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GENETIC VARIABILITY OF *Parkia platycephala* POPULATIONS: SUPPORT FOR DEFINING SEED COLLECTION AREAS[1]

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ABSTRACT - Loss of genetic variability in natural populations affects negatively the adaptive and evolutive process of plant species. In this context, the objective of this work was to evaluate the existing genetic variability between and within natural populations of *P. platycephala*, using biometric characters of fruits and seeds and physiological characters of seeds and seedlings, and, thus, assess the potential for selection of mother trees, indicate areas for seed collection and use, and generate support for conservation and pre-breeding of plant species. A completely randomized experimental design was used, with 45 treatments (progenies) and four replications of 25 seeds. The progenies were evaluated in laboratory, using seeds collected from 45 mother trees sampled in three natural populations. The following characters were evaluated: seed germination percentage, germination speed index, and mean germination time; shoot and main root lengths; and seedling shoot and root dry weights. The data were subjected to RELM/BLUP analysis for estimating genetic parameters and correlations and to analyses of genetic divergence (UPGMA). The populations present genetic differences to each other and a significant variation between progenies for all characters evaluated, and the variation was greater within the populations. The characters evaluated present high genetic control; therefore, they can be used in analysis of genetic variability of populations and progenies of *P. platycephala*, thus assisting in the identification of areas for seed collection, conservation programs, and pre-breeding of the species.

Keywords: Genetic conservation. Genetic parameters. Fava de bolota. Forest restoration. Forest seeds.

VARIABILIDADE GENÉTICA DE POPULAÇÕES DE *Parkia platycephala*: SUBSÍDIO PARA DEFINIR ÁREAS DE COLETA DE SEMENTES

RESUMO - A perda da variabilidade genética de populações naturais implica negativamente no processo adaptativo e evolutivo das espécies. Nesse contexto, objetivou-se avaliar a variabilidade genética existente entre e dentro de populações naturais de *P. platycephala*, a partir de caracteres biométricos de frutos e sementes e fisiológicos de sementes e plântulas, e assim, verificar o potencial para seleção de árvores matrizes e indicar áreas para coleta e uso de sementes, como também gerar subsídios para conservação e pré-melhoramento genético da espécie. O delineamento experimental utilizado foi o inteiramente casualizado, com 45 tratamentos (progênies) e quatro repetições de 25 sementes cada. As progênies foram avaliadas em laboratório, a partir de sementes coletadas de 45 matrizes amostradas em três populações naturais. Para tanto, avaliou-se os seguintes caracteres: porcentagem de germinação, índice de velocidade de germinação, tempo médio de germinação, comprimento de parte aérea e raiz principal, massa seca da parte aérea e do sistema radicular de plântulas. Os dados foram submetidos a análise RELM/BLUP para estimativa dos parâmetros genéticos, correlações e análises de divergência genética (UPGMA). As populações apresentam diferenças genéticas entre si, e variação significativa entre progênies para todos os caracteres avaliados, sendo maior a variação dentro do que entre populações. Os caracteres avaliados apresentam alto controle genético, portanto, estes podem ser utilizados na análise da variabilidade genética de populações e progênies de *P. platycephala*, auxiliando assim na identificação de áreas para a coleta de sementes, programas de conservação e pré-melhoramento genético da espécie.

Palavras-chave: Conservação genética. Parâmetros genéticos. Fava de bolota. Restauração florestal. Sementes florestais.

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INTRODUCTION

Fragmentation of forest ecosystems, combined with the lack of information on genetic resources, has contributed to the loss of diversity and, thus, we live under a high ecological concerning with public policies and measures for forest restoration and better cost-benefit strategies for mitigating climate changes and improving the economy. In the scope of efforts to control climate change, Brazil took on ambitious goals upon the Paris Agreement by committing to restore and reforest 12 million hectares of forests until 2030 (REI; GONÇALVES; SOUZA, 2017) with estimates of using 3,6 to 15,6 thousand tonnes of forest seeds, but, considering the current situation, seed availability is far below this demanded quantity (URZEDO et al., 2020).

Natural forest remnants are secure sources for collection of seeds of native species that meet physical, physiological, and genetic quality parameters (MORI; NAKAGAWA, 2015). However, these areas usually have underwent some changes in the original vegetation, which can directly affect the genetic quality of seeds to be grown. Considering the assumption that differences between individuals can exist within a same species due to the environmental effect and genetic factors (SILVA et al., 2014), studies focused on analyzing physiological and genetic quality of seeds from different mother trees and populations are important and can be used to recommend potential areas and individuals for seed collection.

