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Research article

Phenotypic variability of *Calycophyllum spruceanum* (Benth.) Hook. f. *ex* K. Schum. in the Peruvian Amazonia

Variabilidad fenotípica de *Calycophyllum spruceanum* (Benth.) Hook. f. *ex* K. Schum. en la Amazonía peruana

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Abstract

Calycophyllum spruceanum, commonly known as "*capirona*", is a tree native to the Peruvian Amazonia, with ecological, cultural and economic importance due to its diverse uses. However, gaps remain in understanding of the morphological traits that significantly contribute to its genetic diversity. This study evaluated 18 *C. spruceanum* individuals *in situ* using 34 qualitative and quantitative morphological descriptors (leaf, flower, fruit and seed) and 6 forest descriptors in two forest types in the *Tambopata* province, *Madre de Dios*. The results confirmed high variability in forest characteristics (CV>35 % for height and *DBH*), regardless of forest type (p>0.05). Multiple correspondence analysis revealed a close association between leaf and flower descriptors (41.9 % variability). Simultaneously, principal component analysis explained 44.6 % of the total variance using two axes associated with leaf and reproductive morphology, allowing the grouping of individuals into three distinct morphological groups: one with a vegetative emphasis and two with favorable reproductive potential. Strong correlations (r≥0.7) between leaf and reproductive traits support this classification. These findings validate the use of these descriptors as a baseline for identifying promising phenotypes and constitute an essential contribution to establishing *ex situ* germplasm banks aimed at the conservation and genetic improvement of the species in the Peruvian Amazonia.

Keywords: Germplasm banks, *capirona*, genetic resources conservation, genetic diversity, plant morphology, forests types.

Resumen

Calycophyllum spruceanum, comúnmente conocido como "capirona", es un árbol nativo de la Amazonía peruana, con relevancia ecológica, cultural y económica por sus diversos usos. Sin embargo, persisten vacíos respecto a los rasgos morfológicos que aportan de forma significativa a su diversidad genética. Este estudio evaluó 18 individuos de *C. spruceanum in situ* mediante 34 descriptores morfológicos (hoja, flor, fruto y semilla) cualitativos y cuantitativos, y seis dasométricos en dos tipos de bosque de la provincia de Tambopata, Madre de Dios. Los resultados confirmaron alta variabilidad en caracteres dasométricos (CV>35 % para altura y *DN*), independientemente del tipo de bosque (p>0.05). El análisis de correspondencias múltiples reveló una asociación estrecha entre descriptores de hoja y flor (41.9 % variabilidad). Simultáneamente, el análisis de componentes principales explicó 44.6 % de la varianza total mediante dos ejes asociados a morfología foliar y reproductiva, lo que permitió el agrupamiento de los individuos en tres grupos morfológicos distintos: uno con énfasis vegetativo y dos con potencial reproductivo favorable. Las asociaciones fuertes (r≥0.7) entre rasgos foliares y reproductivos sustentan esta clasificación. Estos hallazgos validan el uso de dichos descriptores como línea base para la identificación de fenotipos promisorios y constituye un aporte esencial para establecer bancos de germoplasma *ex situ* orientados a la conservación y el mejoramiento genético de la especie en la Amazonía peruana.

Palabras clave: Banco de germoplasma, capirona, conservación de recursos genéticos, diversidad genética, morfología vegetal, tipos de bosque.

Introduction

Calycophyllum spruceanum (Benth.) Hook. f. *ex* K. Schum., commonly known as *capirona* (Rubiaceae family, Ixoroide subfamily) is a tree native to the Amazon basin (Reynel et al., 2003). In Peru, it covers key regions such as *Amazonas*, *Huánuco*, *Junín*, *Loreto*, *Madre de Dios*, *San Martín*, *Pasco* and *Ucayali* (Flores-Bendezú, 2018; Saldaña et al., 2021); it forms dense populations called c*apironales* in primary and secondary forests of low, floodable terraces and *terra firme* (Flores-Bendezú, 2018; Freitas-Alvarado et al., 2021). It has remarkable adaptive ability, developing at altitudes below 1 200 m, in alluvial soils and under precipitation regimes exceeding 2 500 mm annually (Reynel et al., 2003).

Capirona has significant ecological, cultural, medicinal, and particularly economic value due to the high quality of its wood and its rapid growth (Duke, 2008; Ugarte-Guerra & Domínguez-Torrejón, 2010; Peixoto et al., 2018; Egoavil-Cueva-Gálvez et al., 2023). In the Peruvian Amazon, the demand for fast-growing timber species for plantations and agroforestry systems has increased (Cornelius et al., 2018), positioning *C. spruceanum* as promising for economic diversification and the recovery of areas degraded by alluvial mining. However, to harness this potential, its conservation and the establishment of genetic improvement programs that ensure the long-term sustainability of the resource are priorities.

