

Agronomic performance and nutritional profiling of *Theobroma grandiflorum* (cupuassu) clones under colombian amazon conditions

Desempeño agronómico y perfil nutricional de clones de *Theobroma grandiflorum* (copoazú) en condiciones de la Amazonía colombiana

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Cite: Velasquez-Vasconez, P. A., Castro, M. I., Criollo, D., Diaz, E., & Zambrano, J. C. (2026). Agronomic performance and nutritional profiling of *Theobroma grandiflorum* (cupuassu) clones under colombian amazon conditions. *Revista de Ciencias Agrícolas*, 43(1), e1285. <https://doi.org/10.22267/rcia.2026431.285>

ABSTRACT

Theobroma grandiflorum (cupuassu) is an Amazonian fruit tree of increasing importance for agro-industrial development in Colombia due to its nutritional value and multiple commercial applications. However, its cultivation still faces limitations due to insufficient knowledge regarding the adaptability and productivity of its genotypes under local conditions. This study aimed to evaluate eight genotypes over a three-year period in an experimental field located in Florencia, Caquetá, Colombia. The trial was established as a monoculture of trees with a repeated-measures design. Data included productive variables (fruit number, weight, pulp, and seed yields) and nutritional composition (minerals, fatty acids, and bromatological parameters). The analysis of variance (ANOVA) and Duncan's test revealed significant differences ($p < 0.05$) among the genotypes, with UNR146 and UNR153 excelling in pulp yield (29.00 kg and 29.97 kg, respectively) and almond yield (12.92 kg and 14.81 kg, respectively). These two genotypes showed a superior number of fruits per tree (65 and 71, respectively), positively influencing total almond and pulp production. Furthermore, UNR146 and UNR153 demonstrated consistent performance across three consecutive years of evaluation, outperforming other genotypes, particularly in almond and pulp yield. Their high productivity is coupled with favorable mineral and fatty acid profiles, with UNR153 achieving the highest almond yield at 14.8 kg per plant. Principal component analysis revealed key relationships between minerals and fatty acids, highlighting differences in pulp and seed quality. Clones UNR146 and UNR153 exhibit strong genetic potential to improve cupuassu yield and quality under tropical conditions in the Colombian Amazon.

Keywords: agro-industrial potential; Amazonian fruits; genetic resources; germplasm; plant breeding; *T. bicolor*; *T. cacao*

RESUMEN

Theobroma grandiflorum es un árbol frutal amazónico de creciente relevancia para Colombia, debido a su valor nutricional y múltiples usos comerciales. No obstante, su cultivo aún presenta limitaciones asociadas al escaso conocimiento sobre la adaptabilidad y productividad de sus genotipos en condiciones locales. Este estudio tuvo como objetivo evaluar el desempeño agronómico de ocho clones de copoazú durante tres años en un campo experimental ubicado en Florencia, Caquetá, Colombia. El ensayo se estableció como un monocultivo de árboles en un diseño de medidas repetidas. Los datos incluyen variables productivas (número de frutos, peso, pulpa y rendimiento de semillas) y composición nutricional

(minerales, ácidos grasos y parámetros bromatológicos). El análisis de varianza (ANOVA) y la prueba de Duncan revelaron diferencias significativas ($p < 0,05$) entre los genotipos, destacando a UNR146 y UNR153 en rendimiento de pulpa (29,00 kg y 29,97 kg, respectivamente) y rendimiento de almendra (12,92 kg y 14,81 kg, respectivamente). Estos dos genotipos mostraron un mayor número de frutos por árbol (65 y 71, respectivamente), influyendo positivamente en la producción total de almendra y pulpa. Además, UNR146 y UNR153 demostraron resiliencia bajo condiciones ambientales variables, superando a otros genotipos, particularmente en rendimiento de almendra y pulpa. El análisis de los componentes principales reveló relaciones entre minerales y ácidos grasos, destacando las diferencias en la calidad de la pulpa y las semillas. Los clones UNR146 y UNR153 presentaron un fuerte potencial genético para mejorar el rendimiento y la calidad del copoazú en condiciones tropicales en la Amazonia colombiana.

Palabras clave: frutales amazónicos; germoplasma; potencial agroindustrial; mejoramiento vegetal; recursos genéticos; *T. bicolor*; *T. cacao*

INTRODUCTION

Theobroma grandiflorum (Willd. ex Spreng.) Schum., commonly known as cupuassu, is a fruit tree native to southeastern Pará and northwestern Maranhão in the Brazilian Amazon. It is estimated that the domestication of cupuassu began around 8,000 years ago, driven by strong selective pressure applied to its wild relative, *Theobroma subincanum* (commonly known as cupuí) (Colli-Silva *et al.*, 2023). Indigenous groups in Amazonia played a pivotal role in this process, as archaeological evidence suggests they actively cultivated and managed useful fruit trees as part of their broad-spectrum diet during the Holocene (Clement *et al.*, 2015). In Colombia, cupuassu appears to have been first introduced in the early 2000s through the Department of Putumayo and later propagated by Corpoica (AGROSAVIA), contributing to its spread across the Amazon–Orinoquia region.