The genetic and physiological qualities of seed lots and grown seedlings can be assured when seed collection procedures are carried out correctly. In this sense, studies on forest species evaluating fruit, seed, and seedling characteristics have been conducted focusing on quantifying genetic variability in progenies from mother trees in natural populations, for example, from *Cedrela fissilis* Vell. (Meliaceae) (BIERNASKI; HIGA; SILVA, 2012), *Apuleia leiocarpa* (Vogel) J. F. Macbride (Caesalpiniaceae) (LOVATEL et al., 2021), and *Olea europaea* L. (Oleaceae) (YILMAZ-DÜZYAMAN, ROSA; LEÓN, 2022).

Information on the origin of these seeds is another issue to be studied because of continuous losses of habitats, which directly result in decreases in genetic availability and diversity and can compromise the sustainability of restored populations. Assuring seed physiological and, mainly, genetic quality is essential for forest restoration; thus, some factors, such as geographical distribution of species, genic flow, endogamy, seed and pollen dispersion methods, reproduction system, and efficiency of pollinating and dispersing agents have been taken into consideration, because they affect the genetic structure of populations (SEBBENN, 2002; LOVATEL et al., 2021). Information on genetic variability of natural populations is essential for defining areas for seed collection, focused on using them in restoration programs and further for active germplasm banks and implementation of base population for conservation and pre-breeding purposes.

Harmonizing conservation and production is still a challenge; however, the choice of native species of multiple uses, fast growth, and wide occurrence, such as *Parkia platycephala* Benth. (Fabaceae), can result in environmental, economic, and social benefits. *P. platycephala* is popularly known in Brazil as fava-de-bolota; it is an allogamous, chiropterophily (long-distance pollination by bats) species, with barochoric primary mechanism of fruit and seed dispersion (short-distance dispersion by the fall of seeds) (CHAVES; SANTOS; SILVA, 2020), and occurrence in areas of the Cerrado biome, Cerrado-Caatinga transitional areas, and Amazonian regions, in Brazil (LORENZI, 2013). This species is excellent for composing ecological restoration projects due to its ecophysiological advantages and its scenic, energy, wood, nutritional, and economic potentials (LORENZI, 2013).

Recent studies have indicated the use of *P. platycephala* fruits for feed supplementation of ruminants, which is a common practice in semiarid regions in the dry season and a viable and low-cost alternative adopted by growers (BATISTA et al., 2020; COSTA et al., 2020). In this sense, promising perspectives for the breeding of this species have been developed, focused on increasing production and improving fruit and seed protein quality, with the main purpose of promoting income and minimize impacts for this species and its natural ecosystems.

Although the social, economic, and environmental importance of research on this issue is a consensus among researchers and the scientific community, there is still gaps of information and, in the case of *P. platycephala*, there is no studies focused on providing information on the genetic diversity of natural populations. Therefore, the objective of this work was to evaluate the genetic variability between and within natural populations of *P. platycephala* by using biometric characters of fruits and seeds and physiological characters of seeds and seedlings, assess the potential for the selection of mother trees, and indicate areas for seed collection and use, generating support for conservation and pre-breeding of this species.

MATERIAL AND METHODS

Tests of progenies were carried out using 45 mother tree samples from three natural populations that showed evidence of some anthropogenic intervention, in a Cerrado-Caatinga transition area, in the municipality of Bom Jesus, Piauí, Brazil (9°04'13"S and 44°21'50"W). Fifteen mother trees were selected, identified, and georeferenced in each population, based on the following criteria: dominance, absence of pathogens, well-developed canopy, good fruit production, distant at least 100 m from each other, and fruit production in a single season (Figure 1).

