

Productivity, adaptability, and stability in *Guazuma crinita* progeny tests across three environments in the Aguaytia River Basin, Ucayali, Perú

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Abstract

Guazuma crinita is a fast-growing tree with potential for use in agroforestry systems, due to its rapid wood production, which can contribute significantly to the livelihoods of small-scale farmers in the Peruvian Amazon. However, indiscriminate logging due to high demand is leading to the disappearance of natural forests. As such, the International Council for Research in Agroforestry (ICRAF) began a domestication program to reduce pressure on natural populations of the species. The objective of the present study was to use analyses of genetic parameters, adaptability (PRVG), productivity (MHPRVG), and stability (MHVG), to select *G. crinita* genotypes from a three-year-old progeny test established in the Aguaytia River Basin, in Ucayali, Peru. The test was established in three different sites, with three blocks, 200 progeny per block, and two individuals per plot. The measured traits were diameter at breast height (DBH), total height (H), and total aerial biomass (B). Significant differences in traits between progenies were detected, but with no genotype $\times$ environment interaction (G $\times$ E). However, the genotypic correlation among sites was important (> 0.702), suggesting that genetic improvement is possible by selecting the same progeny across sites. The mean heritability among progenies was moderate for all traits (0.34–0.369) and selective precision through combined site analysis was relatively high

(0.583–0.608). Based on selection for DBH through combined analysis, MHVG, PRVG, and MHPRVG, 50 superior progenies (25.9 %) were identified for all environments. These should be prioritized in breeding programs as they can offer stable genetic variability for future selection cycles.

Keywords: Biomass, G $\times$ E interaction, native tree species, plantations, tree improvement, White Bolaina.

Introduction

Guazuma crinita Mart. (Malvaceae), commonly known as White Bolaina, is a fast-growing timber forest species that develops in alluvial forests of the Peruvian Amazon (Coral et al., 2020). The range of the species is distributed from Central America to the south of Brazil, Bolivia, and Peru, and individuals can reach more than 30 m in height and up to 0.5 m in diameter (Reynel et al., 2003). The species shows good potential for agroforestry plantations and wood production, as it can be harvested at a very young age and can contribute significantly to the livelihoods of small-scale farmers in the Peruvian Amazon (Rochon et al., 2007; Putzel et al., 2013). It is a versatile species with excellent adaptability to a wide variety of locations (Maruyama

et al., 1997; Flores, 2000). Due to the high workability of its wood, *G. crinita* is widely used in general carpentry, as well as for the manufacture of brooms, toothpicks, medical pallets, and toys. Above all, the wood is used for the manufacture of paneling, which is preferred by consumers with limited economic resources due to the low price. As such, it has cornered a large part of the regional and national market (Aróstegui, 1974; Encarnación, 1983).

In Peru, the species is found at a high density in the regions of Loreto, Amazonas, Ucayali, Huánuco, San Martín, Madre de Dios, Junín, and Cerro de Pasco (Reynel et al., 2003). Because of this abundance, the production of Bolaina increased significantly from 2004 to 2019, growing from 23,110.02 to 70,054.15 m³, as a result of high market demand (SERFOR, 2019). However, to date, the demand for *G. crinita* wood continues to grow, causing concern that such demand might lead to over-exploitation of natural stands through selective extraction and the eventual decimation of the species. Such processes can result in a loss of natural regeneration due to the elimination of seed-trees, leading to genetic erosion and the fragmentation of natural stands in the short and medium term, and reducing the yield of harvesting cycles (Casas et al., 2016). In this context, it is necessary to select productive genotypes that can be successfully used in conservation and improvement programs for reforestation. This requires an understanding of the interaction between genotypes and environments (GxE) in order to minimize or leverage the effects and increase efficiency in the selection of genotypes (Pupin et al., 2018; Murillo et al., 2019).