In addition to its ecological and economic importance, understanding the genetic and phenotypic variation of the species is essential for its conservation, adaptation to climate change, and sustainable use (Flores et al., 2019). Previous studies of genetic diversity in *capirona* describe high variability among individuals of the same population, but low variability among provenances (Russell et al., 1999; Sotelo-Montes et al., 2006; Saldaña et al., 2021). Furthermore, Tauchen et al. (2011) report that the phenotypic variability of *capirona* is greater than its genetic variability due to a strong environmental influence. However, most studies on the phenotypic variability of *capirona* have focused on wood technological properties (color, density, shrinkage) and basic descriptors (Sotelo-Montes et al., 2007a, 2007b), but they leave a significant knowledge gap regarding the morphological variability of vegetative and reproductive structures in natural *in situ* populations, which are crucial indicators for the early selection of superior genotypes.

Morphological characterization using standardized descriptors allows for the identification of variation patterns that may not be evident with descriptors alone, thus facilitating the management of germplasm banks. Therefore, this study had two objectives: (1) To compare the dendrometric variables of *C. spruceanum* between high terrace forests and low terrace forests, and (2) To identify morphological groupings using qualitative and quantitative descriptors of leaf, flower, fruit, and seed to identify phenotypes with vegetative or reproductive potential. In this context, the hypotheses are: (a) There are significant differences in the dendrometric variables between the forest types; and (b) The quantitative and qualitative variables show strong associations that facilitate the grouping of individuals based on their superior vegetative or reproductive characteristics.

Materials and Methods

Study area

The study was conducted between February 2023 and November 2024, corresponding to two complete field seasons in natural populations of *C. spruceanum* located in High Terrace Forests (BTa) and Low Terrace Forests (BTb), situated in the populated areas of *San Bernardo* and *Aguas Negras*, *Tambopata* District, *Tambopata* Province, *Madre de Dios* region, Peru. The study area corresponds to a warm and humid climate (Aw) with an average annual temperature of 26.5 °C, relative humidity of 84.7 %, and annual rainfall exceeding 2 100 mm (1981-2010) (Castro et al., 2021). The area corresponds to low and high terrace formations within the Amazonian rainforest ecoregion (Ministerio del Ambiente, 2015; Britto, 2017). The sample consisted of a total of 18 individuals distributed between both forest types (Table 1).

Table 1. Geographic location of the 18 *capirona* individuals.

Forest type	Code	Sector	Latitude	Longitude	Altitude (m)
BTb	Acc1	*Aguas negras*	12°39'5.838" S	69°26'13.05" W	191
BTb	Acc2	*Aguas negras*	12°39'5.642" S	69°26'13.348" W	200
BTa	Acc3	*Aguas negras*	12°39'5.577" S	69°26'13.480" W	193
BTa	Acc4	*Aguas negras*	12°39'5.414" S	69°26'13.414" W	208
BTb	Acc5	*Aguas negras*	12°39'5.153" S	69°26'13.480" W	195
BTa	Acc6	*Aguas negras*	12°39'3.623" S	69°26'13.941" W	202
BTb	Acc7	*Aguas negras*	12°39'4.861" S	69°26'13.181" W	197
BTa	Acc8	*Aguas negras*	12°39'5.514" S	69°26'11.79" W	198
BTa	Acc9	*Aguas negras*	12°39'4.536" S	69°26'11.796" W	199
BTa	Acc10	*Aguas negras*	12°39'2.454" S	69°26'11.784" W	205
BTa	Acc11	*Aguas negras*	12°39'6.852" S	69°26'9.902" W	192

BTb	Acc12	*Aguas negras*	12°39'9.093" S	69°26'13.188" W	207
BTb	Acc13	*Aguas negras*	12°39'9.288" S	69°26'13.553" W	194
BTb	Acc14	*Aguas negras*	12°39'10.003" S	69°26'13.886" W	201
BTb	Acc15	*Aguas negras*	12°39'10.166" S	69°26'13.919" W	196
BTb	Acc16	*Aguas negras*	12°39'10.493" S	69°26'13.257" W	203
BTb	Acc17	*San Bernardo*	12°39'10.658" S	69°26'11.533" W	206
BTb	Acc18	*Aguas negras*	12°41'8.845" S	69°22'50.048" W	209

BTb = Low terrace forests; BTa = High terrace forests.