Cupuassu has emerged as a valuable resource for small producers in the Colombian Amazon due to its environmental significance, nutritional value, and potential in agroindustry. The fruit's pulp and almonds offer significant economic and nutritional potential (da Silva, Salimo *et al.*, 2024; Pugliese *et al.*, 2013), making it an important crop for sustainable development in the region. The pulp, characterized by its high acidity and strong aroma, is used in juices, confections, and ice cream, with derivatives highly valued in international markets (da Silva, Salimo *et al.*, 2024). Despite its minimal exploration in Colombia, the pulp contributes to local food security by supplying essential nutrients that diversify diets. Furthermore, the fruit exhibits beneficial bioactive properties, including antioxidant and therapeutic effects (da Silva, Salimo *et al.*, 2024; Jean-Marie *et al.*, 2022; Pugliese *et al.*, 2013). On the other hand, almonds can be transformed into “cupulate,” a chocolate alternative appreciated for its resilience to heat and its affordability compared to conventional chocolate (Alves *et al.*, 2020). The lipid-rich components of the almonds have garnered attention in the cosmetic industry, exemplified by the recent export of 250 kg of cupuassu butter to Brazil and an unmet demand exceeding 16 tons (Forbes, 2023), presenting an opportunity for economic growth.

Cupuassu cultivation has garnered attention as a viable alternative for diversifying agricultural production and promoting sustainable land use. The species exhibits adaptability to the acidic and nutrient-poor soils typical of the Amazon, making it suitable for agroforestry systems aimed at environmental conservation and economic development (da Silva, Costa *et al.*, 2024). Furthermore, it is increasingly recognized as a sustainable alternative to illicit crops, providing farmers with a profitable and legal agricultural option. However, research efforts are still needed to develop locally adapted varieties and maximize the crop's potential. There are valuable accessions with the potential to improve the productivity and quality of cupuassu in the Colombian Amazon region. Collections conducted across nine municipalities in Caquetá revealed that the

genetic diversity of cupuassu supports breeding initiatives aimed at enhancing yield and nutritional quality (Velasquez-Vasconez *et al.*, 2025). While promising materials with excellent phytosanitary conditions have been identified, the absence of further regional evaluations limits understanding of their local adaptation.

Evaluating genotypes across different environments and time periods is crucial for understanding the environmental effects on their differential performance. Assessing genotypic adaptability and stability helps identify highly productive and stable genotypes across seasons and locations. Although this is one of the most resource-intensive aspects of long-cycle fruit tree breeding programs, mixed models are typically recommended for quantifying genotype-environment interactions (Coelho *et al.*, 2020). Selection based on the longitudinal performance of individual trees enhances selection efficiency, as demonstrated in cupuassu studies (Alves & Chaves, 2022; Chaves *et al.*, 2021; Moysés Alves *et al.*, 2021). Repeated-measures evaluations have also enabled simultaneous variance component analysis and genetic value prediction (Chaves *et al.*, 2021).

There is a lack of comprehensive studies evaluating the agronomic performance and nutritional composition of cupuassu genotypes under Colombian Amazon region conditions. Accordingly, this research seeks to address this gap by analyzing the performance of eight *T. grandiflorum* clones over three consecutive years and estimating their nutritional value. Therefore, this study aimed to evaluate the agronomic performance and nutritional profiles of eight *Theobroma grandifloru* genotypes over three consecutive years under the Amazonian conditions of Caquetá, Colombia.

MATERIALS AND METHODS

Study area

The study was conducted in an experimental field located in the municipality of Florencia (1°38'44" N, 75°28'23" W; 300 m above sea level), in the Department of Caquetá, Colombia. The region is characterized by a tropical rainforest climate, classified as Afm (Warm-Humid Tropical Forest) under the Köppen climate classification system (Álvarez *et al.*, 2021). The soil is a clay loam Oxisol with a bulk density of 1–1.3 g/cm³ and a pH range of 4.1–5.2 (Suárez *et al.*, 2022). The soil has low organic carbon (1.35%), phosphorus (2.58 mg/kg), and base saturation (7.1%), with minimal levels of essential cations, a CEC of 11.3 cmol/kg, and high aluminum content (6.3 cmol/kg) with 73.4% saturation (Suárez *et al.*, 2022). During the evaluation period, precipitation averaged approximately 288.7 mm/month, solar radiation reached 1318.6 hours per year, and the mean temperature was 30.8 °C. Soil fertilization was carried out according to the nutritional requirements of cupuassu, based on recommendations derived from a soil analysis performed prior to field establishment. These measurements were recorded at the Macagual meteorological station, located within the Macagual Research Center (Table 1).

Table 1. Climatic data summary for the years 2008–2010

Year	Temperature (°C)	Precipitation (mm/month)	Solar radiation (hours/year)
Year 1	30.2	268.1	988.8
Year 2	30.9	271.3	1510.4
Year 3	31.3	326.6	1456.7

Cupuassu cultivation was managed with regular cleaning, fertilization, and pruning to maintain plant health and reduce pest incidence. Daily fruit collection and avoiding infested fruits helped disrupt pest and pathogen cycles, minimizing losses (Santos *et al.*, 2022). Eight promising clones were selected and evaluated from a range of genotypes, which were collected during expeditions conducted among populations throughout the Colombian Amazon region. Of these eight clones, seven were selected for a detailed sensory and biochemical analysis of the pulp and seed.

Experimental design

The experiment was established as a monoculture system of cupuassu trees, planted at a spacing of 4×4 m. The planting was carried out in June 2002. The experimental area was associated with banana plants, which played a key role in providing shade during the initial stages of cupuassu cultivation.

