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Agro morphological variability of cassava varieties cultivated in five regions of Côte d'Ivoire based on quantitative traits

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ABSTRACT
Objective: The objective of this study was to assess the morphological variability of cassava accessions from five regions of Côte d'Ivoire based on quantitative criteria.
Methodology and Results: The material used was composed of cuttings from 200 cassava accessions collected in five agro-ecological zones of Côte d'Ivoire. The experimental set-up was a complete block randomised to one factor (accessions), and established on a fallow plot in the Haut-Sassandra region (Daloa/Gosea). Fourteen quantitative descriptors were measured at different stages of plant development. The data collected were subjected to statistical tests. The principal component analysis applied to the 200 accessions showed a variability of 37.018 % revealed by the first two axis. The dendrogram produced by the UPGMA method highlighted three groups of accessions based on the 12 characters. These three groups were generally constituted independently of the agro-ecological zones of collection.
Conclusion and Application of results: At the end of this study, it should be noted that the 200 cassava accessions collected in the five agro-ecological zones of Côte d'Ivoire are characterised by a strong morphological variability. This variability was structured into three distinct agro-morphological groups with the height of the first branching and the number of branches of the plant as distinctive characters. The genetic variability observed between groups constituted by the accessions is important for varietal selection work.
Key words: Agronomical, cassava, morphological, variability

INTRODUCTION
Discovered in the Amazon and domesticated nearly 7,000 years ago (Dickau *et al.*, 2007), cassava (*Manihot esculenta*) is the third largest source of carbohydrates in the world, with Africa being the largest production centre (Adenle *et al.*, 2012). The carbohydrate production of cassava is about 40 % higher than rice and 25 % higher than maize (Tonukari, 2004). Cassava is grown in more than 100 tropical and subtropical countries around the world. Its nutritional importance lies in its starchy tuberous roots and protein-

rich leaves. It is a crop that serves as a food security crop because of its high source of carbohydrates and it has ability to grow in different climatic conditions (Ceballos *et al.,* 2006; Tumuhimbise *et al.,* 2014). In addition, it has multiple uses including human consumption, animal feed and industrial applications (Rabbi *et al.,* 2012). Moreover, cassava is adapted to several agrosystems; it lends itself to polyculture, in association with cucurbits (Doubi *et al.,* 2016), in association with sweet potato (Ijoyah *et al.,* 2012) and other crops. Thus, cassava is one of the least demanding food crops and is tolerant of ecological conditions that are sometimes marginal for agriculture, and the sustainability of its cultivation will depend on the rational management of the resource. Numerous genetic diversity studies have been carried out for cassava management and breeding; both morphological (N'zue *et al.,* 2014; Adjebeng-Danquah *et al.,* 2016 ; Djaha *et al.,* 2017; Kosh-Komba *et al*., 2017 ; Doubi *et al.;* 2021) and molecular (Beovides *et al.*, 2015 ; Kouakou *et al.,* 2022). In Côte d'Ivoire, cassava is a predominant crop; it is grown on about 4/5 of the national territory (N'Zué *et al.,* 2014). With a tuber production of 6.44 million tonnes in 2020 (FAOSTAT, 2020), cassava is the second most important food crop after yam. Ivorian populations have made it a staple food and the wide variety of varieties favours different types of local dishes such as attiéké, bêdêkouman, placali. However, diversity studies using quantitative traits to characterise local varieties held by farmers have not yet been carried out. The use of morpho-agronomic characterisation to classify accessions according to quantitative plant traits provides useful information on the relationships between breeding clones and the performance of specific traits of agronomic and economic importance, thus facilitating the parental selection process (Elameen *et al.,* 2011; Laurie *et al*., 2013). This study aims to assess the morphological diversity of cassava accessions based on quantitative characteristics.