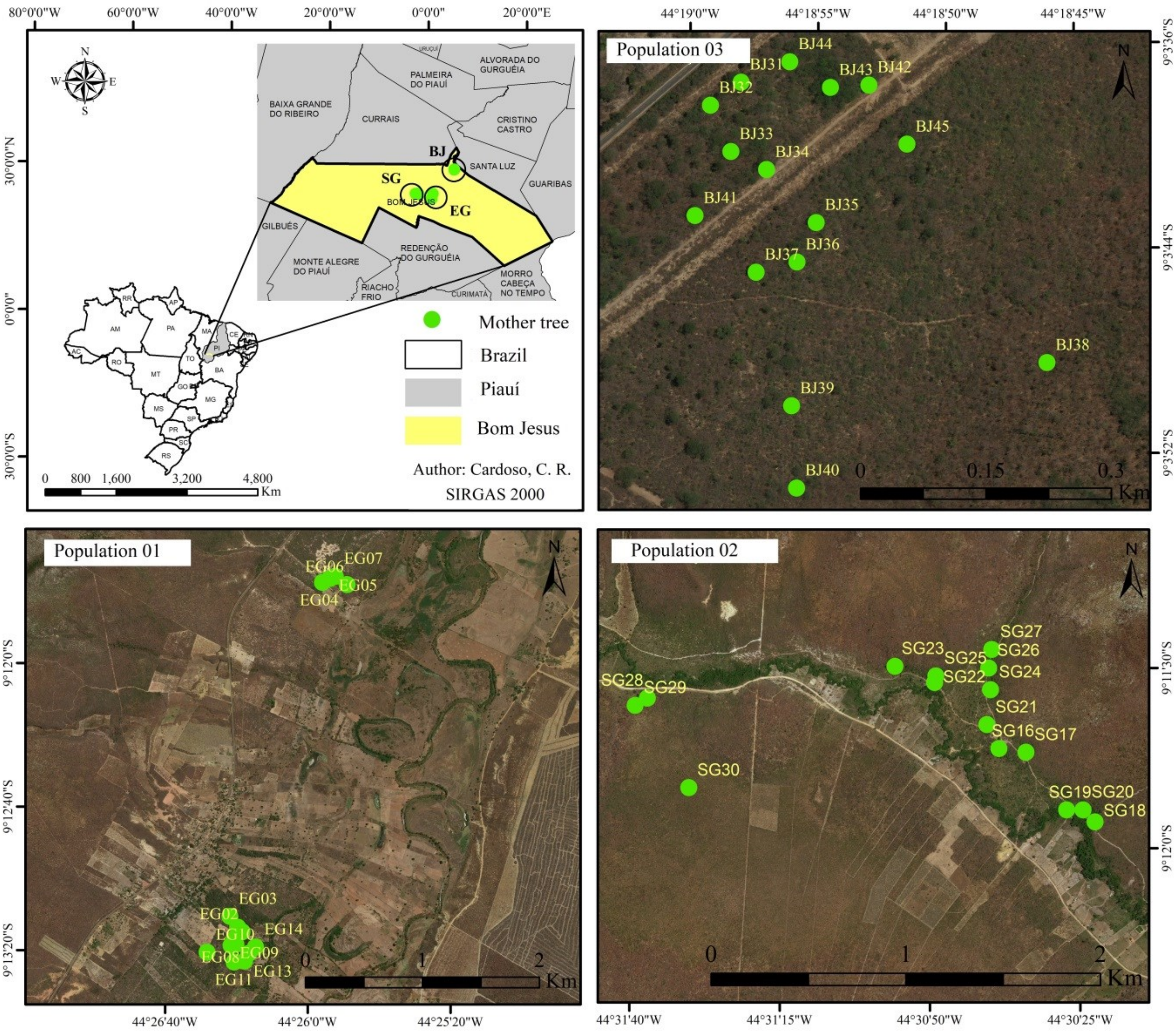


Figure 1. Geographical distribution of three populations of *Parkia platycephala* Benth. and spatial distribution of the 45 georeferenced mother trees sampled in three districts different of the municipality of Bom Jesus, Piauí, Brazil. Population 1 (EG), population 2 (SG), and population 3 (BJ).

The fruits were collected, separated, and identified by mother tree and, then, taken to a laboratory for seed extraction and processing. The progenies were evaluated through germination tests, in a completely randomized experimental design with 45 treatments (progenies) and four replications of 25 seeds. The implementation and conduction of the germination test followed the recommendations proposed by Silva et al. (2017) for the species: use of BOD (Biochemical Oxygen Demand) germinator, germination under light, alternate temperature of 25 to 35 °C, and sowing in vermiculite substrate in Gerbox boxes.

The following quantitative characters were evaluated: biometric characters: length, thickness, and width of fruits and seeds and numbers of seeds per fruit. Fruit length and width (cm) were measured using a millimetric tape ruler, and the fruit and seed length, width, and thickness (mm) were measured using a digital caliper; seed germination and seedling vigor: germination (%) was calculated based on the number of germinated seeds at the end of the test

(15 days after sowing), adopting the following criterion for germination: hypocotyl emergence, with consequent opening of cotyledons and emergence of embryonic leaves; germination speed index was calculated according to the formula proposed by Maguire (1962); mean germination time was calculated according to the methodology proposed by Labouriau and Valadares (1976), with results expressed in days after sowing; seedling main root and shoot lengths (cm) of each replication were measured at the end of the germination test (15 days after sowing), using a millimetric ruler; seedling root and shoot dry weights (mg) were measured by separating seedling parts with a scissor, placing them in kraft paper bags, and taking them to a forced air circulation oven at 60 °C for 24 hours. The dry material was weighed in a precision balance (0.001 g).

