BRAZILIAN
JOURNAL OF
BIOLOGY®

ISSN 1519-6984 (Print)
ISSN 1678-4375 (Online)

Original Article

Genetic diversity of *Peltophorum dubium* (Spreng.) Taub. progenies from the states of Minas Gerais and Mato Grosso do Sul, Brazil

Diversidade genética de progênies de *Peltophorum dubium* (Spreng.) Taub. procedentes de Minas Gerais e Mato Grosso do Sul, Brasil

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Abstract

There is little information regarding the genetic diversity of native species aimed at identifying the best viable progenies for *in situ* and *ex situ* conservation. Furthermore, there is a lack of future forest improvement programs. We aimed to know the genetic diversity of 64 *Peltophorum dubium* (Spreng.) Taub. (Fabaceae) progenies. We determined this species' dendrometric characteristics, and when using multivariate techniques and cluster analysis, we verified the differences between the progenies and groups with less heterogeneity. The progeny and provenance test was installed in Dourados (Mato Grosso do Sul - MS), with seeds collected in three MS regions (Vale do Ivinhema, Serra de Maracaju, and Serra da Bodoquena) and in the micro-region of Lavras (Minas Gerais - MG). The experiment was conducted in an alpha lattice 8 x 8 with four repetitions. We found genetic variability among and within *P. dubium* populations for all height, diameter, circumference at breast height, volume, and basal area characters. We suggest that *P. dubium* populations have high genetic variability, which indicates possible genetic improvement through best progeny selection. The UPGMA and Tocher methods grouped the progenies into three and nine groups, respectively, in which the most divergent individuals come from MG and the Bonito region in MS. Based on morphological characters, *P. dubium* progenies identified as 45, 47, 49, 50, 55, and 59 from MG are the most promising, while progenies 6 and 9 were the least promising.

Keywords: clustering, dendrometric traits, progeny testing, UPGMA.

Resumo

Informações quanto à diversidade genética de espécies nativas visando identificar melhores progênies viáveis para conservação *in situ* e *ex situ*, além de futuros programas de melhoramento florestal são incipientes. Objetivamos conhecer a diversidade genética de 64 progênies de *Peltophorum dubium* (Spreng.) Taub. (Fabaceae). Determinamos os caracteres dendrométricos dessa espécie, e ao utilizarmos técnicas multivariadas e análises de agrupamento verificamos as diferenças entre as progênies e grupos de menor heterogeneidade. O teste de progênies e procedências foi instalado em Dourados (MS), cujas sementes foram coletadas em três regiões de MS (Vale do Ivinhema, Serra de Maracaju e Serra da Bodoquena) e na microrregião de Lavras-MG. O experimento foi conduzido em alfa-látice 8 x 8, com quatro repetições. Constatamos variabilidade genética entre e dentro das populações de *P. dubium* para todos os caracteres altura, diâmetro, circunferência à altura do peito, volume e área basal. Sugerimos que as populações de *P. dubium* tem alta variabilidade genética, o que indicou possibilidade de melhoramento genético pela seleção das melhores progênies. Os métodos UPGMA e Tocher agruparam as progênies em três e nove grupos, respectivamente, em que os indivíduos mais divergentes são procedentes de MG e da região de Bonito em MS. As progênies de *P. dubium* de identificação 45, 47, 49, 50, 55 e 59, todas de MG, são as mais promissoras, enquanto que as progênies 6 e 9, foram as menos promissoras, baseando-se nos caracteres morfológicos.

Palavras-chave: agrupamento, caracteres dendrométricos, testes de progênies, UPGMA.

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Received: February 5, 2022 – Accepted: June 9, 2022

Introduction

A species' diversity involves morphological and genetic variation among individuals in the same population and also among spatially separated populations (Scariot, 2011; Barros et al., 2018). Several anthropogenic practices on natural resources have caused a decrease in the floristic diversity of natural populations in different phytophysiognomies of the most varied biomes. In this context, phenotypic and genotypic studies among and within populations for different characters are the most appropriate ways to determine the genetic structure of a species to conserve populations (Silva et al., 2019). Furthermore, they contribute to breeding or seed production programs, with a broad genetic basis for environmental restoration (Rebrean et al., 2019; Moraes et al., 2020), improving *in situ* and *ex situ* conservation strategies.

However, for many native tree species, such as *Peltophorum dubium* (Spreng.) Taub. (Fabaceae), popularly known as '*canafístula*', genetic information is insufficient, which makes it essential to improve diversity studies on its progenies. The species is found in the phytogeographic domains of Cerrado, Caatinga, Atlantic Forest, and Pantanal in the Northeast, Midwest, Southeast, and South regions (Silva et al., 2020).

