Articles

Methodology for the phenotypic evaluation in *Guazuma crinita* trees in Ucayali, Peru

Metodologia para avaliação fenotípica de árvores de *Guazuma crinita* em Ucayali, Peru

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ABSTRACT

The objective of this study was to present a methodological tool for the phenotypic evaluation in progeny tests of *Guazuma crinita* in producer plots of the Aguaytía river basin, Ucayali, Peru, which allows field technicians to standardize the morphological evaluation criteria of trees in forest plantations. Therefore, the phenotypic traits were evaluated for plant height (m), diameter at the height of the base (cm), number of branches, number of rings, stem form, branch orientation, presence and quantity of leaves. The heritability and genetic and phenotypic correlations between traits were also estimated. Therefore, 32 morphological categories were plotted based on the significant correlations ($p \leq 0.05$) shown between the place of planting, the stem form, the orientation of the branches and the presence of leaves. For the same reason, the progeny showed low morphological patterns, being a low factor of phenotypic variability. It is concluded that the correlations between the biometric and morphological traits evaluated, allowed to validate the phenotypic evaluation procedures of *Guazuma crinita* progeny tests at 36 months of age.

Keywords: Amazon; Aguaytia Basin; Bolaina blanca; Progeny test

RESUMO

O objetivo deste estudo foi apresentar uma ferramenta metodológica para avaliação fenotípica em testes de progênie de *Guazuma crinita* em parcelas de produtores na bacia do rio Aguaytía, Ucayali, Peru, que permite aos técnicos de campo padronizar os critérios de avaliação morfológica das árvores em plantações florestais. Também foi estimada a herdabilidade e as correlações genéticas e fenotípicas entre os caracteres. Dessa maneira, os caracteres fenotípicos foram avaliados para altura da planta (m), diâmetro na altura da base (cm), número de ramos, número de anéis, forma do fuste, orientação do ramo, presença e quantidade de folhas. Sendo assim, 32 categorias morfológicas foram plotadas com base nas correlações significativas (p≤ 0,05) mostradas entre local de plantio, forma do fuste, orientação do ramo e presença de folhas. Conclui-se que as correlações entre os caracteres biométricas e morfológicas avaliadas permitiram a validação dos procedimentos de avaliação fenotípica dos testes de progênies de *Guazuma crinita* aos 36 meses de idade.

Palavras-chave: Amazônia; Bacia Aguaytia; Bolaina branca; Teste de progênie

1 INTRODUCTION

Guazuma crinita Mart. (Malvaceae) is a fast-growing tree, promising for use in agroforestry plantations and improving the quality of life of farmers in the Peruvian Amazon. The species has been subjected to intense logging, which is causing the decline of its will populations, as well as leading to its genetic erosion (Revilla *et al*., 2021). This limits the possibilities of using the species in the recovery of degraded areas and hinders commercial reforestation programs, which require seeds with genetic quality originating from genetic improvement programs (Sebbenn *et al*., 2007; Kubota *et al*., 2015; Aguiar *et al*., 2019; Gerber *et al*., 2021; Silva *et al*., 2023). Much of what we know about the species in Peru arose as a result of the ICRAF Agroforestry Tree Domestication Program in the 1990s, whose philosophy is to promote the conservation of genetic resources through their use by farmers (Sotelo; Weber, 1997; Putzel *et al*., 2013; Sears *et al*., 2018; Tuisima *et al*., 2016, 2020).

The economic criterion associated with productivity is the most important variable in the choice of tree species to be used by farmers in reforestation. For this, the best trees from wild populations are selected based on the phenotypic expression of traits of economic interest for collecting seeds and using them in their plantings.

However, the phenotypic selection of traits in trees from wild populations, due to the interaction of genotypes with the environment, can lead to errors in choosing mother trees that produce seeds with better genetic quality (Aguirre; Fassbender, 2013). To avoid errors in the selection of mother tees, provenance and progeny tests are used, where information is obtained on the heritability of the traits, the genetic and phenotype correlations between the traits and the interaction between the genotype and the environment (Weber; Sotelo-Montes; Labarta-Chávarri, 1997; Oliva; Rimachi, 2017). Therefore, a forest domestication program can provide genetically improved germplasm for the establishment of forest plantations, being necessary to establish seed orchards with individuals with traits that the market wants.

The selection of high-yielding trees is the foundation of forest genetic improvement, and success depends on the quality and rigor that individuals are characterized (Vallejos *et al*., 2010; Gutiérrez-Vásquez *et al*., 2016). Most of the trials consider the types of stems, growth, stability, adaptability, resistance to pests and diseases, as they are directly related to the attributes of the wood (Zobel; Talbert, 1994; Espitia; Murillo; Castillo, 2016). Proof of this is that the reports of genetic gain when using superior material is greater than 15% for the traits growth in height and growth in diameter at breast height (DBH), as well as greater than 35% in volume per unit area (Cornelius, 1994; Espitia; Murillo; Castillo, 2016). Selection works by considering highly heritable traits (Zamudio; Guerra, 2002) such as stem straightness, branching, plant health, tree height, diameter et breast heigh (DBH) and volume (Cornelius, 1994). So, these traits are suggested for selection due to having a higher heritability (Murillo; Rojas; Badilla, 2003; Murillo; Badilla, 2004).