The data were analyzed by the restricted maximum likelihood methodology. The components of variances and genetic parameters for the variables studied were estimated using the following mixed model: $Y_{ijkl} = \mu + b_i + t_j + f_k + e$, where Y_{ijkl} is the phenotypic value of the analyzed variable; μ is the fixed term of the overall mean of the analyzed variable; b_i is the fixed effect of the i-th replication; t_j is the random effect of the j-th population; f_k is the random effect of the k-th progeny in the j-th population; and e_{ijkl} is the effect of the experimental error relative to the l-th seedling within the k-th progeny of the j-th origin in the i-th replication. The mixed model was adjusted in the R software, using the lmer function of the *lme*4 statistical package (BATES et al., 2015). The random effects of the model were tested by the likelihood-ratio test (LRT) and their significances were verified by the qui-square (χ^2) test.

The components of variances estimated were: genetic additive variance (σ_a^2), genetic variance between populations (σ_{pop}^2), residual variance (σ_e^2), and phenotypic variance $(\sigma_f^2 = \sigma_a^2 + \sigma_{pop}^2 + \sigma_e^2)$, according to the Equation 1:

$$\sigma_f^2 = \sigma_a^2 + \sigma_{pop}^2 + \sigma_e^2 \qquad (1)$$

These components of variances were used to estimate the heritability (Equations 2, 3 and 5), coefficients of variation (Equations 6, 7 and 8) (NAMKOONG, 1979), and other genetic parameters (Equations 4 and 9) :

a) individual heritability in the restricted sense:

$$(h_r^2 = \frac{\sigma_a^2}{\sigma_f^2}) \qquad (2)$$

b) mean heritability of progenies:

$$h_m^2 = \frac{0.25\sigma_a^2}{0.25\,\sigma_a^2+\sigma_e^2/r} \qquad (3),$$

where r is the number of replications (RESENDE, 2002).

c) accuracy of the selection of progenies:

$$\hat{r}_{aa} = \sqrt{h_m^2} \text{ (RESENDE, 2002)} \qquad (4)$$

d) heritability within progenies:

$$h_d^2 = \frac{0.75\sigma_a^2}{\sigma_e^2} \qquad (5)$$

e) coefficient of individual additive genetic variation:

$$\mathrm{CV}_{gi\%} = \frac{\sqrt{\sigma_a^2}}{m} \cdot 100 \qquad (6),$$

where m is the mean of the variable analyzed.

f) coefficient of genotypic variation between progenies:

$$\mathrm{CV}_{gp\%} = \frac{\sqrt{0.25\,\sigma_a^2}}{m} \cdot 100 \qquad (7)$$

g) coefficient of environmental variation:

$$CV_{e\%} = \frac{\sqrt{\sigma_e^2}}{m} \cdot 100 \qquad (8)$$

h) coefficient of relative variation:

$$\hat{b} = \frac{CV_{gp\%}}{CV_{e\%}} \text{ (VENCOVSKY; BARRIGA, 1992)} \qquad (9)$$

These components of variance were used to estimate the genetic difference between populations (F_{ST}), according to Equation 10 (RESENDE, 2015):

$$(F_{st} = \frac{\sigma_{pop}^2}{\sigma_{pop}^2 + 2\sigma_a^2}) \qquad (10)$$

Pearson's correlations between phenotypic data of height (H; m) and diameter at breast height (DAP; cm) of mother trees, and phenotypic and genotypic data of seed germination and vigor and seedling initial growth were estimated and the significances were analyzed by the *t* test at 5%

probability level; these analyses were carried out using the *corrplot* package (WEI; SIMKO, 2017). The genetic divergence between *P. platycephala* mother trees was evaluated based on their progenies by using the method UPGMA (Unweighted Pair Group Method with Arithmetic Mean). First, the dissimilarity matrix was estimated based on the quantitative characters evaluated by the mean Euclidean distance, using the *vegdist* function of the *vegan* package (OKSANEN et al., 2018) of the R statistical program; the matrix was used to obtain the UPGMA grouping. The coefficient of cophenetic correlation was calculated to assess the fit between the dissimilarity matrix and the generated grouping, according to Sokal and Rohlf (1962).

RESULTS AND DISCUSSION

The populations and progenies of *P. platycephala* presented significant genetic differences for all characters evaluated by the likelihood ratio test (LRT), except for fruit and seed biometric characters and seedling shoot and root dry weights, which presented significant genetic variances only for the effect of progenies, denoting the existence of genetic variability between and within populations (Table 1).