The experiment was conducted over three years using a one-way repeated measures design, where clones were treated as fixed effects. The clones were randomly arranged in the field to avoid the negative effects of self-incompatibility and, in certain cases, inter-incompatibility within the species (Vieira *et al.*, 2022). The number of replicates per clone was 15, with each plot consisting of a single plant (single-tree plot). Evaluations were performed at the plant level across three consecutive harvest seasons (2008, 2009, and 2010). Data collection focused on key variables, including the average number of fruits produced per harvest, almond percentage, pulp percentage, number of fruits per tree, fruit weight, almond yield per tree, and pulp yield per tree. The fruit characteristics were also evaluated, including the percentages of calcium (Ca), phosphorus (P), and ash (%) in the pulp, as well as the composition of the almond, which included linoleic acid (%), oleic acid (%), palmitic acid (%), and stearic acid (%). Additionally, the bromatological parameters of the almond were analyzed, encompassing ash (%), nitrogen (%), ether extract (%), crude fiber (%), phosphorus (%), sodium (mg/kg), potassium (%), calcium (%), magnesium (%), copper (mg/kg), zinc (mg/kg), iron (mg/kg), manganese (mg/kg), sulfur (%), and boron (mg/kg).

Data analysis

Variables contributing to performance components were analyzed using a linear mixed-effects model with Genotype as a fixed factor and Year as a random effect representing repeated measures. Although mixed-effects models are often used in longitudinal studies, they were not applied in this case because the dataset did not include repeated measurements on the same experimental units across years, justifying the use of a fixed-effects ANOVA. Normality and homoscedasticity assumptions were evaluated through residual diagnostics prior to model interpretation. Mean comparisons were conducted using Duncan's multiple range test ($p < 0.05$). To evaluate relationships between traits, a Pearson correlation matrix was generated. Correlation coefficients (r) were computed to quantify the linear associations between variables such as almond percentage, pulp percentage, number of fruits per tree, fruit weight, almond yield per tree, and pulp yield per tree. The statistical significance of correlations was determined, and a visual representation was created using a heatmap with a gradient color scale. Principal component analysis was performed to explore the multivariate relationships among the chemical and nutritional traits of pulp and almonds. Variables included mineral content (e.g., Ca, P, K), fatty acid composition (e.g., oleic acid, linoleic acid), and bromatological parameters. Because UNR148 presented missing values ('NA') for multiple nutritional variables, this genotype was removed from the PCA, as the method requires a complete matrix free of missing observations. The PCA biplot highlights the contributions of each variable to the principal components and displays the clustering of genotypes (UNR146 to UNR153). All statistical analyses were performed using R software v4.4.2 (R Core Team, 2020).

RESULTS

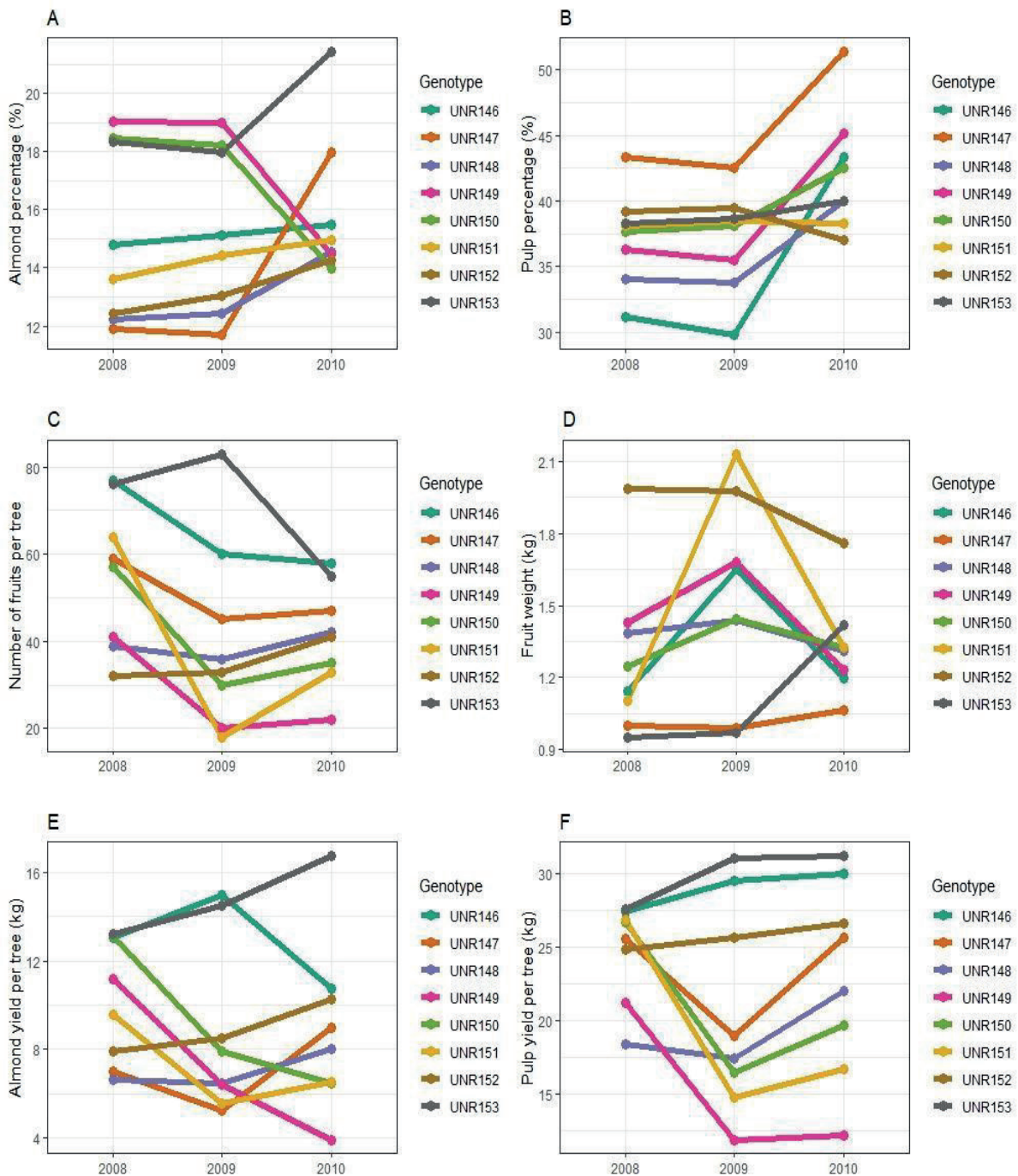
The results showed that the number of fruits, total almond percentage, and total pulp yield exhibited significant differences among genotypes ($p < 0.05$) (Table 2). Moreover, significant differences ($p < 0.05$) were observed for pulp yield, almond yield, and fruit weight, underscoring the notable variability among the evaluated genotypes (Table 1). These findings highlight genetic influence on these traits and the genetic potential of the assessed cupuassu clones for improving key agronomic traits under the environmental conditions of Caquetá, Colombia.