Selection is generally based on growth traits, which present complex patterns of heritability, making it difficult to predict responses of genotypes to different environments (Namkoong et al., 1966). Information on the nature and magnitude of this interaction is essential, particularly for selection based on traits with low levels of heritability (Yan and Kang, 2002). Barros et al. (2008) defined the GxE interaction as the inconsistent performance of genotypes in different environments. While Namkoong et al. (1966) point out that GxE interaction can generate erroneous and inflated estimates of genetic variability. Which directly affects the selection and reduce genetic gain, making it difficult to select genotypes with broad adaptability. One of the alternatives to minimize the effects of GxE interaction is the choice of genotypes with simultaneously high productivity, stability, and adaptability (Torres-Dini et al., 2016; Chaves et al., 2021), which can be done using predictive methods, such as the Harmonic Mean of the Relative Performance of Genotypic Values (MHPRVG). This method allows for the use of unbalanced data and heterogeneity of variances, providing stability values and genotypic adaptability, as well as generating results on the scale or magnitude of the evaluated trait. As such, the method enables direct interpretation of results as genetic values and genetic gain estimation based on its productivity, stability, and adaptability (Resende, 2007; Torres-Dini et al., 2016; Pupin et al., 2018).

Considering that the environment can result in phenotypic variation of up to 80 %, this effect together with genotypic variation are the most relevant for selection if the effects of GxE interaction are considered (Yan and Kang, 2002). The GxE

interaction reduces the correlation between phenotype and genotype (Rao et al., 2011), interferes with genetic gains, and creates greater uncertainty in selection (Vencovsky et al., 2012). Therefore, to study GxE interaction, it is necessary to establish multi-environment experimental trials (Mustapha et al., 2014). The evaluation of GxE interaction can lead to the adoption of two selection strategies: i) stratification of heterogeneous areas into smaller and homogeneous subregions for selection; ii) selection of stable genotypes based on its performance in a variety of environments (Funga et al., 2017; Souza et al., 2020). In this context, Weber and Sotelo (2008) assessed the genetic differences in *G. crinita* biomass yield between provenances and suggested the best provenance to be used in future plantations.

The present study aimed to estimate genetic parameters and select *G. crinita* genotypes from a series of three-year-old progeny tests established in three different environments in the Aguaytía river basin, Ucayali, Peru, based on adaptability (PRVG, relative performance of genetic values), productivity (MHPRVG), and stability analysis (MHVG, harmonic mean of breeding values).

Material and Methods

Sampling and establishment of progeny test

Open-pollinated seeds from 209 mother trees were collected from 14 sites in the Aguaytía and Pachitea River Basins: New Requena – River (17 trees); Neshuya Stream – Carretera Federico Basadre (CFB) Km 49.5 (13 trees); Tahuayo Stream – CFB Km 72 (11 trees); Curimana – River (20 trees); Aguaytía River (19 trees); Yurac Stream – Aguaytía (3 trees); Inca Port (18 trees); Von Humboldt (17 trees); Macuya (49 trees); Santo Alexandre (17 trees); CFB to Km 72 (7 trees); Road to Nueva Requena (4 trees); Road to Curimaná: (7 trees); and Road to Tournavista (7 trees) (Figure 1). This study was carried out on the west side of the Aguaytía River Basin, in lowland forest at elevations between 180 m and 300 m, with terrain ranging from undulating at higher elevations to flat at lower elevation (Ugarte-Guerra and Domínguez, 2010). For the study, we evaluated progeny in plots established by the International Council for Research in Agroforestry (ICRAF), distributed in terraced soils, at three sites in the basin: lower basin between the areas of Pucallpa, Campo Verde, and Nueva Requena (site 1); middle from Neshuya to Curimaná (site 2); and upper basin from Von Humboldt to San Alejandro (site 3) (Figure 2). Sites have predominantly acidic soils and low natural fertility, with rainfall ranging from 1500 mm in the lower basin to 2500 mm in the upper basin. The average annual temperature is 26 °C (Table 1).