Table 1. Estimates of genetic parameters for fruit and seed biometric characters, seed germination and vigor, and seedling initial growth of 45 *Parkia platycephala* Benth. mother trees.

	Genetic parameters												
	σ_a^2	σ_{pop}^2	σ_e^2	σ_f^2	F_{ST}	h_r^2	h_{mp}^2	A_{cprog}	CV_{gi}	CV_{gp}	CV_e	$\hat{b}$	$\bar{x}$
FL	7.57^{**}	---	10.50	18.07	---	0.42	0.95	0.97	20.12	10.06	23.71	0.42	13.67
FW	1.24^{**}	---	0.24	1.48	---	0.84	0.99	0.99	21.90	10.95	9.60	1.14	5.09
FT	4.17^{**}	---	0.92	5.09	---	0.82	0.99	0.99	41.07	20.53	19.35	1.06	4.97
TSF	44.84^{**}	---	54.77	99.62	---	0.45	0.95	0.98	26.60	13.30	29.40	0.45	25.17
SL	0.66^{**}	---	0.45	1.11	---	0.60	0.97	0.99	9.50	4.75	7.82	0.61	8.55
SW	1.24^{**}	---	0.24	1.48	---	0.84	0.99	0.99	21.90	10.95	9.60	1.14	5.09
ST	0.85^{**}	---	0.17	1.02	---	0.83	0.99	0.99	28.30	14.15	12.76	1.11	3.25
G(%)	419.70^{**}	76.85^{**}	39.37	535.92	0.08	0.78	0.91	0.96	21.92	10.96	6.71	1.63	93.47
GSI	2.99^{**}	0.75^{**}	0.20	3.93	0.11	0.76	0.94	0.97	33.38	16.70	8.60	1.94	5.18
MGT	0.25^{**}	1.14^{**}	0.02	1.41	0.69	0.40	0.92	0.96	10.50	5.25	3.16	1.66	4.76
SL	1.07^{**}	2.02^{**}	0.21	3.31	0.48	0.32	0.83	0.91	17.89	8.94	7.99	1.11	5.79
MRL	1.96^{**}	0.83^{**}	0.35	3.13	0.17	0.62	0.85	0.92	23.58	11.79	9.94	1.19	5.93
SDW	100.78^{**}	0.51^{ns}	3.23	104.52	0.002	0.96	0.97	0.98	36.03	18.02	6.45	2.79	27.86
RDW	4.76^{**}	0.11^{ns}	0.34	5.22	0.01	0.91	0.93	0.97	33.10	16.55	8.85	1.87	6.59

σ_a^2 = genetic additive variance; σ_{pop}^2 = genetic variance between populations; σ_e^2 = residual variance; σ_f^2 = phenotypic variance; F_{ST} = genetic quantitative difference between populations; h_r^2 = individual heritability in the restricted sense; h_{mp}^2 = mean heritability of progeny; A_{cprog} = accuracy of the selection of progenies; CV_{gi}% = coefficient of individual additive genetic variation; CV_{gp}% = coefficient of genetic variation between progenies; CV_e% = coefficient of residual variation; $\hat{b}$ = coefficient of relative variation; $\bar{x}$ = mean of the character; FL = fruit length; FW = fruit width; FT = fruit thickness; TSF = total seeds per fruit; SL = seed length; SW = seed width; ST = seed thickness; G(%) = germination percentage; GSI = germination speed index; mean germination time (MGT); MRL = main root length (cm); SL = shoot length (cm); SDW = shoot dry weight (mg); RDW = root dry weight (mg). ** significant at 1% probability level; ^{ns} not significa.

Moderate (F_{STGER}(%)= 0.08 and F_{STIVG}= 0.11) to high (F_{ST}>0.25) genetic divergences (WRIGHT, 1976) were found between the populations for most evaluated characters (Table 1). These values can vary from 0 (absence of genetic difference between populations and genetic structuring) to 1 (characterizing a populational genetic structuring due to occurrence of fixation of alleles in different populations) (GOIS; FERREIRA; SILVA-MANN, 2018). Therefore, the preservation of inter and intrapopulation genetic variability is an efficient strategy of conservation for *P. platycephala* trees.