The morphological descriptors of the samples were measured at the facilities of the Genetic Resources Research Module of the *San Bernardo* Agricultural Experiment Station, of the National Institute of Agricultural Innovation (*INIA*), located in the *San Bernardo* sector, *Tambopata* district and province, *Madre de Dios*, Peru.

Morphological descriptors

For the collection of plant material, 18 mature trees with a diameter at breast height (*DBH*; model Mantax Blue Haglof® caliper) greater than 10 cm were selected to ensure a complete collection from the same individual at different phenological stages (flowering, fruiting, and ripening). In the field (*in situ*), total height (m) and merchantable height (m) were measured using a model RD 1000 Criterion® electronic dendrometer. *DBH*, number of branches, crown diameter (m), and volume (m^3) of each tree were recorded to complement the morphological analysis. Subsequently, 25 samples of leaves, flowers, fruits, and seeds were collected from different parts of the tree.

The samples were immediately transported to the laboratory (Genetic Resources Research Module of the *San Bernardo* Agricultural Experiment Station, of the National Institute of Agricultural Innovation) in labeled plastic bags for subsequent measurement.

Thirty-two descriptors were used to characterize the morphology. These included 24 quantitative descriptors (Table 2) and 8 qualitative descriptors (Table 3), categorized as follows: leaf (7), flower (9), fruit (7) and seed (9). These descriptors and their categories were proposed by Eras-Guamán et al. (2021) and Gutiérrez et al. (2020) for *Cinchona officinalis* L. and *Calycophyllum candidissimum* (Vahl) DC. of the Rubiaceae family and were also adapted from the International Plant Genetic Resources Institute (IPGRI, 1996).

Table 2. Quantitative morphological descriptors evaluated in *Calycophyllum spruceanum* (Benth.) Hook. f. *ex* K. Schum. individuals.

Part of the plant	Descriptor	Abbreviation
Leaf	Leaf blade length (cm)*	LLF
	Leaf blade base width (cm)*	ABL
	Leaf blade area (cm^2)*	AFL
	Petiole length (cm)*	LP
Flower	Flower length from base to apex (mm)	LFA
	Corolla base width (mm)	ABC
	Corolla area (cm^2)	ACF
	Number of stamens	NE
	Average stamen length (mm)*	LPE
	Style length (mm)*	LEF
	Number of petals	NP
Fruit	Fruit length from base to apex (mm)*	LFBA
	Fruit base width (mm)*	ABF
	Total fruit area (mm^2)*	AF
	Average fruit weight (g)*	PF
	Fruit peduncle length (mm)*	LF
Seed	Number of seeds per fruit**	NSF
	Fresh weight (mg)**	MF
	Seed width (mm)**	AS
	Total seed length (mm)**	LS
	Seed length without wing (mm)**	LSSA
	Seed length without wing-total seed length (mm)*	LSSLT
	Ratio of embryo length-internal seed length	LELIS
	Embryo length	LE

*Eras-Guamán et al. (2021); **Gutiérrez et al. (2020).

Table 3. Qualitative morphological descriptors evaluated in *Calycophyllum spruceanum* (Benth.) Hook. f. *ex* K. Schum. individuals.

Part of the plant	Descriptor	Status	Abbreviation
Leaf	Apex shape*	1 Acute	FA
		2 Acuminate	
		3 Mucronate	
	Base shape*	1 Acute	FB
		2 Truncate	
		3 Obtuse	
		4 Rounded	
	Leaf color*	1 Bright yellowish-green	CH
		2 Moderate yellowish-green	
		3 Dark yellowish-green	
		4 Strong yellowish-green	
		5 Grayish-green	
		6 Vivid yellowish-green	
		7 Deep yellowish-green	
		8 Grayish-olive-green	
Flower	Petal color*	1 Greenish-white	CP
		2 Yellowish-gray	
		3 Yellowish-white	
	Pistile shape*	1 Longistila	FP
		2 Mediostila	
		3 Brevistila	
Fruit	Fruit color*	1 Dark grayish-brown	CF
		2 Dark yellowish-brown	
		3 Dark brown	
	Fruit shape*	1 Elliptical	FF
		2 Oblong	
Seed	Seed color*	1 Light brown	CS
		2 Dark grayish-yellowish-brown	

*Adapted from the International Plant Genetic Resources Institute (IPGRI, 1996).

Statistical analysis

Initially, descriptive statistics were calculated for the forest dasometric variables (mean, standard deviation, Coefficient of variation, minimum and maximum values). Subsequently, compliance with the assumptions of normality was assessed using the Shapiro-Wilk test, and homogeneity of variances was assessed using Levene's test for each quantitative variable. To compare the forest dasometric variables between the two forest types (high terrace *vs.* low terrace), the Student's t-test for independent samples was applied when the data met both assumptions. When the assumption of normality was violated, the non-parametric Mann-Whitney *U* test was used.

