Phenotypic and genotypic evaluation of Parkia *platycephala* families: a proposal for pre-selection

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Abstract: *The objective of the study was to determine whether Parkia platycephala families with superior morphophysiological traits perform consistently across four stages of early development (plantlets, seedlings, and juveniles at 34 and 60 months), as a means to assess the possibility of conducting pre-selection. For 21 morphophysiological traits, the following genetic parameters were estimated: heritability, coefficients of variation (genetic, relative, and environmental), accuracy, genetic and phenotypic correlation, percentage of coincidence (PC) of the best families, effective population size, and inbreeding in three progeny tests conducted under laboratory, nursery, and field conditions. Families of P. platycephala showed significant phenotypic and genotypic differences. The traits evaluated show genetic control. The percentage of coincidence between the best families was more accurate when the selection intensity was greater than 50% (PC ≥ 52%). Based on the evaluated traits, a pre-selection strategy at the juvenile stage for P. platycephala was researched to effectively identify superior families.*

Keywords: *Genetic improvement, early selection, genetic variability, genetic correlation, forest species*

INTRODUCTION

Parkia platycephala Benth. is one of 17 neotropical tree species of the *Parkia* genus that is endemic to Brazil, occurs naturally in the North, Northeast, and Midwest regions of the country, and has multiple uses, such as great ecological, landscape, pharmacological, energy, and nutritional potential. The calorific value of 18,282 GJ ton^{-1} for *P. platycephala* classified the wood of this species as a good alternative for use as an energy source (Silva and Vale 2018). It is a hermaphroditic species, but it has self-incompatibility as a favorable mechanism for outcrossing. *P. platycephala* has primary pollination syndromes with bats and bees as primary floral visitors (Chaves et al. 2020). The flowering period begins between five and six years of age, characterizing the beginning of the mature age for *P. platycephala* (Lacerda and Mapeli 2021).

Species with wide geographic distribution that occur across different biomes, such as *P. platycephala*, show several advantages including adaptability, phenotypic plasticity, and high levels of genetic diversity (Castro et al. 2021), which can be a great advantage for breeding programs, specifically when it is
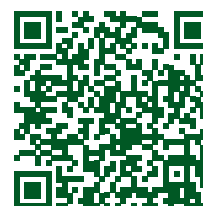
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starting the domestication of the species as for *P. platycephala*. Therefore, to design effective strategies for conservation and/or genetic improvement, the characterization of genetic variability is essential (Spigler et al. 2017). In that case, for breeding programs and conservation proposals, the evaluation of performance and the selection of genetically superior families and individuals must be based on accurate estimates and predictions (Pires et al. 2011).

The implementation of provenance and/or progeny tests is a common practice for native forest species with high economic and ecological value. The goals of implementing such tests include genetic conservation, the formation of seed orchards, pre-breeding, domestication, and the development of genetic improvement programs (Souza et al. 2021). Besides enabling the phenotypic and genotypic characterization of the population of interest, provenance and progeny tests also provide information about genitors based on an evaluation of their descendants (Lustri et al. 2021). These tests indirectly assess the potential of the sampled mother trees and natural populations for use as seed sources.

The process of planning, implementing, evaluating, and identifying families and genetically superior individuals demands time and financial and human resources. Thus, the development of strategies based on highly accurate genetic estimates/predictions that optimize and ensure the identification of superior families and genotypes, even at juvenile stages, can be an effective option for pre-selection of non-domesticated species. Removal individuals that do not perform well can enhance selection efficiency and reduce costs associated with seedling production, planting, development, and families evaluation.

The characterization of the genetic variability of base populations of forest species in the form of progeny tests has been well documented in research carried out under field conditions (Garuzzo et al. 2021, Lustri et al. 2021, Souza et al. 2021). As a way of anticipating this characterization, morphophysiological assessments at the seedling (Kampa et al. 2020) and plantlet stages (Menegatti et al. 2016, Corrêa et al. 2021) have also been conducted. However, the question remains as to whether progenies that stand out phenotypically and genotypically at the plantlet stage also show good phenotypic and genotypic performance at more advanced stages of development, such as the seedling and juvenile stages. Thus, this is the first study for the species to date to compare the performance of the same genetic material at three different stages of development (plantlets, seedlings, and juveniles), and check whether there is correspondence in terms of performance among the best families at different stages of development.

