

SELECTION OF FISÁLIS POPULATIONS FOR HIBRIDIZATIONS, BASED ON FRUIT TRAITS¹

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ABSTRACT - The objective of this study was to characterize the genetic variability in fisális populations and select promising parents based on fruit traits. The experimental design consisted of randomized blocks, with six populations. Five plants per treatment were sampled. The evaluated traits were fruit weight, capsule weight, 1000- seed weight and fruit diameter. The data were subjected to multivariate analysis of variance with error specification between and within ($p < 0.05$). Mahalanobis' distance was used as a measure of genetic dissimilarity. Significant differences for the assessed traits were detected between fisális populations. The ratio error among by within indicated no need for sampling within the experimental unit. Dissimilarity was greatest between Lages and Vacaria. The most discriminating traits were capsule weight, fruit weight and fruit diameter. The multivariate contrasts indicated differences between the populations of Vacaria and from Caçador, Lages and Peru, selected for hybridizations.

Index Terms: *Physalis peruviana* L., genetic variation, selection.

SELEÇÃO DE POPULAÇÕES DE FISÁLIS PARA USO EM HIBRIDAÇÕES, BASEADA EM CARACTERES DO FRUTO

RESUMO - O objetivo do trabalho foi caracterizar a variabilidade genética em populações de fisális e selecionar genitores promissores mediante caracteres relacionados ao fruto. Para tanto, o delineamento utilizado foi o de blocos casualizados, composto por seis populações, com amostragem de cinco plantas da unidade experimental. Os caracteres avaliados foram massa do fruto, massa da cápsula, massa de mil sementes e diâmetros do fruto. Os dados foram submetidos à análise de variância com a especificação do erro entre e dentro ($p < 0,05$). Para estimar a dissimilaridade genética, foi utilizada a distância generalizada de Mahalanobis, e com a técnica de contrastes multivariados foi possível testar as diferenças entre as populações e estimar a contribuição das variáveis para a dissimilaridade. As populações de fisális são diferentes para o conjunto de caracteres avaliados. A relação do erro entre sobre o erro indica a não necessidade de amostragens dentro da unidade experimental. A maior magnitude de dissimilaridade foi entre Lages e Vacaria. Os caracteres responsáveis pela diferença foram massa da cápsula, massa do fruto e diâmetro equatorial do fruto. Os contrastes multivariados apontaram diferença entre a população de Vacaria e as populações de Caçador, Lages e Peru, selecionadas para as hibridizações.

Termos para Indexação: *Physalis peruviana* L., variação genética, Seleção.

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INTRODUCTION

Fisális (*Physalis peruviana* L.) is native to the Andean region and belongs to the nightshade family. The basic chromosome number of the genus *Physalis* is $n = 12$, and the majority of the species are diploid; of the cultivated species, only *P. peruviana* is tetraploid (NOHRA et al., 2006). Pollination is predominantly by allogamy (SANTANA; ANGARITA, 1999), although selfing can occur (FISCHER et al., 2014). The fruits are yellow-orange, have a diameter of 10 to 35.5 mm and an aromatic and sweet flavor. Consumption can be fresh, canned or used for decoration as well. The high vitamins A, B1, B2, B12 and C levels make it an interesting nutritional source (BRIONES-LABARCA et al., 2013).

Fisális is grown mainly in Colombia (HERRERA et al., 2012). In Brazil, it was introduced as cash crop in 1999, in São Paulo State, and later expanded to the south of the country. The good adaptation of the crop to the soil and climatic conditions and acceptance of the fruit were essential for the success of the specie in Brazil. This country is a potential producer of fisális, with prospects to become an exporter of this fruit. However, any crop production chain depends, among a series of factors, on the efforts of research institutions invested in breeding work. Most of the research is intended to develop cultivation techniques, while few studies are focused on breeding.

Characterization studies of accessions, carried out in Colombia (LAGOS et al., 2007), represented the basis for the beginning of a breeding program different fisális accessions were characterized by Leiva-Brondo et al. (2001), who detected genetic differences in fruit yield and quality, which are key traits to be exploited by breeding of the species. In Brazil, the cultivated populations are grown from seeds of unknown origin, with no prior knowledge about the genetic potential they contain. This fact can be confirmed by the lack of registered seeds (MAPA, 2015), reinforcing the importance of initiating a breeding program.