Peltophorum dubium reaches between 15-25 m in height, and has medicinal and silvicultural potential (Lorenzi, 1992; Bertolini et al., 2015; Ciaccio et al., 2020). This legume can be used to restore degraded areas, enrich native forests, and in agroforestry systems due to its potential for biological nitrogen fixation (Carvalho et al., 2016; Caron et al., 2019).

Diversity characterization studies among and within natural populations assist in detecting genetic variability associated to environmental factors and different geographic areas (Canuto et al., 2015; Barros et al., 2018). In progeny tests under field conditions, different quantitative morphological characters are evaluated, and their variation indicates the species' adaptive mechanisms to different conditions, such as management, providing subsidies for forest conservation and improvement (Costa et al., 2020).

Cluster analyses are among the most widely used techniques in genetic divergence studies, and aim to separate high heterogeneity groups and bring together similar groups based on the evaluated characters (Alencar et al., 2013; Vaz et al., 2017). The Tocher optimization method has been widely used in tree species, such as *Copernicia prunifera* (Mill.) H.E. Moore (Silva et al., 2018), *Theobroma grandiflorum* (Willd. ex Spreng.) Schum. (Maia et al., 2011), and *Acrocomia aculeata* (Jacq.) Lodd. Mart. (Manfio et al., 2012). Therefore, progeny selection should be the main selection strategy, and crossings between superior progenies from different groups (Rodrigues et al., 2017).

Considering the species' ecological and economic potential, which makes it part of the Brazilian biodiversity heritage, besides the need for technical information, this study analyzed the genetic diversity of *P. dubium* progenies from different provenances in the states of Minas Gerais and Mato Grosso do Sul to support possible selections for conservation and future genetic improvement.

Material and Methods

The progeny testing experiment was carried out at the Experimental Farm of Agricultural Sciences - FAECA (22º14'08" S and 54º59'13" W, altitude 434 m), of the Universidade Federal da Grande Dourados - UFGD, at Rodovia Dourados/Itahum. The predominant soil is classified as Oxisol (Embrapa, 2018) and the climate is Cwa (temperate rainy with dry winter (Alvares et al., 2013), rainy summer, and average temperature of the coldest month below 18 ºC and the hottest month above 22 ºC) with a 22.7 °C average annual temperature and 1,410 mm rainfall.

In order to install the *P. dubium* progeny and provenance test, open-pollinated seeds were collected from 64 reproductive trees of populations from the states of Minas Gerais (MG) and Mato Grosso do Sul (MS) and located in two biomes (Atlantic Forest and Cerrado). In Mato Grosso do Sul, seeds were collected in June/2012 from populations in three regions in the state: 15 matrices in Vale do Ivinhema (Ivinhema, Angélica, and Deodápolis), 10 reproductive trees in Serra de Maracaju (Nioaque, Guia Lopes, and Maracaju), and 15 reproductive trees in Serra da Bodoquena (Bonito and Porto Murtinho). The municipalities of Ivinhema, Angélica, Deodápolis, and part of Bonito are inserted in the Atlantic Forest biome, while Guia Lopes da Laguna, Nioaque, Maracaju, and part of Bonito are in Cerrado areas (Imasul, 2019). The altitude range in these areas was from 250 to 660 m (Table 1).

In Minas Gerais, seeds were collected in March/2012 from 24 reproductive trees from the Atlantic Forest biome in the micro-region of Lavras, in the municipalities of Lavras, Nepomuceno, Itutinga, Ribeirão Vermelho, Nazareno, Candeias, and Perdões, where the altitude ranged from 850 to 964 m. The reproductive trees were selected based on characters of silvicultural importance, such as height, diameter at breast height, canopy condition, healthiness, spindle shape, and amount of available fruits/seeds. All of them were georeferenced (Table 1), distributed on highways, some isolated and others in grasslands.

The production of *P. dubium* seedlings was carried out in nursery conditions with 50% shade at the School of Agricultural Sciences of the Universidade Federal da Grande Dourados (UFGD), Dourados - MS. Therefore, fruits from the selected reproductive trees were manually harvested and packed in polyethylene bags, which were transported to the Laboratory of Seed Technology at UFGD. The seeds were manually processed and thermally scarified (Davide and Silva, 2008), and sown in 110 cm^3 capacity rigid plastic tubes (three seeds/recipient), with sprinkler irrigation at two daily watering rounds, where the seedlings were kept in tubes for 180 days after emergency until they reached an average height of 25 to 40 cm tall and 3 to 5 mm collar diameter (Terra et al., 2014).