In this context, the objectives of the current study were to: i) phenotypically and genotypically characterize *P. platycephala* progeny tests carried out under laboratory, nursery, and field conditions (34 and 60 months); ii) determine the correlation between the estimates of predicted genetic values (BLUPs) and obtain the degree of association between the four evaluated stages of development; and iii) assess the possibility for pre-selection of *P. platycephala* families.

MATERIAL AND METHODS

The open-pollinated families used in the three progeny tests were collected from 45 mother trees selected from three populations (15 trees population⁻¹) across the natural range of the species: Pop 1 (lat 9° 13' 13.5'' S, long 44° 26' 16.7'' W, alt 268 m asl); Pop 2 (lat 9° 11' 43.4'' S, long 44° 30' 38.5'' W, alt 286 m asl); and Pop 3 (lat 9° 3' 37.6'' S, long 44° 18' 58.1'' W, alt 276 m asl). The three populations are located in the southwestern region of the State of the Piauí, Brazil, in areas of transition between the Cerrado and Caatinga biomes (Figure 1). For the phenotypic selection
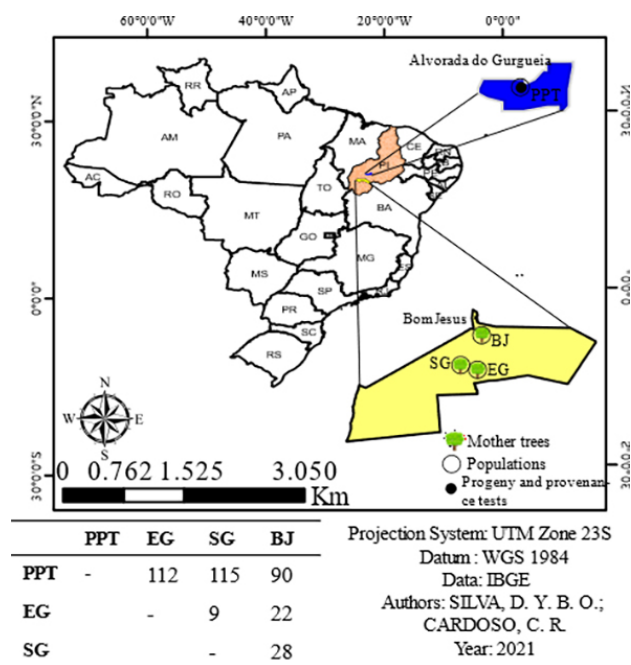

Figure 1. Geographical location of the natural populations where the 45 mother trees were sampled in Bom Jesus, Piauí, and the progenies and provenance test of *Parkia platycephala* Benth. in Alvorada do Gurgueia, Piauí. The matrix shows the geographic distance between populations [Eugenópolis (EG), São Gonçalo (SG), Bom Jesus (BJ)], and the provenance and progeny test (PPT).

of mother trees, phytosanitary, the absence of attacks by pests and disease, a minimum distance of 100 m between trees, and good fruit production were taken into consideration. To assess families' performance, seeds collected from the 45 trees were evaluated at four developmental stages: plantlets at 15 days after germination (Test I); seedlings at six months of age (Test II); and juveniles at 34 and 60 months of age in the field (Test III).

The experimental design used in Test I, conducted in the laboratory, was completely randomized, with 45 treatments (families) and four replicates of 25 seeds each, for a total of 100 seeds per treatment. The germination test followed the recommendations for the species (Silva et al. 2017). In this test, the following traits were analyzed: germination percentage (GERP, %); index of germination speed (IGSP); mean germination time (MGTP, days); total length (TLP, cm plantlet^{-1}); total dry mass (TDMP, mm plantlet^{-1}); and plantlet vigor (VIGP). With the exception of total dry mass of plantlets, all traits were calculated using the statistical package *SeedCal* (Silva et al. 2019).