Qualitative traits often have greater heritability ($h^2 > 0.5$), indicating that they are regulated by a few loci, and are less subject to environmental effects, so that a tree with a qualitative trait superior, it will be superior to a great extent in other environments (Murillo; Rojas; Badilla, 2003). Thus, the bifurcation of a tree is used as a suppression factor for a tree aspiring to a plus tree, since it is considered to have high

heritability (Zobel; Talbert, 1994). Therefore, the stem form is expressed as a result of the interaction between the genotype and the environment (Chambel *et al*., 2005).

Identifying desirable individuals that have more than one trait of interest is a fundamental objective in forest improvement. But this task is not easy, because the traits are associated with each other, where the association between some traits may have a direct relationship and others may have an inverse relationship (Vencovsky; Barriga, 1997). The quantification of the association between traits can be obtained from analysis of phenotypic, genotypic and environmental correlations (Vencovsky; Barriga, 1997). In selection, correlations are useful for the indirect selection of a trait using its relationship with another, based on criteria of greater ease of measurement and identification and greater heritability, which allows inferring that the traits are genetically association and indicates the possibility of developing synchronous selection for several traits simultaneously (Vencovsky; Barriga, 1997; Correa *et al*., 2013). For this purpose, the final product of the tree should be observed based on its intrinsic traits such as growth dynamics and tree morphology. So, the evaluation should collect comprehensive information with which the traits occur in a stand based on to the expected products. For example, in that sense for sawn wood and posts, straight and cylindrical trunks, low conicity factor, without low forks, with fine branches and horizontal position are required. On the other hand, for the production of firewood, the shape of the stem and branches is not very important, as the biomass yield is of greater interest. But, in both cases, fast growth, health is promising in seed production (Vallejos *et al*., 2010).

Therefore, in order to find practical methods of phenotypic selection, it is necessary to validate the use of morphological descriptors and determine the phenotypic variability mainly from the easily observed traits of the tree (Castañeda-Garzon *et al*., 2021). From the qualitative assessment of the trees, it is possible to identify trees with exceptional, average and undesirable traits (Ortiz *et al*., 2017; Ramírez-Garcia *et al*., 2022). Due to that, this study aimed to develop a tool for the
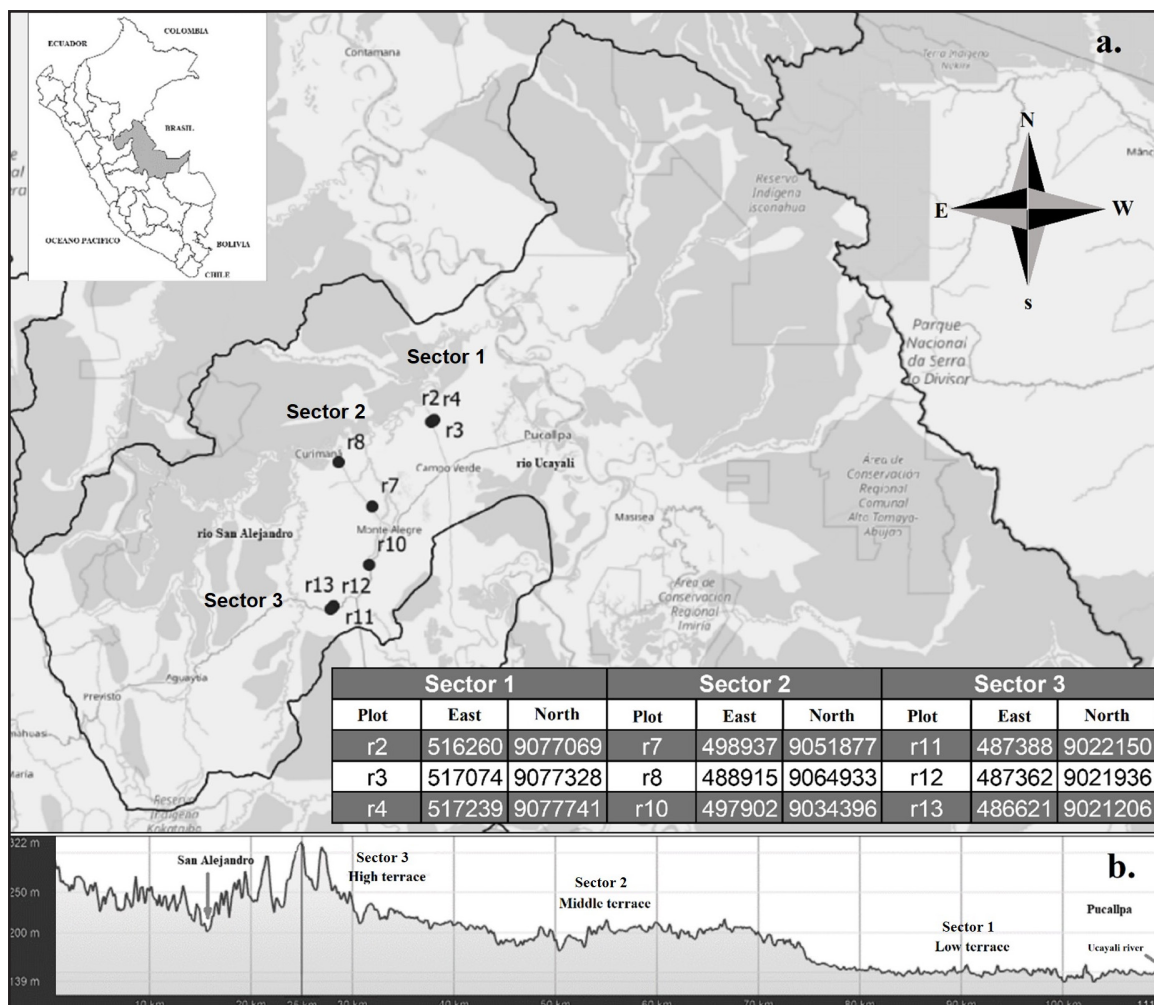
evaluation of qualitative traits of commercial interest, such as stem form, branches and health, as they are variables of high heritability in *Guazuma crinita* progeny test established in the Aguaytia river basin, Ucayali, Peru.

