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Morpho-agronomic diversity of *Manihot esculenta* Crantz accessions: Implications for conservation and genetic management

Diversidad morfo-agronómica de accesiones de *Manihot esculenta* Crantz: Implicaciones de conservación y manejo genético

Del Rosario–Arellano, J.L.[1], Meneses–Márquez, I.[2], Cruz–Moreno, F.Z.[1], Serna–Lagunes, R.[1], Leyva–Ovalle, O.R[1], Andrés–Meza, P.[1], Verdejo–Lara, R.A.[1], Llarena–Hernández, C.R.[1], Diaz–José, J.[1]*

[1] *Facultad de Ciencias Biológicas y Agropecuarias, región Córdoba-Orizaba. Universidad Veracruzana. Calle Josefa Ortiz de Domínguez, S/N, Col. Centro, C.P. 94950, Peñuela, Amatlán de los Reyes, Veracruz, México.*

[2] *Instituto Nacional de Investigaciones Forestales Agrícolas y Pecuarias, Campo Experimental Cotaxtla. Km 34 carretera Veracruz-Córdoba, C.P. 94270, Medellín de Bravo, Veracruz, México.*

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ABSTRACT

The evaluation of variation in plant germplasm is crucial for classifying and identifying desirable traits for the improvement and conservation of crops. The objective of this study was to analyze the morpho-agronomic diversity of cassava accessions in the Las Montañas region of Veracruz, Mexico. The morphogenetic diversity of 11 cassava accessions was determined using the Shannon index (H') and the Jaccard similarity coefficient (J') based on 33 qualitative traits. Principal Components Analysis (PCA) and cluster analysis were applied to 15 quantitative traits. The traits with significant variation included the shape of the leaf's central lobe, petiole orientation, epidermis color, and plant shape. The H' index ranged from 0.13 to 1 ($\bar{X}$ = 0.43), indicating moderate diversity due to variability (J' from 43 to 100 %; $\bar{X}$ = 69 %) among the accessions. The cluster analysis identified 4 contrasting groups, with a variance of 81 % in the first three components of the PCA. The study indicates the presence of sufficient genetic information contributed by the variability of the morpho-agronomic traits, attributed to the diversity of lineages adapted to the geographic origin of the evaluated accessions.

KEY WORDS: Cassava, germplasm, morpho-agronomic traits, principal component analysis, Shannon index.

***Corresponding Author:**

Otto Raúl Leyva–Ovalle. Facultad de Ciencias Biológicas y Agropecuarias, región Córdoba-Orizaba. Universidad Veracruzana. Calle Josefa Ortiz de Domínguez, S/N, Col. Centro, C.P. 94950, Peñuela, Amatlán de los Reyes, Veracruz, México.
Teléfono: (271) 740 4828. E-mail: oleyva@uv.mx

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A B S T R A C T

La evaluación de la variación de germoplasma vegetal es importante para clasificar e identificar las características deseables para mejoramiento y conservación de los cultivos. El objetivo del estudio fue analizar la diversidad morfo-agronómica de accesiones de yuca en la región Las Montañas, Veracruz, México. La diversidad morfogenética de 11 accesiones de yuca se determinó con el índice de Shannon (H') y el coeficiente de similitud de Jaccard (J') a partir de 33 caracteres cualitativos. Un análisis de componentes principales (PCA) y conglomerados se aplicó a 15 caracteres cuantitativos. Los caracteres con variación significativa fueron la forma del lóbulo central de la hoja, orientación del peciolo, color de la epidermis y forma de la planta. El índice H' osciló entre 0.13 y 1 ($\bar{X}$ = 0.43) indicando una diversidad media debida a la variabilidad (J' de 43 a 100 %; $\bar{X}$ = 69 %) entre accesiones. El análisis de conglomerados determinó 4 grupos contrastantes, y una varianza del 81 % en los primeros tres componentes del PCA. El estudio indica la existencia de suficiente información genética aportada por la variabilidad de las características morfo-agronómicas, que se atribuyen a la diversidad de linajes que se encuentran adaptados al origen geográfico de las accesiones evaluadas.

P A L A B R A S C L A V E : Análisis de componentes principales, caracteres morfo-agronómicos, germoplasma, índice de Shannon, yuca.

Introduction

Cassava (*Manihot esculenta* Crantz) is a perennial shrub-like plant characterized by a tuberous root that can reach 1 meter in length and 10 centimeters in diameter, rich in carbohydrates, as well as fats, proteins, multivitamins, and minerals (Li *et al*., 2023). Its cultivation provides a reliable source of economic income through the sale of its tubers and is noteworthy for its industrial value in producing high-value products (Aguilar-Rivera, 2024; Andrés-Meza *et al*., 2024). Additionally, its ecological versatility allows it to thrive in various environmental settings (Ogbonna *et al*., 2021), even under challenging soil and climatic conditions (Imarhiagbe *et al*., 2024). For these reasons, in tropical and subtropical regions, cassava represents a crucial phytogenetic resource for ensuring food security and combating poverty (Thiele *et al*., 2022).