Test II was conducted in the nursery, based on a randomized block design, with 45 treatments (families), 20 blocks, and three plants per plot. The test was carried out in a greenhouse. Seeds were sown in 100 cm³ tubes, filled with commercial substrate Carolina II, and the fertilizer used for nutrition was Osmocote 18:5:9, at dose of 225 g for 8 kg of substrate. Until complete emergence, the seedlings were watered three times a day. After ten days of stabilization post emergence, watering was reduced to twice a day, in the morning and in the evening. The traits evaluated in this test were: total height of aerial part of the plant (HEIS, cm); collar diameter (CDS, mm); number of leaves (NLS); ratio of total height to collar diameter (RHCDS); dry mass of the aerial part of the plant (DMAPS, seedling g^{-1}); dry mass of root system (DMRSS, seedling g^{-1}); total dry mass (TDMS, seedling g^{-1}); ratio of height of aerial part to dry mass of aerial part (HDMAPS); Dickson quality index (DQIS) (Dickson et al. 1960); and survival (SURS).

For Test III, progeny testing in the field, seedlings were produced as detailed in Test II and taken to the field at six months of age. The test was established in February 2017, in the Alvorada do Gurgueia Experimental Farm, Federal University of Piauí, located in the city of Alvorada do Gurgueia, southwestern Piauí (lat 8° 22' 23.34" S, long 43°51' 24.31" W, alt 281 m asl; Figure 1). The test was established with a randomized block design, with 20 blocks, 45 treatments (families), and one plant per plot, for a total of 900 plants. The climate of the region is semi-arid hot, classified as BSh based on the Köppen-Geiger climatic classification (Köppen and Geiger 1928). The average precipitation between the year of installation (2017) and evaluation (2019) ranged from 960 to 1057 mm year^{-1}, with rainfall in the months of October through May. The average minimum and maximum temperatures were 21.5 and 34.2 °C, respectively (INMET 2020). The traits evaluated were total height (HEIF, m), diameter at ground level (DGLF, mm), and survival (SURF, %).

For each test, the restricted maximum likelihood/best linear unbiased predictor (REML/BLUP) method in the software SELEGEN (Resende 2016) was used to estimate the following components of variances and genetic parameters: genetic additive variance (σ_a^2); residual variance (σ_e^2); phenotypic variance (σ_f^2); individual narrow-sense heritability ($h_a^2 = \frac{\sigma_a^2}{\sigma_f^2}$); heritability within families ($h_w^2 = \frac{0.75\sigma_a^2}{\sigma_e^2}$) and average of all families ($h_m^2 = \frac{0.25\sigma_a^2}{0.25\sigma_a^2 + \sigma_e^2/r}$); selection accuracy at the individual level ($Ac_{(h_a^2)} = \sqrt{h_a^2}$) and as an average of all families ($Ac_{(h_m^2)} = \sqrt{h_m^2}$); coefficient of individual additive genetic variation ($CV_{gi} = \frac{\sqrt{\sigma_a^2}}{m} \cdot 100$); coefficient of genotypic variation between families ($CV_{gp} = \frac{\sqrt{0.25\sigma_e^2}}{m} \cdot 100$); residual variation ($CV_e = \frac{\sqrt{\sigma_e^2}}{m} \cdot 100$); and relative variation ($\hat{b} = \frac{CV_{gp}}{CV_e}$). When observing a non-significant effect by the likelihood-ratio test (LRT) for populations, the analyses were performed considering the populations as one. The statistical models, $y = Za + e$, $y = Xr + Za + Wp + e$ and $y = Xr + Za + e$ were used to obtain estimates of variance components and genetic parameters of the evaluated traits for Test I, Test II and Test III, respectively. *X*, *Z*, and *W* incidence matrices. *y*, *r*, *a*, *p*, and *e* are vectors of observations, fixed effects, random additive effects, random plot effect, and random errors, respectively.

Characterization and phenotypic divergence between the families were checked with principal component analysis (PCA), using the *Factorextra* statistical package in the R software environment (Kassambara and Mundt 2020). Pearson's correlation coefficients were estimated between the genetic parameters of the 21 morphophysiological traits and genetic correlations between traits based on the predicted genetic values (BLUP) of the 45 evaluated families, with significance determined by the *t* test at 5% probability level. The *corrplot* package was used for these analyses (Wei and Simko 2017).

For each Test, a "key trait" was defined, with the ranking for this trait used in the subsequent stage of the study. The

criteria considered to select the key trait were the highest values of heritability and accuracy, positive genetic correlations, measurements that are quick and easy to obtain, and a low probability of error. With the ranking of the best families for the defined key trait at each development stage, and disregarding the effect of chance, the percentage of coincidence among the rankings was assessed when selecting 25, 50, and 75% of the best families.