Table 2. Mean square for pulp and almond yield parameters

Source variation	Df	Mean square					
		Pulp yield	Almond yield	Number of fruits	Fruit weight	Total almond percentage	Total pulp yield
Genotype	7	31.71*	15.05*	689.0**	0.21*	26.91**	79.05**
Year/Genotype	2	68.56	1.46	562.7	0.14	5.27	33.93
Residuals	14	8.92	4.48	105.8	0.05	5.48	12.99
Coefficient of variation		7.70%	13.75%	22.38%	16.83%	25.23%	15.76%

Note. Mean square values marked with a single asterisk (*) indicate significance at the $p < 0.05$ level, while values marked with a double asterisk (**) indicate significance at the $p < 0.01$ level.

Genotype UNR147 showed a comparable trend, in contrast to UNR149 and UNR150, which reached their highest almond percentages during the first two years but performed poorly in 2010 (Figure 1A). Elevated rainfall appeared to enhance pulp production in most genotypes, except for UNR152, which displayed a decline of approximately 5% (Figure 1B). The number of fruits per tree tended to be higher during the first year across all accessions, with genotypes UNR146 and UNR153 displaying the highest values (Figure 1C). In contrast, genotype UNR152 produced the largest fruits and demonstrated the greatest stability throughout the evaluation (Figure 1D). Meanwhile, UNR151 produced the heaviest fruits in the second year but experienced a weight reduction of up to 50% in the following two years (Figure 1D). Overall, UNR146 and UNR153 were the highest-yielding genotypes under the environmental conditions evaluated, excelling in both almond and pulp production (Figure 1E-F). Genotypes UNR150 and UNR151 exhibited comparable yields in the first year, but their performance declined by nearly 50% under less favorable conditions. These findings underscore the influence of environmental conditions on cupuassu genotype performance, with UNR146 and UNR153 emerging as the most resilient and productive across varying climatic scenarios.



Note. (A) Almond percentage (%), (B) Pulp percentage (%), (C) Number of fruits per tree, (D) Fruit weight (kg), (E) Almond yield per tree (kg), and (F) Pulp yield per tree (kg) across seven genotypes (UNR146 to UNR153).

Figure 1. Agronomic traits of cupuassu clones during the period between 2008 and 2010

Duncan’s multiple range test confirmed the overall trends observed in the performance of cupuassu genotypes. In terms of pulp percentage, genotype UNR147 achieved the highest value (45.7), surpassing genotypes UNR148 and UNR146 by 27.8% and 31.7%, respectively (Table 3). Similarly, genotypes UNR153 and UNR149 recorded the highest mean almond yield (14.8% and 7.1%, respectively), exceeding the values of the other six genotypes (Table 3). The heaviest fruits were produced by genotypes UNR151 and UNR152, with weights reaching up to 1.7 kg, which was 0.5 kg higher than

the average weight of fruits from the other genotypes (Table 3). Conversely, genotypes UNR153 and UNR146 exhibited the highest fruit production, with up to 32 more fruits per plant compared to the other genotypes (Table 3). This latter attribute positively influenced the total almond and pulp yields, positioning UNR153 and UNR146 among the highest-ranking genotypes in both categories (Table 3).