In February 2013, we transplanted the seedlings in the Experimental Farm (FAECA) area at UFGD. We conducted base fertilization with the 06:30:06 fertilizer (110 g/plant divided into two lateral pits at 15 cm from the seedling) at 10 days after transplanting (DAT). Topdressing fertilization was done with 20:00:20 fertilizer + 0.5% B and 0.5% Zn (90 g/plant) at 180 DAT.

Table 1. Characteristics of the places of provenance of *Peltophorum dubium* (Spreng.) Taub. seeds, 2018-2019.

REPRODUCTIVE	GEOGRAPHICAL COORDENATES		ALTITUDE	LOCALIZATION	MEAN ANNUAL	MEAN
TREES					TEMPERATURE	PRECIPITATION
	Lat.	Long.	mm		(°C)	(mm)
1	21° 4’3.90”S	56°34’35.00”O	466	Bonito/MS	23.7	1363
2	21° 3’55.20”S	56°34’43.40”O	460	Bonito/MS	23.7	1363
3	21° 3’35.70”S	56°35’7.90”O	288	Bonito/MS	23.7	1363
4	21° 3’27.00”S	56°35’28.80”O	250	Bonito/MS	23.7	1363
5	21° 0’27.90”S	56°42’50.30”O	660	Bonito/MS	23.7	1363
6	21° 1’45.10”S	56°43’11.80”O	635	Bonito/MS	23.7	1363
7	21° 2’33.70”S	56°48’48.60”O	552	Bonito/MS	23.7	1363
8	21° 2’31.30”S	56°49’2.70”O	551	Bonito/MS	23.7	1363
9	21° 1’58.80”S	56°52’10.80”O	500	Porto Murtinho/MS	25.0	1282
10	21° 2’17.10”S	56°52’26.00”O	460	Porto Murtinho/MS	25.0	1282
11	21° 4’10.20”S	56°52’41.00”O	288	Porto Murtinho/MS	25.0	1282
12	21° 4’10.30”S	56°53’34.30”O	250	Porto Murtinho/MS	25.0	1282
13	21° 4’5.40”S	56°53’47.40”O	258	Porto Murtinho/MS	25.0	1282
14	21° 2’7.70”S	56°51’55.40”O	532	Porto Murtinho/MS	25.0	1282
15	21° 2’20.20”S	56°51’20.60”O	555	Bonito/MS	23.7	1363
16	21°27’47.76”S	55°47’33.72”O	410	Nioaque/MS	24.1	1391
17	21°27’49.02”S	55°47’36.06”O	418	Nioaque/MS	24.1	1391
18	21°29’9.54”S	55°48’55.74”O	484	Maracaju/MS	24.1	1391
19	21°29’9.42”S	55°50’37.98”O	418	Nioaque/MS	24.1	1391
20	21°28’40.14”S	55°51’12.84”O	397	Nioaque/MS	24.1	1391
21	21°28’31.92”S	55°52’2.28”O	368	Guia Lopes/MS	23.8	1372
22	21°27’45.78”S	55°53’41.22”O	353	Guia Lopes/MS	23.8	1372
23	21°28’29.04”S	55°52’13.02”O	367	Guia Lopes/MS	23.8	1372
24	21°29’10.26”S	55°52’14.46”O	417	Guia Lopes/MS	23.8	1372
25	22°17’33.72”S	53°48’22.92”O	332	Ivinhema/MS	23.0	1534
26	22°12’9.12”S	53°46’12.66”O	341	Angélica/MS	23.1	1501
27	22°10’32.76”S	53°46’10.20”O	363	Angélica/MS	23.1	1501
28	22°10’3.06”S	53°46’35.10”O	373	Angélica/MS	23.1	1501
29	22° 8’29.40”S	53°46’5.82”O	342	Angélica/MS	23.1	1501
30	22° 9’6.60”S	53°46’3.24”O	349	Ivinhema/MS	23.0	1534
31	22°15’15.84”S	53°48’23.88”O	291	Ivinhema/MS	23.0	1534
32	22°16’24.36”S	53°49’4.62”O	334	Ivinhema/MS	23.0	1534
33	22°19’15.42”S	53°47’34.08”O	372	Ivinhema/MS	23.0	1534
34	22°19’16.74”S	53°47’26.28”O	369	Ivinhema/MS	23.0	1534
35	22°19’21.90”S	53°47’13.14”O	399	Ivinhema/MS	23.0	1534

Table 1. Continued...