In addition, to assess the genetic representativeness of *P. platycephala* families in Tests II and III, the effective population size (N_e) was estimated for the total population. We used the formula proposed by Resende and Bertolucci (1995): $N_e = \dfrac{(4N_f k_f)}{k_f + 3 + (\frac{\sigma^2_{kf}}{k_f})}$; where, k_f is the average number of individuals selected per family; σ^2_{kf} is the variance of the number of individuals selected per family; and N_f is the number of families selected. After the identification of inferior families, a new estimate of N_e was performed using only the superior families. The aim was to determine the extent of the impact on N_e if the inferior families were discarded, based on the set of analyses performed at the juvenile stage. The inbreeding coefficient was also calculated based on N_e, as: $F = \dfrac{1}{2N_e}$ (Resende 2007).

RESULTS AND DISCUSSION

There were no genetic differences between populations of *P. platycephala*, as found in the previous study by Morais et al. (2022). The recent study, analyzed by nucleotide polymorphism loci, found that most of the diversity (99.06%) was distributed within populations; so, according to the genetic structure, the two populations could be considered a single population (Morais et al. 2022). No differences between populations of *P. platycephala* could be explained, in that case the gene flow was effective to prevent divergences. Another point is that the arboreal areas analyzed are considerably similar in terms of landscape and climatic characteristics and are geographically close. These characteristics, combined with the reproductive and ecological aspects of the species, contribute to the observed genetic uniformity between the populations (Chung et al. 2020, Vieira et al. 2022). In agreement with these results, the next analysis considered the populations as one.

The *P. platycephala* families showed phenotypic variation for seed and plantlet vigor, seedling quality, and initial growth at 34 and 60 months in the field. Except for the ratio of height to dry mass of the aerial part (HDMAPS), ratio of height to collar diameter (RHCDS), and mean germination time (MGTP), the other traits showed positive interrelationships among them. In Figure 2, the closer the arrows are in the Cartesian plane, the more correlated the traits are. Therefore, we can see that the families that had plantlets with best vigor (VIGP) also showed high values for germination, index of germination speed (IGSP), and total plantlet length in Test I, and total height (HEIF) and diameter at ground level (DGLF) in Test III (Figure 2).

The phenotypic variation observed between families may indicate the possibility of identifying important morphophysiological traits (Lustri et al. 2021). Families 20, 22, 23, 27, 29, and 30 had low phenotypic mean values for the 21 evaluated traits and appear more to the left of the graph. When compared to the other families, they are the
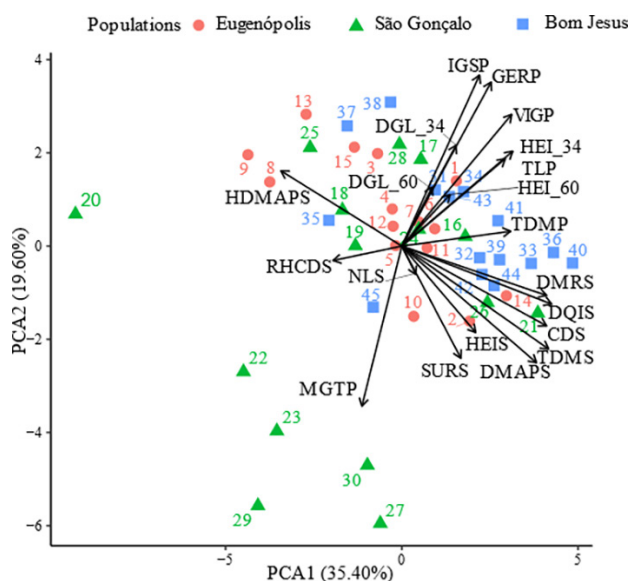

Figure 2. Phenotypic characterization and graphic dispersion of 45 *Parkia platycephala* Benth. families based on 21 morphophysiological traits evaluated at the plantlet stage at 15 days (suffix P), seedling stage at six months (suffix S), and juveniles at 34 and 60 months in the field (suffix F_34 and suffix F_60, respectively). [GERP (%) - percentage of germination; IGSP – index of germination speed; MGTP (days) – mean germination time; TLP (cm plantlet^{-1}) – total length; TDMP (mm plantlet^{-1}) – total dry mass of plantlet; VIGP – plantlet vigor; HEIS (cm) – total height of the aerial part of the seedling; CDS (mm) – collar diameter; NLS – number of leaves; RHCDS – ratio of total height to collar diameter; DMAPS (g seedling^{-1}) – dry mass of the aerial part; DMRSS (g seedling^{-1}) – dry mass of the root system; TDMS (g seedling^{-1}) – total dry mass; HDMAPS – ratio of height to dry mass of the aerial part; DQI – Dickson quality index; SURS – survival at the seedling stage; HEIF (m) – total plant height; DGLF (cm) – diameter at ground level; SURF– families survival in the field].

