SHORT COMUNICATION – Silviculture

Genetic Variation of Trees of *Caryocar brasiliense* for Fruit Morphometric Traits

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This study aimed to verify the genetic variability of matrix trees of *Caryocar brasiliense,* best known by the popular name of "pequi", in a completely random delineation, with 20 treatments (matrices), and 50 repetitions (collected fruits in each matrix). We have evaluated the following traits of each fruit: weight (g), diameter (cm), length (cm), width (cm), and thickness (cm). As results we obtained a coefficient of experimental variation (CV_e(%)) that showed advantageous values of 2.82 to 7.80, and the genotype heritability (h_g^2 (%)) of 55 to 95; both results can indicate favorable genetic control in the traits of the fruit. At the same time certain traits have significant genotypic and phenotypic correlations, which can be understood as an advantage for the improvement of the specie. In conclusion, we have noted that the population of *Caryocar brasiliense* has a high genetic variation, these results support the planning for genetic improvement programs.

Keywords: pre-breeding, genetic variability, fruit, pequi, Cerrado.

Caryocar brasiliense Cambess, commonly known by the popular name of "pequi", is a typical native specie of the Brazilian Cerrado, it can be found in the states of Minas Gerais, Goiás, Mato Grosso, Tocantins, Bahía, Pará and Maranhão (Carvalho, 2009). It is an allogamous specie, with fruits rich in oils and vitamin A, which are very well appreciated by people and wild animals of the Brazilian cerrado (Collevati et al., 2001). Besides its importance, we still have little research on *Caryocar brasiliense's* genetic variability and its natural populations across the Cerrado, one reason for that may be the great extension of this biome (Moura et al., 2013).

Many different species of the Cerrado have been reported as of favorable genetic variability (Ganga et al., 2009; Carmargo et al., 2010), this information is a good indication to start breeding trials. Due to the lack of information on various aspects of *Caryocar brasiliense*, progeny tests, mainly used to estimate genetic parameters and select individuals, are an important tool (Aguiar et al., 2011) to calculate the genetic variability of the matrices, respecting the morphological traits of the fruits (Ramos et al., 2015).

Over the years the "Pequi" has shown great economic and social potentials, however, the agricultural expansion and the disorderly exploitation of timber resources has threatened the natural populations and communities that used to depend on it; because of that, the need to start genetic enhancement studies (Giordani et al., 2012) has become essential. Based on all these reasons, this research aimed to study the genetic parameters, and analyze the genetic variability of matrix trees of *Caryocar brasiliense* through the morphometric traits of its fruits.

The experiment was conducted at the Experimental Farm of the Federal University of Tocantins (UFT), campus of Gurupi, located under the coordinates 11° 43'5 S and 49° 04' W, and at 280 meters above sea level. Accordingly to the Koppen's

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classification, the climate in the region is Aw (tropical with dry season) and the soil is classified as a dystrophic Red-Yellow Oxisol (Embrapa 2018). We collected 50 fruits for each matrix tree of *C. brasiliense*, with a minimum distance of 50 meters between individuals to avoid kinship. For the study of the genetic variability, we used the following quantitative genetic parameters: fruit weight (FW (g)), width (FW2 (cm)), thickness (FT (cm)), diameter (FD (cm)) and length (FL (cm)). The experiment was conducted in a specie's natural population, under a completely randomized design, with 20 treatments (matrix trees) and 50 fruits per tree.

The statistical significance was evaluated in accordance to the likelihood ratio test (LRT), the results were analyzed by the SELEGEN REML / BLUP (restricted maximum likelihood) a statistical-genetic *software* (Resende, 2007) used for completely random delineations, expressed in the mathematical equation: $y = Xu + Zg + Wp + e$, where, "y" is the data vector, "u" is the general average, "g" represents the genotypic effects of the matrices (assumed as random), "p" is the plot effects (random), "e" is for the vectors of the effects of random errors, and the uppercase letters represent the matrices of incidence.

The likelihood ratio test (LRT) showed significant variance at 5% in the characters of FW, FL, FT, FD and FW2, indicating genetic variability between the materials (individuals), which is favorable at the time of selection (Table 1).

Table 1. Likelihood ratio test (LRT) for traits of fruits of *Caryocar brasiliense*: weight (FW), width (FW2), thickness (FT), diameter (FD) and length (FL).