REPRODUCTIVE	GEOGRAPHICAL COORDENATES		ALTITUDE	LOCALIZATION	MEAN ANNUAL	MEAN
TREES					TEMPERATURE	PRECIPITATION
36	22°21'2.10"S	53°43'16.74"O	395	Ivinhema/MS	23.0	1534
37	22°19'35.52"S	53°46'9.12"O	430	Ivinhema/MS	23.0	1534
38	22°16'33.36"S	54° 9'6.96"O	416	Ivinhema/MS	23.0	1534
39	21°27'7.92"S	55°53'18.66"O	363	Guia Lopes/MS	24.1	1391
40	22°15'32.82"S	53°48'30.84"O	292	Ivinhema/MS	23.0	1534
41	21°13'12.35"S	45°13'49.44"O	873	Nepomuceno/MG	20.6	1357
42	21°13'56.49"S	45°13'44.10"O	851	Nepomuceno/MG	20.6	1357
43	21°11'48.20"S	45° 2'13.57"O	798	Lavras/MG	19.9	1486
44	21°13'46.12"S	44°59'33.32"O	850	Lavras/MG	19.9	1486
45	21°13'56.53"S	44°59'32.45"O	854	Lavras/MG	19.9	1486
46	21°19'25.26"S	44°36'56.08"O	900	Itutinga/MG	19.6	1593
47	21°19'21.23"S	44°36'53.97"O	896	Itutinga/MG	19.6	1593
48	21°13'38.51"S	44°58'45.76"O	924	Lavras/MG	19.9	1486
49	21°13'38.25"S	44°58'47.46"O	925	Lavras/MG	19.9	1486
50	21°16'18.37"S	44°58'18.88"O	929	Lavras/MG	19.9	1486
51	21°19'9.69"S	44°36'57.09"O	915	Itutinga/MG	19.6	1593
52	21°19'9.01"S	44°36'58.21"O	907	Itutinga/MG	19.6	1593
53	21°19'9.67"S	44°37'5.81"O	932	Itutinga/MG	19.6	1593
54	21°17'50.61"S	44°37'11.15"O	929	Itutinga/MG	19.6	1593
55	21°17'50.88"S	44°37'13.71"O	912	Itutinga/MG	19.6	1593
56	21°16'39.34"S	44°36'27.36"O	956	Nazareno/MG	24.5	1551
57	21°16'36.91"S	44°36'27.71"O	964	Nazareno/MG	24.5	1551
58	20°50'7.21"S	45°17'19.73"O	947	Candeias/MG	19.9	1475
59	21° 7'0.80"S	45° 5'39.03"O	856	Perdões/MG	20.4	1455
60	21° 9'54.23"S	45° 7'24.29"O	796	Ribeirão Vermelho/MG	20.7	1405
61	21°12'27.76"S	45° 0'12.49"O	913	Lavras/MG	19.9	1486
62	21°16'16.20"S	44°58'20.82"O	929	Lavras/MG	19.9	1486
63	21°13'12.67"S	45°13'50.69"O	883	Nazareno/MG	24.5	1551
64	21°13'12.67"S	45°13'50.69"O	887	Nazareno/MG	24.5	1551

The experiment was conducted in an alpha lattice 8 x 8 design with four repetitions. The *P. dubium* seedlings were arranged in a 3.0 m x 2.0 m spacing, with 6 plants/plot, and the treatments comprised 64 *P. dubium* progenies distributed in 08 blocks with 8 plots/each and 4 repetitions (a total of 1,536 plants), occupying an area of approximately 9,300 m^2. The altitude on the plot is 390 m.

Dendrometric data, represented by plant height (PH, m), diameter at breast height (DBH, cm), circumference at breast height (CBH, cm), base area (BA, m^2/ha), and volume (VOL, m^3) were measured in August/2018 and June/2019, five and six years after planting, respectively.

The PH was measured with a Criterion RD 1000 dendrometer, measuring the length from the collar to the top of the tree. The DBH was measured at 1.30 m from the ground, using caliperd. When the plant presented bifurcations at 1.30 m height, the diameter of the circumferences of all branches was taken to obtain the average. The CBH was measured at 1.30 m from the ground using a diametric tape. Values for BA and VOL were calculated according to Poggiani et al. (1996) and Couto et al. (1989), respectively.

For the analysis of the progeny effect in several environments or locations, we used the statistical model as, $y = Xb + Zc + Pd + Mf + Tg + Wh + e$. Where y, b, c, d, f, g, and h correspond, respectively, to the vectors of each response variable, fixed effects (overall average of the experiment), year effects (random), provenance effects (random), progeny effects (random), progeny x provenance interaction effects (random), block effects (random), and random errors, and X, Z, P, M, T, and W correspond to the reproductive trees of incidence for b, c, d, f, g, and h, respectively.