For the qualitative morphological descriptors, Multiple correspondence analysis (MCA) was applied to explore patterns of association between categories. To evaluate associations among the 24 quantitative morphological descriptors, Spearman's correlation was used, which was visualized graphically using the Corrplot package (Wei & Simko, 2017).

Subsequently, a Principal Component Analysis (PCA) was performed based on the means of the quantitative descriptors of the 18 evaluated individuals. To classify the individuals according to their morphological similarity, a hierarchical clustering analysis was carried out using Euclidean distance as a measure of dissimilarity and Ward's method (Ward, 1963) as agglomeration criterion, generating a classification dendrogram (Maechler et al., 2026). Once the clusters were identified, the means of the quantitative variables were compared between groups using ANOVA followed by Tukey's *post-hoc* test when normality and homogeneity of variances were met. Welch's ANOVA followed by the Games-Howell test was used when the assumption of homogeneity of variance was violated; and the Kruskal-Wallis test followed by the Dunn-Holm test was used for variables that did not meet the assumptions of normality.

All statistical analyses were performed using R software version 4.4.1 (R Core Team, 2023). The graphical representation and visualization of the multivariate results were carried out using the FactoMineR (Lê et al., 2008), Factoextra (Kassambara & Mundt, 2020) and Ggplot2 (Wickham, 2016) packages.

Results

Although the dendrometric variables did not significantly differentiate the forest types ($p>0.05$), high variability was recorded in total height and diameter at breast height (*DBH*) among the sampled *capirona* trees (Table 4).

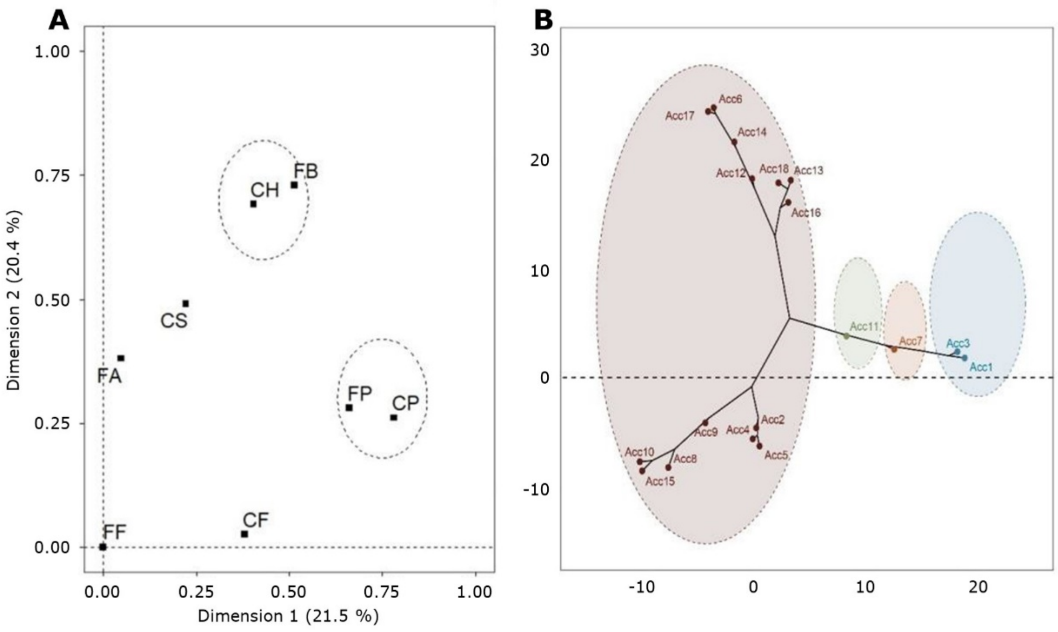
Table 4. Minimum, maximum, mean, coefficients of variation and standard deviation values for the quantitative mensuration characteristics of *Calycophyllum spruceanum* (Benth.) Hook. f. *ex* K. Schum in two forest types.