Currently, the intraspecific genetic diversity of cassava is attributed to ongoing processes of selection, exchange of native materials, natural hybridization, introduction of new genotypes, and translocation of genetic lineages (Laila *et al*., 2021; Tovar *et al*., 2016). In this context, while the use of improved varieties is common in conventional agriculture (Obare *et al*., 2023), local

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production systems continue to utilize and conserve numerous morphotypes (Wooding & Payahua, 2022). These morphotypes are characterized by high yield, flavor, commercial demand, drought tolerance, resistance to pests and diseases, or high starch content (Mutoni *et al*., 2023; Ferguson *et al*., 2024). However, materials lacking desirable traits are often discarded (Obayelu *et al*., 2015; Le *et al*., 2019), despite the potential for unknown uses (Pérez *et al*., 2019; Hoogerheide & Tiago, 2023); therefore, it is crucial to preserve the genetic pool.

In this context, the International Center for Tropical Agriculture conserves 5,760 South American and Asian accessions, along with 883 wild relatives of cassava; similarly, the International Institute of Tropical Agriculture maintains a collection of 2,712 accessions from West Africa (Ferguson *et al*., 2019). Meanwhile, in Mexico, *ex situ* conservation programs for cassava are limited, except for findings reported by Del Rosario-Arellano *et al*. (2022[a]), who highlighted the MMEXV40 material for its agricultural productivity, starch extraction yield, and excellent properties to produce biodegradable films.

In this approach, the collection, conservation, and characterization of plant germplasm emerge as actions that significantly contribute to reduce the impacts of genetic erosion, with the potential for use in the development of improved materials (Devi *et al*., 2022; Carvajal-Yepes *et al*., 2024). Based on this, studies that combine the analysis of quantitative and qualitative traits associated with indicators of intraspecific genetic variation, such as the Shannon index (H’) and the Jaccard similarity index (J’), facilitate better exploration and understanding of the divergence among cassava varieties (Afonso *et al*., 2020).

In this regard, there is ecological, biological, and cultural evidence concerning cassava diversity in the southeastern region of Mexico (Del Rosario-Arellano *et al*., 2017; Salinas-Cach *et al*., 2019; Li *et al*., 2023). Specifically, in the state of Veracruz, there are records of collections from the coastal area at an altitude range of 20 to 500 masl (Meneses *et al*., 2014). Meanwhile, in the Las Montañas region, a prospecting study (112 and 1 391 masl) identified 13 cassava clones, whose phenotypic characteristics, potential diversity, and uses remain unknown (Del Rosario-Arellano *et al*., 2024). Thus, this research aimed to evaluate the genetic diversity of cassava germplasm present in the Las Montañas region of Veracruz, Mexico, to provide valuable/useful information for future breeding programs, conservation initiatives, food security promotion, and the development of resilient agricultural strategies.

Material and Methods

Collection and establishment of cassava accessions

Cassava accessions were collected in February 2023 through surveys conducted in various municipalities of the Las Montañas region, Veracruz (Figure 1). Additionally, cuttings were requested as donations from students at the Facultad de Ciencias Biológicas y Agropecuarias (FCBA), region Orizaba-Córdoba de la Universidad Veracruzana. A total of 13 accessions were established on March 21st, at the experimental field of the FCBA (Figure 1). The area has a semi-

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warm humid climate classified as (A)C(m)(f) (García, 2004), with an average temperature of 22.9 °C and annual precipitation of 2,372 mm based on a historical series spanning 30 years (Harris *et al*., 2020). The soil type is vertisol (INEGI, 2022), characterized by a loam texture, pH of 4.4, and organic matter content of 1.47 %. Additionally, nitrogen and phosphorus levels were recorded at 0.04 % and 77.28 mg kg^{-1}, respectively.

Agronomic management

Soil preparation was carried out mechanically through weeding, plowing, and furrowing. For planting, cuttings measuring 20 cm in length were prepared and then submerged in a solution of Agromil®V AdStrong (1 ml L^{-1}) and Promyl® (Methyl 1-(butylcarbamoyl) benzimidazol-2-ylcarbamate, 0.3 g L^{-1}). A planting distance of 1 x 1 m was maintained between plants and furrows, resulting in a density of 10,000 plants per hectare. The experimental plots consisted of an area of 25 m^2, weeds were controlled manually, and nutrient management involved applying 10 g of diammonium phosphate (18-46-00) to the soil at 60 days after sowing (das) and 20 g of Blaukorn® (12-8-16 (Mg+S+B+Fe+Zn)) at 100 das. Harvesting was performed manually at 300 das. During the experiment, temperature and precipitation data were recorded and analyzed, allowing for the creation of a climogram to visualize the variation patterns of these two climatic variables (NASA, 2024).