Deviance analyses were performed using this model to investigate the significance of the factors in the model through the likelihood ratio test (LRT). Moreover, genetic parameters were estimated using restricted maximum likelihood (REML) and, for provenance, additive genetic values were estimated using best linear unbiased prediction (BLUP). The BLUPs were obtained by the composition of the random effects and the estimation of the general average for each response variable.

For the genetic diversity analyses, multivariate techniques were employed by grouping the progenies using the average linkage method among groups (UPGMA) and the hierarchical clustering optimization method proposed by Tocher (Cruz and Carneiro, 2006). We adopted the average Euclidean distance as a dissimilarity measure considering the degree of dependence among the variables studied. Principal component analysis was also performed followed by graphical dispersion of the genotypes. Statistical analyses were performed using the R *software* (R Development Core Team, 2020), with the assistance of the *lme4* (Bates et al., 2015), *ggplot2* (Wickham et al., 2016), *lmerTest* (Kuznetsova et al., 2016), and *NbClust* (Charrad et al., 2014) libraries.

Results

We observed significant progeny effect on all traits with the LRT test (LRT= 0.001). Regarding provenance, all characters were significant except PH (LRT= 0.6117) and BA (LRT= 0.03) (Table 2). The high LRT statistic value indicates a pronounced difference in the models' deviance, and that the evaluated component explains a significant portion of the observed variation. This statistic for the variance component associated with the random effect of Progeny was high, indicating the existence of genetic variability among the progenies.

We can infer the existence of differentiated performance of progenies from different locations for CBH (LRT= 0.001), DBH (LRT= 0.001), and VOL (LRT= 0.001) as a function of *P. dubium* provenances. However, for the Progeny x Year interaction, the non-significant effect ($p<0.001$) (PH: LRT= 1.0; CBH: LTR= 0.999; DBH: LTR= 0.999; BA: LTR= 1.0; VOL: LTR= 0.999) for the characters shows there was no change in the progeny rank over the evaluation years (2018 and 2019). Therefore, the selective accuracy values obtained for all the characters studied were below 0.50, suggesting a low accuracy value, except for PH, which was classified as moderate.

Considering that the BLUP estimates are the closest to the genotypic value, we used the individual BLUP for the superior progenies' *rank*. Figure 1 shows the performance of each progeny for each character evaluated as a function of random effects. We emphasize that the predicted values of each progeny (BLUPs) are obtained by adding their random effect to the overall average estimate (Table 2).

Progenies 57, 49, and 47 (MG) were among the progenies that showed superior performance for all the characters studied, followed by progenies 55 and 50 from MG and 1 from MS, which were superior in at least four characters. Regarding the progenies that showed inferior performance for all the characters studied, we can highlight 56, 52, and 42 (MG), and 17 and 6 (MS). Progenies 64 (MG), 23, and 9 (MS) showed inferior performance in at least four characters.

Table 2. Summary of deviance analysis of 64 *P. dubium* progenies evaluated in two years. Dourados/MS, 2018-2019.

Effects	H	CBH	DBH	BA	VOL
Replicate	1.8363	3.3479	3.5029	2.8351	5.0863
	(0.1754^{ns})	(0.0672^{ns})	(0.0612^{ns})	(0.0922^{ns})	(0.0241^{ns})
Block /Replicate	68.5198	25.2489	25.2295	18.0651	25.1834
	(<0.001**)	(<0.001**)	(<0.001**)	(<0.001**)	(<0.001**)
Provenance	0.2577	8.127	7.6634	4.5911	7.0878
	(0.611^{ns})	(0.004**)	(0.005**)	(0.03^{ns})	(0.0077**)
Progeny (P)	78.1402	56.6944	56.4816	41.5145	51.8023
	(<0.001**)	(<0.001**)	(<0.001**)	(<0.001**)	(<0.001**)
Year (Y)$^{+}$	0.0187	16.0497	16.5656	10.4457	9.8812
	(0.8912^{ns})	(<0.001**)	(<0.001**)	(0.001**)	(0.001**)
P x Y	1.82 x 10^{-12}	3.64 x 10^{-12}	1.09 x 10^{-11}	2.73 x 10^{-11}	9.09 x 10^{-12}
	(1.0^{ns})	(0.9999^{ns})	(0.9999^{ns})	(1.0000^{ns})	(0.9999^{ns})
Overall mean	7.8379	29.9967	9.5407	0.0077	0.0649
Accuracy	0.54	0.45	0.45	0.4	0.44

(value) Likelihood ratio tests (LRT). ^{ns} – not significant; **Significance of the LRT, with distribution with 1 degree of freedom for x^2. $^{+}$Mean square and significance by F test. Accuracy: Very High (AC: >0.90); High (AC: 0.70 - 0.90); Moderate (AC: 0.50 - 0.70); Low (AC: <0.50).