Table 1. Estimates of genetic parameters of 22 morphophysiological traits for 45 open-pollinated families of *Parkia platycephala* Benth. evaluated at four stages of development, plantlets at 15 days (in a laboratory environment, suffix P), seedlings at six months (in a nursery environment, suffix S), and young plants at 34 and 60 months in a progeny test

E*	Traits	h^2_a	h^2_m	h^2_w	$AC_{(h^2_a)}$	$AC_{(h^2_m)}$	CV_{gi}	CV_{gp}	CV_e	$\hat{b}$	$\bar{x}$
Laboratory	GERP	0.78	0.91	0.89	0.88	0.96	21.76	10.88	6.69	1.63	93.58
	IGSP	0.90	0.94	0.92	0.95	0.97	29.95	14.98	7.76	1.93	5.75
	MGTP	0.91	0.91	0.89	0.96	0.96	11.37	5.68	3.49	1.63	4.17
	TLP	0.73	0.89	0.86	0.86	0.94	18.65	9.32	6.63	1.41	11.73
	TDMP	0.96	0.97	0.96	0.98	0.98	34.09	17.05	6.04	2.82	34.45
	VIGP	0.57	0.97	0.96	0.76	0.98	24.06	12.03	4.29	2.80	666.6
Nursery	HEIS	0.27	0.72	0.32	0.52	0.85	10.27	5.14	14.22	0.36	26.57
	CDS	0.51	0.87	0.52	0.72	0.93	11.33	5.67	9.76	0.58	5.72
	NLS	0.39	0.85	0.35	0.62	0.92	9.01	4.50	8.57	0.53	8.44
	DMAPS	0.48	0.85	0.55	0.70	0.92	18.99	9.50	18.13	0.52	4.46
	DMRS	0.46	0.85	0.50	0.68	0.92	29.09	14.55	27.72	0.52	1.28
	RHCDS	0.24	0.73	0.25	0.49	0.86	11.26	5.63	15.24	0.37	4.75
	HDMAPS	0.29	0.79	0.27	0.54	0.89	21.83	10.92	25.05	0.44	6.46
	TDMS	0.50	0.85	0.58	0.71	0.92	19.78	9.89	18.63	0.53	5.75
	DQIS	0.44	0.84	0.47	0.67	0.92	27.11	13.55	26.34	0.51	0.72
Field	HEIF_34	0.11	0.37	0.09	0.34	0.61	6.77	3.39	19.80	0.17	3.04
	DGLF_34	0.20	0.51	0.16	0.45	0.71	9.78	4.89	21.39	0.23	63.52
	SURF_34	0.19	0.50	0.15	0.43	0.70	31.59	15.79	71.34	0.22	0.64
	HEIF_60	0.10	0.21	0.08	0.32	0.46	4.58	2.29	13.98	0.16	4.76
	DGLF_60	0.14	0.26	0.11	0.37	0.51	7.84	3.92	20.69	0.19	11.80
	SURF_60	0.11	0.22	0.08	0.33	0.47	24.65	12.32	73.62	0.17	0.63

* Environment; Individual narrow-sense heritability (h^2_a); Heritability of family means (h^2_m); Within-family heritability (h^2_w); selection accuracy at the individual level ($AC_{(h^2_a)}$) and as an average of all families ($AC_{(h^2_m)}$); Coefficient of individual additive genetic variation (CV_{gi}); Coefficient of genotypic variation between families (CV_{gp}); coefficient of environmental variation (CV_e); coefficient of relative variation ($\hat{b}$); mean ($\bar{x}$). [GERP (%) - percentage of germination; IGSP – index of germination speed; MGTP (days) – mean germination time; TLP (cm plantlet⁻¹) – total length; TDMP (mm plantlet⁻¹) – total dry mass of plantlet; VIGP – plantlet vigor; HEIS (cm) – total height of the aerial part of the seedling; CDS (mm) – collar diameter; NLS – number of leaves; RHCDS – ratio of total height to collar diameter; DMAPS (g seedling⁻¹) – dry mass of the aerial part; DMRSS (g seedling⁻¹) – dry mass of the root system; TDMS (g seedling⁻¹) – total dry mass; HDMAPS – ratio of height to dry mass of the aerial part; DQI – Dickson quality index; SURS – survival at the seedling stage; HEIF (m) – total plant height; DGLF (cm) – diameter at ground level; SURF– families survival in the field].

