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RESEARCH ARTICLE

Resilience of progeny of *Swietenia macrophylla* to the simulated attack of *Hypsipyla grandella* in nursery

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Abstract

The resilience of seedlings from four open-pollinated families of *Swietenia macrophylla* to simulated attacks by *Hypsipyla grandella* was evaluated at the nursery stage to determine the possibility of early selection of individuals from the most resilient families and establish sustainable forest plantations in the Peruvian Amazon. Significant differences were detected among families for diameter (D), sprout length (SL), and basal sprout area (BA). The coefficient of determination for genotypic effects was moderate (range: 0.248 – 0.457) for H (plant height), D, SL, and BA, and low (< 0.15) for plant base height (HB), number of sprouts (NR), number of branches (NB), and number of leaves (NL). The genetic correlation for the traits H, D, SL, BA, NR, NB, and NL ranged from 0.228 to 0.996, indicating that an increase in one of these traits can result in an increase in the other. This is important because there is the possibility of early selection of families for the traits D, SL, and BA for the development of plantations with families resistant to attack. Therefore, the genetic and phenotypic variation observed in the families suggests the possibility of early selection as a promising strategy for genetic improvement programs, using a larger number of families than those used in the present study, since theoretically larger samples may contain greater genetic variation between and within families.

Keywords: Amazonia; early selection; progeny; shoot borer; mahogany.

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1. Introduction

Mahogany, *Swietenia macrophylla* King (Meliaceae) is one of the most valuable large, deciduous Neotropical tree species on the world market (Gullison et al., 1996; Degen et al., 2012; Sebbenn et al., 2012). Its wood has excellent aesthetic, physical, and mechanical characteristics, remarkable workability, and is used in the manufacture of luxury furniture, interior decoration for civil construction, and musical instruments (Carvalho, 2006; André et al., 2008). The geographic range of *S. macrophylla* extends from southern Mexico to the southern Amazon basin in Bolivia, Brazil, and Peru (Lamb, 1966). In adulthood, individuals can reach a diameter at breast height > 2 m and a tree height of up to 50 m (Gullison et al., 1996), but population density is generally low, <1 tree/ha (Grogan et al., 2008). Logging of *S. macrophylla* began in the 16th century in Central American populations (Mejía et al., 2008), but large-scale harvesting began in South American populations in the 20th Century (Grogan et al., 2008), where due to over-exploitation during the 1970s and 1980s resulted in a decline in their natural populations (Alcalá et al., 2015). In Peru, the species has been exploited since the 1920s (Mejía et al., 2008). As a result, many natural *S. macrophylla* populations have become spatially isolated, resulting in a loss of genetic diversity (Novick et al., 2003; Breed et al., 2012; Degen et al., 2012; Sebbenn et al., 2012; Alcalá et al., 2015; Oliveira et al., 2020; Andrade et al., 2022). Due to that, *S. macrophylla* was included on the list of endangered species of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) Appendix II (CITES, 2019).

Across the geographic range of *S. macrophylla* natural distribution, demand for its timber has exceeded available supply due to extinction or decreases in natural population sizes throughout its range (Reynel et al., 2003; Campos et al., 2009; Castro et al., 2019; Andrade et al., 2022; Arlacon-Méndez et al., 2023). The future of mahogany as a commercial timber species is at risk due to overexploitation and deforestation (Verwer et al., 2008). For this reason, the use of the species in commercial reforestation and degraded area restoration programs has been gaining prominence in various places across the Americas (Barrena & Vargas, 2004; Kurihara et al., 2005). However, insects such as *Hypsipyla grandella* Zeller (Lepidoptera: Pyralidae) have been identified as the main pest and the most important barrier to establishing and developing *S. macrophylla* commercial plantations (Grijpma & Gara, 1976; Lunz et al., 2009). The caterpillar attacks the terminal bud of the plant causing bifurcations (Grijpma & Gara, 1976; Lunz et al., 2009), or it can feed on the fruits and seeds of the plant (Castro et al., 2019).