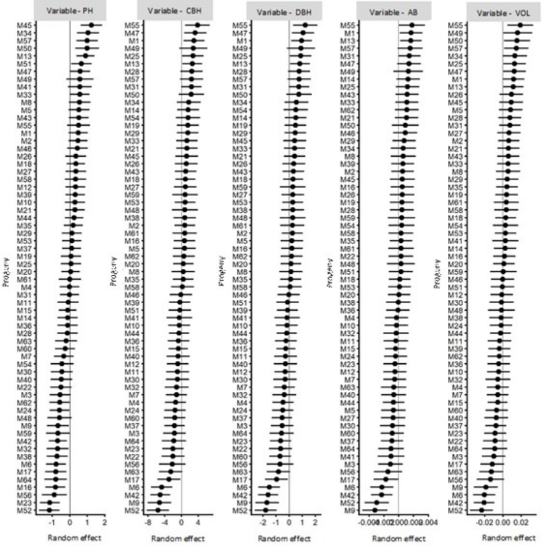

Figure 1. Caterpillar plots for random effects in *P. dubium* progenies for the traits plant height (PH), circumference at breast height (CBH), diameter at breast height (DBH), basal area (AB), and volume (VOL). Dourados/MS, 2018-2019.

In the dissimilarity dendrogram, three progeny groupings were suggested as a function of the analyzed characters (Figure 2). The group in blue included 53 individuals from different locations, representing 82% of the analyzed progenies, where 16 individuals are from MG and 37 from MS. The red group included five progenies of distinct provenance that showed low performance for the characters studied (Figure 1): progenies 6 from Bonito/MS, 9 from Porto Murtinho/MS, 17 from Nioaque/MS, and 42 and 52 from Lavras/MG. The green group included six progenies (45, 47, 49, 50, 55, and 57) from MG that stood out regarding silvicultural characters. Considering the 40 progenies studied from MS, only 3 progenies (6, 9, and 17) are not in the blue group. Among the groups formed, the most divergent were the red and green groups. While among the progenies, the greatest divergence occurred between 9 and 55.

The Cophenetic Correlation Coefficient (CCC) obtained was high (0.756), representing a good adjustment between the Cophenetic matrix and the dissimilarity matrix built based on the Euclidean distance, which indicates a high reliability.

The progenies showed high divergence as a function of the reproductive trees' provenance (MG and MS), with the green group representing reproductive trees from MG and the red group representing reproductive trees from MS (Figure 3). The reproductive trees from MG showed greater dispersion than the reproductive trees from MS. Among the MS progenies, we found that the most distant progenies were 9, 6, and 17, which showed inferior performance for the evaluated characters, while progeny 34 showed high performance. On the other hand, progenies 45, 57, 50, 47, 49, and 55 from MG showed the best performance.

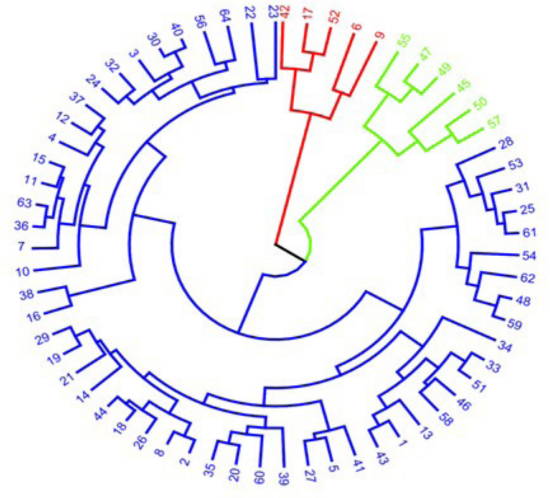

Figure 2. Dendrogram representing the genetic dissimilarity among the 64 *P. dubium* progenies, obtained by average linkage clustering method and using the Euclidean distance as a measure of dissimilarity. Cophenetic correlation coefficient (0.756). Dourados/MS, 2018-2019.

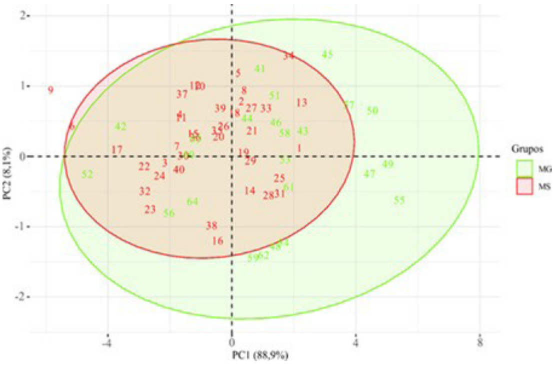

Figure 3. Scatter plot obtained through principal component analysis considering the provenance of the 64 *P. dubium* progenies. Dourados/MS, 2018-2019.