Factors inherent to the species, such as geographical distribution, pollination dynamics, dispersion, and reproduction system, can explain the genetic variability found between and within populations of tree species (SEBBENN et al., 2011; BIERNASKI; HIGA; SILVA, 2012). In this sense, considering that *P. platycephala* is an allogamous, chiropterophily (long-distance pollination by bats) species with barochoric primary mechanism of fruit and seed dispersion (short-distance dispersion by the fall of seeds) (CHAVES; SANTOS; SILVA, 2020), the hypothesis in the study was confirmed, as the F_{ST} values denoted the existence of low to moderate genetic differences between populations of *P. platycephala* for most characters evaluated.

The hypothesis of the structuring in families in these populations can be confirmed in the new population to be originated, as a decrease in density of *P. platycephala* individuals can favor the crossing between related individuals, thus increasing the population endogamy level; however, the loss of individual vigor, low adaptability, and reproduction problems are negative implications. In addition, the populations studied may descend from one common ancestral and differentiated in mosaics due to high anthropogenic intervention, since deforestation in areas with this species is evident, either for implementation of pastures or opening of roads.

Genetic differences between populations for adaptive characters define different seed collection zones (BIERNASKI; HIGA; SILVA, 2012). Thus, seed collection can be carried out between and within *P. platycephala* populations to obtain a high genetic representativeness. However, in situations of logistical and financial difficulties, the collection in a single population is viable, when considering the basic principles of sampling of genetic resources proposed by Sebbenn (2002) for an adequate seed collection intended to forest restoration.

Genetic parameters were estimated to determine whether the observed phenotypic characteristics can be used as genetic indicators for the species and identifiers of superior mother trees, and whether they are inheritable. The heritability values (h_r^2 and h_{mp}^2) varied from 0.32 to 0.99 (Table 1); which can be considered median (0.15 to 0.50) to very high (>0.80) (RESENDE; ALVES, 2020), denoting that the phenotypic and genetic values found for the characters present high correspondence (VENCOVSKY; BARRIGA, 1992). High heritability values represent lower environmental effect on the performance of progenies, denoting high genetic control on the characters evaluated and, thus, higher possibility of genetic gains with the selection of phenotypically superior mother trees.

The selection at progeny level ($h_{mp}^2 > 0.50$) can provide significant genetic gains in conservation and breeding programs for the species (RESENDE; ALVES, 2020). Considering this high genetic control, the characters analyzed can be used in studies of genetic variability focused on obtaining information about genetic variability of natural populations and selection of superior individuals as mother trees for seed collection.

Individual heritability estimates in the restricted sense (h_r^2) were high for most characters, and were close to the mean heritability values of progenies (h_{mp}^2); thus, it is recommended to adopt the selection level of mother trees between and within the best populations of *P. platycephala*, focused on reaching the maximum possible genetic variance, to obtain higher gains in a genetic selection, considering that populations can present private alleles. Kampa et al. (2020) found similar results for seedlings of *Campomanesia xanthocarpa* (Mart.) A. Berg. (Myrtaceae) and recommended the selection between and within progenies and mass selection as good strategies.

The high heritability values found can be connected to the controlled conditions of the experiment, as the study was conducted in a laboratory with high control of environmental variations, where the environmental effect on the phenotype expression was lower. It explains the expressive genetic control on the characters evaluated and the reliability of the results presented. Analyses of seed physiological characteristics of *Ceiba speciosa* (A.St.-Hil.) Ravenna. (Bombacaceae) also showed, through coefficients of heritability, that the environmental effect on phenotypic characteristics such as germination and germination speed index is low; thus, these characteristics are promising for the indication of superior mother trees and progenies (ROVERI NETO; PAULA, 2017).

