino 1-3; 18 - Vitorino 2-1; 19 - Vitorino 2-2; 20 - Vitorino 2-3; 21 - Vitorino 2-4; 22 - Vitorino 2-5; 23 - Vitorino 3-1; 24 - Vitorino 3-2; 25 - Vitorino 3-3; 26 - Vitorino 4-1; 27 - Vitorino 4-2; 28 - Vitorino 4-3; 29 - Vitorino 4-4; 30 - Vitorino 4-5; 31 - Vitorino 5-1; 32 - Vitorino 5-2; 33 - Vitorino 5-3; 34 - Vitorino 5-4; 35 - Vitorino 6-1; 36 - Vitorino 6-2; 37 - Vitorino 6-3; 38 - Vitorino 6-4; 39 - Vitorino 7-1; 40 - Vitorino 7-2; 41 - Vitorino 7-3; 42 - Chopinzinho 1-1; 43 - Chopinzinho 1-2; 44 - Chopinzinho 2-1; 45 - Chopinzinho 2-2; 46 - Chopinzinho 2-3; 47 - Chopinzinho 4-1; 48 - Chopinzinho 4-2; 49 - Chopinzinho 4-3; 50 - Coronel Vivida 1-1; 51 - Coronel Vivida 1-2; 52- - Coronel Vivida 1-3; 53 - Coronel Vivida 2-1; 54 - Coronel Vivida 2-2; 55 - Coronel Vivida 2-3; 56 - Coronel Vivida 2-4; 57 - Coronel Vivida 2-5; 58 - Coronel Vivida 3-1; 59 - Coronel Vivida 3-2; 60 - Coronel Vivida 4-1; 61 - Coronel Vivida 4-2; 62 - Coronel Vivida 4-3; 63 - Coronel Vivida 4-4; 64 - Coronel Vivida 5-1; 65 - Coronel Vivida 5-2; 66 - Coronel Vivida 5-3; 67 - Sabará-1; 68 - Sabará-2; 69 - Sabará 1-1; 70 - Sabará 1-2; 71 - Sabará 2-1; 72 - Sabará 2-2; 73 - Sabará 2-3; 74 - Pato Branco 1-1; 75 - Pato Branco 1-2; 76 - Pato Branco 1-3; 77 - Pato Branco 4-1; 78 - Pato Branco 4-2; 79 - Pato Branco 4-3; 80 - Silvestre-1; 81 - Silvestre-2; 82 - Dois Vizinhos-1; 83 - Dois Vizinhos-2; 84 - Dois Vizinhos-3; 85 - Dois Vizinhos-4; 86 - Açú-1; 87 - Açú-2; 88 - Açú-3; 89 - Imbituva-1; 90 - Imbituva-2; 91 - Imbituva-3; 92 - Imbituva-4.