2 MATERIAL AND METHODS

2.1 Site and establishment of the progeny test

The study was carried out in *Guazuma crinita* progeny test of 36 months of age, established in the Aguaytia river basin developed by the World Agroforestry Center (ICRAF), in the department of Ucayali. The region physiography has terraces low, medium and high (Figure 1b), with varied drainage conditions; riverbank complexes, predominantly acidic high terrace soils with low fertility; the floodable alluvial zone has soils of greater fertility; the low terraces with sandy and very clayey soils on the upper terraces of the basin; rainfall ranges from 1,400 mm in the lower part to 2,500 mm closer to the eastern Andes mountain range with the presence of 2 life zones, Tropical Humid Forest (bh–T), Premontane Tropical Humid Forest (bh–PT) (Goreu, 2017). The trial was established with 209 open-pollinated progenies, collected in 14 sites in the Aguaytia and Pachitea River Basins: New Requena – River (17 trees), Neshuya Stream – Federico Basadre Road (CFB) Km 49.5 (13 trees), Tahuayo Stream – CFB Km 72 (11 trees), Curimana – River (20 trees), Aguaytia River (19 trees), Yurac Stream – Aguaytia (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) (Revilla-Chavez *et al*., 2022). The progeny test was planted in three different sites (sectors 1, 2 and 3) (Figure 1a), each trial established in a randomized complete block design with three blocks (repetitions) distributed in three environments, 200 progenies per block and two individuals per plot (400 plants per evaluable block). Each block has 0.25 ha, with a density of 1,600 trees/ha, spacing between trees of 2.5 x 2.5 m, and with two lines of non-evaluable plants at the edge of the plots (Revilla-Chavez *et al*., 2021).

Figure 1 – a. Geographical location of plots (repetitions); b. Physiography of the study area

Sector 1			Sector 2			Sector 3		
Plot	East	North	Plot	East	North	Plot	East	North
r2	516260	9077069	r7	498937	9051877	r11	487388	9022150
r3	517074	9077328	r8	488915	9064933	r12	487362	9021936
r4	517239	9077741	r10	497902	9034396	r13	486621	9021206

Source: Authors (2023)

2.2 Evaluation of traits

The phenotypic evaluation of the trees was performed for biometric and morphological traits. Seven procedures were used to evaluate the biometric traits total height of the tree, diameter, number of branches, number of rings, location and arrangement of branches with or without leaves (Figure 2). The tree height (cm) was measured with a telescopic ruler from the base to the upper end of the apex (Figure 2a). The evaluation of stem form was performed using the table of traits from the World Agroforestry Center's domestication of agroforestry tree Project (Table 1). The

height of the tree (H, cm), the diameter at the height of the base (DAB, cm) and the diameter at breast height (DBH, cm) were measured; when it is the case (DAB< 2 cm) two diameters are measured perpendicular to each other (Figure 2b) with the help of a caliper, while with DAB or DBH> 2 cm, the diameter tape was used. The branches were evaluated by counting them separately at three levels of the tree crown, lower, middle and upper (Figure 2c, c1, c2, and c3), and at the same time it was observed whether they had leaves, axillary leaves or no leaves (Figure 2f, g and h). As morphological traits, stem form and stem health were evaluated using a graphic template of 32 most frequent stem morphotypes (Figures 3 and 4, Table 1) correlated with their biometric traits, because a qualitative trait varies from the observer's point of view, so the graphic descriptors are intended to reduce the evaluation error. For the evaluation of the symptoms, the description described in Table 1 was be used.