Each of the three trials was established with a randomized complete block design, with five repetitions (blocks) per site, for a total of 15 repetitions with 200 progenies. For the present study, we used only nine repetitions (Figure 1). Each progeny test in replicate was randomly in a two seedlings (half-sibs) plot, for a total of 400 plants, spaced at 2.5 x 2.5 m, over an area of 2500 m². All replicates had perimeter of two tree rows which

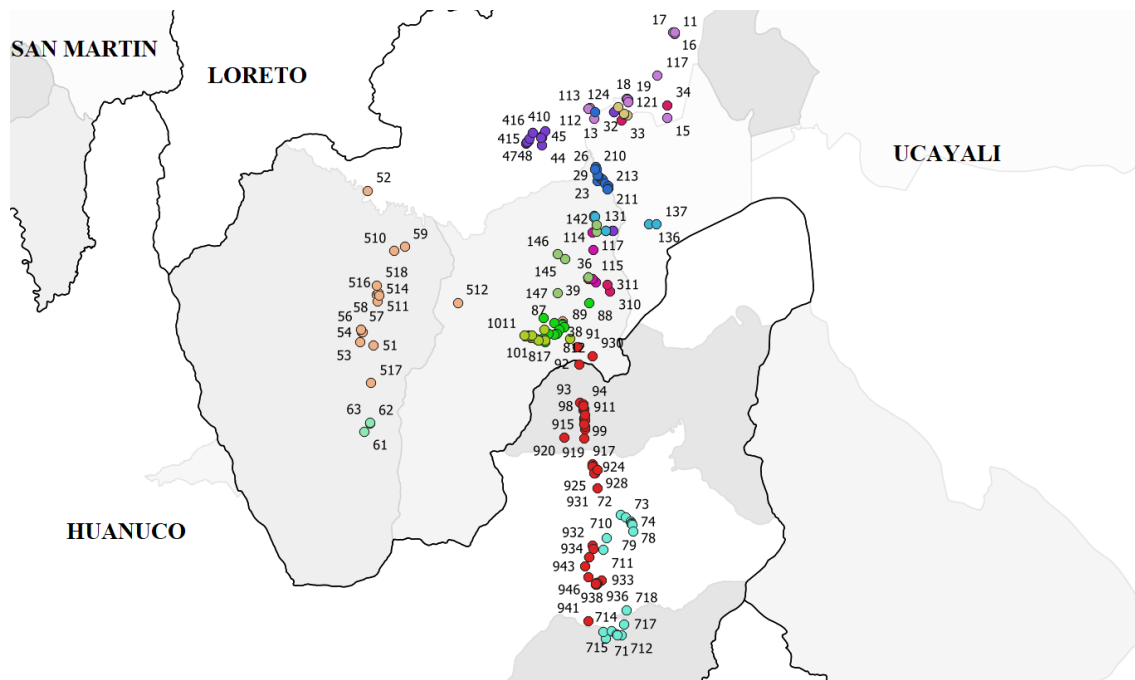


Figure 1

Collection of seeds from 209 trees for progeny testing *Guazuma crinita*: 1= New Requena – River (17 trees); 2= Neshuya Stream (13 trees); 3= Tahuayo Stream (11 trees); 4= Curimana – River (20 trees); 5= Aguaytia River (19 trees); 6= Yurac Stream (3 trees); 7= Inca Port (18 trees); 8= Von Humboldt (17 trees); 9= Macuya (49 trees); 10= Santo Alexandre (17 trees); 11= CFB up to Km 72 (7 trees); 12= Road to Nueva Requena (4 trees); 13= Road to Curimaná (7 trees); 14= Road to Tournavista (7 trees).