The graphical dispersion of the progenies as a function of the dendrometric characteristics formed three groups, with the greatest variability occurring among individuals in the blue group (Figure 4). The red group was formed by individuals from MG with the greatest performances for the analyzed characteristics. However, there was less variability within the group.

The Tocher clustering method allowed the progenies to be put into nine groups, of which three groups (I, II, and III) had a significant number of progenies (Table 3). Group III has the largest number of progenies, with 14 coming from MS and four from MG. Group I comprised a total of 17 progenies, 13 of which were from MS. Group II presents 12 progenies, five from MS and seven from MG. Group VII includes progenies that showed low performance for the characters studied (6 and 9), and group V included progenies 50, 57, 47, 49, and 55. Among the nine clusters obtained using Tocher, groups V and VII clustered exclusively progenies of the same provenance, MG and MS (Bonito and Porto Murtinho), respectively.

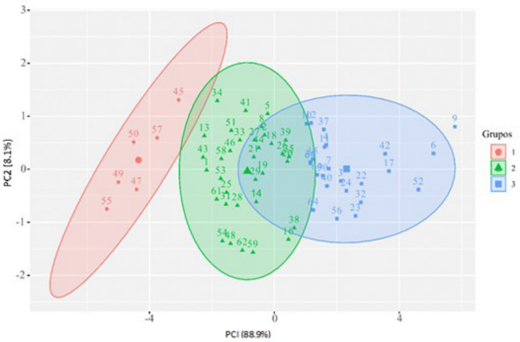

Figure 4. Scatter plot obtained through principal component analysis based on the evaluation of dendrometric traits of the 64 *P. dubium* progenies. Dourados/MS, 2018-2019.

Table 3. Grouping of 64 *P. dubium* progenies by Tocher's optimization method. Dourados/MS, 2018-2019.

Groups	Reproductive trees					
I	26	27	21	44	19	35
	33	29	14	51	41	20
	46	18	5	2	8	
II	31	61	28	25	62	53
	1	43	58	13	48	59
III	11	63	36	7	15	40
	30	32	12	39	64	60
	56	24	37	4	3	10
IV	16	38				
V	50	57	47	49	55	
VI	17	42	22	23	52	
VII	6	9				
VIII	34	45				
IX	54					

The greatest distance among groups was between groups V and VII (15.02) and the greatest similarity between groups I and IV (1.55) (Table 4). Within groups, the greatest genotype distance occurred within group VIII (2.01) and the least variability among individuals in group IV (0.22). Groups I and II also showed low variability among individuals (0.86).

Discussion

Considering the variability of PH, DBH, and CBH as a function of *P. dubium* progenies, we suggest using fewer progenies per reproductive tree and a larger number of collection sites to form populations for genetic improvement programs. Several genetic diversity studies among progenies of native tree species, such as *Cedrela fissilis* Vell. (Navroski et al., 2016), *Mimosa scabrella* Benth. (Menegatti et al., 2016), *Schinus terebinthifolia* Raddi. (Bertonha et al., 2016), and *Handroanthus vellosoi* (Toleto) Matos (Batista et al., 2012) have been conducted through provenance tests and between progenies with evaluation of dendrometric characters. The observed accuracy is important when there are significant differences between progenies for the characteristics under study, because in this case it is possible to obtain gains through selection (Senna et al., 2012).

In the progeny performance analysis, we verified the superiority of the progenies from MG, while the ones with the lowest performance were those from the Bonito region (MS). These results are in line with those observed by Terra et al. (2014) in a study conducted at the site at 16 months post-planting of the *P. dubium* progeny test. According to Silva et al. (2018), monitoring at adult plant stages in the field should be conducted since the sampled genotypes may be suitable for use in genetic improvement and ecological restoration programs if their genetic variability persists at adulthood.

In the progeny cluster analysis, the number of groups formed expresses the genetic variability observed among the genotypes, allowing us to state there is dissimilarity among genotypes from distinct provenances within the same group, and there is also dissimilarity among progenies of the same provenance for the characters studied. Overall, there was dissimilarity in most progenies, which showed

Table 4. Average distances inside (main diagonal) and between (outside the main diagonal) groups formed by 64 *P. dubium* progenies. Dourados/MS, 2018-2019.

z	I	II	III	IV	V	VI	VII	VIII	IX
I	0.86	2.30	2.99	1.55	5.97	5.68	9.07	2.42	4.10
II		0.86	5.07	2.82	3.95	7.76	11.20	1.81	1.97
III			1.14	2.58	8.88	2.81	6.19	5.27	6.84
IV				0.22	6.64	5.10	8.58	3.55	4.41
V					1.55	11.59	15.02	3.88	2.58
VI						1.27	3.51	7.98	9.50
VII							1.29	11.32	12.97
VIII								2.01	2.86

average performance for the characteristics analyzed, regardless of provenance. We also highlight the clustering of MG progenies, which showed high performance for the characters studied, and the low genetic diversity within the MS populations. According to Silva et al. (2020), *P. dubium* has wide geographic (Northeast, Midwest, Southeast, and South regions) and phytophysiognomic distributions in the Cerrado, Caatinga, Atlantic Forest, and Pantanal.