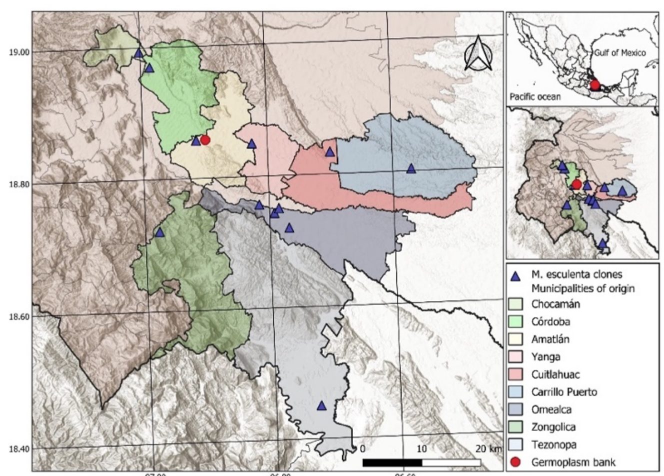

Figure 1. Origin of cassava germplasm in the Las Montañas region, Veracruz.

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Morpho-agronomic characterization

The characterization of the genetic material was conducted following the manual proposed by Fukuda *et al*. (2010), in which 48 morpho-agronomic descriptors were recorded at 3, 6, 9, and 12 months after planting in 11 cassava accessions, measuring between 1 and 5 plants depending on the availability of vegetative material. It is noteworthy that two clones did not thrive due to a lack of material at the beginning of planting, and that clone MMEXV4 originated from a sugarcane field that had previously been burned for harvest (Del Rosario-Arellano *et al*., 2024).

For the study of genetic diversity contained in the phenotypic traits of the accessions, the evaluation of 33 qualitative traits was considered using the Shannon-Weaver diversity index (H'). This indicator facilitates the assessment of morphotype characteristics by analyzing the various forms that reflect their genetic diversity (Dong *et al*., 2004). It operates under the hypothesis that agro-morphological patterns are manifestations of genes that have adapted to the environmental conditions specific to the locality of origin, where these accessions were collected and cultivated over multiple generations (Sing *et al*., 2016; Desheva & Valchinova, 2023). The Shannon index indicates a value ranging from -1 to 1 as low diversity, from 1 to 2 as medium diversity, and greater than 2 as high diversity (Zambrano *et al*., 2003). Additionally, the Jaccard similarity coefficient (J') was calculated, which relates morpho-agronomic, biochemical, and molecular characteristics of genetic diversity in crops (Guidoti *et al*., 2018; Nogueira *et al*., 2021). This coefficient varies from 0 to 1, with a value of 1 representing maximum similarity among the set of discrete traits. These indicators were calculated using Real Statistics Using Excel software (Zaiontz, 2023). It is important to note that both indicators are useful for evaluating the diversity of qualitative traits in crops (Dong *et al*., 2004).

The recorded 15 quantitative variables related to cassava accessions, including: number of leaf lobes (NLL), length of the central leaf lobe (LCLL), width of the central leaf lobe (WCLL), leaf length/width ratio (LLWRA), petiole length (PETL), plant height (PLAH), height to the first branching (HBRAN), levels of branching (LBR), angle of branching (ABR), number of storage roots (NSROOT), root weight (ROOTW), number of commercial roots (CROOT), cortex thickness (CORT), dry matter content (DMC), and starch content (STC). These variables were analyzed using Principal Component Analysis (PCA) based on the correlation matrix. The primary aim of this analysis was to elucidate the variation among accession groups and their associated morpho-agronomic traits, which can be effectively visualized through a two-dimensional biplot. Additionally, a cluster analysis was performed utilizing Ward's method and Euclidean distance to classify groups exhibiting similarities in morpho-agronomic patterns. All analyses were conducted using InfoStat software version 2020 (Di Rienzo *et al*., 2020).

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Results and Discussion

Climatic condition

During the 300-day cultivation cycle, the average maximum and minimum temperatures recorded were 27.01 and 15.87 °C, respectively, with a total precipitation of 1,627.76 mm (Figure 2). The climatic data indicate the feasibility of introducing a cassava germplasm bank, as the optimal temperature requirements for the species range from 20 to 29 °C, with tolerance extending up to 35 °C, and rainfall levels between 1,000 mm and 2,500 mm (Del Rosario-Arellano *et al*., 2022[b]). It is noteworthy that the evaluation site features soil characterized by high moisture retention due to its clayey texture; prolonged saturation could lead to tuber root rot (Cock *et al*., 2018). Therefore, it is essential to consider elevated furrows to mitigate potential damage.

Distribution of qualitative traits

The cassava accessions exhibited variable ranges in the frequency of qualitative traits (Table 1). The traits demonstrating the highest variability were the shape of the central leaf lobe, with 36.36 % classified as lanceolate, 27.27 % as elliptical-lanceolate, and 18.18 % as obovate-lanceolate and linear-pandurate. Obare *et al*. (2023) found that in a population of 256 cassava accessions in Kenya, 43.5 % exhibited an oblong-lanceolate shape, 35.7 % were lanceolate, and 8.2 % displayed an elliptical-lanceolate form. Due to the diversity of this trait, it is utilized to discriminate among cassava phenotypes. Additionally, the reddish-green color of the petiole was observed most frequently (36.36 %), followed by yellowish-green (27.27 %) and green with red (9.09 %).