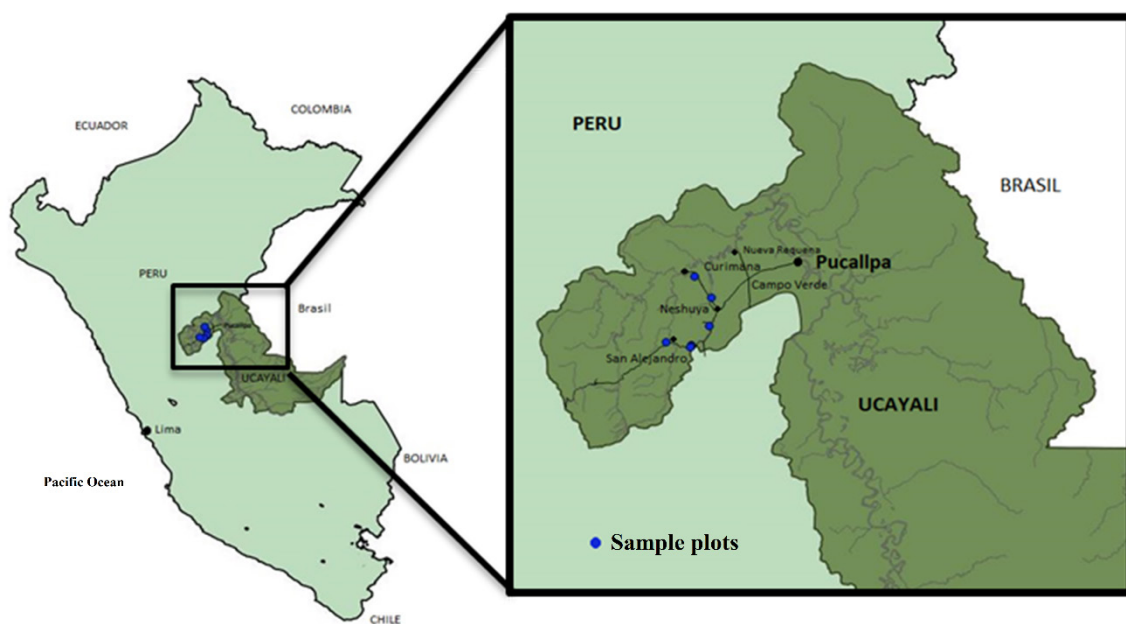


Figure 2

Location of the study area.

Table 1
Environmental variables of the Aguaytia River Basin.

Parameter	Site 1	Site 2	Site 3
Soil*			
Type of soil	Sandy Franc	Clay Franc	Clayey
Clay (%)	21.1	35.7	52.4
Loam (%)	33.8	38.5	27.5
Sand (%)	45.1	25.8	20.1
pH	4.63	5.34	6.52
Phosphor: P (ppm)	3.79	7.76	3.46
Acidity (pH)	2	2.08	0.2
Potassium: K (ppm)	0.23	0.22	0.2
AC	1.43	10.2	32.3
Magnesium: Mg	0.84	2.02	3.43
Cation exchange capacity: CICE (meq/100g)	4.5	14.52	36.14
Sat. To (%)	39.7	18.5	0.6
Organic matter content: C.O. (%)	0.8	1.2	1.6
Physiography	Low terrace	Medium terrace	High terrace
Elevation (masl)	160	172	232
Climate**			
Precipitation (mm/ha/year)	1504	1997	2545
Mean annual temperature (°C)	25.4	25.4	25.8

Source: *ICRAF (2003); **USAID PERU (2012).

were excluded from the assessment. At the time of planting, 1600 kg ha⁻¹ of earthworm humus and 320 kg.ha⁻¹ of phosphate rock were applied (1 kg of earthworm humus and 200 g of phosphate rock per plant applied at a 2.5 x 2.5 m distance). During the second and third year, the experiment was fertilized with 112 kg of urea.ha⁻¹, 316 kg.ha⁻¹ of phosphoric rock, and 160 kg.ha⁻¹ of potassium chloride, corresponding respectively to 70, 185, and 100 g of each product per plant (Ugarte-Guerra and Domínguez, 2010). In the third year, 50 % thinning was conducted, resulting in approximately 200 individuals within each repetition; the remaining planting density was maintained until year six (Revilla-Chávez et al., 2021a). At 36 months-old were evaluated: i) total height (H, m); ii) diameter at breast height (DBH, cm); iii) total aerial biomass (B, kg); and iv) survival (SUR, %). Total aerial biomass was determined through applying the allometric model $B=0.04253*DBH^{2.5027}$ (Revilla-Chavez et al., 2021b) for trees up to 21.8 cm in DBH.

