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Article

Morphological characterization of the national cassava collection for conservation purposes at the NIAI, Peru

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Abstract

The research aimed to morphologically characterize the national collection of cassava (*Manihot esculenta* Crantz) of the National Institute of Agrarian Innovation (NIAI), Peru for conservation purposes. The study was conducted at the NIAI experimental station in Huaral (Lima); observation plots were installed with a systematic distribution of 741 accessions in the experimental field. Depending on the development of the crop, the evaluation and characterization were carried out using descriptors prepared by the curators of the National Institute of Agrarian Innovation. Hierarchical cluster analysis was used for the parameters used in the characterization and absolute and relative frequencies were calculated for the qualitative descriptors. Subsequently, a principal component analysis was performed to examine the association between the traits. The quantitative and qualitative parameters allowed discrimination between genotypes and establishing groups of accessions according to their similar characteristics using descriptors developed by the National Institute of Agrarian Innovation. Morphological variability was found among the conserved accessions of the cassava germplasm bank, and 12 promising accessions with potential for use for genetic improvement, suitable for human consumption and for food security, were identified.

Palabras clave:

Manihot esculenta, accessions, clustering analysis, germplasm, principal component analysis.

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Introduction

Cassava (*Manihot esculenta* Crantz) belongs to the family Euphorbiaceae (Ceballos and De La Cruz, 2002); it is a traditional crop native to Latin America and of great value for food security (Quispe-Jacobo *et al*. 2021). It has grown in tropical areas for the production of roots, which are the most important for human and animal consumption, for starch, and for use as a raw material for ethanol industries (Soto-Veiga *et al*., 2016).

In Peru, cassava crops represent a source of energy and are part of the family's economic livelihood; in 2023, 1 508 281 t of cassava were produced in Peru, with Loreto being the region with the highest production (34%), followed by Amazonas (11%), San Martín (9%), Ucayali and Junín (8%) and Lima (2%) at the national level. The national average yield is around 12.6 t ha^{-1} (Ministerio de Desarrollo Agrario y Riego, 2023).

Germplasm banks should ensure that the accessions they maintain are kept viable and in good condition for as long as possible. Nevertheless, even following the highest management standards, germplasm deteriorates over time and must be regenerated to maintain the original genetic diversity and structure of the accession or collection and to produce sufficient numbers of healthy and viable seeds, roots, or other vegetative propagules (Dulloo *et al*., 2008).

Regarding morphological characterization, descriptors can be used to define plant attributes that are quantifiable and identifiable, and these can be highly heritable to allow a rapid discrimination of phenotypes. Likewise, when evaluating polygenic inheritance, traits can be affected by the influence of the environment, such as yield and resistance to diseases, which are of great importance in crop improvement (Demey *et al*., 2003).

Alulema (2014) used nine quantitative descriptors and 24 qualitative descriptors to determine genetic diversity in 195 cassava accessions in Ecuador, resulting in the formation of three groups. In 87 accessions from the cassava germplasm bank in Ghana, agromorphological traits analyzed using principal components showed that plant height, branching levels, petiole length and color, yield, leaf mosaic severity, and aerial biomass contributed to the variability between the cassava genotypes evaluated (Adu *et al*., 2020).

This research aimed to morphologically and agronomically characterize 741 accessions of the national cassava collection of the germplasm bank of the National Institute of Agrarian Innovation (NIAI), Peru, for the purpose of conservation and improvement of the crop.

Materials and methods

The experiment was installed in lot nine of the Donoso Agricultural Experimental Station in Huaral. This station is located at km 5.6 of the Chancay-Huaral highway, Lima region. The experimental field is located at 11° 31' 22.8" south latitude and 77° 13' 53.6" west longitude, at 160 masl. The characteristics of the soil were slightly inclined topography with an approximate slope of 5%, deep horizon and sandy loam texture.