The genetic potential of a species depends largely on the availability of genetic variability (CECCARELLI, 2015). Genetic variability is the basis of breeding and can facilitate the selection of productive populations adapted to local conditions (WAMSER et al., 2012). Based on genetic resources, breeders can select populations with large distance or with pre-defined characteristics, perfecting cloning work and mass multiplication of plants with the desired traits or combinations thereof (LIGARRETO et al., 2005). In characterization studies, morphological

descriptors are used to estimate the variability, which is the first step to deepen the knowledge of the genetic potential of a species.

In this sense, the purpose of this study was to characterize the genetic variability in fisális populations and select promising parents by fruit-related traits.

MATERIAL AND METHODS

The study was carried out in the experimental area of Instituto de Melhoramento e Genética Molecular of the Universidade do Estado de Santa Catarina – UDESC in Lages, SC (lat 27 ° 48 ' S, long 50 ° 19' W, mean 916 m asl). The climate is Cfb (temperate climate with cool summer) and the mean annual temperature 15°C, with an average rainfall of 1.500 mm.

The data were adopted from an experiment consisting of six fisális populations, from Fraiburgo, Vacaria, Caçador, Lages, Colombia, and Peru. These populations are representative of the genetic variability of the varieties cultivated in municipalities in the Midwest region and Planalto Serrano of the State of Santa Catarina. Seeds were taken randomly from ripe fruits from each population, sown in trays with commercial substrate for nightshade plants, and maintained in a greenhouse. Seedlings were planted in the field 45 days after sowing in trays, at a plant height of 15 to 20 cm.

The experiment was arranged in a randomized block design with two replications. Five plants per experimental unit were sampled. The measured traits were fruit weight without capsule (FW, in g) capsule weight (CW, in g) 1000- seed weight (TSW, in g), equatorial fruit diameter (EFD, in mm) and polar fruit diameter (PFD, in mm).

For data analysis, multivariate variance was comprehensively tested ($p < 0.05$) by Wilks' lambda criterion, by the Generalized Linear Model (GLM) procedure of SAS 9.2. In the analysis, the error between and the error within were considered. The following statistical model was used: Y_{ijl} indicates the set of assessed traits; μ is the general mean; b_i : the block effect; pop_j : the effect associated with the j -th population level; e_{ij} : effect of the error between (experimental error); d_{ijl} : effect of the error within (sampling error), which are data obtained by evaluation of the plants of the experimental units.

The genetic dissimilarity was estimated by the coefficients of Mahalanobis' distance (D^2) between all pairs of populations. Based on the genetic distance matrix, a dendrogram was constructed using the unweighted pair-group method based on

arithmetic averages (UPGMA) grouping method. The adjustment between the distance matrix and the dendrogram was estimated by the cophenetic correlation coefficient (r_{cof}) (SOKAL E ROHLF, 1962). The procedure of multivariate contrasts considering Wilks' lambda test ($p < 0.05$) was performed to test for significance between the populations of interest. With this procedure, the relative contribution of traits could be determined by standardized canonical coefficients. The GLM procedure of SAS 9.2 was used to test the contrasts.

RESULTS AND DISCUSSION

The result of the multivariate analysis of variance showed a significant difference for the population (at 5% error probability), indicating the existence of variability between at least two *fisális* populations (Table 1). Thus, the origin of variation between *fisális* populations as well as which traits are contributing to the variation are addressed here. When the average vectors of the treatments show significant variation, complex inferences must be derived, requiring multivariate techniques. It is worth emphasizing that the multivariate analysis of variance considers the phenomenon of mutual dependence between the response variables, which was not taken into consideration in the univariate analysis (COIMBRA et al., 2007a).

The occurrence of variability can be explained by different selection pressures (natural and artificial) to which each population was naturally subjected, inducing changes in genotype frequencies. Therefore, it is of paramount importance to know the genetic variability, which allows the exploitation of the genetic potential of the population for the selection and fixation of agronomically important traits (RAMALHO et al., 2012). Plant breeders are interested in wide genetic variability for the application of selective processes resulting in significant genetic gains (ALLABY et al., 2014).

In the analysis of variance the ratio of the variance of error among by the variance of error within was not significant (Table 1). Therefore, the variation affecting the sample values was purely random and evenly distributed between the five plants in the experimental unit. Therefore, sampling within the unit is not indicated, since the variation is evenly distributed in the unit and contains no additional information to be exploited (SILVA, 2003).