Table 3. Mean comparison of cupuassu genotypes' performance conducted using Duncan's multiple range test

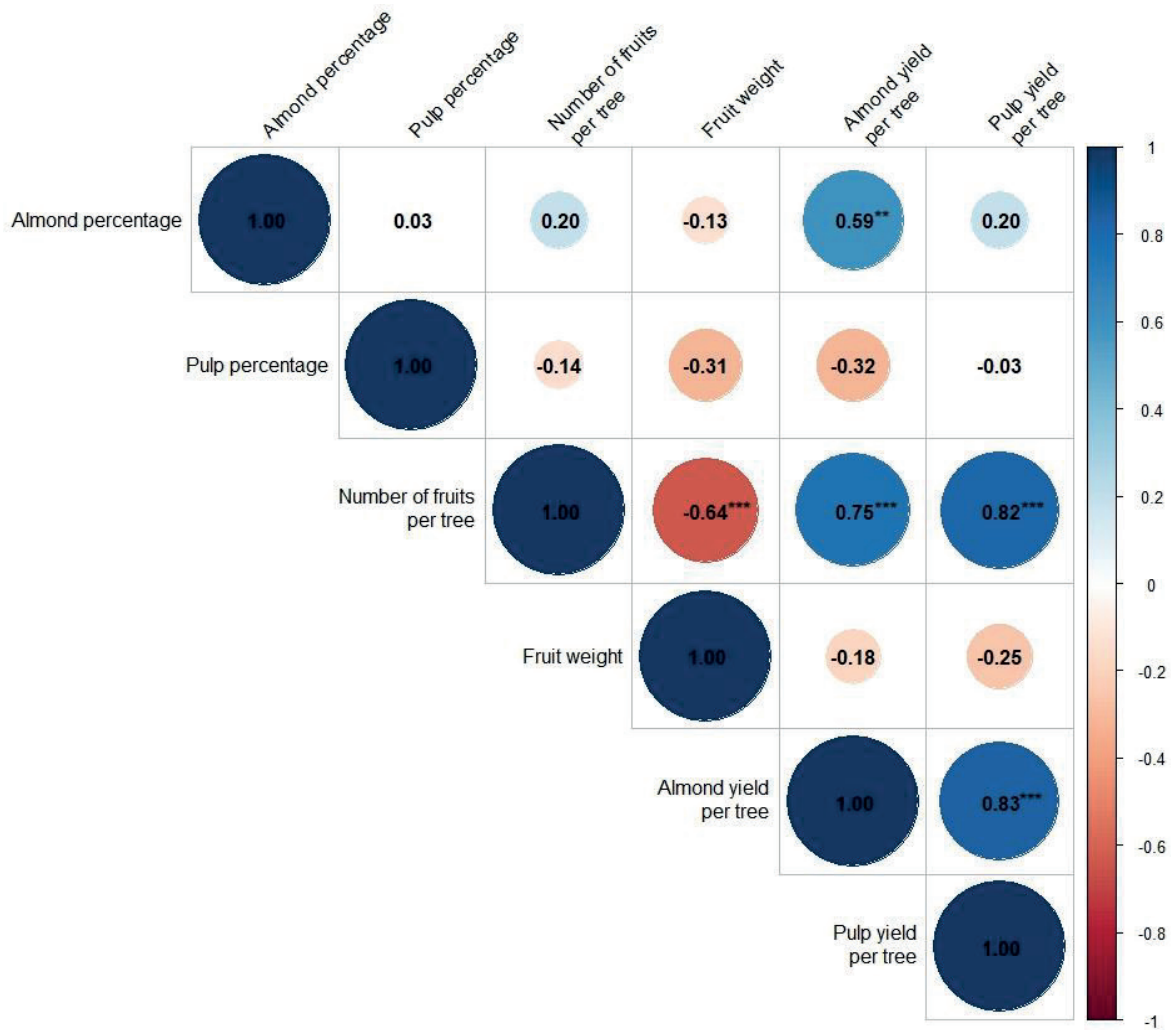
Genotype	Pulp percentage		Almond percentage		Number of fruits		Fruit weight (kg/plant)		Almond yield (kg/plant)		Pulp yield (kg/plant)	
UNR147	45.78	a	13.85	bc	50.33	ab	1.02	c	7.06	c	23.4	ab
UNR150	39.45	ab	16.89	abc	40.67	b	1.34	bc	9.16	bc	20.99	bc
UNR149	38.95	ab	17.50	ab	27.67	b	1.45	abc	7.15	c	15.12	c
UNR153	38.95	ab	19.24	a	71.33	a	1.11	bc	14.81	a	29.97	a
UNR152	38.53	ab	13.25	c	35.33	b	1.91	a	8.89	bc	25.74	ab
UNR151	38.30	ab	14.32	bc	38.33	b	1.52	ab	7.21	c	19.45	bc
UNR148	35.93	b	13.07	c	39.00	b	1.38	bc	7.02	c	19.31	bc
UNR146	34.76	b	15.13	bc	65.00	a	1.33	bc	12.92	ab	29.00	a

Note. Values followed by the same letter within each column are not significantly different according to Duncan's multiple range test ($p < 0.05$).

The correlation analysis revealed significant relationships between key agronomic traits of cupuassu. Significant correlations are highlighted, with almond yield per tree and pulp yield per tree showing strong positive correlations with the number of fruits per tree (0.75 and 0.82, respectively) (Figure 2).

This indicates that an increase in the number of fruits directly contributes to higher yields of both pulp and almonds. Almond percentage showed a moderate positive correlation with almond yield per tree ($r=0.59$, $p < 0.01$), suggesting that genotypes with a higher almond percentage tended to produce greater almond yields (Figure 2). Conversely, fruit weight exhibited a significant negative correlation with the number of fruits per tree ($r=-0.64$, $p < 0.001$), possibly due to competition for assimilates (Figure 2). This indicates that an increase in the number of fruits likely reduces the availability of photoassimilates per fruit, leading to a corresponding decrease in individual fruit weight.