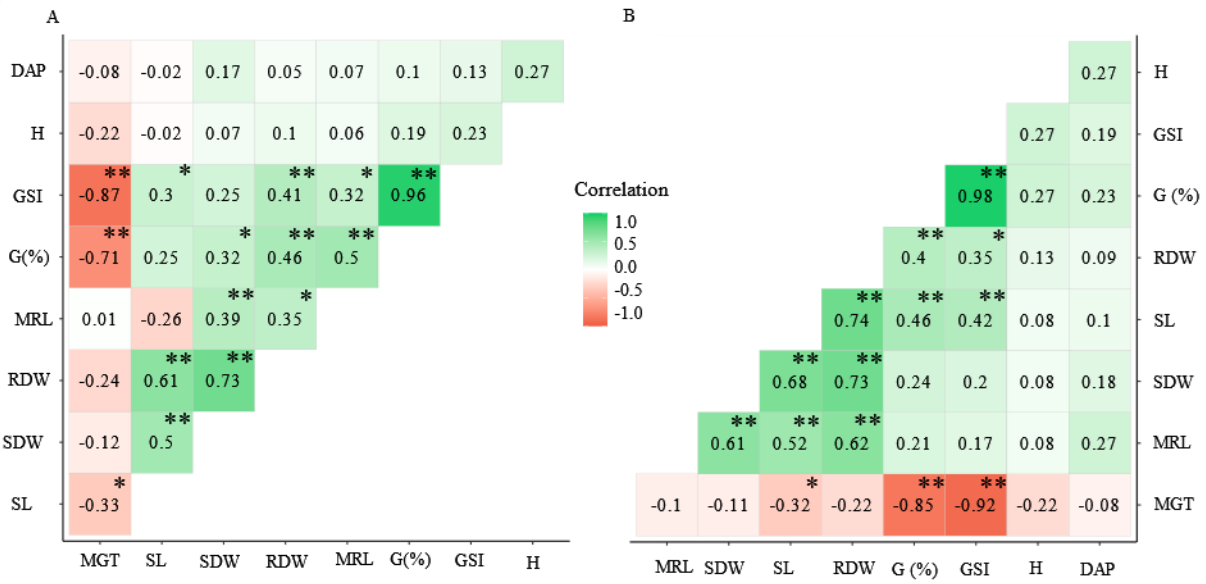
The accuracy values were high ($A_{cprog} \geq 90\%$), denoting high correlation between the predicted and observed genetic values, efficiency in the selection, and adequacy of the experimental design used (Table 1). The high values obtained denote the high reliability of the results (RESENDE; ALVES, 2020), thus, the characters evaluated present reliability and can be used to determine the existing genetic variability between mother trees in similar studies for *P. platycephala* and other forest species. Studies developed with other forest and agricultural species, such as *C. speciosa* (ROVERI NETO; PAULA, 2017), *Helianthus annuus* L. (Asteraceae) (SANTOS et al., 2017), and *Euterpe oleracea* Mart. (Arecaceae) (YOKOMIZO; FARIAS NETO; OLIVEIRA, 2016) are consistent with the present study and point out that these seed physiological characteristics can be used as parameters for the evaluation of genetic variability.

The coefficients of genotypic variation, individual and between progenies (CV_{gi} and CV_{gp}, respectively), show the magnitude of the genetic variability in a population (CARVALHO et al., 2016). The quantitative characters fruit thickness and shoot dry weight presented the highest CV_{gp} (20.53% and 18.02%. respectively) and CV_{gi} (41.07% and 36.03%, respectively) for *P. platycephala* progenies; thus, they stood out among the characters evaluated by presenting higher variability between *P. platycephala* progenies.

The coefficients of genetic variation showed the existence of genetic variability between and within (CV_{gi}% and CV_{gp}%, respectively) *P. platycephala* progenies for all evaluated characters (Table 1). The genetic variance within families (CV_{gi}%), i.e., progenies from the same mother tree, was higher than the genetic variance between families (CV_{gp}%); it is a similar result to those found for allogamous species, which presented higher genetic variability within than between families (BIERNASKI; HIGA; SILVA, 2012). Thus, all characters of seed biometry, germination, and seedling initial growth can be used as indicative of success for the selection of populations and mother trees with higher genetic variability, enabling the definition of areas for seed collection, which is important for conservation and breeding programs for this species.

The coefficients of experimental variation (CV_e) were low, which is positive, since it denotes the experimental quality of the study (Table 1). The lowest and highest values were shown by the variables: mean germination time (CV_e=3.16%) and total seeds per fruit (CV_e=29.40%), respectively (Table 1). The amplitude of CV_e is associated with the experimental precision and the measurements of characteristics evaluated (BATISTA et al., 2012), which is confirmed by the high accuracy (A_{cvroa}) and heritability values (Table 1), denoting that the genetic value was responsible for the existing variation between progenies and not the environmental effect.

The phenotypic data of height and diameter of mother trees were correlated to each other and presented positive values for the most correlations when correlated with phenotypic (Figure 2A) and predicted genetic values (Figure 2B) of seed and seedling germination and vigor of *P. platycephala* progenies.



Green = positive correlation; Red = negative correlation; the color intensity represents the magnitude of the correlations. G (%) = germination percentage; GSI = germination speed index; MGT = mean germination time (days); SL = shoot length; MRL = main root length (cm); SDW = shoot dry weight; and RDW = root dry weight (mg).

Figure 2. Pearson's correlations between phenotypic characters of height (H) and diameter (DAP) of mother trees and phenotypic (A) and predicted genetic (B) values of seed and seedling germination and vigor of *P. platycephala* progenies.