MATERIAL AND METHODS

Presentation of the study site: The study was conducted in the Haut Sassandra region of Côte d'Ivoire, specifically on a plot in the village of Gosea, 14 km from Daloa on the Man axis. This village in the sub-prefecture of Gboguhé, in the department of Daloa, is located in the centre-west of Côte d'Ivoire, about 397 km from Abidjan, between 7°00' and 7°26' north latitude and between 6°00' and 6°30' west longitude (**Figure 1).** The soils of the Haut-Sassandra region are ferrallitic. They are characterised by their humus horizon, which is thin but rich in organic matter, weakly acidic and well structured. In this region dry and wet seasons alternate with temperatures ranging from 24.65°C to 27.75°C on average (Adjiri *et al.,* 2018).

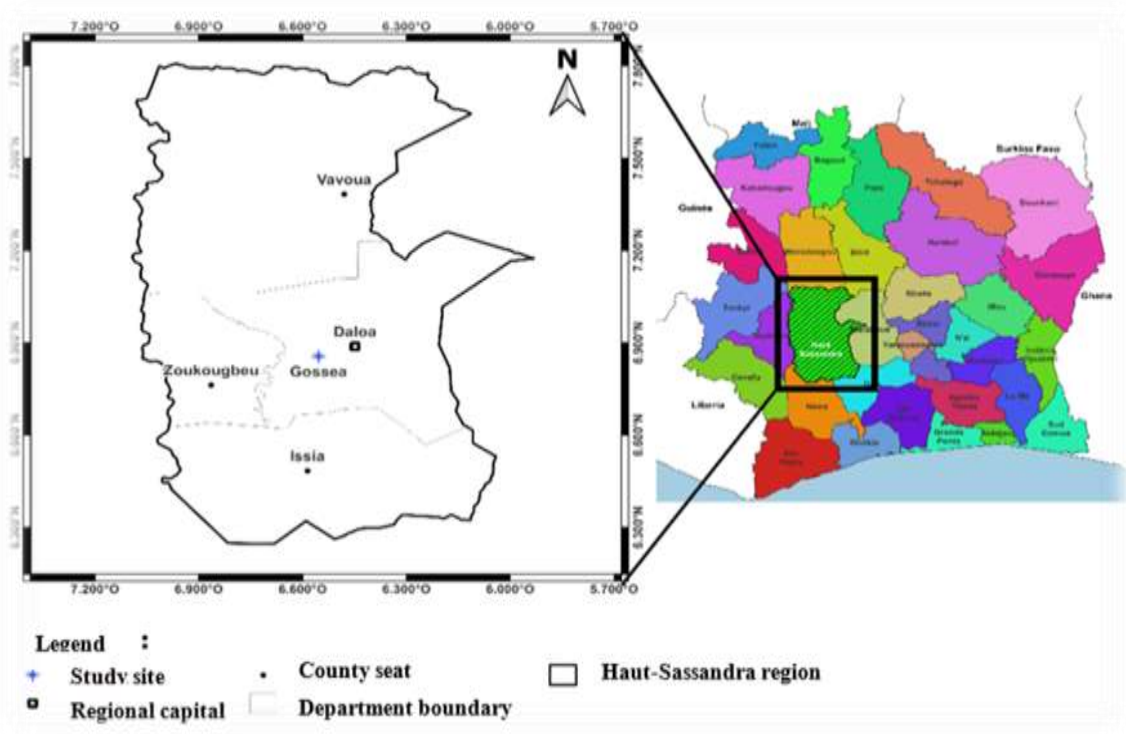

Figure 1: Location of the study site

Material: The material used is composed of cuttings from 200 cassava accessions collected in five agro-ecological zones of Cote d'Ivoire. An accession corresponds to the cassava stem collected from a farmer according to defined criteria. These characteristics are the colour of the petioles; the colour of the stem; the colour of the phelloderma of the tuberous root and the colour of the starchy parenchyma. The number of accessions collected in the regions are summarised in the **table 1.**