To determine the genetic distance between one population and the other, the coefficients of Mahalanobis' distance were estimated (Table 2). The population from Lages diverged significantly from

the other populations, demonstrating that the trait set allowed a discrimination of this population (Table 2). The population with greatest genetic distance from Lages was Vacaria (4.641) and therefore, less similar populations. The population of Vacaria was also dissimilar from Caçador (1.192) and Peru (2.210). The greater genetic distance between parents can increase the chances of genetically superior combinations (ZAMORA-TAVARES et al., 2015). With the complementation of different alleles the hybrid vigor can be exploited, and for *fisális* this seems to be a viable alternative since vegetative propagation provides efficient results (MORENO et al., 2009). In addition, artificial hybridization ensures a high number of seeds per fruit (200 to 250 seeds).

The populations from Colombia and Peru did not differ by the distance of Mahalanobis (Table 2), this similarity may be due to the common origin of these populations. In spite of being a species with predominance of allogamy, the gene pool for the traits may be similar in the population of Colombia and Peru. In a study on the morphological characterization of *Physalis peruviana*, of Betancourt et al. (2008) in Colombia, 10 (ten) *fisális* accession with very close phenotypic distances were identified, forming a group with minor differences. This is possibly a single accession, with wide dispersion in the Andean region.

The visual analysis based on the dendrogram supports the results of genetic dissimilarity between the population of Lages and the other populations (Figure 1). A cut performed at a distance of 70% (x-axis) formed a dissimilarity group of the population from Lages. The dendrogram also showed the similarity between Colombia and Peru, by the close grouping. In addition, the cophenetic correlation coefficient (r_{cof}) had a magnitude of 0.76. The more this value approaches 1, the smaller is the distortion caused by the population grouping based on UPGMA (CARGNELUTTI-FILHO et al., 2010). Comparisons between the mean vectors generated by multivariate contrasts ($p < 0.05$), showed differences only between the combinations involving the population of Vacaria (Table 3), differing from those from Caçador, Lages and Peru. The range of distances between the populations of Lages and Vacaria, proved by Mahalanobis' distance, suggested the selection of both populations for future hybridizations. The choice of parents for hybridization with a view to expanding the species variability must take into account the genetic divergence, *per se* performance of the parents and the allelic complementation (DA COSTA et al., 2014).

Nevertheless, the traits that contributed to the variation among populations were identified

using standardized canonical coefficients (Table 3). Among the significant contrasts, the traits that contributed to the differentiation were CW, FW and EFD. Conversely, standardized canonical coefficients with negative values can be interpreted similarly, but with the opposite direction to the effect, i.e., a negative value reduces the effect of the trait in question (COIMBRA et al., 2007b). Thus, the traits TSW and PFD contributed to the similarity between the population of Vacaria with those from Caçador, Lages and Peru.

The results showed that the traits responsible

for discriminating populations can be prioritized in *Physalis* breeding for the region of the highland plateau of Santa Catarina. In a study of morphological characterization of *Physalis peruviana* accessions, Bonilla and Espinosa (2005) pointed out that the fruit weight and diameter were decisive to identify promising accessions for fresh market consumption and the fruit processing industry. Among the important traits for selection, fruit weight is considered the key trait for marketing (ANZANELLO et al., 2013). The commercial value of fruits is related to appearance, size and post-harvest quality (TAVARINI et al. 2008).

TABLE 1 - Multivariate analysis of variance ($p < 0.05$), indicating the degrees of freedom of the numerator (DFN) and denominator (DFD), Wilks' lambda criterion, value of the F test and significance for the traits: fruit weight, capsule weight, 1000- seed weight, equatorial fruit diameter and polar fruit diameter, among six *Fisális* populations, with the utilization of errors to test the hypothesis.

Source of variation	DFN	DFD	Λ value	F value
Block	5	1	0.001	123.91 ^{ns1}
Population	25	5.21	0.001	8.37*
Error among	25	164.95	0.606	0.95 ^{ns}

^{1/*}: significant at 5% error probability. ^{ns/}: non significant. Null hypothesis tested: $H_0: \mu_1 = \mu_2 = \dots = \mu_k$.

TABLE 2 – Estimates of the genetic divergence between two *Fisális* populations, established by the coefficients of the Mahalanobis' distance (D^2), considering the traits fruit weight, capsule weight, 1000- seed weight, equatorial fruit diameter and polar fruit diameter.