The highest correlation values were found when the phenotypic data of mother trees were correlated with predicted genetic values (Figure 2B). The obtaining of progenies that present good germination speed indexes and germination percentages is expected when selecting mother trees with good DAP, as these characters are genetically correlated (Figure 2B). Thus, considering a design of strategies focused on obtaining *P. platycephala* seeds with good genetic quality, the phenotypic and genetic performances of mother trees can be observed based on the evaluation of the germination speed index of their progenies.

The groups were formed by progenies collected in a single population (Figure 3, group II), and progenies collected in different populations (Figure 3, groups III, VI, VIII, and X). This division into different groups is positive, since it confirms the existence of genetic variability between and within populations. The progenies are grouped in these groups according to their dissimilarity degree, denoting a higher genetic similarity within than between groups. In the context of genetic conservation, which in this case is focused on sampling that optimizes access a high genetic variability of natural populations of *P. platycephala*, seed collection from a large number of mother trees between and not within groups is an excellent strategy and may result in higher genetic gains.

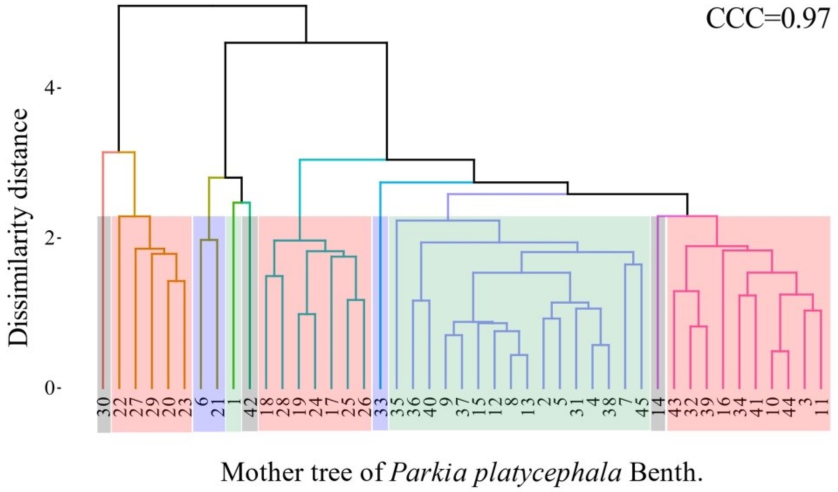


Figure 3. Dendrogram representing the genetic dissimilarity of 45 mother trees of the species *Parkia platycephala* Benth., by the method Unweighted Pair Group Method with Arithmetic Mean (UPGMA), using the Euclidean distance as a dissimilarity measured.

The information obtained in the present study is important for the adaptation and evolution of species, and provides information related to the natural capacity of *P. platycephala* plants to respond to climate changes and common biotic and abiotic stress conditions in environments to be restored. The *P. platycephala* populations and mother trees analyzed can be used as seed sources, as they present physiological and genetic qualities and their seeds can be used to produce seedlings for reforesting programs, environmental restoration, commercial crops, silvopastoral systems, implementation of base population, ex situ conservation, and implementation of progeny and precedence tests focused on domestication and breeding programs for the species.

The methodological approach used showed that the experiments were relatively fast when using germination tests, compared to the time of experiments under nursery or field conditions, and provide accurate and representative information on population and individual genetic variability. The methodology was efficient for genetically discriminating *P. platycephala* populations and mother trees and can, therefore, be applied to other forest species and contribute to define areas for seed collection, selection of mother trees, and pre-evaluations of seeds to produce seedlings in progeny tests, thus avoiding the use of seeds with low genetic variability and composition of seed lots with low genetic quality due to the choice of genetically similar mother trees.

The results found were consistent with the Brazilian public policies for promotion of production chains related to the recovery of native vegetation and fulfillment of goals and international commitments assumed by the country to solve local and global problems. In addition, these results can be recommended by public and private agencies, such as the Ministry of Agriculture, Livestock and Supply (MAPA), as a complementary analysis of seed physiological quality to support actions for recovery and restoration of native vegetation and conservation, pre-breeding, and breeding of native species.

CONCLUSIONS

Populations of *Parkia platycephala* are genetically different from each other, as well as their progenies, presenting higher variation within than between populations, denoting their potential as adequate seed collection sources for forest restoration. Seed collection between and within populations is recommended for accessing a high genetic representativeness. The characters evaluated present high genetic control; therefore, they can be used for analysis of genetic variability of natural populations and progenies of *P. platycephala*, thus assisting in strategies of seed collection for forest restoration programs, ex situ conservation, and pre-breeding of this species.

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