(*) LRT	Features				
	FW (g)	FW2 (cm)	FT (cm)	FD (cm)	FL (cm)
Fruit	81.85*	94.23*	97.34*	5.72*	12.04*

(*) LRT fruit: Reason for likelihood in fruit characters; *: significant at 5% of probability.

The coefficient of experimental variation (CV_e (%)) has indicated that the adopted experimental design was adequate. The fruit had a weight of (7.8%), which is in accordance to the values found in the literature (Moura et al., 2013). The Genotypic inheritance, in the broad sense, (h_g^2(%)) varied from 55% to 95%, these results indicate high genetic control in the morphometric traits of the fruits (Table 2). The selective accuracy ($r_{âa}$) is an important parameter for maximizing genetic progress, for this trait the values were greater than 0.50, which corroborates with Resende (2007), that says that $r_{âa}$ values greater than 0.50, is ideal for a good accuracy in genotype selection. The value of the coefficient of individual additive genetic variation (CV_{gi} (%)) varied from 2.90% to 6.12%, and was low for the traits FW (3.88%) and

FL (2.90%), this can indicate that the studied individuals of *Caryocar brasiliense* have genetic variability available. The genetic gain (G_s (%)), was of 5.56% for FW, 12.20% for FW2, 14.33% for FT, 15.12% for FD and of 5.12% for FL. The fruit's thickness (FT) was the most outstanding value.

Table 2. Genotypic parameters for fruit weight (FW), width (FW2), thickness (FT), diameter (FD) and length (FL) of *Caryocar brasiliense*.

Genetic parameters	Features				
	FW (g)	FW2 (cm)	FT (cm)	FD (cm)	FL (cm)
h_g^2(%)	55	94	95	95	68
$r_{âa}$ (%)	74	96	97	97	82
CV_{gi} (%)	3.88	5.00	5.80	6.12	2.90
G_s (%)	5.56	12.20	14.33	15.12	5.12
CV_e (%)	7.80	2.82	2.89	3	4.50
Average	15.38	2.88	2.69	2.51	3.83

Genotypic heritability in broad sense (h_g^2), selective accuracy ($r_{âa}$ %), coefficients of genotypic variation (CV_{gi} (%)), genetic gain (G_s (%)), coefficient of residual variation (CV_e(%)) and averages for each character.

The correlations can guide the selection of a set of traits as a total, not for each character in isolation (Vencovsky & Barriga, 1992). Our results showed a strong correlation between fruit weight ($rf \geq 0.72$), and width ($rg \geq 0.94$) (Table 3). The correlations between the fruit's weight and its dimensional traits are interesting, specially because when selecting matrices that have fruits with larger transverse diameters, consequently it will be selected heavier fruits (more weight). The phenotypic correlations are useful in indirect selection, where gains can be made without restricting selection (Zobel & Talbert, 1984). The significant unfavorable correlations were found between fruit weight ($rg \geq 0.87$) and thickness ($rf \geq 0.60$), because this implies a high proportion of fruit peel, which in small or medium productions would result in low yield.

Table 3. Phenotypic (*rf*) and Genotypic (*rg*) correlations for fruit's characteristics in matrices of *Caryocar brasiliense*.

*Characters	FW	FW2	FT	FD	FL
FW	–	0.723**	0.599ns	0.516ns	0.546ns
FW2	0.948**	–	0.712*	0.635*	0.557ns
FT	0.877**	0.952**	–	0.715*	0.488ns
FD	0.454ns	0.613*	0.637*	–	0.755*
FL	0.392ns	0.407ns	0.324ns	0.699*	–

Phenotypic correlation (*rf*) above the diagonal and genetic correlations (*rg*) below the diagonal, for fruit weight (FW), width (FW2), thickness (FT), diameter (FD) and length (FL) of *Caryocar brasiliense*.

The integral maintenance of natural populations is important to preserve the viability of the species. The pairing system and the flow of the species' genes can be altered, resulting in a possible fragmentation of the natural populations of *Caryocar brasiliense*, which can decrease the population

size (Collevati et al., 2001), reduce genetic variability, and increase endogamy (Tambarussi et al., 2017).

More researches aiming to study the genetic control of native species are necessary for the preservation and pre-improvement of the species (Faleiro et al., 2008). In conclusion, the trees of *Caryocar brasiliense* of the southern region of Tocantins has shown significant genetic variation; and high heritability according to the traits of its fruits, which has demonstrated more than sufficient potential to be explored in a genetic improvement program.

SUBMISSION STATUS

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