Table 1: Origins size and of the accessions collected Geographical area

	Regions	**Number of accessions collected**
	Haut-Sassandra	56
Centre-West	Marahoué	10
	Gôh	10
West	Guémon	6
	Gbêkê	40
Centre	Bélier	6
South-West	Nawa	15
	Agnéby- tiassa	15
	Lagune	10
	Grand-pont	11
South	La Mé	9
	Sud-Comoé	7
	Lôh Djiboua	5

Methods

Experimental Design: The trial was set up on a plot of 1573 m^2 equivalent to the dimensions of 60.5 m length and 26 m width in a completely randomised block. Each accession was replicated five times and randomly placed on the plot rows. This consisted of 40 lines, each with 25 sowing points. The rows were 1.5 m apart and the sowing points within the rows were 1m apart. Regular weeding was carried out to avoid competition with weeds. **Data collection and analysis:** Fourteen (14) quantitative traits were selected in standard descriptors for cassava (Fukuda *et al.*, 2010) to characterize agro morphological diversity **(Table 2).**

Table 2: List of agro-morphological descriptors used for the characterisation of 200 cassava accessions

Traits considered	Codes	Description and measurement period
Diameter of principal stem (mm)	DTiPr	Diameter of the most developed stem at the colet (2cm above ground level); measured over three periods: three months; six months and ten months after planting.
Length of stipules (mm)	LodS	Three measurements per plant in the third month after planting
Number of leaf lobes	NoLF	Number of lobes observed on each plant (3 leaves/plant): observed in the third month after planting on mature leaves
Number of stems per cutting	NoTB	Total number of stems emitted per cutting: observed at the third month after planting
Number of branchings	NoRm	Number of branching observed on the main stem: measured over three periods; three months; six months and ten months after planting.
Numbers of Branching habit	NoBr	Observed at the lowest or first branching. Record three periods; three months, six months and ten months after planting.
Length of the Central leaflet (Cm)	LoLC	It is the distance between the point of insertion of the lobes and the upper tip of the central lobe. It is measured at the sixth month after planting on three leaf samples.
Width of the Central leaflet (Cm)	LaLC	This is the largest width of the central lobe. It is measured at the sixth month after planting on three leaf samples
Petiole length (Cm)	LoPe	It corresponds to the distance between the point of insertion of the petiole on the stem and the base of the leaf; measured at the sixth month after planting on three petiole samples.
Height of the principal stem / Plant height (Cm)	HTiPr	It corresponds to the distance from the collar (0Cm from the ground) to the top of the main stem. It is measured over the three periods: three months; six months and nine months after planting.
Distance between the leaf scars / Length between knots (mm)	LoEN	This is the distance between two nodes (10cm above the ground) of the main stem. Measured over the two periods: six months and nine months after planting.
Height to first branching(cm)	HPRm	It corresponds to the distance from the collar (0Cm from the ground) to the point of the first branching of the main

		stem. It is measured at the sixth and ninth month after planting.
Number of storage roots/plant	NoRa	Total number of consumable roots of each plant
Fresh weight of accumulated roots per plant (kg)	PoRa	Total root weight of each plant weighed with an electronic scale. Measured at harvest

The matrix of morphological data composed of the means of the quantitative variables was used for the statistical analysis. First principal component analysis was performed to identify the active variables. The variables which contribute most to the formation of the axis, and the remain as supplementary variables. The PCA was preceded to Pearson correlation r who permed to evaluate the relation existing between the variables two by two. The groupings of individuals were then obtained by hierarchical ascending classification (HAC) on the factorial axis of the previous analysis. This HAC was established based on the Euclidean distance according to Ward's (1963) aggregation criterion. Finally, discriminant factor analysis (DFA) was performed to determine the most discriminating traits and to give the characteristics of the groups obtained by the HAC. All analysis was conducted using the statistical software R version 4.1.2 (2021-11-01) (Core Team, 2021). Before the analyses, the values were standardised according to the following formula:

$$\text{standardised data} = \frac{\text{sample value} - \text{average of the parameter}}{\text{standard deviation}}$$

RESULTS

Analysis of correlations between measured quantitative characteristics: Pearson's r correlation was significant (≥ 0.70) and positive for four variable pairs. The variables pairs who had greater than or equal to 0.70 are the following: PoRa-NoRa (0.966), NoBr-HPRm (0.839), LoLC-LaLC (0.75) and LoLC-LoPe (0.869). To avoid redundancy, one of the characters in each pair was eliminated in the further analyses. A total of eleven traits out of the fourteen traits enabled us to carry out the rest of the statistical tests.