Hypsipyla grandella is difficult to control, which is why multiple methods were tested with different results, even though they could significantly reduce populations, although even low population levels could cause important damage to the plantation, among the most commonly used ones are silvicultural management, chemical, bioecological control, integrated systems, resistance to hosting and combinations between methods, are some of them (Álvarez et al., 2021; Guerra-Arevalo et al., 2022; Dueñas, 2022; Borges et al., 2022; Ávila-Arias et al., 2023; Domínguez et al., 2023; García et al., 2024; Ávila-Arias et al., 2025).

One way to address this problem is to establish commercial plantations with seedlings that are resistant to *H. grandella* attacks (Newton et al., 1993; Mayhew & Newton, 1998; Schabel et al., 1999). To develop a selection strategy, the three aspects of coexistence, prevention, and sustainability must be considered, alongside the use of resistant or tolerant trees based on the antixenosis of *H. grandella* to the Meliaceae family throughout the Americas (Jiménez, 2007). In terms of improving tree response to *H. grandella* attacks, the terminal bud of the plant can be eliminated by pruning so that it does not bifurcate or emit several regrowth sprouts, with subsequent selection of the most vigorous plants (Navarro et al., 2004; Revilla-Chávez et al., 2024).

In this context, the use of techniques such as the predictive decapitation of *S. macrophylla* regrowth can help genetic selection by identifying trees with greater tolerance to *H. grandella* attacks, resulting in improved commercial plantation viability (Cornelius, 2009). Based on this technique, studies have observed genetic differences at the individual level, where *S. macrophylla* from Panama produced an average of 2.2 regrowth sprouts per tree after decapitation with scissors, while those from Costa Rica had 3.1 regrowth sprouts per tree (Hilje & Cornelius, 2001). In the case of Meliaceae species such as *Cedrela* sp. and *S. macrophylla*, the number of regrowth sprouts produced after an *H. grandella* attack represents an important component of attack tolerance, as species show a wide range of responses, from a single regrowth to 10 or more (Hilje & Cornelius, 2001). Thus, simulated attacks using scissors can be conducted across different genotypes early in the nursery phase for later establishment in the field. The results suggest that it is feasible to identify genotypes that are more tolerant to attack by using the decapitation test (Hilje & Cornelius, 2001; Revilla-Chávez et al., 2024).

The aim of this study was to assess the vegetative regrowth of *S. macrophylla* plants from four different families to simulated attacks by *H. grandella* in a nursery and examine the possibility of early selection of individuals more suitable for the development of forest plantations in the Peruvian Amazon. We emphasize that the present study represents an exploratory investigation (pilot study) to assess the possibility of early selection of *S. macrophylla* individuals for vegetative regrowth before *H. grandella* attack in the nursery phase. This is not an empirical study aimed at using the selected plants in a program of genetic improvement of the species, as a progeny test with only four *S. macrophylla* families is insufficient to conduct selection between and within progenies in a breeding program.

2. Methodology

The study was carried out in the Forest Nursery at the Faculty of Forestry and Environmental Sciences of the National University of Ucayali, Manantay district, Coronel Portillo Province, Ucayali Region, Peru. For the study, open-pollinated seeds from four seed-trees were sampled at four locations: Juanjui (UTM 326823E, 9055066N; elevation of 283 m) and Sisa (326878E; 8767893N; elevation of 430 m), representing families from the San Martin region; and

Primavera (558797E; 8779586N; elevation of 164 m) and Unión (559748E; 8801935N; elevation of 164 m), representing families from the Ucayali region (Figure 1). On September 6, 2018, 175 seeds per family were sown directly into polyethylene bags with fertile substrate, composed of two volumes of black soil, one of sand and one of worm humus, with a texture of 40% silt, 30% clay and 30% sand. Of the sown seeds, 27 Juanjui seeds, 16 Sisa seeds, 143 Primavera seeds, and 25 Unión seeds germinated. On December 29, 2018, when the plants reached an average height of 30 cm, 50% of the crowns of 77 plants selected for their best phenotypic characteristics in the nursery were decapitated with pruning shears to simulate an attack by *H. grandella* (Figure 2). A completely randomized design with unbalanced repetitions was applied, with 22 from the Juanjui family, 22 from the Primavera family, 22 from the Unión family, and 11 from Sisa. After decapitation, the plants were evaluated at 194 days of age. Plant height (H, cm), plant base height (HB, cm), stem diameter (D, cm), number of regrowth sprouts (NR), sum of regrowth length (RL, cm), regrowth basal area (BA, mm^2), number of branches (NB), and number of leaves (NL), were evaluated until robust regrowth sprouts were obtained.