The material under study was made up of 741 cassava accessions from the germplasm bank of NIAI, which are the product of collections carried out in different regions of the country as well as from some international collections. The study was conducted in observation plots that were systematically distributed with seven replications for each accession; planting was done manually from October 4 to 6, 2021.

The planting distance used was 1.2 m between rows, 0.6 m between plants, seven plants per 4.2 m row and one row for each accession. Seven plants were used for each sample, but only the five central plants were characterized, excluding the two plants of the edge to avoid the edge effect. The appropriate agronomic work was carried out in order to provide the right conditions for the development and growth of the crop; the harvest was done between July and August 2022.

Information on commercial and non-commercial roots was obtained from each of the cassava accessions, but only commercial roots (healthy roots, average size and diameter, without deformations or striations in the pulp) were considered for the classification. Passport data from the accessions for cassava germplasm bank are presented in Table 1.

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Table 1. Descriptors used in the morphological characterization of the national cassava collection of the germplasm bank of NIAI, Peru.

Number		Descriptors
1	Qualitative traits	Mature stem color
2		Root peduncle
3		Root position
4		External color of the root
5		Internal color of the root
6		Pulp color
7	Quantitative traits	Number of commercial roots per plant
8		Weight of roots per plant
9		Total weight of roots per plants
10		Yield per hectare

The evaluations and characterization of cassava accessions used the descriptor developed by NIAI curators (Quispe-Jacobo *et al*., 2021; Marcelo *et al*., 2023), which is described in Table 1.

Data analysis

Hierarchical cluster analysis was used for the parameters utilized in the characterization, employing Ward's minimum variance clustering method (Ward, 1963; Núñez and Escobedo, 2015). For the qualitative descriptors, absolute and relative frequencies were calculated. A principal component analysis was then performed to examine the association between the traits and show the similarity between the accessions.

This procedure was used to calculate a similarity matrix to calculate eigenvalues and scores for accessions. The principal component analysis (PCA) was expressed in a correlation matrix of eigenvalues for each of the quantitative variables used in the description of the national cassava collection. The information was processed with the Infostat software version 2020 (Di Rienzo *et al*., 2020) and R studio version 3.0.1.

Results and discussion

Cluster analysis

Through the data obtained from the characterization, morphological variability was found among the accessions studied, because the quantitative and qualitative traits analyzed allowed discriminating between genotypes and establishing groups of accessions according to their association characteristics (Figure 1). According to the outstanding accessions in the research, one of the variables with the greatest discriminating power was root yield.

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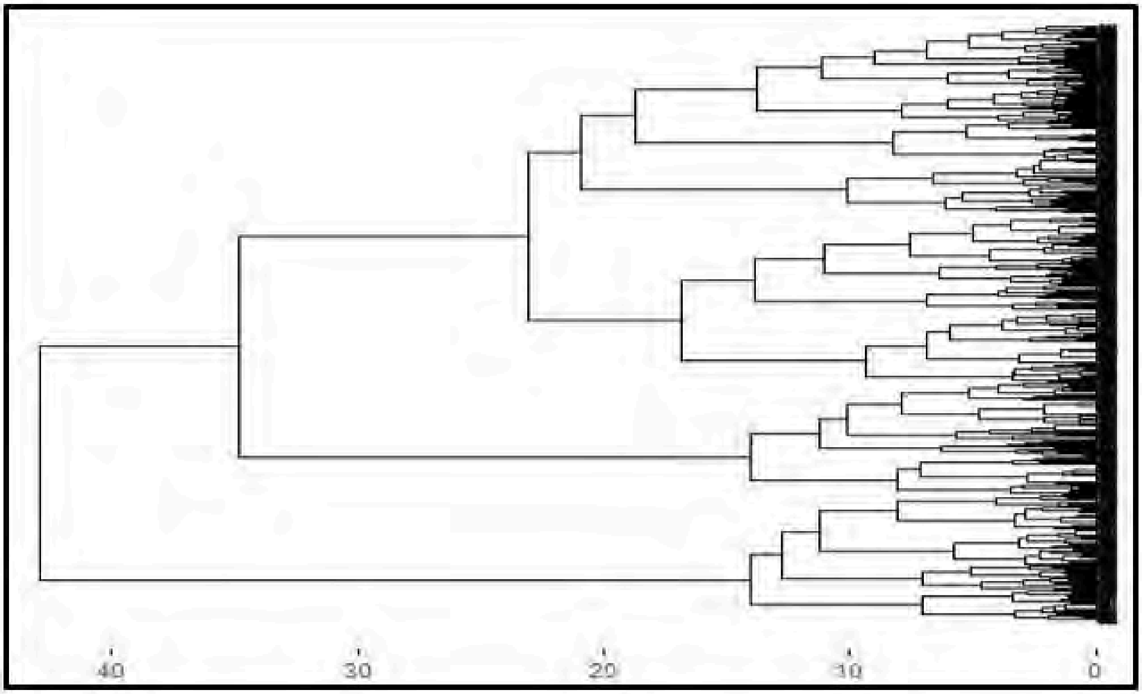
Figure 1. Dendrogram of clustering by the hierarchical method in the national cassava collection of the germplasm bank of NIAI, Peru.