Figure 2 – Graphic diagrams of trait evaluation
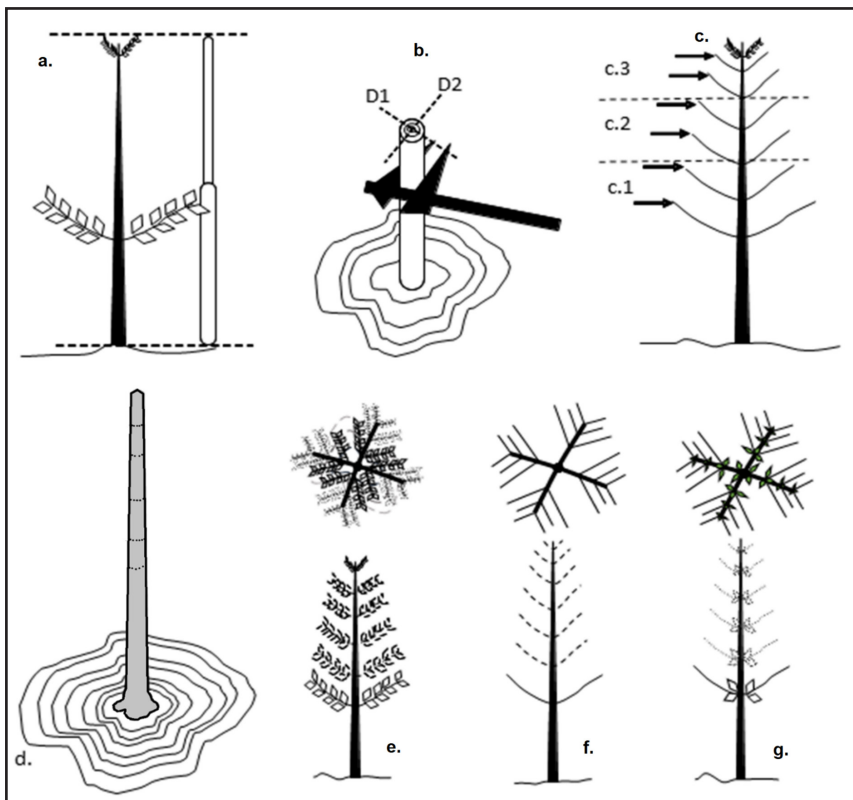
Source: Authors (2023)

In where: a. measurement of the total tree height (Height); b. diameter measurement: diameter 1 (D1) and diameter 2 (D2); c. branch count: c.1. upper branches; c.2. middle branches; c.3. lower branches; d. branches with leaves; f. leafless branches; g. branches with axillary leaves.

Table 1 – Stem form type, forked stem, inclined stem form, and plant symptoms of the trees

Class	Terminal bud		Branches		Stem	Code
	Presence	Dominance	Orientation	Positions		
Stem form	yes	yes	vertically	different	straight	F10
	yes	yes	horizontally	different	straight	F11
	yes	yes	vertically	different	crooked	F12
	yes	yes	horizontally	different	crooked	F13
Forked stem	yes	yes	vertically	different	-	F20
	yes	yes	horizontally	different	-	F21
	yes	yes	vertically	single plane	-	F22
	yes	yes	horizontally	single plane	-	F23
	no	yes	vertically	different	-	F24
	no	yes	horizontally	different	-	F25
	no	yes	vertically	single plane	-	F26
	no	yes	horizontally	single plane	-	F27
	yes	no	vertically	different	-	F28
	yes	no	horizontally	different	-	F29
	yes	no	vertically	single plane	-	F210
	yes	no	horizontally	single plane	-	F211
	no	no	vertically	different	-	F212
	no	no	horizontally	different	-	F213
	no	no	horizontally	single plane	-	F214
	no	no	vertically	single plane	-	F215
Inclined stem form	yes	yes	veritcally	different	-	F30
	yes	yes	horizontally	different	-	F31
	yes	yes	veritcally	single plane	-	F32
	yes	yes	horizontally	single plane	-	F33
	no	yes	veritcally	different	-	F34
	no	yes	horizontally	different	-	F35
	no	no	veritcally	single plane	-	F36
	no	no	horizontally	single plane	-	F37
	yes	no	veritcally	different	-	F38
	yes	no	horizontally	different	-	F39
	yes	no	veritcally	single plane	-	F310
	yes	no	horizontally	single plane	-	F311

Class	Fungal attack	Insect attack	Nutritional deficiencies	Animal damage	Code
Plant symptoms	no	no	no	no	0
	yes	no	no	no	1
	no	yes	no	no	2
	no	no	yes	no	3
	no	no	no	yes	4

To be continued ...

Table 1 – Conclusion

	Fungal attack	Insect attack	Nutritional deficiencies	Animal damage	Code
Plant symptoms	yes	yes	no	no	5
	no	yes	yes	no	6
	no	no	yes	yes	7
	yes	yes	yes	no	8
	no	yes	yes	yes	9
	yes	yes	no	yes	10
	yes	no	yes	yes	11
	yes	yes	yes	yes	12

Source: Adapted from the World Agroforestry Center's domestication of agroforestry tree Project (2023)