The data were arranged in an unbalanced completely randomized design, and the following steps were applied for processing. For analysis of variance, the trait number of regrowth (NR) was transformed by $\sqrt{x + 0.5}$. The REML/BLUP procedure (restricted maximum likelihood/best unbiased linear prediction), via linear mixed model methodology was used in individual analyzes to estimate the variance components and genetic parameters of each of the trait evaluated in the progeny test, using the SELEGEN software, according to the statistical model 82 (Resende, 2016), y= Xt + Zb + e, where y is the data vector, t is the vector of treatment effects assumed to be fixed added to the general average, b is the vector of random repetition effects, and e is the vector of (random) errors or residuals.

Capital letters represent the incidence matrices for the effects. From the analysis, we also estimated the components of quadratic function among families (Φ_f) and environmental variance (σ_e^2). The quadratic additive genetic variance (C_A^2) was estimated by assuming that the open-pollinated families originated from a mixed mating system, as $C_A^2 = \Phi_f / r_{xy}$, where r_{xy} (0.359) is the mean coefficient of relatedness among plants within families, estimated from mating system parameter reported for *S. macrophylla* (Sebbenn, 2002). The coefficient of determination of genotypic effects (C_i^2) was estimated as $C_i^2 = C_A^2/(C_A^2 + \sigma_e^2)$ and coefficient of individual genetic variation as $CV_{gi}(\%) = 100(\sqrt{C_A^2}/\bar{x}_o)$ (where $\bar{x}_o$ is the mean of the measured trait under analysis). Expected genetic gain by mass selection of 20 (26%) out of 77 seedlings was estimated as $G(\%) = 100[(\mathrm{S}h_i^2)/\bar{x}_o]$, where S is the selection differential index ($S = \bar{x}_s - \bar{x}_o$, where $\bar{x}_s$ is the mean of the trait for selected individuals). All parameters, as well as the mean standard error of C_i^2 (SE), coefficients of genetic correlation (r_g) and phenotypic correlation (r_f) were estimated based on Resende (2002).