The hierarchical cluster analysis of the parameters used in the characterization shows that most of the cassava accessions exhibited great similarity in terms of the qualitative characteristics related to the storage roots (external and internal color, pulp color, peduncle, position and stem color) and for this reason, the dendrogram does not show very well-defined groups (Figure 1) unlike what was found by León *et al*. (2013); Alulema (2014).

This analysis was carried out based on six morphological characters in 741 accessions of the collection; the associations allowed the identification of some duplicates among the accessions, highlighting the fact that the morphological traits grouped in different states expressed the variability and the nature of the groupings.

Figure 2 shows the clustering analysis for the external color of the root, with four very differentiated groups, where group A (light brown external color) and group B (dark brown external color) made up the largest number of accessions, and group C (white or cream external color) and group D (yellow external color) had a lower number of accessions.

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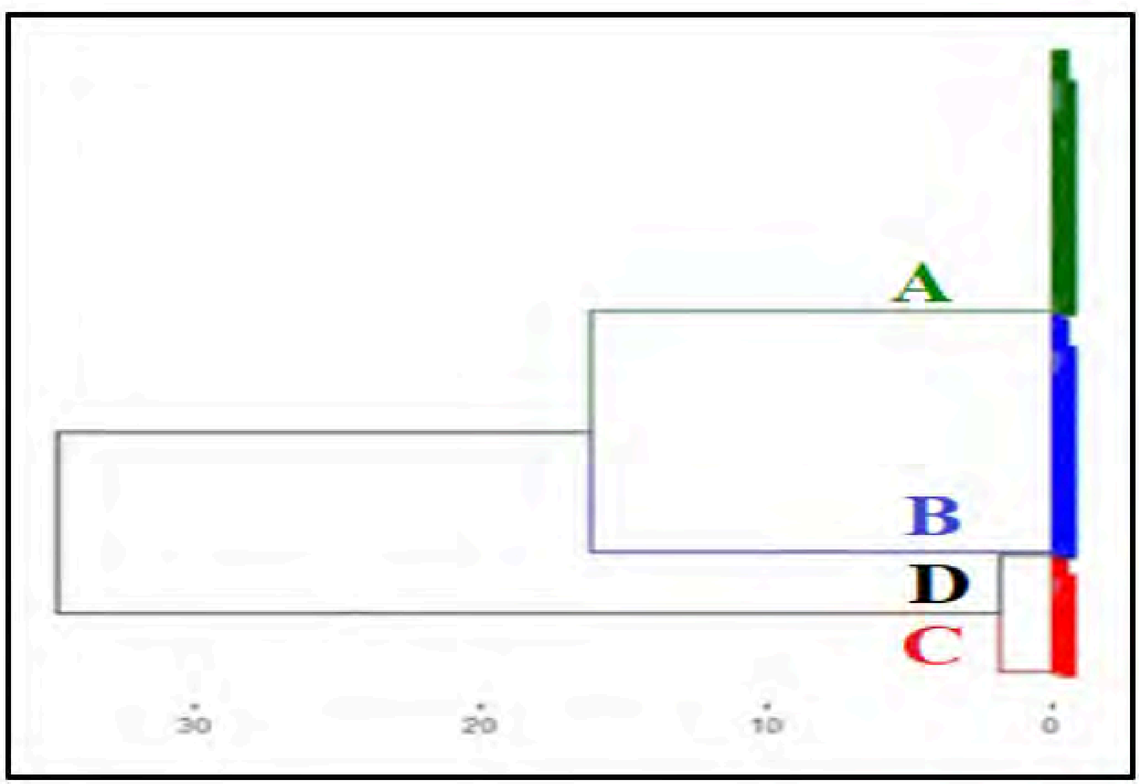
Figure 2. Dendrogram of clustering for external root color. External color of the storage root: group A (light brown external color); group B (dark brown external color); group C (white or cream external color) and group D (yellow external color).