most divergent and phenotypically inferior. Therefore, they are not recommended, as they did not show satisfactory results for the physiological quality of seeds, plantlet vigor, seedling quality, and growth traits in the field.

The estimates of genetic parameters of the progeny tests show that there is genetic control of the analyzed traits, genetic variability between *P. platycephala* families, and the possibility of obtaining genetic gains by selecting families with superior performance (Table 1).

The greater the environmental influence in the tests (CV_e), the lower the genetic values observed (h^2_a, h^2_w, h^2_m and $\hat{b}$) (Table 1), which is consistent with results obtained in studies on other forest species (Menegatti et al. 2016, Kampa et al. 2020, Corrêa et al. 2021, Garuzzo et al. 2021). As noted, these estimates may vary according to populations, environments, traits, nature of the traits, age, and estimation methods used (Pires et al. 2011). Until the plant reaches a complete development and balance in the field, greater or lesser environmental influence can occur on the expressiveness of the growth characteristics (Ettori et al. 2006).

Among the genetic parameters evaluated, the coefficients of genetic variation (CV_{gi} and CV_{gp}) and accuracy ($AC_{h^2_a}$ and $AC_{h^2_m}$) showed the lowest amplitude of variation (Table 1). These results are interesting for what this study proposes; regardless of the environmental conditions under which the progeny tests were installed and the evaluated stage of development, the coefficients of genetic variation showed that there is genetic variability. Thus, there is potential to obtain genetic gains and increase the level of improvement of the test by selecting superior families and individuals (Pires et al. 2011). The good values for accuracy, which ranged from 0.46 (Test III) to 0.98 (Test I), demonstrate the

correlation between the observed and predicted genotypic value, a key parameter that is indispensable in this type of study (Henderson 1984).

In Table 1, we can also see that the lowest estimates of genetic parameters were identified in the traits evaluated at the juvenile stages (34 and 60 months). This result is understandable, as the tests were carried out under completely contrasting environmental conditions. Germination tests were carried out under controlled laboratory conditions, where the influence of the environment on the phenotypic value is very low (Table 1), and consequently there is a greater expressiveness of the genetic value. In contrast, the environmental influence is high among tests carried out in the field and is even more intense in the initial years of plant establishment (Resende 2015).