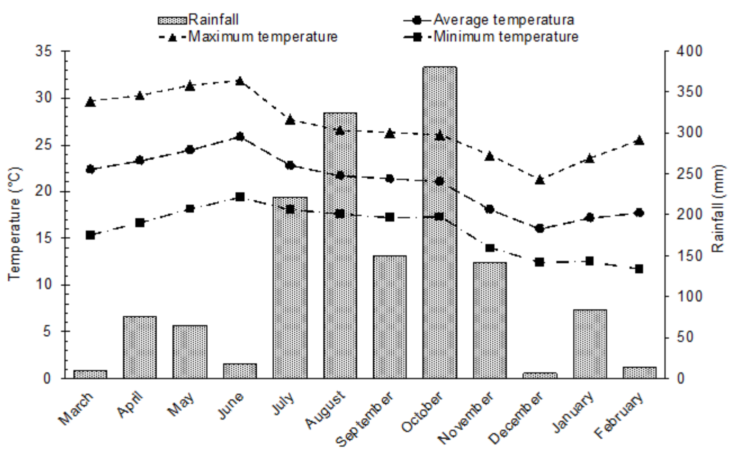

Figure 2. Climogram during the cassava development period.

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Regarding the tuberous root, the cream color of the pulp was the most predominant trait, observed in 72.73 % of the accessions. The significance of this variable lies in its association with the dietary habits of different regions, which ultimately influences commercial sales (Mezette *et al*., 2013). It is important to note that accessions MMEXV3 and MMEXV7 exhibited a yellow pulp color (18.18 %), a characteristic linked to a high concentration of β-carotenes, provitamin A precursors (Tize *et al*., 2021; Mutoni *et al*., 2023). Therefore, these accessions could be valuable in breeding programs aimed at enhancing the nutritional quality of new genotypes.

On the other hand, the green color of the leaf vein, semi-prominent foliar scars, erect stem growth, and green color of the terminal branches were the traits exhibiting the lowest variability, as these characteristics were present in 100 % of the accessions. This contrasts with a characterization study of 52 cassava accessions in Tanzania, which reported that only 50 % of the germplasm displayed green venation (Mtunguja *et al*., 2017). It has been noted that dark green coloration plays a significant role in identifying genotypes with high tuber root yields (Khumaida *et al*., 2015).

It is noteworthy that 72.73 % of the accessions exhibited pubescence on the apical leaf, contrasting with findings by Ferguson *et al*. (2024), who reported this characteristic in only 7 % of 118 cassava accessions studied. Additionally, the results from Pierre *et al*. (2022) corroborate this low frequency. Genotypes with a higher density of trichomes have been shown to facilitate the oviposition and development of whitefly nymphs, depending on the species; however, leaf color parameters also closely correlate with insect incidence (Pastório *et al*., 2023). Consequently, these traits are valuable for selecting cassava clones with a degree of tolerance to pest attacks of agronomic significance and hold promise for advancing genetic improvement programs.

On the other hand, flowering, pollen, and fruiting were observed in 36.36 % of the germplasm. Clones of cassava that exhibit early flowering are preferred by breeders, as this facilitates timely crosses and the subsequent development of new genotypes. However, flowering is influenced by several factors, including the accumulation of degree-days (Santos *et al*., 2024), photoperiod (Pineda *et al*., 2020), genotype, and even agronomic practices such as grafting techniques (Silva *et al*., 2018).

Shannon-Weaver Diversity Index and Jaccard Similarity Index

It is noteworthy that the Shannon diversity index (*H'*) ranged from 0.13 to 1 ($\bar{X}$ = 0.43). An H' value of 0.43 indicates intermediate diversity among the evaluated morphotypes, reflecting variability in the morphological traits across the accessions. This finding aligns with the Jaccard similarity coefficient (J'), which varied from 43 to 100 % ($\bar{X}$ = 69 %) across 22 qualitative traits, resulting in a 41 % variability in these traits (Table 1). It is important to clarify that traits with a J' value of 1 do not imply that the collections are genetically identical; rather, they indicate similarity based on the categories used for each characteristic. A closer examination (Table 1) reveals that for most variables (at least 22), the Shannon diversity index is less than 0.5, while the J' value depends on the observed classes for each variable. For instance, variables with a low H' index may exhibit over 90 % similarity in J' if they only possess two classes. These indicators demonstrate the variability in the qualitative morpho-agronomic traits of the harvested accessions, such as leaf and stem color, which exhibit a diverse range of colors. Although the frequency of occurrence for each trait corresponds to a 41 % variation, this is considered intermediate and may be influenced by genetic factors (Collado *et al*., 2004). The variation in H’ and J’ indices is associated with genetic factors that define heterogeneous evolutionary lineages resulting from backcrossing between local or regional varieties. Therefore, further research should incorporate molecular markers such as single-nucleotide polymorphisms (SNPs), as phenotypic traits determined by genes can be identified using this tool; additionally, its implementation is valuable in genetic improvement programs and genomic association studies (Cardoso *et al*., 2023).