These results are consistent with Beovides *et al*. (2002), who point out that characteristics such as the presence of a peduncle in the root and the color of the root bark are usually discriminating; on the other hand, Pincay (2010) obtained a greater number of accessions with a dark brown external coloration, with 62.14% (87 accessions), followed by light brown with 19.28% (27 accessions), out of a total of 141 accessions under study.

Figure 3 shows the grouping of accessions according to the color of the root pulp, with four different groups observed. Group C is made up of accessions with cream pulp, this group being the most frequent, followed by group D with white pulp, and the groups with the lowest number of accessions were group A (yellow pulp) and group B (pink pulp).

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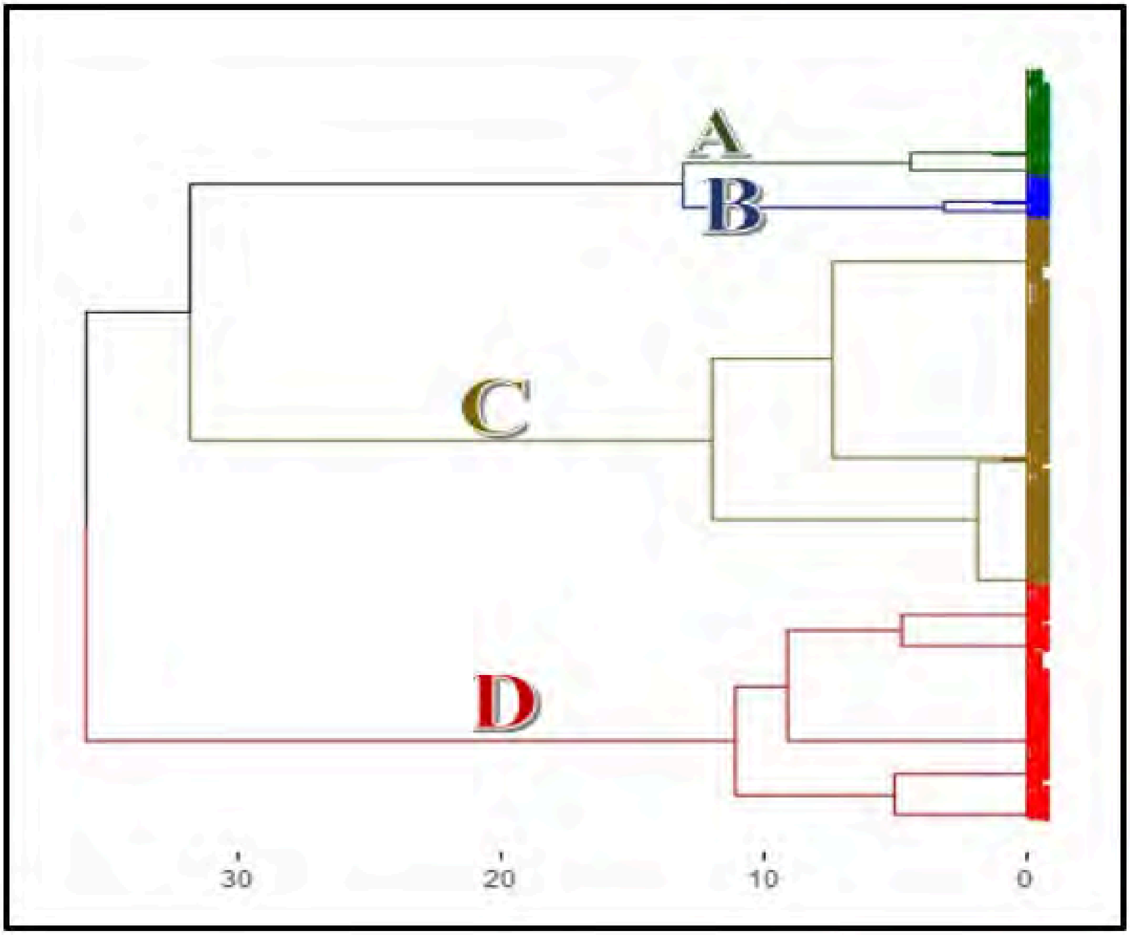
Figure 3. Dendrogram of clustering for pulp color. Pulp color: group C-accessions with cream pulp, group D-white pulp, group A-yellow pulp and group B-pink pulp.