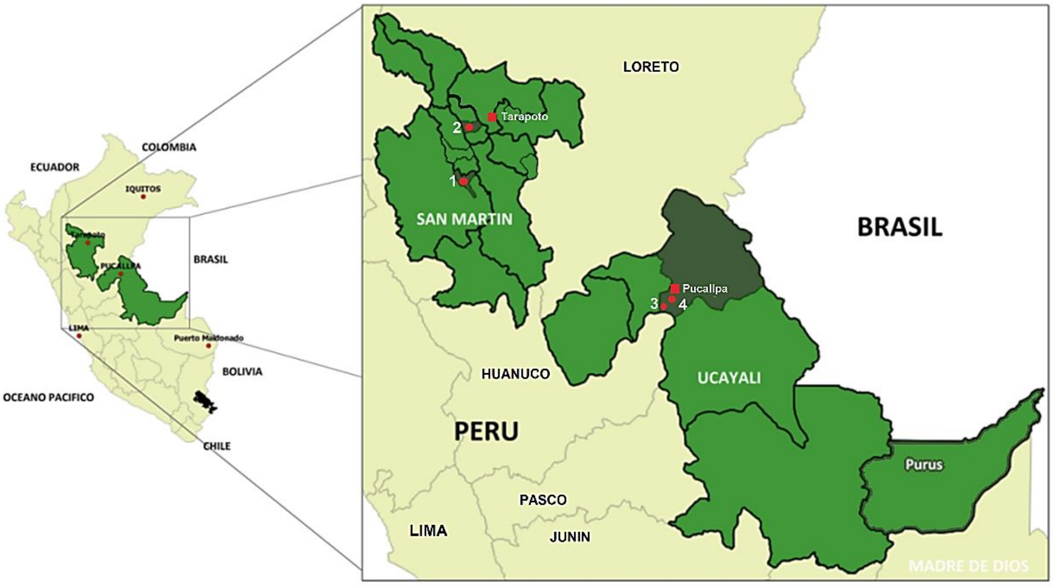

Figure 1. Map of *Swietenia macrophylla* germplasm collection and area of the project; 1=Juanjui (San Martín); 2=Sisa (San Martín); 3=Primavera (Ucayali); 4=Unión (Ucayali).

Figure 2. Decapitation of 50% of the crown of plants in the nursery to simulate the attack of *Hypsipyla grandella;* a: plants in nursery; b, c: decapitation of the plant; d: disinfection and cut sealing; e, f: regrowth 23 days after decapitation.

A multivariate analysis was conducted to evaluate the genetic and phenotypic correlations among the variables of interest. The variables considered in the study were: plant height (H), plant base height (HB), stem diameter (D), number of regrowths (NR), sum of regrowth length (RL), regrowth basal area (BA), number of branches (NB), and number of leaves (NL).

Initially, the phenotypic data corresponding to these traits were subjected to a cleaning process, which included the elimination of missing values and the correction of potential outliers using standard statistical procedures. Subsequently, a phenotypic correlation matrix was constructed using Pearson's correlation coefficient, as the variables exhibited distributions approximately close to normality. This coefficient is widely used to quantify the linear association between quantitative variables in studies focused on the prediction of plant quantitative traits (Pan et al., 2024).

In parallel, to address genetic correlations, the data were grouped according to their genetic origin or provenance. Phenotypic means were calculated by provenance, and a genetic correlation matrix was developed based on these means, again applying Pearson's correlation coefficient. This methodology allowed for the analysis of the average behavior of genetic groups and the detection of association patterns among the different traits.

Additionally, a Principal Component Analysis (PCA) was performed on the phenotypic data matrices. This technique facilitated the reduction of data dimensionality, allowing a graphical representation of individuals and variables based on the principal sources of variability. Variables were interpreted according to their contributions to each principal component, highlighting those that explained the highest percentage of total variability. The optimal number of components retained was determined using the elbow method, a widely employed technique for identifying the appropriate number of components in clustering and dimensionality reduction analyses (Crista et al., 2024).

Finally, the results derived from the multivariate analysis were interpreted comprehensively, identifying the most relevant phenotypic and genetic traits, the patterns of association among them, and their relationship with the different provenances analyzed. This methodological strategy provided a robust basis for understanding the existing phenotypic and genetic diversity, as well as for designing strategies aimed at selecting and conserving superior genetic materials.

3. Results and discussion

From the evaluation it is observed that the Juanjui, Primavera, Unión and Sisa origins had the best growth in descending order, while Primavera, Sisa, Juanjui and Unión in descending order had the greatest standard deviations (Figure 3). In the same way significant differences between at least two means of families were detected for stem diameter (D), regrowth length (RL), and regrowth basal area (BA), suggesting the possibility of genetic improvement through selection between families (Table 1). These results show that before the attack of *H. grandella* in the nursery stage, it is possible to conduct early selection of *S. macrophylla* families to quickly obtain genetic gains to establish experimental and commercial plantations.

Swietenia macrophylla is commonly used in reforestation projects (Barrena & Vargas, 2004; Kurihara et al., 2005; Ríos-Saucedo et al., 2017). Among the evaluated traits, the regrowth length (RL) is important for the management of *S. macrophylla* seedlings for reforestation purposes since individuals with greater RL can reach 6 m in height more quickly (Hilje & Cornelius, 2001). When experiencing recurrent attacks, this means healthy segments can develop until the next attack, thus improving wood quality (Cornelius, 2009). As the simulated *H. grandella* attack resulted in significant differences between families for regrowth length (RL) and other traits (D, BA), RL should be considered an important variable for early selection, rather than just considering growth in height and diameter for seedling selection.