The predominant fatty acids in cupuassu butter were oleic acid (42.8%), stearic acid (30.4%), palmitic acid (8.9%), and linoleic acid (4.2%), which together account for approximately 86.3% of the butter's composition (Table 4). The ether extract ranged from 14.4% to 54.8%, highlighting significant differences in the lipid composition among the genotypes. The crude fiber ranged from 2.3% to 5.0%, and the ether extract from 14.4% to 54.8% (Table 4). Important differences were observed in mineral content, including high levels of copper (24.6–40.1 mg/100g), boron (22.2–48.4 mg/100g), sodium (64.0–223.0 mg/100g), and manganese (0.0–16.5 mg/100g). In contrast, potassium, calcium, magnesium, and sulfur were present in minimal amounts.



Note. The size and color intensity of the circles indicate the strength and direction of the correlation, with blue representing positive correlations and red representing negative correlations. Values marked with a single asterisk (**) indicate significance at the $p < 0.01$ level, while values marked with a double asterisk (***) indicate significance at the $p < 0.001$ level.

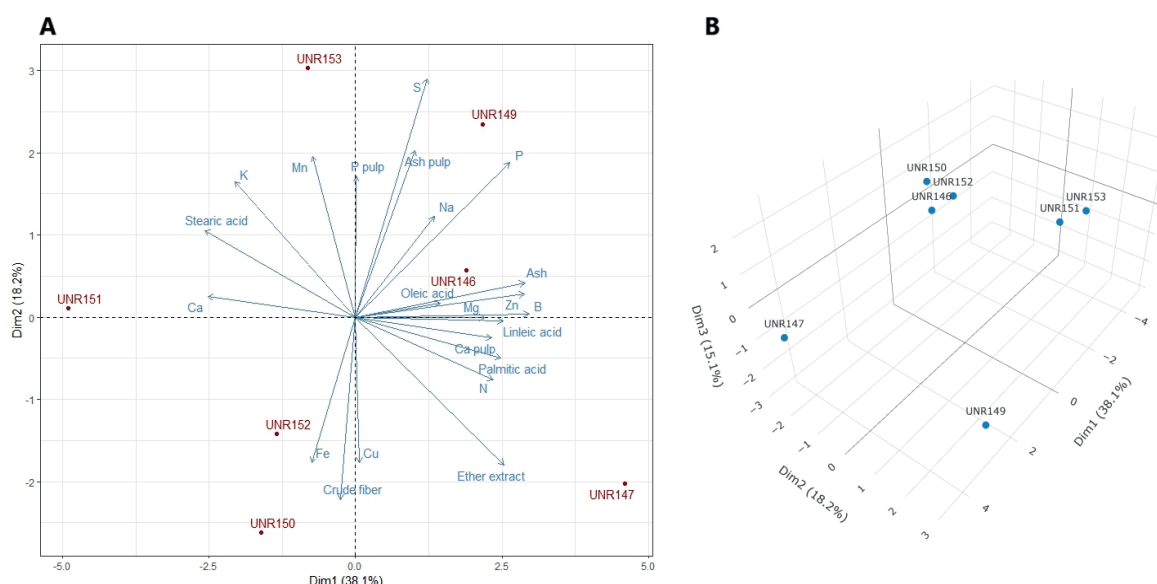
Figure 2. Pearson correlation matrix among agronomic traits of cupuassu clones

The principal component analysis identified distinct groupings of genotypes based on almond and pulp quality traits. Genotype UNR147 exhibited a strong association with ether extract, pulp calcium, nitrogen, palmitic acid, and linoleic acid (Figure 3A). Similarly, genotypes UNR149 and UNR146 were closely linked to pulp-related traits, including ash content in pulp and almond, as well as phosphorus, sodium, boron, zinc, magnesium, sulfur, and oleic acid, emphasizing their potential for enhancing pulp quality (Figure 3A). Conversely, genotypes UNR151 and UNR153 displayed lower mineral content but were enriched in calcium, potassium, magnesium, and stearic acid (Figure 3A). In contrast, genotypes UNR152 and UNR150 were characterized by higher levels of iron, copper, and crude fiber but exhibited lower mineral and fatty acid content compared to the other genotypes (Figure 3A).

Table 4. Chemical composition of pulp and almond from eight cupuassu genotypes (UNR146 to UNR153)