Population	Vacaria	Caçador	Lages	Colômbia	Peru
Fraiburgo	1.022 ^{ns}	0.558 ^{ns}	3.313*	0.514 ^{ns}	0.691 ^{ns1}
Vacaria		1.195*	4.641*	0.853 ^{ns}	2.21*
Caçador			1.617*	0.206 ^{ns}	0.372 ^{ns}
Lages				1.972*	1.375*
Colômbia					0.477 ^{ns}

^{1/*}: significant at 5% error probability. ^{ns/}: non significant.

TABLE 3 - Multivariate contrasts obtained the information of generalized Mahalanobis' distances (D^2) with their standardized canonical coefficients and statistics of the traits likelihood ratio: capsule weight (CW), fruit weight (FW), weight of thousand seeds (TSW) equatorial diameter of fruits (EFD), polar diameter of fruits (PFD).

Contrasts	CW	FW	TSW	EFD	PFD	F
Fraiburgo vs Lages	0.569	0.866	-0.502	-0.444	-0.374	0.115 ^{ns1}
Vacaria vs Caçador	0.193	0.794	-0.129	0.355	-0.433	0.025 [*]
Vacaria vs Lages	0.339	0.709	-0.393	0.356	-0.338	0.001 [*]
Vacaria vs Peru	0.056	0.608	-0.370	0.543	-0.352	0.002 [*]
Caçador vs Lages	0.493	0.156	-0.781	0.176	0.046	0.751 ^{ns}
Lages vs Colômbia	0.492	0.634	-0.192	0.362	-0.504	0.416 ^{ns}
Lages vs Peru	0.930	0.241	-0.054	-0.434	0.029	0.596 ^{ns}

^{1/} * : significant at 5% error probability. ^{ns/} : non significant.

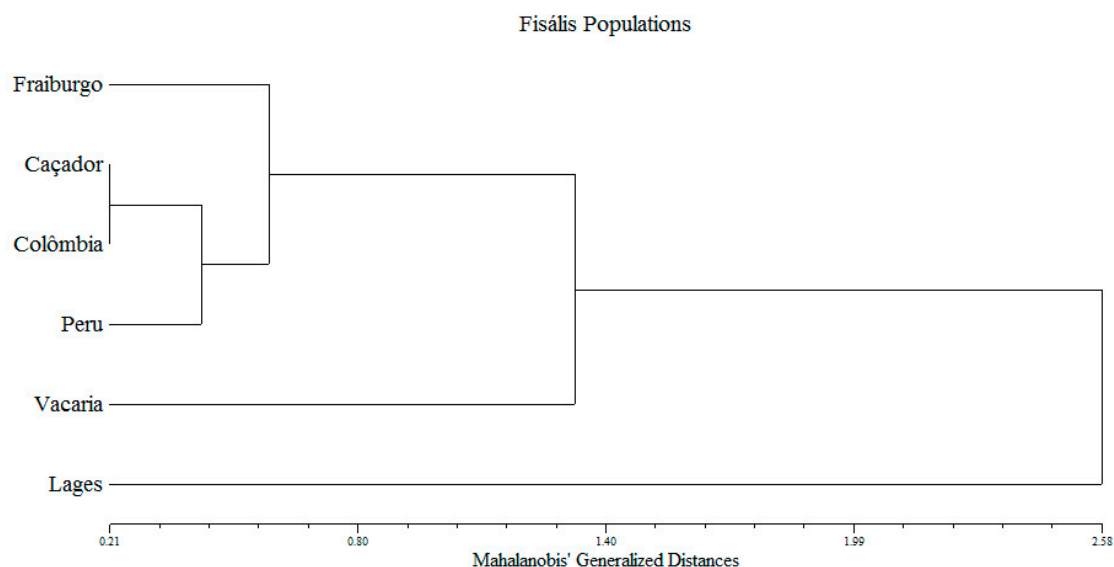


FIGURE 1- Dendrogram illustrating the dissimilarity pattern, established by the UPGMA clustering method based on Mahalanobis' generalized distances for six *Physalis* populations.

CONCLUSIONS

The fisális populations analyzed in this study differ genetically. There is homogeneity within fisális populations, indicating that sampling within plots is unnecessary. Crosses between the population of Vacaria with populations of Caçador, Lages and Peru are recommended, to obtain segregating fisális populations and to possibly exploit hybrid vigor. Hybridizations between individuals of these populations could give rise to superior individuals from parents that are genetically different for the studied traits.

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