Principal component analysis

The principal component analysis estimated that three components accounted for 81 % of the total variation, with eigenvalues of 46, 23, and 12 %, respectively, and eigenvalues greater than 1 (Table 2). Consequently, the variations in the data can be explained by these components (Jeffers, 1996; Laila *et al*., 2021), with traits located along the axes having a significant impact on the phenotype of the accessions. The variation observed was greater than that reported by Carine *et al*. (2016), who recorded 57.56 % of the total variation in the first three components during a genetic diversity study involving 89 cassava accessions assessed for 14 quantitative traits. Similarly, Kamanda *et al*. (2020) found that five principal components accounted for 70.44 % of the phenotypic variation among 183 accessions cultivated in Taiama, Sierra Leona, Africa.

Table 1. Frequency distribution of 33 qualitative characters and values of the Shannon-Weaver diversity index (*H’*) and Jaccard similarity coefficient (J’) from 11 cassava accessions.

Qualitative character	Variants	Scoring	Frequency (%)	H´	J’
Color of apical leaves	Light green	3	54.55	0.39	83
	Dark green	5	36.36		
	Purplish green	7	9.09		
	Purple	9	0		
Pubescence on apical leaves	Absent	0	27.27	0.25	85
	Present	1	72.73		
Shape of central leaflet	Ovoid	1	0	0.58	96
	Elliptic-lanceolate	2	27.27		
	Obovate-lanceolate	3	18.18		
	Oblong-lanceolate	4	0		
	Lanceolate	5	36.36		
	Straight or linear	6	0		
	Pandurate	7	0		
	Linear-piramidal	8	0		
	Linear-pandurate	9	18.18		
	Linear-hostatilobalate	10	0		

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Continuation

Table 1. Frequency distribution of 33 qualitative characters and values of the Shannon-Weaver diversity index (*H'*) and Jaccard similarity coefficient (J') from 11 cassava accessions.

Qualitative character	Variants	Scoring	Frequency (%)	H´	J'
Leaf retention	Very poor retention	1	0	0.44	74
	Less than average retention	2	9.09		
	Average leaf retention	3	9.09		
	Better than average retention	4	18.18		
	Outstanding leaf retention	5	63.63		
Petiole color	Yellowish-green	1	27.27	0.63	91
	Green	2	9.09		
	Reddish-green	3	18.18		
	Greenish-red	5	36.36		
	Red	7	9.09		
	Purple	9	0		
Leaf color	Light green	3	54.54	0.29	99
	Dark green	5	45.45		
	Purple-green	7	0		
	Purple	9	0		
Lobe margins	Smooth	3	18.19	0.2	68
	Winding	7	81.81		
Color of leaf vein	Green	3	100	1	1
	Reddish-green in less than half of the lobe	5	0		
	Reddish-green in more than half of the lobe	7	0		
	All red	9	0		
Orientation of petiole	Inclined upwards	1	36.36	0.54	91
	Horizontal	3	36.36		
	Inclined downwards	5	9.09		
	Irregular	7	18.19		
Flowering	Absent	0	63.64	0.28	0.95
	Present	1	36.36		
Pollen	Absent	0	63.36	0.28	0.95
	Present	1	36.36		
Prominence of foliar scars	Semi-prominent	3	100	1	1
	Prominent	5	0		
Color of stem cortex	Orange	1	9.09	0.4	85
	Light green	2	45.45		
	Dark green	3	45.45		

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Table 1. Frequency distribution of 33 qualitative characters and values of the Shannon-Weaver diversity index (*H'*) and Jaccard similarity coefficient (J') from 11 cassava accessions.

Qualitative character	Variants	Scoring	Frequency (%)	H´	J'
Color of stem epidermis	Cream	1	45.45	0.45	94
	Light brown	2	18.19		
	Dark brown	3	0		
	Orange	4	36.36		
Color of stem exterior	Orange	3	0	0.38	63
	Greeny-yellowish	4	9.09		
	Golden	5	9.09		
	Light brown	6	0		
	Silver	7	72.73		
	Gray	8	9.09		
	Dark brown	9	0		
Growth habit of stem	Straight	1	100	1	1
	Zig- zag	2	0		
Distance between leaf scars	Short ≤ (8 cm)	3	0	0.29	99
	Medium (8–15 cm)	5	45.46		
	Long ≥ (15 cm)	7	54.54		
Color of end branches of adult plant	Green	3	100	1	1
	Green-purple	5	0		
	Purple	7	0		
Stipule margin	Entire	1	72.73	0.25	84
	Split or forked	2	27.27		
Length of stipules	Short	3	90.9	0.13	43
	Long	5	9.10		
Fruit	Absent	0	36.36	0.28	94
	Present	1	63.64		
Seed	Absent	0	45.46	0.29	99
	Present	1	54.54		
Branching habit	Erect	1	27.27	0.37	78
	Dichotomous	2	9.09		
	Trichotomous	3	63.64		
	Tetrachotomous	4	0		
Shape of plant	Compact	1	36.36	0.47	99
	Open	2	27.28		
	Umbrella	3	36.36		
	Cylindrical	4	0		

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Continuation

Table 1. Frequency distribution of 33 qualitative characters and values of the Shannon-Weaver diversity index (*H'*) and Jaccard similarity coefficient (J') from 11 cassava accessions.