Estimate of variance components and genetic parameters

REML/BLUP procedure using mixed linear models was used, in order to estimate the genetic parameters for each trait across the three sites. SELEGEN-REML/BLUP software (Resende, 2016) was employed with statistical model 93, $y = X_r + Z_a + W_p + e$, where: y , r , a , p , and e are the vectors data, replication, genetic, plots, and error, respectively. The incidence matrices for the above effects are represent by the uppercase letters X , Z , and W (Resende, 2007). The following variance components were estimated: genetic variance among progeny (σ_p^2), additive genetic variance ($\sigma_a^2 = 4\sigma_p^2$), environmental variance among plots (σ_c^2), residual variance (environmental + non additive) (σ_e^2), variance of genotype x environmental interaction (σ_{ge}^2), and

individual phenotypic variance, $\sigma_f^2 = \sigma_a^2 + \sigma_c^2 + \sigma_e^2$. From the variance components, the following parameters were estimated:

Narrow-sense individual heritability, $h_i^2 = \sigma_a^2 / \sigma_f^2$;

Mean heritability among progeny,

$$h_m^2 = \frac{0.25\sigma_a^2}{0.25\sigma_a^2 + \frac{\sigma_c^2}{r} + \frac{0.75\sigma_a^2 + \sigma_e^2}{nr}};$$

Coefficient of individual genotypic variation,

$$CV_{gi}(\%) = 100 \left(\frac{\sqrt{\sigma_a^2}}{m} \right);$$

Coefficient of experimental variation,

$$CV_e(\%) = 100 \left(\frac{\sqrt{[0.75\sigma_a^2 + (\sigma_e^2/n)] + \sigma_c^2}}{m} \right),$$

where n is the number of plants per plot;

Selective accuracy among progeny, assuming full survival, $r_a = \sqrt{h_m^2}$;

Genotypic correlation between progeny in various environments,

$$r_g = \sigma_a^2 / (\sigma_a^2 + 4\sigma_{ge}^2);$$

Coefficient of determination of the plot effect, $C_p^2 = \sigma_c^2 / \sigma_f^2$;

Coefficient of determination of the genotype x environment interaction (GxE) effect, $C_{ge}^2 = \sigma_{ge}^2 / \sigma_f^2$.

Analyses of adaptability (PRVG), productivity (MHPRVG), and stability (MHVG) were conducted using all three progeny tests (sites). For this, the MHPRVG method predicted by BLUP (Resende, 2007) was used, based on SELEGEN-REML/BLUP software, according to mathematical model 51: $y = X_r + Z_a + W_p + T_i + e$, where y , r , a , p , i , and e are the vectors data, replication, genetic, plots, GxE interaction, and error term. The incidence matrices for the above effects are represented by uppercase letters X , Z , W , and T (Resende, 2007).

Results

Genetic parameters

At three years of age, *G. crinita* progeny in site 1 presented lower mean DBH, H, and B than in site 2 and site 3 (Table 2). The chi-square test (χ^2) on deviance analysis was statistically significant ($P < 0.05$) among progenies for all traits in site 1 and 2, indicating the possibility for genetic improvement by selection among progenies. For the site combined analysis, mean DBH was 12.6 cm, H was 11.2 m, and B was 27.55 kg. The χ^2 was statistically significant ($P < 0.05$) for all traits among progenies and plots, indicating the possibility of genetic improvement through selection among progenies (Table 3).