Genotype	Pulp						Almond													
	Ash	P	Linoleic acid	Oleic acid	Palmitic acid	Stearic acid	Ash	N	Ether extract	Crude fiber	P	Na	K	Mg	Cu	Zn	Fe	Mn	S	B
UNR146	5.1	1.0	4.4	46.1	9.2	30.6	2.8	1.3	38.8	4.8	4.9	223.0	0.0	0.2	30.8	29.4	0.0	7.8	0.1	35.0
UNR147	5.0	1.3	4.9	43.5	10.4	26.9	3.2	1.3	54.8	5.0	5.0	67.0	0.0	0.2	40.1	31.0	0.0	0.0	0.1	48.4
UNR149	7.1	1.4	5.0	40.8	8.9	29.2	2.7	1.2	39.1	2.3	5.2	154.0	0.0	0.2	29.4	27.9	0.0	0.0	0.1	41.8
UNR150	5.0	0.8	3.6	42.0	7.6	31.4	2.4	1.2	46.9	4.6	4.0	74.0	0.0	0.2	32.7	27.2	0.6	0.0	0.1	22.4
UNR151	5.1	1.5	3.4	40.7	7.3	35.9	2.2	1.2	14.4	4.8	3.7	64.0	2.3	0.1	39.7	22.5	0.0	3.7	0.1	22.3
UNR152	4.2	1.0	4.8	43.0	10.0	27.6	2.1	1.2	40.0	3.7	3.9	83.0	0.0	0.1	27.8	23.4	0.0	6.1	0.1	35.7
UNR153	5.3	1.2	3.8	44.1	8.5	32.4	2.7	1.2	27.2	3.3	5.1	79.0	2.3	0.2	24.6	28.3	0.0	16.5	0.1	29.1
UNR148	5.0	1.0	4.1	42.6	9.6	29.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Note: The table presents the content of ash, calcium (Ca), phosphorus (P), and fatty acids (linoleic, oleic, palmitic, and stearic acids) in the pulp, with values reported in percentages. For the almond, it includes ash, nitrogen (N), ether extract, crude fiber, phosphorus (P), sodium (Na), potassium (K), calcium (Ca), magnesium (Mg), copper (Cu), zinc (Zn), iron (Fe), manganese (Mn), sulfur (S), and boron (B), with values reported in mg/kg. Missing data is indicated as "NA." UNR148 data not available due to insufficient sample for analysis. The nutritional composition analysis of pulp and almonds was conducted using samples harvested during the 2010 season.



Note. (A) The biplot illustrates the distribution of seven cupuassu genotypes along the first two principal components, which explain 56.3% of the total variation. (B) The 3D plot shows the distribution of genotypes along the first three principal components (explaining 71.4% of the total variance), revealing four distinct clusters among the genotypes.

Figure 3. Principal Component Analysis of nutritional properties from almond and pulp of cupuassu (*T. grandiflorum*) fruits

On the other hand, the concentration of minerals such as magnesium, zinc, boron, and nitrogen was correlated with the composition of fatty acids, except for stearic acid. Stearic acid showed a stronger positive correlation with increased potassium, manganese, and calcium content in the almond (Figure 3A). The concentrations of phosphorus and pulp ash appear to be independent of the nutritional values of the almond, although they exhibited a negative relationship with the levels of iron, copper, and crude fiber (Figure 3A). A 3D plot of genotype distribution based on the first three

dimensions of the PCA, which collectively explain 71.4% of the total variance, revealed four well-defined groups (Figure 3B). The results highlighted the distinct separation of UNR147 and UNR149, characterized by unique nutritional profiles (Figure 3B). In contrast, genotypes UNR150, UNR152, and UNR146 clustered closely together, indicating shared traits (Figure 3B). Similarly, genotypes UNR153 and UNR151 formed a separate group, suggesting common associations with the evaluated nutritional attributes (Figure 3B). These findings highlight distinct mineral and fatty acid associations among genotypes, emphasizing their potential for targeted selection in breeding programs.

DISCUSSION

The observed variability in yield components among the evaluated clones underscores the importance of genotype selection in optimizing cupuassu production. Several studies demonstrate that the number and weight of cupuassu fruits are attributes governed by quantitative traits (Chaves *et al.*, 2021; Mournet *et al.*, 2020). The most promising clones for pulp and kernel yield production were UNR146 and UNR153. The high productivity of these materials was primarily attributed to their elevated fruit production. Among the two, UNR153 demonstrated greater stability and maintained higher production even under unfavorable environmental conditions, characterized by elevated temperatures (31.3 °C) and high monthly rainfall (268–326 mm) (Table 1). In contrast, UNR151 and UNR152 were the most desirable for fresh consumption due to their larger fruit size, making them attractive for premium market segments (Alves *et al.*, 2021). On the other hand, the genotype UNR147 exhibited strong potential for enhancing pulp quality in terms of its fatty acid and mineral profile. Previous studies have demonstrated that selecting genotypes rich in essential fatty acids and minerals is crucial for meeting the nutritional demands of consumers (Jean-Marie *et al.*, 2022; da Silva, Costa *et al.*, 2024). Meanwhile, the genotypes UNR149 and UNR146 emerged as ideal candidates for breeding strategies aimed at enhancing the emollient properties, which make them highly suitable for cosmetic applications (Bezerra *et al.*, 2024; Kolodziejczyk-Czepas, 2024). Additionally, their high content of polyphenols, anthocyanins, and flavonoids provides antioxidant benefits, protecting against cellular damage caused by free radicals (Bezerra *et al.*, 2024; Kolodziejczyk-Czepas, 2024).

The genotypes UNR151 and UNR153 exhibited a reduced overall mineral profile but showed higher concentrations of potassium, magnesium, and stearic acid in the almond. The latter is associated with specific physical properties of the kernel and potential industrial applications (Bangar *et al.*, 2024). Additionally, the genotypes UNR150 and UNR152 were characterized by high levels of iron, copper, and crude fiber. The high crude fiber content offers significant health benefits, including improved digestive health, better regulation of blood sugar levels, and enhanced cardiovascular support, making them valuable for developing functional foods aimed at populations with specific dietary needs (Mar *et al.*, 2024).