Qualitative character	Variants	Scoring	Frequency (%)	H´	J'
Extent of root peduncle	Sessile	0	54.55	0.39	83
	Pedunculate	3	36.36		
	Mixed	5	9.09		
Root constrictions	Few to none	1	36.36	0.45	94
	Some	2	45.45		
	Many	3	18.19		
Root shape	Conical	1	0	0.29	99
	Conical-cylindrical	2	45.45		
	Cylindrical	3	0		
	Irregular	4	54.56		
External color of storage root	White or cream	1	9.09	0.48	80
	Yellow	2	54.55		
	Light brown	3	27.27		
	Dark brown	4	9.09		
Color of root pulp	White	1	9.09	0.32	69
	Cream	2	72.73		
	Yellow	3	18.18		
	Orange	4	0		
	Pink	5	0		
Color of root cortex	White or cream	1	45.45	0.4	85
	Yellow	2	9.10		
	Pink	3	45.45		
	Purple	4	0		
Cortex: ease of peeling	Easy	1	54.54	0.29	99
	Difficult	2	45.46		
Texture of root epidermis	Smooth	3	9.10	0.37	78
	Intermediate	5	63.63		
	Rough	7	27.27		
Root taste	Sweet	1	4		
	Intermediate	2	6		
	Bitter	3	1	0.39	0.83
Overall average				0.43	0.83

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The contribution of characters in a principal component is identified by finding loadings close to one (Bhanupriya *et al*., 2014). The variables that indicated a significant contribution in the first principal component PC1 were leaf width (WCLL) with a loading of 0.370, total root weight (ROOTW) at 0.358, petiole length (PETL) at 0.340, and cortex thickness (CORT) with a value of 0.334, while LLWRA exhibited a negative loading (-0.283). These variables are associated with leaf dimensions and yield. In PC2, NLL (0.433), LCLL (0.315), PLAH (0.356), and HBRAN (0.454) showed significant contributions, while a negative load was observed in LBR (-0.408) and CROOT (-0.290). The PC3 was influenced by the variable NSROOT (0.424), DMC, and STC (0.396), categorized as productivity parameters and quality indicators. From the above, In a diversity study conducted by Daemo *et al*. (2023), they estimated that the PCI was associated with the width of the leaf lobe, the length of the petiole, the height of the plant, the stem diameter, the aerial biomass, and the fresh yield of the storage root, while the PC2 was related to the length of the leaf lobe, the width of the leaf lobe, the number of storage roots, the length of the storage root, and the aerial biomass.

Table 2. Eigenvalues and explained and cumulative variance in 3 principal components of 11 *M. esculenta* clones from the Las Montañas Region, Veracruz, Mexico.

Character	CP1	CP2	CP3
Number of leaf lobes (NLL)	0.074	0.433	-0.246
Length of central leaf lobe (LCLL)	0.277	0.315	0.148
Width of central leaf lobe (WCLL)	0.370	0.085	0.022
Leaf length/ width ratio (LLWRA)	-0.283	0.238	0.225
Petiole length (PETL)	0.340	0.176	0.162
Plant height (PLAH)	0.193	0.356	0.096
Height to first branching (HBRAN)	0.019	0.454	-0.046
Levels of branching (LBR)	0.222	-0.408	0.093
Angle of branching (ABR)	-0.211	-0.019	-0.523
Number of storage roots (NSROOT)	0.246	-0.119	0.424
Root weight (ROOTW)	0.358	-0.130	0.005
Number of commercial roots (CROOT)	0.177	-0.290	-0.173
Cortex thickness (CORT)	0.334	-0.054	-0.154
Dry matter content (DMC)	-0.247	-0.021	0.396
Starch content (STC)	-0.247	-0.021	0.396
Eigenvalues	6.84	3.48	1.80
Explained variance (%	0.46	0.23	0.12
Cumulative variance (%)	0.46	0.69	0.77

The characters and accessions were plotted in a biplot to visualize their relative contributions to the total variation. From the distribution plot of PC1 against PC2 (Figure 3), the variables

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positively correlated with the first axis, indicated by the angular separation of their projections, were the HBRAN, NLL, PLAH, LCLL, PETL, and WCLL, which are characteristic of the clones MMEXV5 and MMEXV2, as they exhibited larger dimensions. It was also found that MMEXV3, MMEXV8, and MMEXV13 are accessions with larger branch height.