The coefficient of determination of the effects of plots (C_p^2) was low for all traits in sites 2 and 3 (≤ 0.106), for DBH and B in site 1 (≤ 0.239), and DBH in the combined analysis (0.025), but intermediate in the combined analysis for H (0.528) and B (0.63). Thus, no strong environmental heterogeneity was found within pairwise blocks for the studied traits. For the site combined analysis, the coefficient of determination of GxE interaction (σ_{ge}^2) was low for all traits (< 0.03) and the genotypic correlation by environment (r_{ge}) was high for all traits (0.702–0.743), indicating that the interaction is simple. The individual heritability (h_i^2) was moderate for all traits in sites 1 and 3 (ranging from 0.226–0.27 and 0.374–0.494, respectively), as was heritability at the mean progeny level (h_m^2 : site 1, 0.218–0.263; site 3, 0.36–0.435). In site 2, h_i^2 and h_m^2 were low for all traits (< 0.06). Consequently, the selective accuracy (r_a) was higher for all traits in sites 1 and 3 (0.466–0.66) than site 2 (0.181–0.228), indicating that there is greater possibility for obtaining genetic gains with the selection of progenies within sites 1 and 3, with highest mean for all traits. For the site combined analysis for all traits, h_i^2 was lower (0.041–0.049) than h_m^2 (0.34–0.369), and r_a was relatively high (0.583–0.608), indicating the possibility for improvement through selection among progenies across all sites. The coefficient of genotypic variation ($CV_{gi}(\%)$) was variable among traits and sites. The as a mean across all sites was higher for B (7.2–28.7 %, mean of 8.7 %) than DBH (2.6–12 %, mean of 3.7 %) and H (2.6–14.8 %, mean of 3.5 %). However, for all traits, $CV_{gi}(\%)$ was lower in site 2 (2.6–7.2 %) than in site 1 (12–28.7 %) and site 3 (8.2–25.3 %), indicating high variation among progenies for all traits in site 1 and 2. The coefficient of experimental variation ($CV_e(\%)$) was higher for all traits in site 1 (19.6–41.5 %) than sites 2 and 3, where the values were similar for all traits

(9.4–26.9 %). The B trait showed the highest $CV_e(\%)$ in all sites and as a mean across sites (24.9–41.5 %).

Adaptability, productivity, and stability

From the evaluations carried out based on the sources of variation (progeny, plot, and progeny x plot interaction), we found that there are significant differences in the evaluated DBH, H, and B traits at 5 % probability in the progenies and plots. But no differences were found for the GxE interaction (Table 3). In the simultaneous selection by DBH through the combined analysis (MHVG, PRVG, and MHPRVG), individual analysis for MHVG, PRVG, and MHPRVG, 50 progenies (25.9 %) stood out (Table 4). The ranking of these progenies considering all four methods was relatively consistent. Based on a combined analysis, it is possible to select genetic materials across all sites with a consistent adaptability, productivity, and stability.

Discussion

Genetic parameters

At three years of age, *G. crinita* progenies showed variation among traits and sites. These results indicate the possibility for improvement by selecting the best progenies within sites and across all sites. The low values for h_i^2 , h_m^2 , r_a , and $CV_{gi}(\%)$ and the absence of significant differences among progenies for all traits in site 2, indicates that the possibilities of obtaining genetic gains in this site, with selection within and among progenies is limited. In contrast, for site 1 and 3, there are significant differences among progenies. The h_i^2 in sites 1 and 3 showed a moderate genetic control for all *G. crinita* traits, with results falling within the range of those reported for other tropical tree species at an early age (i.e. Aguiar et al., 2019; Murillo et al., 2019; Machado et al., 2021; Resende et al., 2021). The h_m^2 was also moderate for traits (0.34–0.369), and r_a in the combined analysis was relatively high (0.466–0.513). Despite of the low number of blocks and plants per progeny in the test, enough and large genetic variation was presented among progenies to enable performing selection and to expect genetic progress. These results indicate that genetic gains can be obtained by selecting progenies with the highest mean for the studied traits in sites 1 and 3. Therefore, to implement a second-generation progeny test, or for the genetic conservation of the species, the selection of progenies will be effective.

The $CV_{gi}(\%)$ for B was at least twice that for DBH and H in all sites, indicating large variation among progenies for B. Theoretically, B is indicated as an effective trait for selection. However, because DBH and B are directly related (Lima et al., 2016; Araujo et al., 2021; Revilla-Chávez et al., 2021a), with a higher DBH resulting in greater B, and DBH is an easy to measure, we chose to use DBH as the variable for selection. Furthermore, the coefficient of determination of the effects of plots (C_p^2) was lower for DBH (0.246) than for H and B (> 0.5). Thus, in this experimental trial, no environmental heterogeneity was found within the pairwise blocks for DBH.