Within the qualitative traits, the color of the pulp was also a discriminating value, but of lesser capacity for the selection of accessions; these results do not coincide with Lenis (1988), who mentions that the color of the mature stem, color of the rib and the pulp of the root are the most differentiating characteristics.

Likewise, it must be considered that farmers incline their preferences towards agronomic and productive aspects, but the selection criteria are also based on plant attributes, root size, and pulp color (Aquino, 2006). Of ten parameters studied, four had the highest discriminating power (number of commercial roots/plant, root weight/plant, total root weight and yield), these being quantitative characteristics.

The variation regarding some discriminant quantitative characteristics can be explained because they are characteristics determined by many genes and have a lot of interaction with the environment (Lobo, 2004).

Identification of promising accessions

Figure 4 shows the analysis of commercial roots, where a group of accessions with an average of two roots per plant and a smaller group of accessions that have more than five commercial roots per plant are observed; these results are related to low production because non-commercial roots with a range of less than 15 cm in length were not included.

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Figure 4. Frequency distribution of accessions for number of commercial roots per plant.

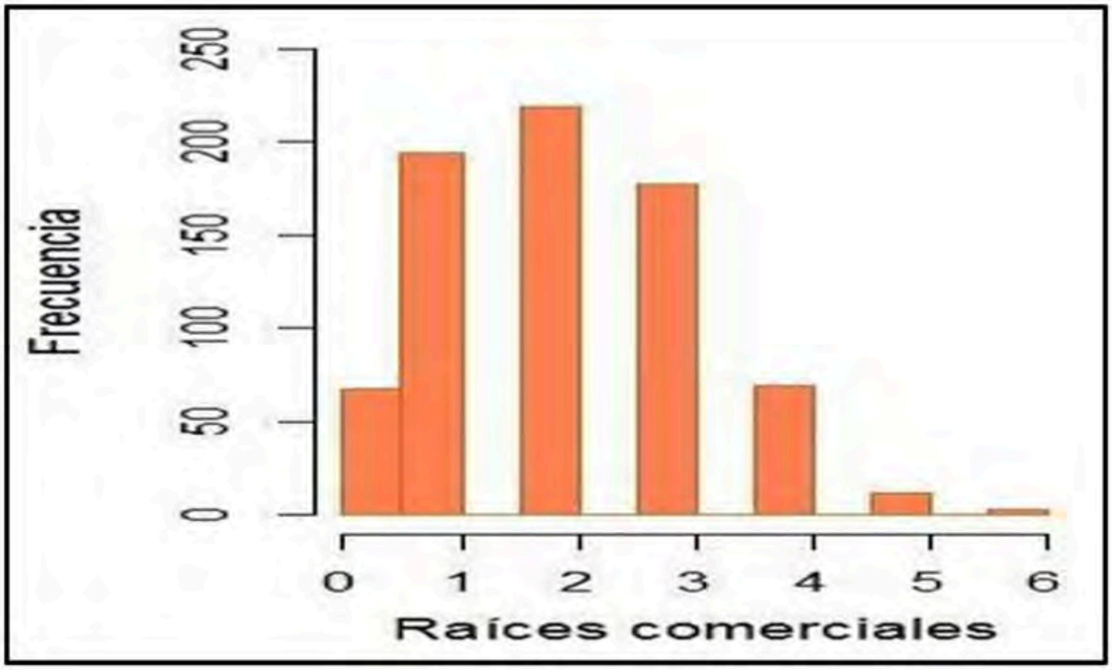

Figure 5 shows the yield per hectare of cassava accessions; 12 of the accessions had a high production (60 to 90 t ha^{-1}), followed by 108 accessions (40 to 60 t ha^{-1}) and 621 accessions with a production of less than 40 t ha^{-1}. Lobo (2004) determined that these quantitative characteristics are influenced by factors such as soil fertility, salinity, drainage, pests and diseases, vigor and age of the plant.

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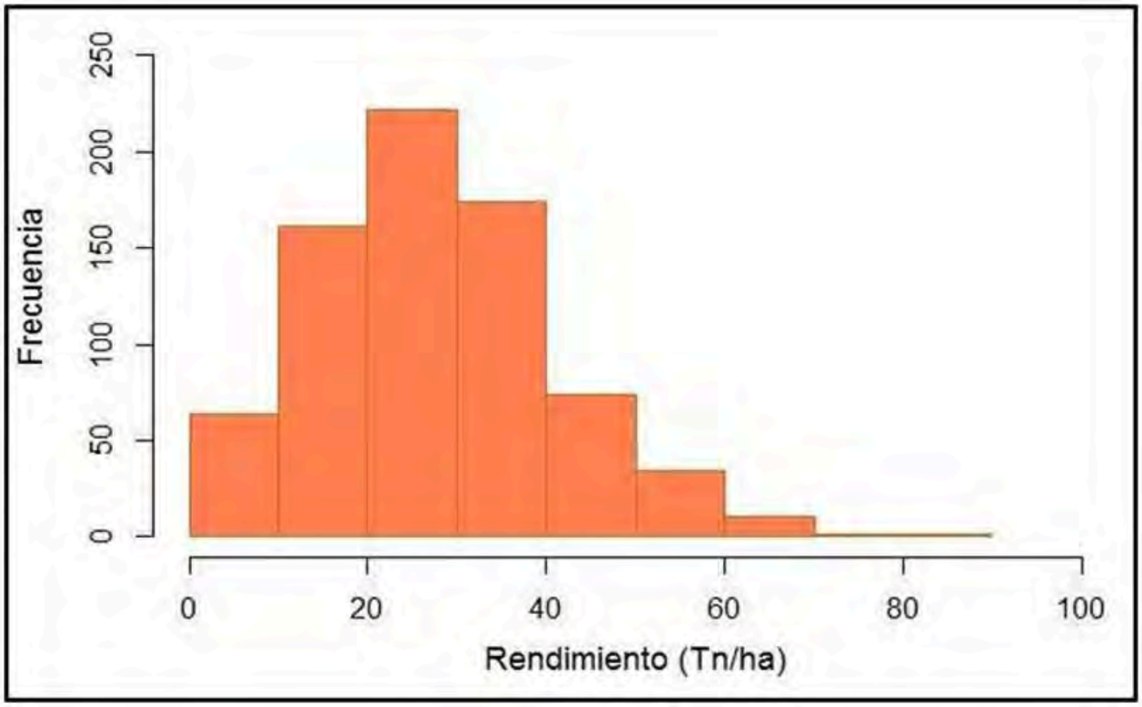
Figure 5. Frequency distribution for root yield (t ha^{-1}).