On the other hand, when plotting PC1 against PC3, a negative correlation was observed between CROOT and LLWRA, DMC and STC, although accessions MMEXV1, MMEXV2, and MMEXV5 were characterized by higher field yields, they exhibited poor DMS and STC, indicating that materials with high agricultural yield do not necessarily achieve high industrial value. Meanwhile, accessions MMEXV1, MMEXV3, MMEXV6, MMEXV7, and MMEXV8 were characterized by having open branch angles, which negatively correlated with RALM, suggesting that accessions with trichotomous and tetracotomous branching habits will present a lower NSROOT (Figure 4).

The length and yield of storage roots are traits characterized by high heritability and genetic advancement, indicating the presence of additive effect genes (Daemo *et al.*, 2023). This is similarly observed in quality parameters such as starch content and dry matter. Consequently, the quantification of heritability guides plant breeders in developing new genotypes with high yield potential within heterogeneous populations (Sivan *et al.*, 2023). In this context, the variability observed suggests the existence of traits of interest, which will facilitate the selection of parental combinations aimed at enhancing genetic gain during selection, advancement, and potentially the release of elite clones (Kamanda *et al.*, 2020; Laila *et al.*, 2021). Furthermore, by identifying the genetic variability of materials collected from different geographical areas, it is anticipated that these regions will significantly contribute to the conservation and utilization of germplasm.

Cluster analysis

The cluster analysis classified the 11 cassava genotypes into four groups based on 15 quantitative traits (Figure 5). The first group includes accessions MMEXV2, MMEXV5, and MMEXV11, which exhibited the largest plant height (ranging from 2.12 to 3.21 m). This trait is beneficial for implementation in intercropping systems, as these plants typically have an erect growth habit with minimal canopy diameter development, making it a useful characteristic for defining population density (Rós *et al.*, 2011). Reports indicate a wide phenotypic diversity associated with plant height, varying from low-stature clones at approximately 0.65 m (Kamanda *et al.*, 2020) to those approaching 5 m in height (Wooding & Payahua, 2022). Additionally, this group is characterized by a thicker cortex (ranging from 3.11 to 3.55 mm). The second group consists of MMEXV8 and MMEXV13, which are distinguished by a higher LLWRA (6.94 to 7.46) but a lower NBR (1.50 to 2.60).

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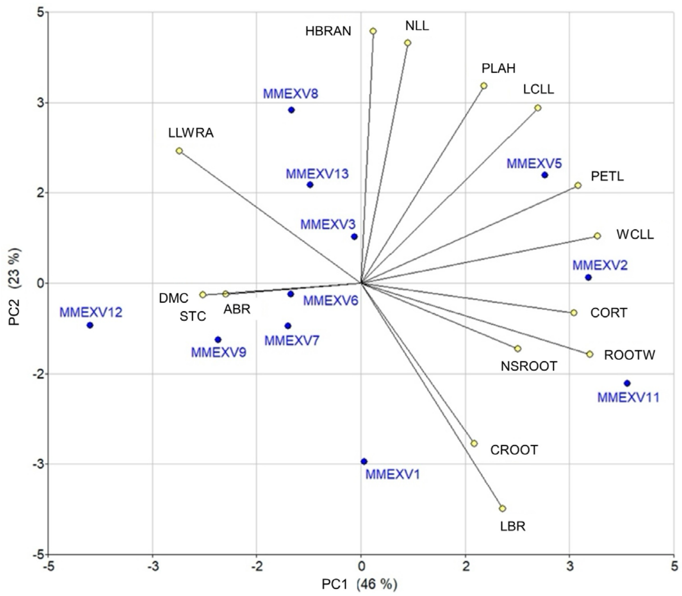

Figure 3. Biplot of 15 quantitative traits against 11 cassava accessions (PC1 and PC2).

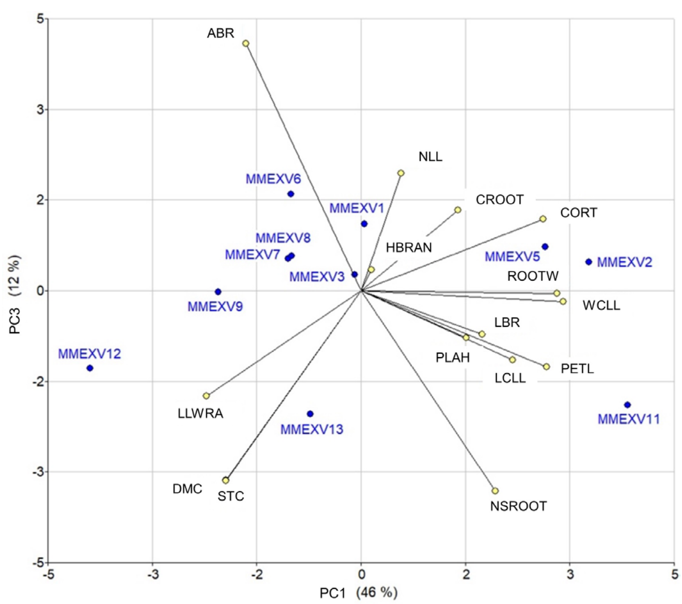

Figura 4. Biplot of 15 quantitative traits against 11 cassava accessions (PC1 and PC3).