For the traits plant base height (HB), number of regrowths (NR), number of branches (NB), and number of leaves (NL), the coefficient of genotypic determination (C_i^2) was low (ranged from 0.002 – 0.144), where for the plant height (H), diameter (D), regrowth lengths (RL), and regrowth basal area (BA) traits C_i^2 was moderate (ranged from 0.248 – 0.457, Table 1). These results indicate that H, D, RL, and BA may be more effective in increasing the population mean of traits by mass selection at the nursery trial stage and 194 days after the simulated *H. grandella* attack. This is particularly the case with RL which showed the highest values of C_i^2. However, the mean standard error of C_i^2 (SE) was generally high for all traits (SE: ranging from 0.028 – 0.46), which is related to the low total number of evaluated families (4) and individuals (77) in the progeny test. Thus, we strongly recommend that future studies include at least 500 individuals in the progeny test.

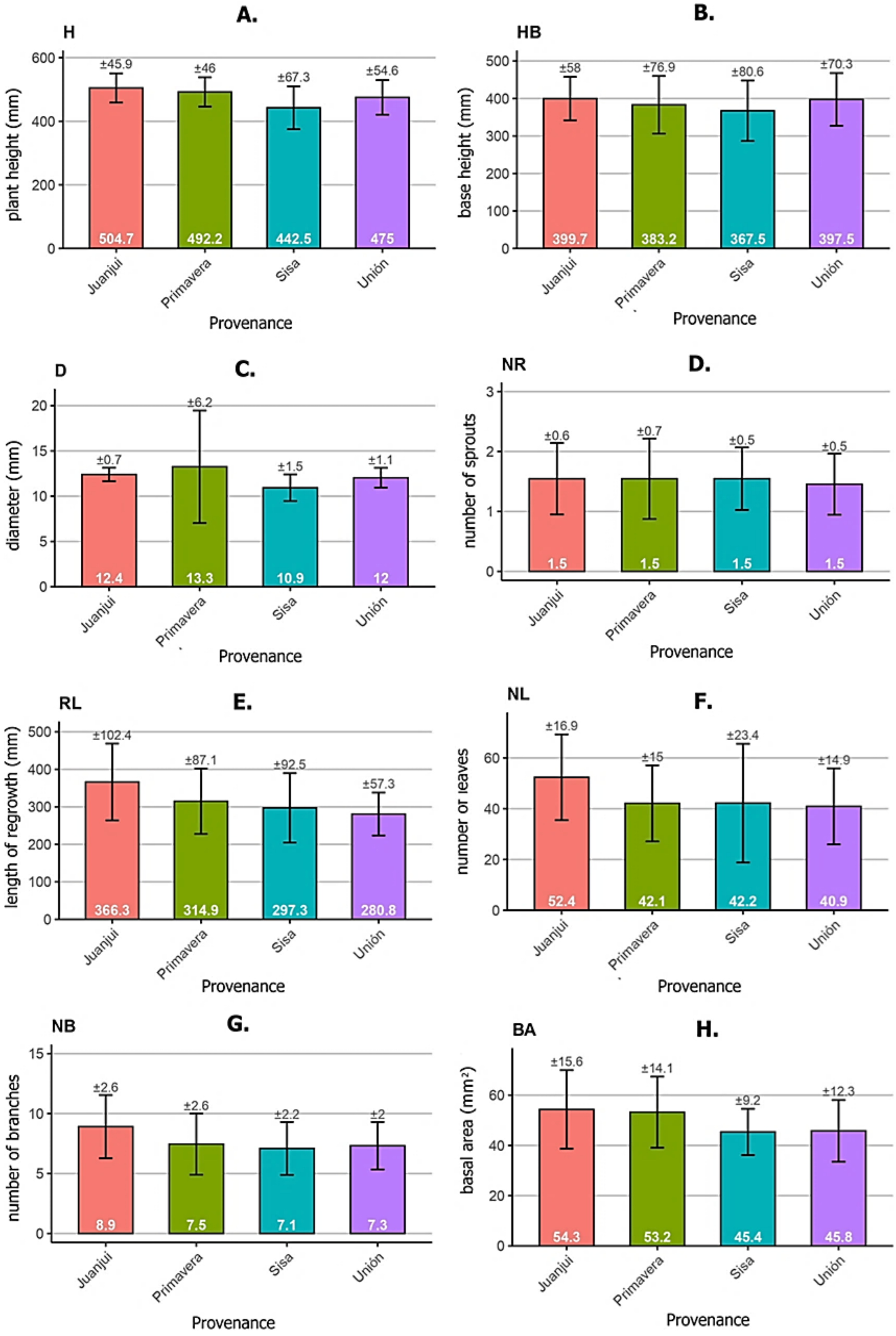

Figure 3. Means and standard deviations of *Swietenia macrophylla* provenances for the variables A. plant height (H, cm), B. plant base height (HB, cm), C. stem diameter (D, cm), D. number of regrowth sprouts (NR), E. sum of regrowth length (RL, cm), F. number of leaves (NL), G. number of branches (NB) and H. regrowth basal area (BA, mm^2) at 114 days in the nursery.

Table 1
Mean, coefficient of genotypic determination (C_i^2), coefficient of individual genetic variation ($CV_{gi}(\%)$) and expected genetic gain by massal selection ($G(\%)$) of traits

	Mean	LRT (χ^2)	$C_i^2 \pm SE$	CV_{gi} (%)	G (%)
Height (H, cm)	48.2	2.16	0.387 ± 0.445	6.8	2.9