Table 2

Estimation of genetic parameters for the traits diameter at breast height (DBH), height (H), and total aerial biomass (B), per site and for all sites, of *Guazuma crinita* progeny tests.

Parameters	Site 1			Site 2			Site 3			All sites		
	DBH (cm)	H (m)	B (kg)	DBH (cm)	H (m)	B (kg)	DBH (cm)	H (m)	B (kg)	DBH (cm)	H (m)	B (kg)
Coefficient of determination of the plot effects: C_p^2	0.239	0.522	0.189	0.106	0.104	0.104	0.088	0.089	0.085	0.246	0.528	0.63
Coefficient of determination of GxE interaction effects: C_i^2	-	-	-	-	-	-	-	-	-	0.014	0.015	0.021
Individual heritability: h_i^2	0.226	0.27	0.267	0.025	0.04	0.04	0.42	0.374	0.494	0.041	0.045	0.049
Mean heritability at progeny level: h_m^2	0.222	0.218	0.263	0.033	0.052	0.051	0.39	0.36	0.435	0.369	0.34	0.343
Selective accuracy: r_a	0.472	0.466	0.513	0.181	0.228	0.227	0.625	0.6	0.66	0.608	0.583	0.586
Genotypic correlation among sites: r_{ge}	-	-	-	-	-	-	-	-	-	0.743	0.742	0.702
Coefficient of individual genetic variation: $CV_{gi}(\%)$	12	14.8	28.7	2.6	2.6	7.2	10	8.2	25.3	3.7	3.4	8.7
Coefficient of experimental variation: $CV_e(\%)$	19.6	24.3	41.5	12.2	9.5	26.9	10.8	9.4	24.9	14	13.7	34.9
Overall mean: m	8.9	6.3	11.6	14.3	13.5	34.7	14.6	13.9	36.5	12.6	11.2	27.5
LRT: Likelihood ratio test, χ^2 deviance chi-square	3.7*	3.6*	5.3*	0.02	0.07	0.06	6.5*	5.4*	8.8*	10.3*	10.4*	11.1*

*P < 0.05, with 0.5 degree of freedom.

Table 3

Deviance analysis (ANADEV).

Source of variation	DBH (cm)		Height (m)		Total aerial biomass (kg)	
	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)
Progeny	5956.46	10.31*	25409.19	10.37*	12676.85	11.11*
Plot	5974.87	28.72*	25557.11	158.29*	12767.08	101.34*
Progeny x Plot	5946.59	0.44	25399.28	0.46	12666.48	0.74
Complete Model	5946.15	-	25398.82	-	12665.74	-

*P < 0.05, with 0.5 degree of freedom; LRT: Likelihood ratio test, χ^2 deviance chi-square.

In the combined site analysis, h_i^2 was low for all traits (< 0.05), suggesting an unfavorable situation for improvement by mass selection in the experiment. Although h_i^2 values for all traits in *G. crinita* were low, they were within the range of values reported for other young tropical trees, such as *Calyculophyllum spruceanum* (Sotelo et al., 2006), *Dipteryx alata* (Pagliarini et al., 2016), *Myracrodruon urundeuva* (Canuto et al., 2017), and *Theobroma grandiflorum* (Chaves et al., 2021). In contrast, h_m^2 was moderate for traits (0.34–0.369), and r_a in the combined analysis was relatively high (0.583–0.608). These results indicate that genetic gains can be obtained with the selection of progenies with the highest mean for all traits. Thus, selection precision was high compared to the $CV_{gi}(\%)$, h_m^2 and r_a , respectively. This again suggests that selection to implement a second-generation progeny test, or for genetic conservation of the species, would be effective. The observed absence of significant difference for the coefficient of determination of GxE interaction (C_{ge}^2) and the high genotypic correlation by environment (r_{ge}) for all traits (0.702–0.743) indicates that the interaction is simple. Thus, in a breeding program, this type of interaction would be easier to be managed than that of a complex interaction (Vencovsky et al., 2012; Pupin et al., 2018; Souza et al., 2020).