Mensuration features	**Low terrace forests**					**High terrace forests**					***P***
	Min	***Max***	***Mean***	***SD***	***VC***	***Min***	***Max***	***Mean***	***SD***	***CV***	
Crown Diameter (m)	1.50	17.60	4.06	1.27	5.17	3.75	18.00	5.20	1.14	5.93	0.17
Number of branches	1.00	3.00	2.27	0.79	1.79	2.00	3.00	2.14	0.38	0.81	0.58
Plant height (m)	7.30	17.60	12.90	3.07	39.64	10.78	18.00	14.51	2.48	35.97	0.26
Marketable height (m)	3.60	11.00	6.28	2.18	13.67	3.45	11.01	5.71	2.63	15.03	0.62
Diameter at breast height (cm)	13.10	23.70	17.73	3.99	70.76	14.50	26.50	19.46	4.37	85.04	0.40
Volume (m^3)	0.07	0.56	0.27	0.17	0.05	0.13	0.63	0.35	0.20	0.07	0.36

Min = Minimum value; *Max* = Maximum value; *SD* = Standard deviation; *CV* = Coefficients of variation.

Qualitative descriptors

Multiple correspondence analysis of qualitative descriptors (Figure 1A) identified associations between foliar descriptors, where the first two dimensions together explained 41.9 % of the total variability. The close association between leaf base color and shape was evident, contributing to the morphological differentiation among the 18 *C. spruceanum* individuals. Likewise, the relationship between pistil shape and petal color was observed, suggesting possible morphological groupings.



A = Multiple correspondence analysis (MCA); B = Hierarchical dendrogram. CH = Leaf color; FB = Base shape; FP = Pistil shape; CP = Petal color; CS = Seed color; FA = Apex shape; FF = Fruit shape; CF = Fruit color. Codes Acc1, Acc2, …, Acc18 = Table 1.

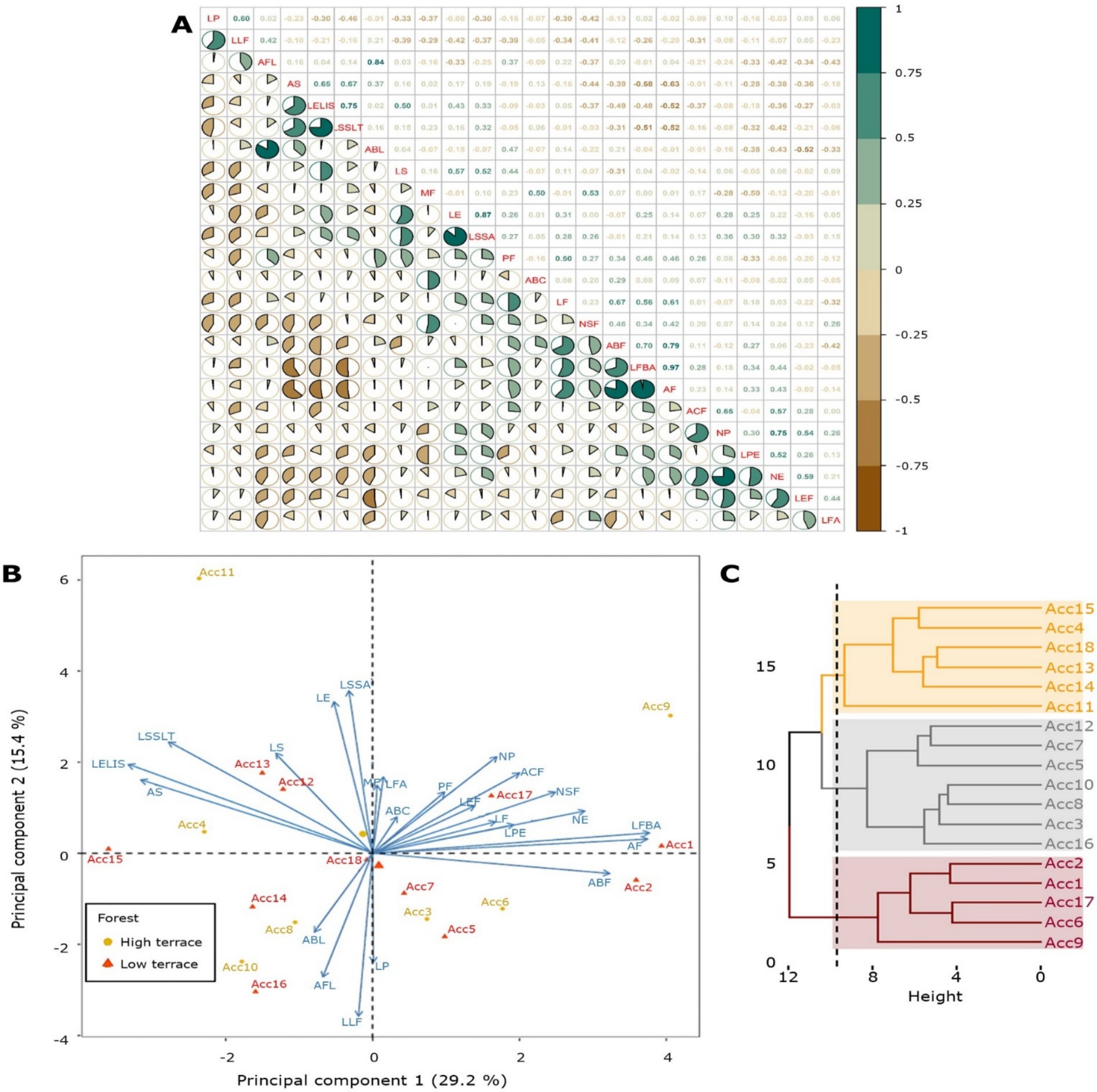
Figure 1. Results of multivariate analysis of qualitative characteristics in 18 *C. spruceanum* (Benth.) Hook. f. *ex* K. Schum. individuals, *Madre de Dios*, Peru.