Therefore, it was determined that during the morphological characterization of cassava germplasm, both quantitative and qualitative descriptors can be used, both types of descriptors would have the power to discriminate differently through phenotypic expression. This coincides with what was expressed by Cruz (2002), who mentions that quantitative morphological characteristics are those that have the greatest action in the manifestation of a trait and are determined by many genes that interact with the environment.

Principal component analysis

The results obtained in the principal component analysis (PCA) were expressed in a correlation matrix of eigenvalues of each of the variables used in the description of the collection; the PCA generated a number of components equal to the number of descriptors used in the characterization. Therefore, in Table 2 93.34% variation was observed in component 1 of the four descriptors used. According to the eigenvalues obtained, PC1 is shown with a value of 3.734 and the other components are shown with eigenvalues less than 1.

Table 2. Eigenvalues for each of the traits used in the cassava collection

PC	Eigenvalue	Variation (%)	Cumulative variation (%)
PC 1	3.734	93.342	93.342
PC 2	0.26	6.497	99.839
PC 3	0.006	0.151	99.99
PC 4	0.0004	0.011	100

Table 3 exhibits the correlation of the variables related to the first identified principal component; these values are interpreted by the contribution coefficient; that is, higher coefficients will be more efficient in discriminating accessions.

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Table 3. Eigenvectors in four principal components of the variables studied.

Traits	PC 1	PC 2	PC 3
Number of roots/plant	0.892	0.452	0.0004
Weight of roots/ plant	0.99	-0.136	-0.034
Total weight of roots	0.988	-0.138	0.063
Yield	0.99	-0.134	-0.029

According to the values obtained in Table 2 related to Table 3, there are traits of greater interest in the first component, such as yield (0.99), weight of roots/plant (0.99), total weight of roots (0.988), and number of commercial roots/plant (0.892).

The result obtained in the principal component analysis is not similar to the results by Torres (2010), where it was found that five components determined the existing variability in at least 72% of the accessions due to the fact that their results were 25.4% of variability in PC1 and 18.4% in PC2, with the sum of these two components making only 43% of the variability for the quantitative variables. In the qualitative variables, at least nine PCs were found to explain the 73% variability (PC1 explained 15.2% variability and PC2 12.2%, where these two components only reflected 27.4% of the variability between cassava accessions).

On the other hand, Beovides *et al*. (2014) found that the qualitative variables allowed discriminating the variability in three dimensions, explaining 76.3% of the total variance and 66.62% of the total variance for the quantitative variables with the first four principal components of the analysis, which indicates that the variability is probably widely distributed among all the descriptors that represent the wide diversity of the cultivars under study.

Conclusions

The accessions of cassava (*Manihot esculenta*) preserved in the germplasm bank of NIAI (Peru) show the existence of variability in various morphological characteristics of interest that are useful for the genetic improvement of the crop. It was determined that during the morphological characterization in crops, both quantitative and qualitative descriptors should be used.

The hierarchical cluster analysis allowed the identification of some duplicates among the accessions of the germplasm bank. Twelve promising accessions with a production of 60 to 90 t ha^{-1} were primarily identified, which exceeded the national average; these accessions can be used for human and industrial consumption due to their high productive potential once the information on the interaction of the genotype by environment has been estimated.

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