Expression of variability significance of the two axis expressing the most variability in the PCA: The eigenvalue matrix showed that all 11 descriptors contributed significantly to the formation of at least one of the first five axis, which presented a value greater than 1. Only one of the variables presented a correlation greater than 0.7 with the axes, therefore the value of 0.5 was retained as the threshold of significance for the rest of the analysis. Of the 11 parameters selected, all were significantly correlated with at least one of the axes at the 0.5 threshold. They could therefore be used to explain the variability within the 200 cassava accessions **(Table 3)**. For the following of this study, we focused our analysis in the first two principal components accounted for 37.018 % of the total variability. The first component explained 23.944 % of the variability. It was defined by the number of stem branches, principal stem height, petiole length, central lobe width, central lobe length and stem diameter. These variables were positively correlated with axis 1. Concerning axis 2, it accounted for 13.074 % of the total variability. Petiole length and central lobe length were the two parameters that contributed most to the formation of axis 2. These parameters are negatively correlated with axis 2.

Table 3: Eigenvalues, correlations between traits and the first five-component axis

Principal component	***Axis 1***	***Axis 2***	***Axis 3***	***Axis 4***	***Axis 5***
Eigen value	2.634	1.438	1.157	1.091	0.976
Variance. Percent	23.944	13.074	10.515	9.917	8.870
Cumulative.Variance.percent	23.944	37.018	47.533	57.450	66.320
LoEN	-0.080	0.437	-0.367	**0.571**	-0.276
NoRm	**0.632**	0.320	-0.056	-0.280	-0.047
HPRm	0.424	0.242	-0.363	0.085	**0.637**
HTiPr	**0.712**	0.349	-0.204	0.143	-0.064
PoRa	0.226	0.306	**0.591**	-0.287	-0.257
LodS	0.414	-0,06	-0.283	**0.610**	-0.052
LoPe	**0.580**	**-0.553**	0.285	0.496	-0.088
LoLC	**0.653**	**-0.680**	0.453	0.480	0.097
NoTB	0.104	0.336	**0.640**	-0.076	0.492
NoLF	0.470	-0.495	-0.136	-0.300	**-0.630**
DiTPr	**0.787**	0.198	0.125	-0.055	-0.290

In bold, significant contributions values

Structuring the morphological variability of 200 cassava accessions: The dendrogram produced by the UPGMA (Unweighted Pair Group Method with arithmetic Average) method highlighted three groups of accessions (**Figure 2**). Analysis of the dendrogram showed that, in general, accessions were grouped independently of the agro-ecological zones from which they were collected **(Table 4)**. At least one accession from each zone was represented in one group. Groups G2 and G3 constituted the largest percentages; respectively 40 % and 44.5 % compared to group G1, which recorded the lowest rate of individuals (15.5 %).