Base height (HB, cm)	39.8	0	0.118 ± 0.259	4.7	0.5
Stem diameter (D, cm)	11.9	5.45*	0.248 ± 0.4	7.7	1.3
Number of regrowths (NR)	1.52	0	0.002 ± 0.028	1.4	0.02
Regrowth length (RL, cm)	31.6	3.69*	0.457± 0.436	17.0	5.9
Regrowth basal area (BA, mm^2)	0.51	3.73*	0.42 ± 0.46	15.9	6.9
Number of branches (NB)	7.82	0.94	0.144± 0.284	12.1	1.2
Number of leaves (NL)	45.2	0.69	0.117 ± 0.257	13.0	1.7

LRT: Likelihood ratio test, χ2 deviance chi-square; *$p < 0.05$, with 0.5 degree of freedom; $\pm SE$ is the mean standard error.

The coefficient of individual additive genotypic variation (CV_{gi}) was moderated for RL, BA, NB, and NL (ranging from 12.1% – 17%), and low for H, HB, D, and NR (ranging from 1.4 –7.7%). These results reinforce the possibility of obtaining genetic gains by mass selection due to the presence of additive genetic inheritance for the traits. For example, the mass selection of 26% of plants suggests an expected genetic gain ranging among traits from 0.02 – 6.9%. There are no other studies on *S. macrophylla* that report C_i^2 (or h_i^2) and CV_{gi} values for all traits evaluated in the present study, and most have focused mainly on plant H and DBH. Estimates of h_i^2 and CV_{gi} for height and DBH in *S. macrophylla* have shown variation across sites and age of trees. Estimates s on h_i^2 between 1.6 and 5 years of age have reported values ranging from 0.05–0.6 for H and from 0.07 – 0.55 for DBH, while estimates of CV_{gi} have ranged from 5.1–20.1% for H and from 0.5% – 21.9% for DBH (Navarro & Hernández, 2004; Wightman et al., 2008; Abarquez et al., 2015). The results for C_i^2 and CV_{gi} are within the observed ranges identified in previous studies for h_i^2 and CV_{gi}.