The hierarchical dendrogram (Figure 1B) showed four morphological groupings among the 18 accessions of *C. spruceanum*. Group I comprised 14 accessions (77.78 %) with similarity in eight characteristics related to leaves, flowers, and fruits; these included short or long pistils, yellowish-gray to greenish-white petals, and yellowish-green leaves with a truncate base and acuminate apex.

Group II (5.55 %) included one accession with leaves with a rounded base and acute apex. Group III (5.55 %) included one accession with yellowish-purple green leaves and light brown seeds. Finally, group IV (11.11 %) comprised two accessions with similarity in leaves, flowers, and fruits, characterized by short pistils, yellowish-white petals, dark grayish-brown fruits, and an obtuse leaf base.

Quantitative descriptors

Spearman's rank correlation analysis ($p<0.05$) revealed strong positive associations ($r\geq0.70$) between several foliar and reproductive traits. In seeds, correlations between embryo length (LE) and wingless seed length (LSSA) ($r=0.87$) were prominent, as were those between the wingless seed length-total seed length ratio (LSSLT) and the embryo length-internal seed length ratio (LELIS) ($r=0.75$). In flowers, the number of petals (NP) and the number of stamens (NE) ($r=0.75$) showed strong associations. In fruits, fruit length (LFBA) was associated with fruit base width (ABF) ($r=0.70$) and fruit area (AF) ($r=0.97$), suggesting larger fruits. While leaf blade area (AFL) correlated with leaf base width (ABL) ($r=0.84$), negative correlations were also observed between seed width (AS) and fruit area (AF) ($r=0.63$), and between AS and LFBA ($r=0.58$) (Figure 2A).



A = Spearman's rank correlation coefficient: teal tones represent positive correlations and dark brown, negative correlations; the size of the semicircles indicates the magnitude of the correlation. Acronyms: see Table 2. B = Principal component analysis (PCA). C = Hierarchical dendrogram.

Figure 2. Results of the descriptive and multivariate analysis for 24 quantitative descriptors of *Calycophyllum spruceanum* (Benth.) Hook. f. *ex* K. Schum., *Madre de Dios*, Peru.

Principal component analysis (PCA) revealed structural patterns in the phenotypic variability among the 18 *C. spruceanum* accessions from high and low terraces. The first two components explained 44.6 % of the total observed variability (Figure 2B). The results showed that both groups were mixed in the plane defined by the first two principal components, without evidence of a clear separation by ecological origin, indicating that quantitative traits do not significantly discriminate between forest types (Figure 2B). The first principal component (PC1), which explained 29.2 %, was related to fruit and seed parameters, such as LFBA, AF, NSF, and average fruit weight (PF), as well as floral variables such as number and length of stamens (NE, LPE) and style length (LEF), largely representing the productive and reproductive dimension. The second principal component (PC2), with 15.4 %, was associated with foliar traits such as blade length (LLF), basal area (ABL), and with seed parameters such as the ratio of wingless seed length to total seed length (LSSLT). Individuals Acc1 and Acc2 showed a greater contribution from reproductive variables (LFBA, ABF, NSF). Tree Acc11 stood out for its positive position in PC2, linked to greater development in LE and LSSA.

The results of the hierarchical clustering analysis allowed the 18 *C. spruceanum* individuals to be grouped into three clearly defined morphological groups (Figure 2C). The classification, which integrated foliar, floral, fruit, and seed traits, revealed consistent phenotypic patterns.