Positive, but weak, genetic correlations between traits considering different developmental stages were observed (Figure 3). The highest values of genetic correlations obtained were related to total plant height (HEIF) and diameter at ground level (DGLF) with seedling vigor (0.46 and 0.25, respectively) and seedling collar diameter (0.41 and 0.24, respectively) (Figure 3). Obtaining a positive genetic correlation between morphophysiological traits of plantlets, seedlings at six months, and juveniles at 34 and 60 months is an interesting and promising result. Thus, we can infer that there
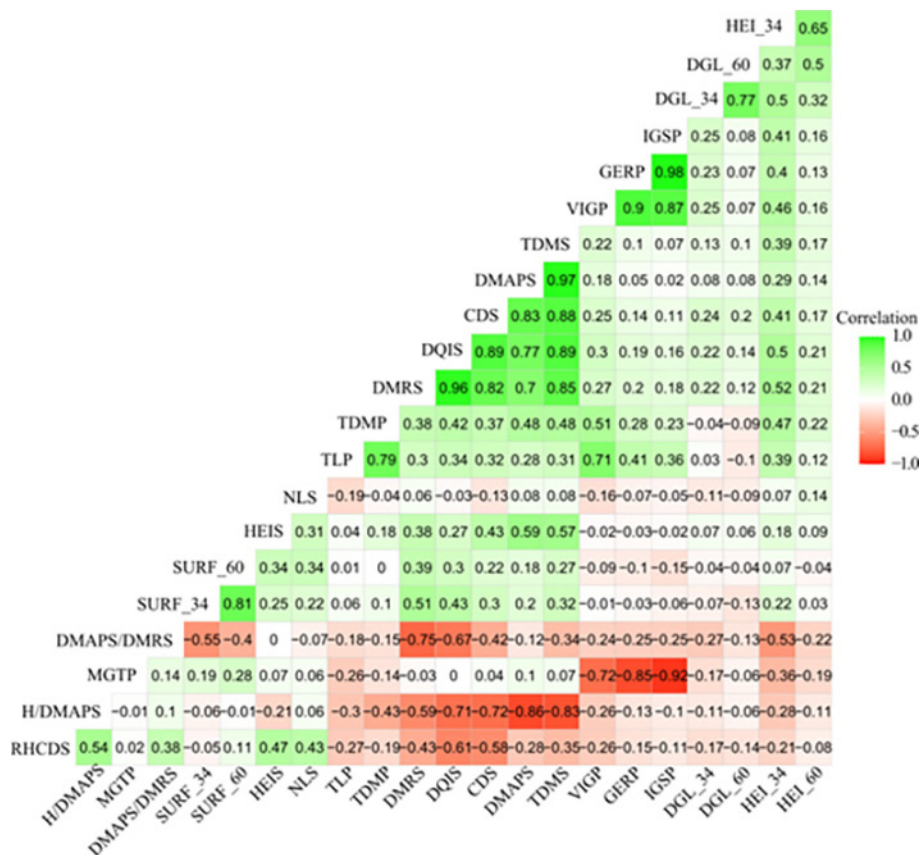

Figure 3. Correlation between predicted genetic values (BLUPs) of 21 morphophysiological traits of open-pollinated *Parkia platycephala* Benth families evaluated at the plantlet stage at 15 days (suffix P), seedlings at six months (suffix S), and juveniles at 34 and 60 months in the field (suffix F_34 and F_64, respectively). Significance via *t* test at 5% probability level. Green corresponds to a positive correlation, and red to negative, with more intense colors indicating greater magnitude of correlation. [GERP (%) – percentage of germination; IGSP – index of germination speed; MGTP (days) – mean germination time; TLP (cm plantlet^{-1}) – total length; TDMP (mm plantlet^{-1}) – total dry mass of plantlet; VIGP – plantlet vigor; HEIS (cm) – total height of aerial part of the seedling; CDS (mm) – collar diameter; NLS – number of leaves; RHCDS– ratio of total height to collar diameter; DMAPS (g seedling^{-1}) – dry mass of the aerial part; DMRSS (g seedling^{-1}) – dry mass of the root system; TDMS (g seedling^{-1}) – total dry mass; HDMAPS – ratio of height of aerial part to dry mass of aerial part; DQIS – Dickson quality index; SURS – survival at the seedling stage; HEIF (m) – total plant height; DGLF (cm) – diameter at ground level; SURF – progenies survival in the field].

is a possibility to proceed with strategies of pre-selection of families that show best performance at juvenile stages.

To pre-select plants and identify genetic materials with great genetic quality when they are still young, it is essential to determine whether families' performance is consistent across each test and developmental stage. For this analysis, and following the established criteria, the coincidence index was determined based on the ranking of the families considering plantlet vigor (VIGP), collar diameter (CDS), total height (HEIF), and diameter at ground level (DGLF) at 34 and 60 months. These traits showed high levels of genetic control, good accuracy, and with the exception of height are easy to measure with a low probability of error. The percentage of coincidence between the rankings of the best families was more consistent when the selection intensity applied was greater than 50% (Table 2).

When selecting 25, 50, and 75% of *P. platycephala* families with the best predicted genetic values, at least one (PC =25%) and at most 25 (PC =75%) families were consistent across the six rankings (Table 2). The percentage of coincidence found by selecting 25, 50, and 75% of the best families in only two test environments were: laboratory and nursery 25, 56.5, and 79.4%; laboratory and field 8.3 to 33.3, 52.2 to 69.6, and 79.4 to 85.3%; nursery and field 33.3 to 41.7, 47.8 to 65.2 and 79.4 to 85.3%; and field and field 75, 82.6 and 82.3%, respectively. When selecting 50 to 75% of the families that perform best for morphophysiological traits of plantlets, seedlings, and juvenile plants in the field, the percentage of coincidence reached up to 85% between rankings.