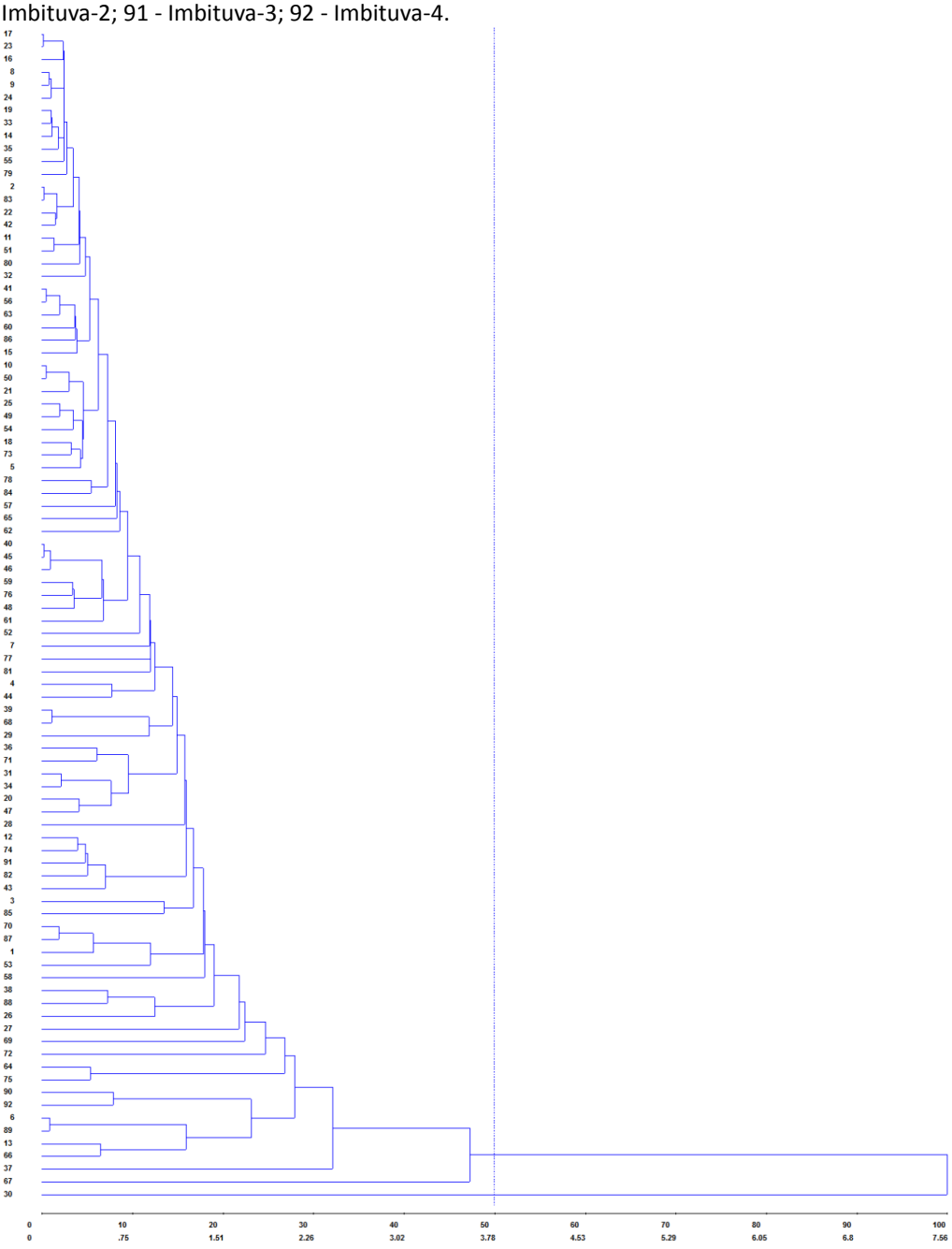
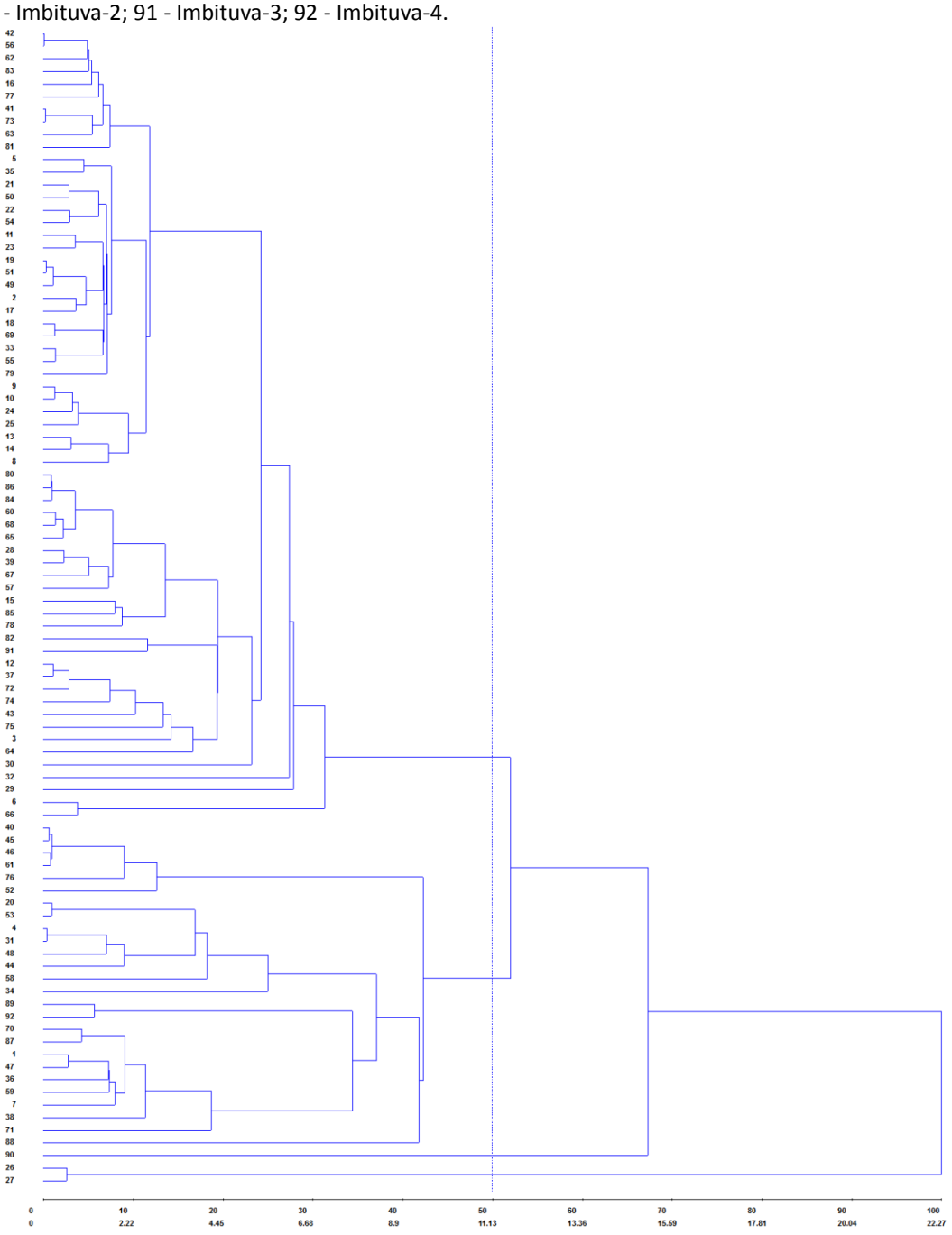