Figure 3 – a. Branches in different positions; b. Branches in a single plane
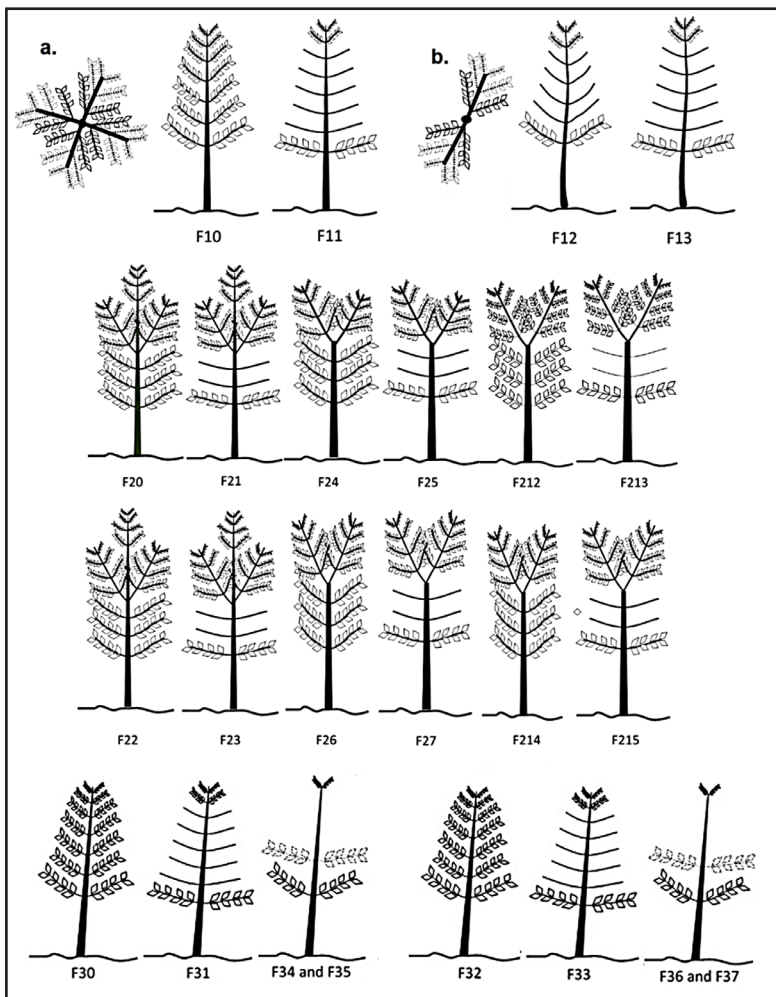
Source: Authors (2023)

In where: Normal stem form with branches in different positions F10 to F13; Forked stem: F20, F21, F24, F25, F212, F213 to F215 and shape of inclined stem with branches in different positions F30, F31, F34 and F35. Inclined stem form with branches in a single plane F32, F33, F36, and F37.

2.3 Graphic of stem classification

For the evaluation of the types of stem of the tree, an alphanumeric coding system was established, which has as first digit „F" corresponds to the abbreviation of stem, plus the shape code that corresponds to „1" for the normal stem, "2" forked stem and "3" for a sloping stem and a correlative code of the existing variants regarding the form of insertion of the branches in the stem ranging from 1 to 15, resulting in the following code, for example F212 breaks down to: F212= F+2+12, where, F is the shaft, 2 is the forked stem and, 12 is no terminal bud, no dominance, branches in vertical orientation, branches in different positions. The method shows how the counting of the rings formed by the presence of dry knots caused by the fall of tree branches was carried out (Figure 2e). The graphs of tree types with normal and bifurcated stems (Figure 3), with variants in the form of arrangement of branches, which appear as branches in different positions, when they project into more than two directions opposite to each other and in more than one plane, being observed from above as a cross or more edges (Figure 3a); while the variant with branches arranged in a single plane, is observed in a single line of branches opposite each other, seen from above is a line (Figure 3b), this type of stem is presented similarly to how the rachis in a branch. The inclined tree type plots (Figure 3) maintain the variants of branch arrangement similar to the previous models.

2.4 Statistical analysis

To determine whether the data were normally distributed, the Kolmogorov-Smirnova (degree of freedom > 50) and Shapiro-Wilk (degree of freedom < 50) tests were applied using the SPSS statistical software (02-03-2022). To determine the correlations between quantitative and qualitative traits, Spearman's correlation coefficient analysis was applied between pairwise traits at level of sector, plot, progeny, diameter, height, stem form, branches and health, using RStudio software 2022.12.0 Build 353.

Site-level and joint-site analyzes of variance were performed based on the incomplete randomized block design, using the SAS program (SAS, 1999) and the GLM procedure to determine significant differences between treatments. The variance

components were estimate using the REML (Restricted Maximun Likelihood) method, in combination with the VARCOMP command of the SAS statistical program due to the experimental imbalance in terms of the unequal number of surviving trees per plot. For site-level analysis, the following mixed model was use – Equation (1):

$$Y_{ijk} = \mu + b_i + t_j + e_{ij} + d_{ijk} \tag{1}$$

Where: Y_{ijk} is the phenotypic value of the k-th individual of the j-th progeny of the i-th replication; μ is the fixed term of the total mean; b_i is the fixed effect of the i-th replication; t_j is the random effect of the j-th progeny; e_{ij} is the effect of the random interaction between the j-th progeny and the i-th replication; d_{ijk} is the random effect of the k-th tree within the j-th progeny of the i-th replication; $i = 1 \ldots b$ (b is the number of replication); $j = 1 \ldots t$ (t is the number of progeny); $k = 1 \ldots n$ (n is the number of plants within the progeny).

For joint analysis, the following mixed model was used – Equation (2):

$$Y_{ijkl} = \mu + l_i + b_{j(i)} + t_k + lt_{ik} + e_{ij(k)} + d_{ijkl} \tag{2}$$

where: Y_{ijkl} is the phenotypic value of the l-th individual of the k-th progeny of the j-th replication at the i-th site; l_i is the fixed effect of the i-th site; μ is the fixed term of the total mean; $b_{j(i)}$ is the fixed effect of the j-th replication within the i-th site; t_k is the random effect of the k-th progeny; lt_{ik} is the effect of the random interaction between the k-th progeny with the i-th site; $e_{ij(k)}$ is the effect of the random interaction between the k-th progeny in the j-th replication within the i-th site; d_{ijkl} is the random effect of the l-th tree within the k-th progeny of the j-th replication at the i-th site; $l = i \ldots s$ (s is the number of sites evaluated).