Group I comprised five individuals (Acc1, 2, 6, 9, and 17) with the highest values for reproductive traits such as NE, fruit length and area (LFBA, AF), and NSF, reflecting high reproductive potential. Group II, with seven individuals (Acc3, 5, 7, 8, 10, 12, and 16), showed higher values for petiole length (LP) and leaf blade length (LLF), but lower values for fruit descriptors (ABF, AF, PF, LF), suggesting a predominance of vegetative traits over reproductive ones. Group III, made up of six individuals (Acc4, 11, 13, 14, 15 and 18), was characterized by high values in reproductive traits, highlighting the greatest seed width, fruit weight and total seed length.

Post-hoc tests revealed significant differences ($p<0.05$) between groups, primarily in reproductive (ACF, AF, ABF, NSF, LFBA) and foliar (LLF, LP) descriptors (Table 5). The high coefficients of variation (>40 %) for flower and fruit descriptors confirm the marked phenotypic differentiation among *capirona* individuals, although this is possibly not influenced by their origin.

Table 5. Descriptive analysis and comparison of means between morphological clusters for quantitative traits in *capirona* accessions.

Feature	Group I	Group II	Group III	Test	*p*	*CV* (%)
LLF	10.0b	10.8a	9.7b	Tukey	0.003*	6.9
ABL	4.5a	4.5a	4.5a	Tukey	0.910	6.8
AFL	27.1a	27.9a	27.9a	Tukey	0.922	11.8
LP	1.8ab	2.0a	1.7b	Tukey	0.034*	13.3
LFA	8.4a	8.4a	8.4a	Dunn-Holm	0.906	10.6
ABC	1.8a	1.6a	1.7a	Games-Howell	0.444	19.7
ACF	18.0a	11.5a	10.2a	Tukey	0.419	78.0
NE	6.3a	6.0a	5.0b	Tukey	0.020*	15.2
LPE	5.2a	4.6a	4.4a	Dunn-Holm	0.111	14.5
LEF	5.8a	6.2a	5.5a	Tukey	0.275	11.7
NP	5.6a	5.6a	5.2a	Tukey	0.507	11.8
LFBA	9.8a	7.4b	7.7b	Tukey	0.00*	15.1
ABF	3.1a	2.3b	2.3b	Tukey	0.001*	18.4
AF	32.6a	15.6b	16.4b	Games-Howell	0.013*	44.0
PF	0.2ab	0.2b	0.2a	Tukey	0.072	10.5
LF	1.3a	1.0b	1.2ab	Tukey	0.016*	19.5
NSF	31.3a	23.8b	24.2b	Tukey	0.055	23.0
MF	0.2a	0.2a	0.2a	Tukey	0.144	4.9
AS	0.5b	0.6ab	0.6a	Tukey	0.026*	13.1
LS	4.2ab	4.1b	4.6a	Tukey	0.041*	9.4
LSSLT	0.7b	0.8b	0.9a	Tukey	0.006*	13.1
LSSA	0.8a	0.7a	0.8a	Games-Howell	0.142	12.6
LELIS	0.7b	0.8b	0.9a	Tukey	0.002*	10.8
LE	0.8a	0.7a	0.8a	Tukey	0.154	10.2

CV = Coefficient of variation. *Significant difference ($p<0.05$). Different letters in the same row indicate significant differences according to the corresponding *post-hoc* test.

Groups I and III include individuals mostly aligned with PC1 in terms of their reproductive and productive traits; while group II is more aligned with PC2 in terms of its vegetative traits.

Discussion

This study constitutes the first *in situ* morphological characterization of *C. spruceanum* in the *Madre de Dios* region of Peru, based on qualitative and quantitative descriptors of vegetative and reproductive organs. The values obtained for the morphological descriptors of *C. spruceanum* align with the ranges documented by dendrological studies for the Peruvian Amazon (Flores-Bendezú, 2018; Reynel et al., 2003). Furthermore, the significant variability observed in total height and diameter at breast height (*DBH*) can be attributed to the different ages of the sampled individuals and the lack of control over environmental variables inherent in *in situ* sampling.

However, studies conducted in *capirona* plantations of different ages, resulting from low-intensity phenotypic selection, suggest that height and *DBH* are effective traits for maintaining genetic variation within populations (Weber et al., 2009). Furthermore, these dendrometric variables show a positive correlation with wood density at both the genetic and phenotypic levels, as demonstrated in progeny tests performed on *capirona* (Sotelo-Montes et al., 2006). Therefore, it is essential to include these variables to ensure genetic representativeness, for example, in the characterization of *ex situ* germplasm banks, where there is greater control over variables.

Environmental factors have a greater impact on the phenotype of *C. spruceanum* depending on origin, planting zone (high, low), and growth variables. Based on drought tolerance, variability in the species' physiological characteristics, such as leaf abscission, could be more expected in low-lying areas than in high-lying areas, which would also generate greater variation in growth by reducing the photosynthetic rate among neighboring individuals (Sotelo-Montes et al., 2006; Tauchen et al., 2011).