The results indicate that the traits evaluated herein have high genetic control (Table 1), and despite the contrasting environmental conditions of the tests, no substantial diversions were observed in families ranking. That is, the *P. platycephala* families that showed the best performance in the laboratory, also stood out in the tests carried out at more advanced stages, as seedlings in the nursery and young plants in the field.

Families 1, 2, 4, 14, 16, 17, 21, 24, 26, 31, 32, 33, 34, 36, 38, 39, 40, and 41 coincided in the rankings, as they had plantlets with good vigor and high values for diameter and total height. Coincidentally, and consistent with the phenotypic characterization, six families (20, 22, 23, 27, 29, and 30) did not show satisfactory genotypic values for the evaluated traits. The families that stood out are excellent candidates for pre-selection, as they performed well from the plantlet stage and show a coincidence across rankings of 61% (Table 2). The efficiency of a genetic improvement program can be expressed by the genetic gain over time (Lustri et al. 2021); therefore, the selection of potential mother trees should be based on well characterized families with positive genetic gains (Garuzzo et al. 2021).

Considering the estimates of effective population size (*Ne*) and inbreeding coefficient (*F*), we observed significant genetic representativeness in the progeny tests installed in the nursery and field (*Ne*=171 and 140, respectively), and an inbreeding coefficient ranging from 0.004 to 0.003. To determine the impact of discarding the poorly performing families (20, 22, 23, 27, 29, and 30) at the seedling and/or nursery stage on the genetic representativeness of the population in Test III, the *Ne* was estimated only for the 39 families with the best performance at all studied stages. We found an average reduction of 12.66% for *Ne* and the inbreeding coefficient (*F*) went from 0.003 to 0.004.

Low values for the inbreeding coefficient in the base population are fundamental to avoid the loss of alleles via genetic drift (Nogueira et al. 2019). Based on the evaluated traits, pre-selection in the juvenile stage for *P. platycephala*

Table 2. Percentage of coincidence (PC) between the ranking of the "key traits" plantlet vigor and seedling collar diameter, with the total height (HEI) and diameter at ground level (DGL) of *Parkia platycephala* Benth. families at 34 and 60 months, when selecting 25, 50, and 75% of the 45 families with the best performance

Test environment	Selection intensity (%)											
	25				50				75			
	34 months		60 months		34 months		60 months		34 months		60 months	
	HEI	DGL	HEI	DGL	HEI	DGL	HEI	DGL	HEI	DGL	HEI	DGL
Laboratory-Nursery-Field	16.67	8.33	0.00	8.33	43.48	30.43	39.13	34.78	73.53	61.76	67.65	61.76
Laboratory - Nursery	25.00				56.52				79.41			
Laboratory - Field	33.33	33.33	8.33	33.33	69.57	52.17	56.52	52.17	85.29	79.41	79.41	76.47
Field - Nursery	41.67	33.33	33.33	41,67	56.52	47.83	65.22	56.52	85.29	82.35	82.35	79.41
Field- Field	75.00				82.60				82.35			

proved to be effective in identifying superior families. Therefore, we believe that the aforementioned study will serve as a basis for conducting new research, either with the species under study or with other species, so that we can contribute to the advancement of genetic improvement of native forest species, which are still far behind when compared to species of the genera Eucalyptus and Pinus, which together total about 9.46 million hectares of planted area in Brazil (IBÁ 2022). In addition, the analysis in juvenile stages of families through germination tests can be an effective tool to be implemented by inspection agencies for the preliminary genetic evaluation of seeds before their selection and use, since the germination tests are fast, efficient and low cost.

CONCLUSIONS

Estimates of correlations between phenotypic and predicted genetic values are effective in identifying *P. platycephala* families that consistently perform well between the plantlet, seedling, and juvenile development stages.

Evaluating genetic materials during the early stages of development is a viable alternative that should be explored in future studies, as there is high probability of matching the performance of genotypes at the juvenile and later development stages. In addition, the analysis of phenotypic and genetic characterization in juvenile stages can provide some useful information about the exploration and identification of genetic resources, as well as ensuring the use of seeds of forest species with high genetic quality, reducing costs and optimizing time across selection cycles in genetic improvement programs of native species with limited or no improvement.

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