The estimated components of variance were, equations (3) and (4)

$$h_f^2 = \frac{\sigma_f^2}{\sigma_f^2 + \frac{\sigma_e^2}{J} + \frac{\sigma_w^2}{JK}} \tag{3}$$

$$h_{f(s)}^2 = \frac{\sigma_f^2}{\sigma_f^2 + \frac{\sigma_{fxe}^2}{L} + \frac{\sigma_e^2}{LJ} + \frac{\sigma_w^2}{LJK}} \tag{4}$$

where: σ_f^2 = genetic variance between progenies; σ_{fxs}^2 = variance of genotype x site interaction; σ_e^2 = environmental variance; σ_w^2 = environmental variance; From the components of variance were estimated the additive genetic variance ($\sigma_a^2 = 4\sigma_f^2$) and mean heritability among progeny (h_f^2, $h_{f(s)}^2$) for each site and joint sites.

Coefficients of genetic and phenotypic correlations were estimated between DBH and plant height *versus* stem form, braches, and health for each site and joint-site, based on Namkoong (1979).

3 RESULTS AND DISCUSSION

The development of methodologies for the phenotypic evaluation of *Guazuma crinita* trees at 36 months of age is based on the principle that the traits plant height, diameter, stem form and health have a greater heritability, so these are the traits most suggested for the selection of trees in domestication programs (Vallejos *et al*., 2010; Gutierrez-Vasquez *et al*., 2016). From an adequate evaluation of these traits, the phenotypic plasticity of the species can be determined, being this fundamental in adaptation, survival, development, reproduction and evolution in ecosystems in permanent changes (Parejo-Farnés; Aparicio; Albaladejo, 2019).

According to normality tests for growth and stem form traits, the data did not show a normal distribution at the sector level (P< 0.005, Table 2). Therefore, applying Spearman's correlation test, it was found that there was significant correlation between traits at sector, plot level with diameter, plant height, stem form, branches and health, while progeny had correlation with diameter, plant height, stem form and branches; on the contrary there was no correlation between sectors and stem form with health (Figure 4), having sector and plot a low correlation and inversely with stem form (ρ: -0.10 and -0.09, respectively). According to Murillo *et al.* (2003), qualitative characters such as stem shape respond to a reduced number of alleles, making shape a more stable trait, since a regular stem frequency (81-95%) is observed despite the diversity of environments. In contrast, quantitative traits such as plant diameter and height may respond better to genotype-environment interactions, as shown by the effect of sector and plot with diameter (ρ: 0.55 and 0.58, respectively) and height (ρ: 0.63 and 0.67, respectively).

Table 2 – Test of normal distribution for stem form

	Kolmogorov-Smirnova			Shapiro-Wilk		
Sector	Test	df	P-value	Test	df	P-value
1	0.392ª	1060	<0.001	0.345ª	1060	<0.001
2	0.427ª	599	<0.001	0.191ª	599	<0.001
3	0.368ª	596	<0.001	0.378ª	596	<0.001

Source: Authors (2023)