Progeny dispersion through the principal components validates the results obtained by the average linkage method. The large progeny overlap denotes the dissimilarity of most progenies for the characters studied, regardless of their provenance (MG and MS) and the progeny clustering into three groups as a function of the characters analyzed. Furthermore, the most genetically distant progenies, both in the grouping performed by the "Average linkage" method and through the principal components were 9 and 55, from MS and MG, respectively. Although reproductive trees from MS show a larger number of progenies and a larger range in latitude than MG for the populations studied, we observed less genetic variability among the progenies.

Clustering through the Tocher method also supports the existence of variability in the germplasm and divergence among the progenies. The Tocher method presents an average distance within groups, which is always smaller than the average distance between groups, so there is more homogeneity between accessions of the same group than between those of different groups (Vasconcelos et al., 2007; Vaz et al., 2017). We found nine groups, with emphasis on group V, which grouped progenies 50, 57, 47, 49, and 55, and group VI (progenies 6 and 9), reinforcing the previous analyses.

The Tocher method has been successfully used in clustering progenies of native species. Based on the genetic values of height, diameter, and survival of *C. prunifera* seedlings, Silva et al. (2018) grouped 97.5% of the progenies into a single group. Based on the genetic variability of the growth and leaf number characters, Manfio et al. (2012) separated *A. aculeata* progenies into two groups according to provenance (São Paulo and Minas Gerais).

Using the UPGMA and Tocher clustering methods, the 64 progenies were grouped into three and nine clusters, respectively. The separation into distinct groups is important for the genetic breeding of the species, because from them heterosis for quantitative traits of economic interest can be obtained when crossing progenies belonging to different groups (Manfio et al., 2012). We also emphasize the need and importance of evaluating the genetic diversity of reproductive trees and progenies with molecular markers. It is a very important tool for advancing perennial tree improvement programs and it cannot be neglected.

The distances data within and between the groups formed underline the results previously found, showing a low variability within a large group of individuals even though the provenances are distant and, in the case of MG and MS comparison, the climate is also different and there is high variability between groups of high performing and low performing progenies for the dendrometric characteristics.

According to Carvalho (2002) and Silva et al. (2020), P. dubium is a pioneer species to early secondary, usually found in several phytogeographic domains, but with few individuals, a fact that justifies its variability. Within groups, the greatest distance of the genotypes occurred within group VIII, comprised only by two progenies from Ivinhema/MS and Lavras/MG (progenies 34 and 45) and the lowest variability occurred between individuals from Nioaque/MS and Ivinhema/MS.

Considering the data analysis, we can infer that the dendrometric characteristics studied are indicated for conservation and use in breeding programs since they showed genetic variation for progenies, which evidences the possibility of success in the selection of individuals. The most promising individuals are found in the MG population, with progenies 50, 57, 47, 49, and 55 showing the best performance when comparing the averages of the evaluated characters.

There was low genetic diversity in the MS populations, of which, progenies 6 and 9 showed the lowest performance. Regardless of the method used to analyze the genetic divergence among the progenies, the most promising MG progenies and the poor performing MS progenies were always allocated into the same group. When introducing genotypes from MG, we obtained an increase in genetic variability, and genotypes with higher performance, in favorable alleles and in selection gain for the characteristics studied.

Considering this study's results, we confirm there is genetic variability in *P. dubium* populations for the quantitative characters evaluated. In the clustering and dispersion methods used, the progenies were gathered into three and nine groups, respectively. Progenies from MG (50, 57, 47, 49, and 55) had higher genetic diversity, and also higher performance for the morphological characters. Progenies 6 and 9 from the region of Bonito and Porto Murtinho/MS showed inferior performance.

Acknowledgements

The authors thank the Foundation for the Development of Education, Science, and Technology of State of Mato Grosso do Sul (FUNDECT) and the Coordination for the Improvement of Higher Education Personnel (CAPES) and the National Council for Scientific and Technological Development (CNPq) for the research scholarship and financial support associated with the development and dissemination of this work

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