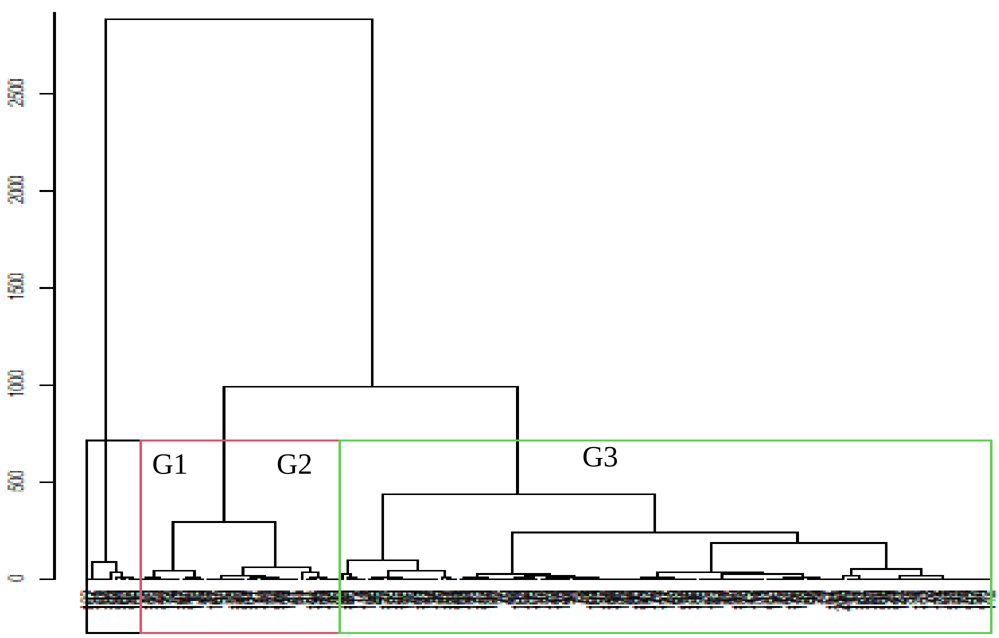

Figure 2: Dendrogram (UPGMA) of 200 cassava accessions based on Euclidean distances
Black=G1; red=G2 and green=G3

Table 4: Distribution of accessions in HAC groups by origin

Groups	Central	Central - West	West	South	South - West	Number of accessions	%
G1	7	11	1	8	4	31	15.5
G2	16	30	4	22	8	80	40
G3	23	35	1	27	3	89	44.5

The groups formed by the Hierarchical Ascending Classification (HAC) and the variables that contributed to their differentiation were assessed using Discriminant Factor Analysis. The individuals in the groups were represented in the plan generated by the Discriminant Factor Analysis (DFA), whose two dimensions expressed 98.99 % of the variability, of which 79.48 % for the first dimension (dim1) and 19.42 % for the second dimension (dim2) **(Figure 3)**. The formation of these two factorial dimensions shows that out of the eleven variables analysed, five variables contribute significantly to the discrimination of agro-morphological groups constituted by the HAC **(Table 5)**.

Table 5: Percentage discrimination and definition of dimensions in the DFA conducted on 200 cassava accessions

	Eigen value	Discrimination (%)	%cumulated	NoRm	HTiPr	LodS	NoLF	DTiPr
Dim 1	1.84	79.48	79.48	0.67	0.62	0.59	0.57	0.75
Dim 2	1.04	19.42	98.9	-0.37	-0.33	0.53	0.42	-0.16