In where: df is the degree of freedom; a Lilliefors significance corrections

Figure 4 – Probability values (Pvalue) and Spearman's correlation coefficient (ρ) of for the main quantitative and qualitative traits of *Guazuma crinita* progeny test at 36 months of age in the Aguayita river basin, Ucayali, Peru
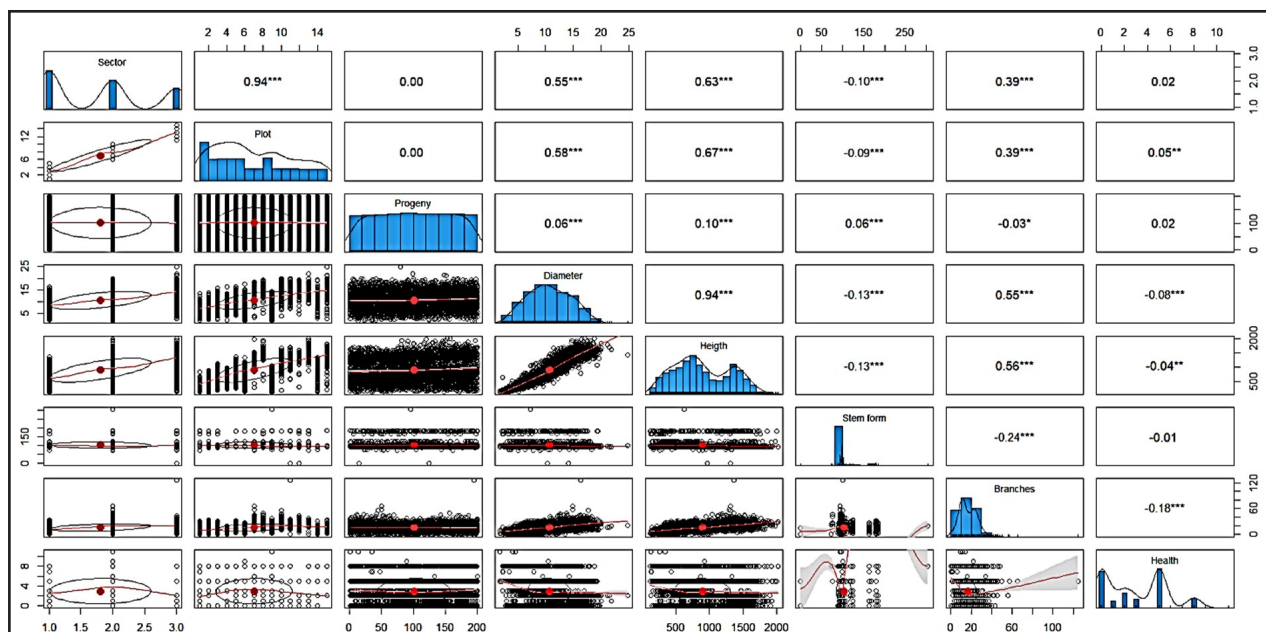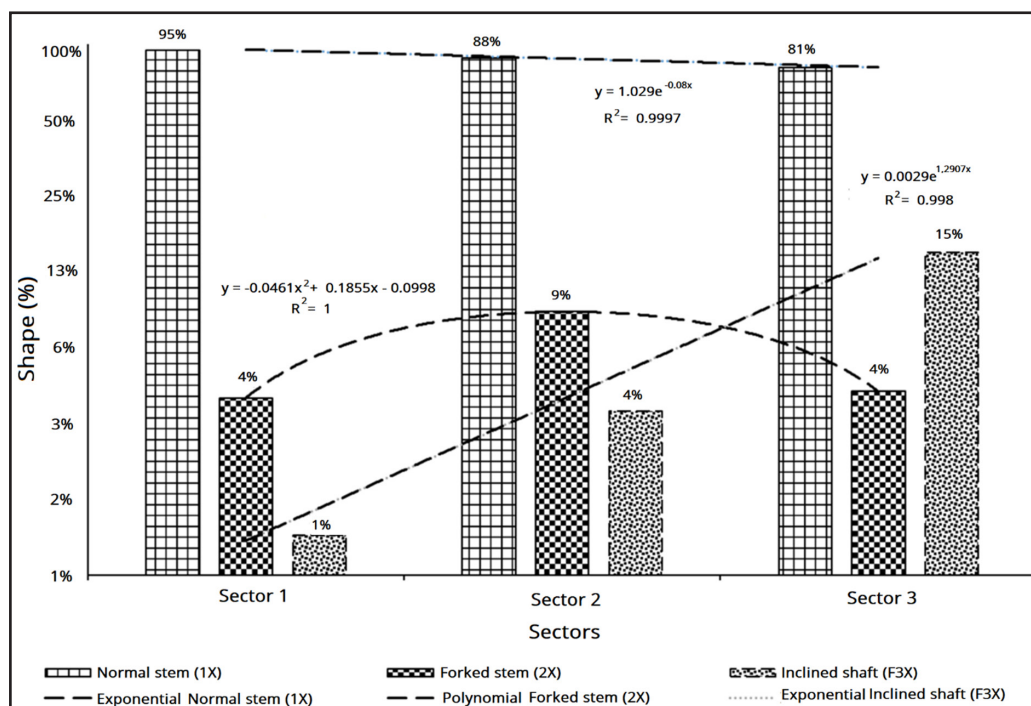

Source: Authors (2023)

In where: **P< 0.05; ***P< 0.01

Taking into account that the sectors and plot were correlated with the main selection traits such as diameter, height, stem form and branches (Figure 5), we can see that in all sectors there is a higher prevalence of trees with normal stems, which is expressed by the exponential regression model Y= 1.029e-0.08x (R²= 0.9997) and is

inversely proportional to the rise of the sector in the basin (Figure 1b and 6), while trees with inclined stems have exponential behavior directly proportional to the rise of the sector in the basin expressed with the exponential regression model Y= 0.0029e1.2907x (R²= 0.998), which could be attributed to the increase in the slope of the soil; while the trees with bifurcated stems have a downward concave polynomial behavior as they ascend in the basin expressed by equation Y=-0.0461x2+0.1855x-0.0998 (R²= 1). According to the evaluations resulting from this methodology, it is observed that the traits under analysis have a strong correlation with each other, due to the fact that there is an intrinsic natural relationship between them, product of the expression of their genotypes in their interaction with the environment (Parejo-Farnés; Aparicio; Albaladejo, 2019), as applied in the present study.

Figure 5 – Occurrence of normal (F1X), bifurcated (F2X) and inclined (F3X) bole types in *Guazuma crinita* progeny test at 36 months of age by site (sectors) in the Aguaytia river basin, Ucayali, Peru

Significant differences were detected between progenies for DBH, height, branches and health at site 1, and for all traits at sites 2 and 3 (Table 3). Significant differences between sites were also detected for all traits, although no significant genotype-environment interactions were detected for traits. These results indicate that, although the traits have different performance between sites, in terms of growth, stem forme and tree health, due to the absence of genotype-environment interaction, there is the possibility of genetic improvement through the simultaneous selection of the same progenies for all sites. In addition, the trees in the three study sites have generally straight boles, lack of bifurcation, and low rates of attack by fungi, insects, nutritional deficiency, and damage caused by animals.