However, the morphological descriptors evaluated in this study did not reveal significant phenotypic differences between the forest types analyzed. This finding is consistent with the genetic structure described for the species, in which variation within *C. spruceanum* populations considerably exceeds variation between populations (Saldaña et al., 2021). This distribution of diversity suggests that morphological differentiation does not necessarily reflect clear geographic or ecological groupings, underscoring the need to complement these studies with robust molecular evidence to discern patterns of population differentiation.

It should be noted that the geographic scope of the sampling used in this research may not encompass the full phenotypic variability of *C. spruceanum* within its natural distribution area, given that statistical robustness in cross-pollinated tropical forest species, high intraspecific diversity, and complex population structure generally require extensive and stratified sampling designs to ensure the statistical robustness of the characterizations (Sotelo-Montes et al., 2006). The proper recording of these descriptors allows for ensuring the traceability of plant material, guiding the selection of seed trees with confirmed local adaptations, and providing a basis for the establishment of *ex situ* germplasm banks under rigorous biological criteria, thus maximizing the potential for conservation and sustainable use of the species (Fajardo-Vizcayno et al., 2014).

The analysis of morphological characteristics revealed that reproductive and vegetative descriptors constitute the main axes of differentiation in *C. spruceanum*. The observed association between leaf and flower characteristics suggests that, while vegetative traits are highly susceptible to environmental conditions, floral traits tend to act as more stable markers for taxonomic and varietal identification. This pattern is consistent with that reported for tree species such as *Malus* spp., in which floral morphology provides key criteria for cultivar differentiation, while vegetative variation largely reflects the adaptive response to the environment (He et al., 2025).

The usefulness of morphological and dasometric descriptors for establishing preliminary phenotypic groups for use in genetic improvement has been validated in various tropical forest species. Research on *Juglans pyriformis* Liebm., *Simarouba amara* Aubl. and *Pseudosamanea guachapele* (Kunth) Harms have shown that characterization based on crown, stem, leaf and fruit traits allows for the discrimination of individuals with potential for specific uses, such as timber production, silvopastoral systems, agroforestry, or ecosystem services (Acosta-Hernández et al., 2011; Castañeda-Garzón et al., 2021, 2024). Based on this background, the identification of contrasting morphological groups in *C. spruceanum* suggests a high potential for the pre-selection of candidates for plus trees, facilitating the prioritization of materials for conservation and sustainable use programs.

However, if phenotypic variability in natural populations is considered the result of genotype×environment (G×E) interaction, the superiority observed in certain morphological traits does not guarantee a heritable genetic basis, and may instead be a product of phenotypic plasticity in response to favorable local conditions (Kageyama & de Souza-Dias, 1985).

To effectively discriminate between genetic and environmental advantages, it is imperative to complement *in situ* characterization with assays under controlled conditions (*ex situ*). This strategy not only guarantees the traceability of accessions but also prevents genetic erosion due to insufficient sampling (Fajardo-Vizcayno et al., 2014). Consequently, *in situ* characterization acts as an efficient filter for building germplasm banks by optimizing the resources allocated to conservation (Núñez-Colín & Escobedo-López, 2014). The findings of this study establish a fundamental baseline for designing strategies to ensure potential genetic diversity, enabling the selection of representative individuals through the evaluation of phenotypic responses from early stages. Furthermore, the future incorporation of health, phytochemical, and wood quality descriptors, along with the estimation of heritability parameters, will facilitate early selection and consolidate a genetic improvement program for *capirona* based on solid genetic evidence.

Conclusions

The study confirmed high phenotypic variability in the dendrometric variables (height and *DBH*); however, forest type did not influence this variation. The analysis of qualitative descriptors showed a close association between foliar and floral characteristics, indicating common morphological patterns predominant in the evaluated population. The strong positive correlations of the quantitative descriptors allowed the classification of individuals into three distinct morphological groups, differentiated by their vegetative (group II) or reproductive (groups I and III) emphasis. This classification validates the use of these descriptors as a baseline for identifying promising phenotypes and constitutes an essential contribution to establishing *ex situ* germplasm banks aimed at the conservation and genetic improvement of the species in the Peruvian Amazon.

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Conflict of interest

The authors have declared no conflicts of interest.

Contribution by author

Gorky Florez-Castillo and Yicelia Maura Mamani Mariaca: conceptualization, formal analysis, research, writing, and review; Sharmely Hilares Vargas: research, data curation, writing, and review. All authors have read and accepted the published version of the manuscript.

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