Analysis of adaptability, productivity, and stability

Significant differences were observed among progenies for DBH, H, and B, but no differences were found for GxE interaction across sites. These results are probably related to several factors, including the fact that the species occurs across a wide natural range. Thus, the species–environment interaction is probably minimal within a restricted area. Results suggest that such an environmental interaction is only found if there is a significant variation in climate and edaphic conditions. On the other hand, species that have a limited distribution and small population size usually present low levels of genetic diversity (White et al., 2007). Coral et al. (2016) reported differences with limited clustering of 44 superior *G. crinita* individuals based on DBH and H from the same experimental unity and that utilized in the present study.

Progeny selection

In the simultaneous selection by DBH considering the combined analysis, MHVG, PRVG, and MHPRVG, 50 progenies stood out. The consistent ranking of these progenies across the four methods applied is related to the positive correlation between genotypic behavior and environments. Therefore, the progeny selected based on the combined analysis are the most

Table 4

Best progeny of *Guazuma crinita* with selection intensity of 25.9 %, based on DBH, in the combined analysis of genotypic stability (MHVG), genotypic adaptability (PRVG), and productivity (MHPRVG).

Ranking	Combined	MHVG	PRVG	MHPRVG
1	76	76	76	76
2	134	134	134	134
3	416	416	416	416
4	77	77	77	77
5	29	61	29	29
6	61	29	61	61
7	515	515	515	515
8	58	38	58	58
9	38	58	38	38
10	71	110	71	71
11	911	74	110	110
12	110	113	911	911
13	113	71	113	113
14	1014	911	74	74
15	74	35	1014	1014
16	1011	1014	35	35
17	35	943	943	943
18	943	1011	1011	1011
19	935	45	45	45
20	144	513	513	513
21	45	55	935	935
22	513	935	55	55
23	55	946	144	144
24	946	144	946	946
25	945	916	916	916
26	417	945	945	945
27	136	136	136	136
28	137	46	46	46
29	916	137	137	137
30	46	1016	417	417
31	1016	918	1016	1016
32	918	417	918	918
33	28	28	28	28
34	42	31	31	31
35	31	42	42	42
36	942	12	942	942
37	107	942	12	12
38	932	512	932	932
39	12	932	107	107
40	420	810	420	420
41	131	420	512	512
42	936	131	131	131
43	512	107	810	810
44	11	813	813	813
45	813	11	936	936
46	810	936	11	11
47	32	53	811	811
48	108	811	53	53
49	39	32	39	39
50	811	39	32	32

productive, the most stable, and the most adaptable. Both for a genetic improvement program and for the genetic conservation of the species, the most productive progenies are not significantly influenced by the environment and, consequently, do not present GxE interaction. These progenies should be prioritized as they present genetic traits that will help maintaining the species in the face of adverse conditions and contribute to *ex situ* gene conservation of this tree species.

Based on combined adaptability, productivity, and stability for DBH trait, it is possible to select genetic materials across all environments in these progeny tests. Fifty progenies with the highest DBH were selected (25.9 % of the total progeny in the combined analysis of all environments), providing a good representation of all genetic material across all environments. These progenies showed adequate adaptability, productivity, and stability across all sites.

These results were similar to those found for stability, which is the variation in genotypic performance in different environments (Resende, 2007; Moraes et al., 2012; Pupin et al., 2018). This selection is consistent with that reported by Dawson et al. (2012), who argue that the genetic variation of a trait in a given area is high and the environmental variation is low, then selecting genetically superior individuals is possible. Similar results were reported for *C. spruceanum* which were sampled and analyzed in the same river basin (Sotelo et al., 2006).

Conclusions

We found genetic variation among *G. crinita* progenies for all traits, but no GxE interaction for the studied traits, indicating that the same group of progenies can be selected for all three sites. Compared to H and B, DBH was the most effective variable to select the best progenies in the assessment of genotypic adaptability, productivity, and stability of 200 *G. crinita* progenies at three years of age. Based on the combined analysis of genotypic adaptability, productivity, and stability, with a selection intensity of 25.9%, and considering the highest DBH values, 50 progenies are indicated as ideal for the development of a genetic improvement program.

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