Figure 3. Dendrogram obtained by the nearest neighbor method, from the distance of Mahalanobis to the 92 genotypes of jabuticaba tree of the UTFPR Native Fruit Trees collection, Campus Dois Vizinhos in the third genotype growth cycle. 1 - Clevelândia 1-1; 2 - Clevelândia 1-2; 3 - Clevelândia 1-3; 4 - Clevelândia 1-4; 5 - Clevelândia 2-1; 6 - Clevelândia 2-2; 7 - Clevelândia 2-3; 8 - Clevelândia 3-1; 9 - Clevelândia 3-2; 10 - Clevelândia 6-1; 11 - Clevelândia 6-2; 12 - Clevelândia 7-1; 13 - Clevelândia 7-2; 14 - Clevelândia 7-3; 15 - Vitorino 1-1; 16 - Vitorino 1-2; 17 - Vitorino 1-3; 18 - Vitorino 2-1; 19 - Vitorino 2-2; 20 - Vitorino 2-3; 21 - Vitorino 2-4; 22 - Vitorino 2-5; 23 - Vitorino 3-1; 24 - Vitorino 3-2; 25 - Vitorino 3-3; 26 - Vitorino 4-1; 27 - Vitorino 4-2; 28 - Vitorino 4-3; 29 - Vitorino 4-4; 30 - Vitorino 4-5; 31 - Vitorino 5-1; 32 - Vitorino 5-2; 33 - Vitorino 5-3; 34 - Vitorino 5-4; 35 - Vitorino 6-1; 36 - Vitorino 6-2; 37 - Vitorino 6-3; 38 - Vitorino 6-4; 39 - Vitorino 7-1; 40 - Vitorino 7-2; 41 - Vitorino 7-3; 42 - Chopinzinho 1-1; 43 - Chopinzinho 1-2; 44 - Chopinzinho 2-1; 45 - Chopinzinho 2-2; 46 - Chopinzinho 2-3; 47 - Chopinzinho 4-1; 48 - Chopinzinho 4-2; 49 - Chopinzinho 4-3; 50 - Coronel Vivida 1-1; 51 - Coronel Vivida 1-2; 52- - Coronel Vivida 1-3; 53 - Coronel Vivida 2-1; 54 - Coronel Vivida 2-2; 55 - Coronel Vivida 2-3; 56 - Coronel Vivida 2-4; 57 - Coronel Vivida 2-5; 58 - Coronel Vivida 3-1; 59 - Coronel Vivida 3-2; 60 - Coronel Vivida 4-1; 61 - Coronel Vivida 4-2; 62 - Coronel Vivida 4-3; 63 - Coronel Vivida 4-4; 64 - Coronel Vivida 5-1; 65 - Coronel Vivida 5-2; 66 - Coronel Vivida 5-3; 67 - Sabará-1; 68 - Sabará-2; 69 - Sabará 1-1; 70 - Sabará 1-2; 71 - Sabará 2-1; 72 - Sabará 2-2; 73 - Sabará 2-3; 74 - Pato Branco 1-1; 75 - Pato Branco 1-2; 76 - Pato Branco 1-3; 77 - Pato Branco 4-1; 78 - Pato Branco 4-2; 79 - Pato Branco 4-3; 80 - Silvestre-1; 81 - Silvestre-2; 82 - Dois Vizinhos-1; 83 - Dois Vizinhos-2; 84 - Dois Vizinhos-3; 85 - Dois Vizinhos-4; 86 - Açú-1; 87 - Açú-2; 88 - Açú-3; 89 - Imbituva-1; 90 - Imbituva-2; 91 - Imbituva-3; 92 - Imbituva-4.



Conclusions

The results obtained showed that the diversity among the genotypes changed as time passed, since in each cycle different groups were clustered, according to each technique used. Genotypes from Minas Gerais tend to remain in distinct groups, since they had low similarity with the others, what it can be interesting for future breeding program. 'Vitorino' genotype showed a high divergence among individuals from the same place. However, for possible recommendation of controlled hybridization, Vitorino 4-2 with Vitorino 4-5, Sabará 2-2 or Clevelândia 7-1 is our recommendation for future breeding program.

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