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The third group identified the collections MMEXV3, MMEXV6, MMEXV7, MMEXV9, and MMEXV12, which are associated with high dry matter content (31.16 to 43.36 %) and starch content (16.25 to 24.89 %). This is significant for potential applications in human nutrition and agro-industry, as the variables that enhance the selection of genotypes include size, total number of roots, and dry matter (Adetoro *et al*., 2021). Additionally, these accessions are characterized by a low growth habit (1.96 to 2.72 m), with between 1.5 and 3.6 branches, and small leaf dimensions, measuring 19.52 to 28.64 cm for LCLL and 2.86 cm to 4.12 cm for WCLL; however, they exhibited a lower weight of tuberous roots compared to other materials (1.08 to 5.36 kg). These findings align with a study characterizing 30 cassava genotypes in India, which indicated a negative correlation between tuber root yield and dry matter and starch content (Sivan *et al*., 2023), presenting a challenge in the development of improved varieties.

The fourth group was formed by MMEXV1, an accession notable for having the highest number of branches and narrow angle, along with large leaf dimensions and long petioles, as well as a greater quantity of storage roots. These characteristics are associated with a high yield (11.37 kg).

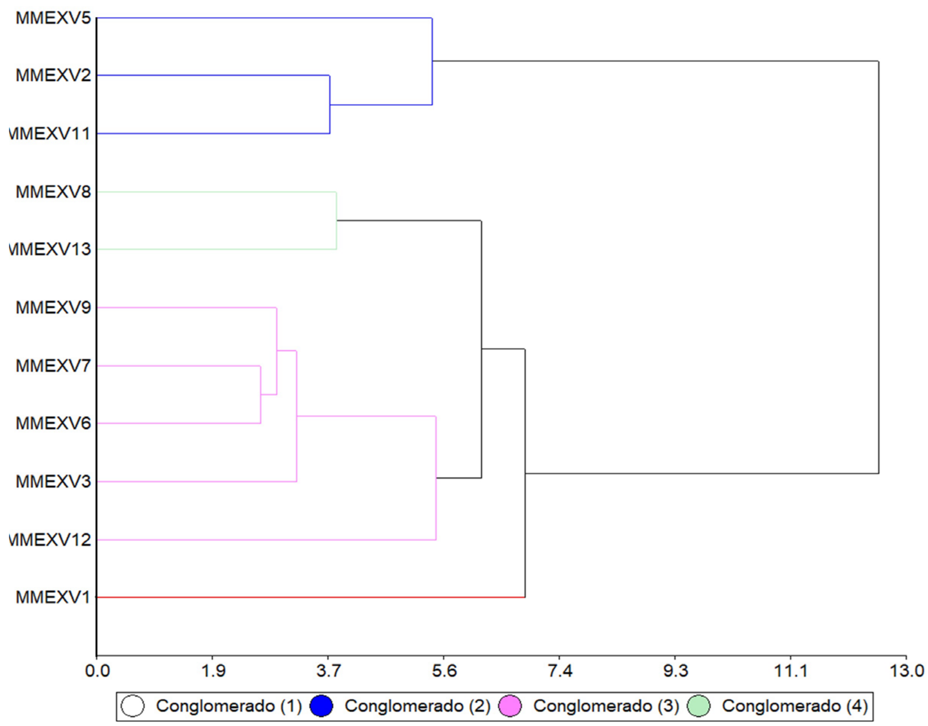

Figure 5. Dendrogram of 11 cassava collections in the Las Montañas Region, Veracruz, Mexico.

Conclusions

There is a genetic diversity reservoir of cassava in the Las Montañas region of Veracruz, reflected in morpho-agronomic traits of interest such as yield, leaf dimensions and shape, flowering, plant height, and parenchyma coloration, among others. These traits are significant for consideration in conservation and genetic improvement programs.

Notably, exploratory studies like this research elucidate materials with unknown potential; specifically, some collections were identified for food use in both livestock and human sectors, and these might have high nutritional profiles. This could pave the way for their promotion in support of nutritional security and contribute to the diversification of local production systems.

Author contributions

Experimental development and conceptualization of the work: José Luis Del Rosario–Arellano; manuscript writing and preparation: Otto Raúl Leyva–Ovalle; experimental validation: Rafael Antonio Verdejo–Lara; results analysis and software management: Pablo Andrés–Meza; writing, review, and editing: Isaac Meneses–Márquez; software management and data analysis: Ricardo Serna–Lagunes; experimental development and data recording: Félix Zahid Cruz–Moreno; writing, review, and editing: Régulo Carlos Llarena–Hernández.

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Conflict of Interest

The authors declare no conflict of interest.

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