The genetic (r_g) and phenotypic (r_f) correlation coefficients between pairs of traits ranged from -0.727 – 0.996 (Table 2). The r_g and r_f correlations between HB and H and D were higher than zero (ranged from 0.64 – 0.881), where between HB and NR, RL, BA, NB, and NL were lower than zero (ranged from -0.059 to -0.727). For the other pairwise traits, the r_g and r_f correlations were higher than zero (0.028 – 0.996). We arbitrarily classified the magnitude of r_g and r_f values higher than zero as low ($r < 0.3$), moderate ($0.3 \leq r < 0.6$), and strong ($r \geq 0.6$). The r_g and r_f correlations were generally moderated or high (90.5%). The r_g correlation was low between RL x NL (0.228), and the r_f correlation was low between H x NR, H x NB, and NR x NL (ranging from 0.195 – 0.282). For the other pairs of traits, the r_g and r_f correlations were moderate or high (ranging from 0.302 – 0.996). These results indicate that an increase in one of the traits results in an increase in the other, especially for pairwise traits showing high genetic correlations.

Regrowth length (RL) is an important trait for the recovery of plants after decapitation or simulated attacks by *H. grandella* (Ríos-Saucedo et al., 2017). Thus, RL is a key trait consideration in early selection strategies because it helps individuals quickly surpass the critical phase (6 m in height), which occurs in the first three years (Hilje & Cornelius, 2001). After this phase, the risk of *H. grandella* attack decreases significantly. Because attacks occur in periodic and recurrent episodes, the selection of individuals with more vegetative regrowth can lead to improved growth with intact sections and relatively long stems (Hilje & Cornelius, 2001). The generally moderate to high genetic correlation (r_g) found between RL and H, D, NR, BA, NB traits (0.441 – 0.996) indicates that selecting plants with a higher RL will result in indirect selection for other traits. Furthermore, due to the substantial phenotypic correlation (r_f) found between RL with H and D (0.893 and 0.526, respectively), traits that are easily measured, early selection strategies for vegetative regrowth before *H. grandella* attacks at the nursery stage are expected to be effective.

Principal Components Analysis (PCA) allowed for the graphical representation of the relationships between the phenotypic variables and the evaluated provenances. The first two principal components (Dim1 and Dim2) explained 64.2% and 22.2% of the total variability, respectively, together accounting for 86.4% of the observed phenotypic variation (Figure 4). The vectors of the variables indicated patterns of association: the sum of shoot lengths (RL) and the number of leaves (NL) showed a strong positive correlation, projecting in similar directions. Likewise, the basal shoot area (BA) and the number of branches (NB) showed a moderate positive association. In contrast, the number of shoots (NR) was located almost in the opposite direction to plant height (H) and the height at the base of the plant (HB), suggesting a negative correlation between regrowth frequency and plant size.

Table 2
Genetic (upper diagonal) and phenotypic (lower diagonal) correlation between pairwise traits

	H	HB	D	NR	RL	BA	NB	NL
H		0.728	0.996	0.312	0.886	0.834	0.92	0.865
HB	0.606		0.64	-0.623	-0.164	-0.183	-0.207	-0.209
D	0.856	0.881		0.416	0.441	0.87	0.662	0.632
NR	0.195	-0.727	0.304		0.671	0.4	0.505	0.302
RL	0.893	-0.059	0.526	0.655		0.996	0.9	0.228
BA	0.447	-0.284	0.361	0.81	0.491		0.894	0.846
NB	0.231	-0.212	0.665	0.393	0.594	0.578		0.81
NL	0.889	-0.242	0.642	0.282	0.516	0.481	0.87	

Plant height (H), plant base height (HB), stem diameter (D), number of regrowth (NR), sum of regrowth length (RL), regrowth basal area (BA), number of branches (NB), and number of leaves (NL).

In relation to the provenances, Sisa projected toward the positive side of Dim1, suggesting a greater influence of traits associated with a high number of regrowth (NR). Juanjui was located toward the negative side of Dim1, indicating contrasting traits, likely related to greater plant height (H) and base height (HB). Primavera was positioned near the origin of the coordinate plane, indicating intermediate phenotypic values for most variables. Unión, meanwhile, separated along Dim2, suggesting particular traits possibly related to stem diameter (D) and other secondary variables. Overall, PCA facilitated the identification of key traits that differentiate the provenances, with NR, RL, and NL contributing the most to the observed variation. These results provide valuable information for selecting materials with greater regrowth potential and for understanding the genetic structure among the provenances studied.