The fatty acids in cupuassu seed oil exhibited a more balanced composition of unsaturated and saturated fatty acids compared to cocoa butter (da Silva, Costa *et al.*, 2024). The results are consistent with those reported in other studies, which have found up to 10% higher levels of oleic and stearic acids compared to cocoa butter (Benlloch-Tinoco *et al.*, 2024). This composition suggests greater potential for anti-inflammatory properties, likely through the modulation of immune responses and the reduction of inflammatory markers (Santamarina *et al.*, 2021). The PCA plot shows a clear negative correlation between stearic acid and other fatty acids (oleic, linoleic, and palmitic acids). This pattern suggests that genotypes with higher stearic acid content, such as UNR151 and UNR153, tend to have lower levels of the other fatty acids.

The correlation analysis revealed significant relationships essential for selection strategies in breeding programs. The number of fruits per plant showed the highest correlation values with cupuassu pulp and almond yield (Figure 2). This demonstrates why this attribute is one of the most prioritized objectives for cupuassu improvement programs (Alves & Chaves, 2022). On the other hand, the number of fruits has a strong negative influence on their individual weight, as reported by Alves and Chaves (2022), and Velasquez-Vasconez *et al.* (2025), with similar findings observed in cacao by Doaré *et al.* (2020). The partitioning of photoassimilates is distributed either among a larger number of smaller fruits or among a smaller quantity of larger fruits.

These findings suggest that gene linkage, pleiotropy, and epistatic interactions may play a critical role in regulating the trade-off between fruit number and size (Santos *et al.*, 2022). Understanding these interactions is crucial for developing effective breeding strategies to optimize both fruit yield and quality. For instance, a cross between UNR153 and UNR152 is particularly promising because their agronomic profiles are highly complementary: UNR153 combines high productivity with a large number of fruits per plant, whereas UNR152 produces larger and heavier fruits with superior pulp and almond proportions. These contrasting yet advantageous traits provide an opportunity to exploit both complementarity and transgressive segregation in the progeny.

Another economically important attribute to consider is the almond percentage. The almond proportion of the fruit can be improved by selecting fruits with a lower proportion of shell and placenta biomass, which exhibit significant phenotypic variability within cupuassu populations. For instance, some trees have been found to produce fruits with shell thicknesses ranging from 2 to 18 mm (Velasquez-Vasconez *et al.*, 2025). Although a lower shell proportion can be advantageous for yield, achieving a balance between these phenotypic attributes is essential. The shell serves as a physical barrier, protecting the fruit from environmental factors, pests, and diseases, while also preventing damage from falling when ripe.

The heritability of traits is another critical criterion to consider when selecting materials in breeding programs. The total genotypic heritability for the number of fruits is higher (0.47) than the heritability for fruit weight (0.31) (Alves & Chaves, 2022). This suggests that the number of fruits is more strongly influenced by genetic factors, while fruit weight may be more affected by environmental factors or genotype-environment interactions. Consequently, the number of fruits is likely to respond more effectively to selection in early generations, whereas improving fruit weight may require prolonged selection efforts and more sophisticated breeding strategies. However, the heritability values are influenced by the genetic basis of the study population. Therefore, the extrapolation of these values and their conclusions must be approached with caution.

The polygenic characteristics evaluated are influenced by the interplay of multiple genes and environmental conditions. It is important to emphasize that the genotypes must be evaluated across diverse environments to reduce uncertainty regarding regional adaptation. Adaptability and stability tests are even more critical for populations derived from sexual reproduction in species with high genetic variability (Garg *et al.*, 2025). In the case of cupuassu, its self-incompatibility promotes increased genetic diversity through cross-pollination (Alves *et al.*, 2024; Ramos *et al.*, 2005). This mechanism enhances the potential for selecting superior genotypes while maintaining a broad genetic base, crucial for long-term breeding and adaptation strategies. Understanding these interactions is crucial for breeding programs to develop superior cupuassu varieties adapted to the local region.

CONCLUSIONS

The multi-year evaluation of eight *Theobroma grandiflorum* genotypes under Amazonian conditions identified clear differences in productivity and nutritional composition. UNR146 and UNR153 were the most productive materials, combining high fruit numbers with superior pulp and almond yields and maintaining stable performance despite variable environmental conditions. Nutritional profiling revealed distinct genotype-specific patterns, with UNR147, UNR149, UNR150, UNR151, UNR152, and UNR153 each expressing unique mineral and fatty-acid characteristics relevant to different agro-industrial applications. Overall, the integration of agronomic and nutritional traits demonstrates that careful genotype selection is essential for improving yield, fruit quality, and resilience in cupuassu cultivation. These results provide a foundation for breeding strategies focused on enhancing productivity and nutritional value while supporting the development of adapted and competitive cupuassu varieties for the Colombian Amazon.

AUTHOR CONTRIBUTIONS

Pedro Alexander Velasquez-Vasconez contributed to Conceptualization, Methodology, Formal Analysis, Investigation, Visualization, Writing – Original Draft Preparation, and Writing – Review & Editing, with a lead contribution in the overall design of the study and manuscript preparation. María Isabel Castro Zambrano contributed to Investigation, Validation, Visualization, and Writing – Review & Editing. Dagoberto Criollo Cruz contributed to Resources, Methodology, Investigation, and Validation. Esteban Diaz Gaviria contributed to Software, Formal Analysis, Data Curation, and Visualization. Juan Carlos Zambrano Arteaga contributed to Review & Editing.

ACKNOWLEDGMENTS

Funding: This research was funded by “Ministerio de Ciencia Tecnología e Innovación – MIN-CIENCIAS”, grant number 106866 and program number 106735.

CONFLICTS OF INTEREST

The authors declare that they have no conflict of interest.

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