Table 3 – Estimates of mean among family heritability (h_f^2) for trees at 36 months of age for DBH, height (H), stem form (SF), braches (BR), and health (HE), per site and joint sites

	DBH (cm)	H (m)	SF	BR	HE
Mean					
Site 1	8.6**	6.2*	97.2	12.4**	2.76*
Site 2	11.8**	10.7**	93.6*	19.8*	2.97*
Site 3	14.0**	13.0**	95.0**	19.1*	3.16**
Joint	11.5**	9.97**	95.1	17.9	4.03
P-value-Site	<0.001	<0.001	<0.001	<0.001	<0.001
P-value-GxE	0.943	0.328	0.381	0.685	0.872
h_f^2					
Site 1	0.281	0.094	0.407	0.065	0.118
Site 2	0.273	0.352	0.409	0.094	0.127
Site 3	0.198	0.304	0.695	0.189	0.087
Joint	0.293	0.356	0.524	0.158	0.123

Source: Authors (2023)

In where: *Pvalue< 0.05; **Pvalue< 0.001; P-value-Site and P-value-GxE for F test among sites and genotype by enviromental interaction (GxE).

Mean heritability among progenies (h_f^2) was variable across locations and traits, with values ranging from low ($h_f^2 \leq 0.2$) to moderate ($0.2\ h_f^2 \leq 0.7$), where stem form presented the highest values and branches and health generally showed the lowest values. In addition, joint analyzes generally show the highest heritability values, which, associated with the fact that the genotype by environmental interaction did not alter the classification of progenies between environments, the same progenies can be selected for the production of improved seeds to meet the demand for seeds for commercial reforestation in the three locations. Stem form, tree height and DBH are the most suitable traits for selection, as they have the highest heritability values.

Genetic (rg) and phenotypic (rp) correlations were estimated between trait pairs at each site and joint site (Table 4). Genetic and phenotypic correlations show a direct association between DBH, height, stem form and branches and an inverse relationship between DBH and height with health. Results show generally higher (or similar) genetic correlations than phenotypic correlations between traits. Genetic and phenotypic correlations were high (> 0.7) between DBH and altura, and moderate ($0.2\ r \leq 0.7$) between DBH and tree height with stem form and branch. Genetic and phenotypic correlations between DBH and health ranged from low (-0.04) to moderate (-0.35) and from low (-0.06) to high (-0.91) between tree height and health. These results indicate a very positive picture for selection of multiple traits in the progeny test and that it is possible to construct a selection index for simultaneous selection of progenies. For example, the results indicate that the selection of progenies with high DBH will select taller trees with straighter stamens. In addition, the inverse relationship observed between DBH health and tree height indicates that larger trees have a low incidence of fungal attack, insects, nutritional deficiency and damage caused by animals and low branches. Thus, the selection of progenies with high DBH will result in indirect selection for progenies with high sanity.

Table 4 – Genetic (rg) and phenotypic (rp) correlations between DBH, height (H), stem form (SF), braches (BR), and health (HE), per site and joint sites

	Site 1		Site 2		Site 3		Joint	
	rg	rp	rg	rp	rg	rp	rg	rp
DBH vs H	0.93**	0.92**	0.89**	0.83**	0.87**	0.88**	0.85**	0.93**
DBH vs SF	0.72**	0.64**	0.41*	0.45*	0.45*	0.41*	0.64**	0.63**
DBH vs BR	0.6**	0.55**	0.47*	0.3*	1.0**	0.36*	0.64**	0.33*
DBH vs HE	-0.13	-0.08	-0.36*	-0.07	-0.04	-0.04	-0.29*	-0.2*
H vs SF	1.0**	0.54**	0.51**	0.23*	0.73**	0.42*	0.55**	0.5**
H vs BR	1.0**	0.5**	0.55**	0.56**	0.55**	0.34*	0.86**	0.31*
H vs HE	-0.65**	-0.12	-0.91**	-0.06	-0.35*	-0.08	-0.16*	-0.15*

Source: Authors (2023)

In where: **$P < 0.01$; *$P < 0.05$.

The methodological development for the phenotypic evaluation in 36-month-old *Guazuma crinita* progeny test, is especially important, because by developing practical evaluation methods it can support the early selection of better phenotypes and help in genetic gain in a shorter time and in turn improve the profitability of the plantations what is preferable during the juvenile stage (De Grado; Diez; Alia, 1999; Gorbitz *et al*., 2020). Therefore, evaluating this trait establishes a form of classification that allows the trees to be assessed quickly and consistently (Gutiérrez-Caro *et al*., 2018) and as corroborated in the present study. We concluded that the morphological traits measured allowed to graph the procedures for the phenotypic evaluation of *Guazuma crinita* progeny test, maintaining the correlations that exist between them.

4 CONCLUSIONS

Considering the strong phenotypic correlation between biometric and morphological traits in forest species, the graphical evaluation methodology used in the evaluation of *Guazuma crinita* progeny test at 36 months of age in the Aguaytia river basin, Ucayali, Peru, maintained correlations between the traits evaluated, which allows the use of this methodology in experiments of other tropical tree species. There

are genetic differences among progenies for both growth and morphological traits, which can be exploited by selecting the best progenies and establishing an orchard to meet the demand for improved seeds for commercial plantings in the three study sites. The growth rate differed between the three study sites, but due to the simple genotype-environment interaction, it is possible to establish only one seed orchard to meet the demand for improved seeds in the three sites. Based on the highest heritability values, the most suitable traits for selection are DBH, height and stem shape. The genetic correlations observed between growth and morphological traits indicate that selection in any one of them can promote direct or indirect genetic gains in the others.

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