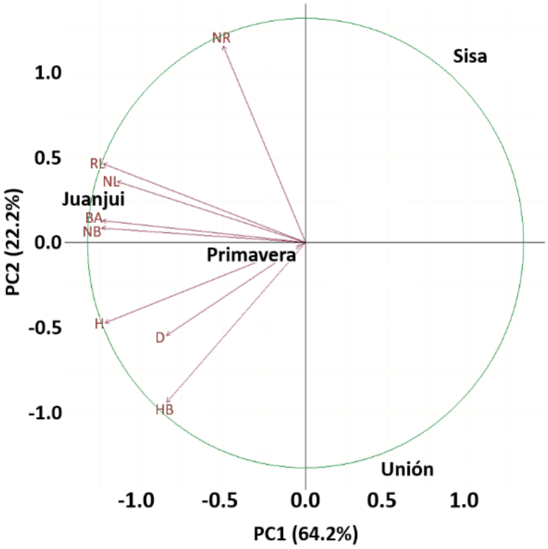

Figure 4. Principal component analysis (PCA) for the Juanjui, Primavera, Unión and Sisa provenances for the variables plant height (H, cm), plant base height (HB, cm), stem diameter (D, cm), number of regrowth sprouts (NR), sum of regrowth length (RL, cm), regrowth basal area (BA, mm^2), number of branches (NB), and number of leaves (NL).

The results of the Principal Component Analysis (PCA) show clear patterns of phenotypic differentiation among the evaluated provenances, based on variables primarily related to regrowth behavior and plant structural growth. Sisa's separation toward positive values of the first principal component (Dim1) suggests greater regrowth vigor, characterized by a greater number of regrowth (NR) and greater total regrowth length (RL), which could be associated with adaptive strategies in the face of environmental disturbances. In contrast, Juanjui's position on the negative side of Dim1 indicates a phenotypic profile centered on larger structural size, such as plant height (H) and base height (HB), but with a lower propensity for regrowth. This pattern could reflect adaptations to more stable environments, where height growth represents a competitive advantage.

Primavera's proximity to the origin suggests a provenance with intermediate behavior, while Unión, with its separation along Dim2, could represent a particular phenotypic variability, possibly associated with stem diameter (D) or traits related to bole robustness. These findings are consistent with recent studies highlighting the importance of phenotypic variability in genetic conservation strategies and the selection of superior materials (Zhou et al., 2021; Silva et al., 2023). The identification of key traits, such as the number of shoots and the sum of shoot lengths, provides a solid basis for future breeding programs aimed at enhancing the resilience and productivity of the study populations. Furthermore, the combined use of genetic and phenotypic correlations, along with PCA, proves to be an effective tool for exploring intraspecific diversity and for outlining management and conservation strategies tailored to the genetic characteristics of each provenance.

4. Conclusions

The conclusions should be interpreted with caution, as the study was based on a limited sample of four open-pollinated families of *Swietenia macrophylla*.

After simulating an attack by *Hypsipyla grandella*, genetic differences were observed in stem diameter, regrowth length, and basal area, suggesting potential for genetic improvement through early selection. Regrowth length emerged as the most relevant trait, showing genetic correlations with plant height and diameter, enabling indirect selection at the nursery stage. Furthermore, height, diameter, and basal area of regrowth showed moderate genotypic determination coefficients, supporting their use in mass selection. Principal Component Analysis (PCA) revealed structured differentiation among provenances, with plant height, basal height, number of regrowth, and regrowth length contributing most to multivariate discrimination, indicating underlying genetic patterns that could be strategically exploited in breeding and conservation programs.

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Contribution from authors

J. M. Revilla-Chávez: *Writing – original draft*. R. D. Manturano-Pérez: *Acquisition of financing, Methodology and review*. A. C. Gonzales-Alvarado: *Data curation*. R. Casas-Reátegui: *Conceptualization, formulation or evolution of general research goals and objectives*. L. I. Briceño Dueñas: *Data curation*. J. A. Mori-Vásquez: *Methodology, Development or design of methodology; Model Creation*. A. M. Sebbenn: *Proofreading and editing, Formal analysis*.

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