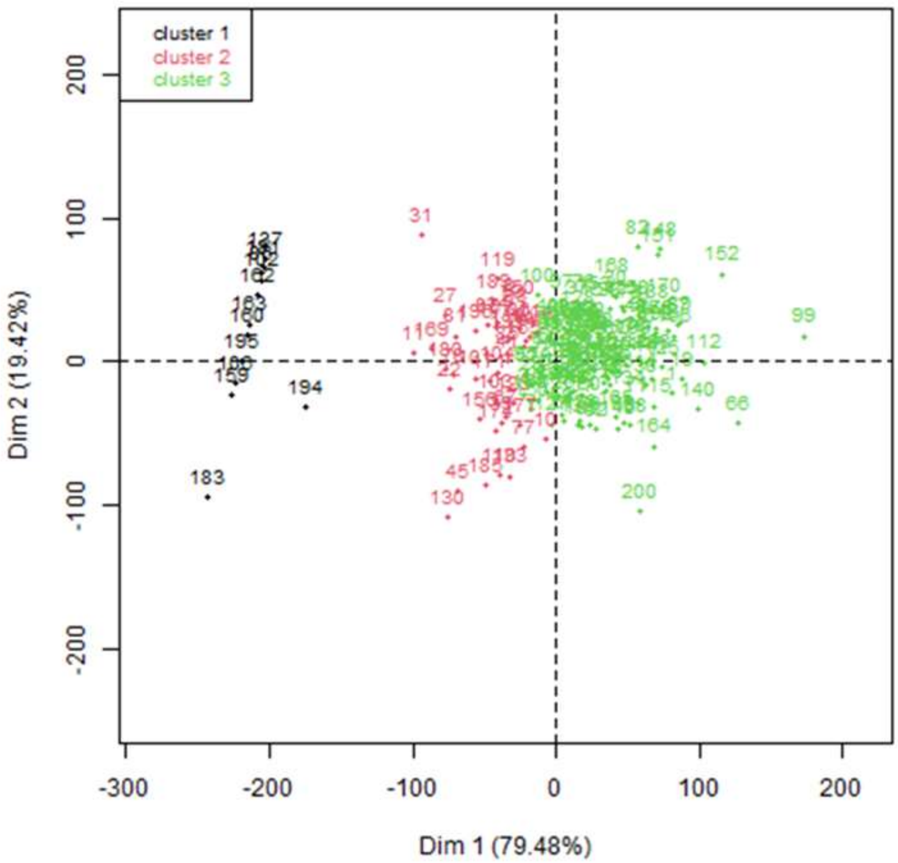

Figure 3: Representation of the groups of cassava accessions in the discriminant factorial plane formed by the canonical axes

Table 6 shows the characteristics of the three clusters. The results show that the three clusters are clearly distinguished by the diameter of the principal stem (DTiPr). Individuals from group (G1) are characterised by small stem diameters compared to individuals from the other two groups G2 and G3, which have medium and large diameters respectively. Individuals from groups G2 and G3 have the largest and identical branching and principal stem heights compared to individuals from group G1. The number of lobes per leaf, the width of the central lobe and the length of the petiole allow to distinguish two groups. The first group contains G1 and G2 which have a reduced number of lobes, central lobe width and petiole length compared to the G3 accessions. G1 accessions are characterised by reduced number of branches, height of the first branch and height of the principal stem compared to G2 and G3 accessions, which have the same criteria for these parameters.

Table 6: Characteristics of the groups resulting from the Ascending Hierarchical Classification

	G1	**G2**	**G3**
LoEN	31.31 ± 5.83^b	34.50 ± 5.08^a	31.04 ± 4.62^b
NoRm	1.03 ± 0.96^b	2.22 ± 0.6^a	2.38 ± 0.5^a
HPRm	138.68 ± 113.01^b	232.62 ± 40.98^a	223.28 ± 44.95^a
HTiPr	301.57 ± 41.55^b	352.37 ± 27.4^a	359.99 ± 29.87^a
DTiPr	20.85 ± 3.08^c	26.04 ± 3.07^b	28.36 ± 3.68^a
NoLF	6.29 ± 0.59^b	6.28 ± 0.56^b	6.93 ± 0.4^a
NoTB	2.19 ± 0.76^a	2.53 ± 0.78^a	2.29 ± 0.74^a
LaLC	4.77 ± 0.59^b	4.69 ± 0.57^b	5.13 ± 0.75^a
LoPe	31.2 ± 3.51^b	31.86 ± 4.71^b	35.36 ± 4^a
LodS	7.82 ± 1.56^b	7.42 ± 1.29^b	9.91 ± 1.84^a
PoRa	0.81 ± 0.94^b	1.70 ± 1.21^a	1.53 ± 1^a

In the rows, the means followed by the same letter are statistically identical at the $\alpha = 5\%$ threshold: Mean ± standard error.

DISCUSSION

The analysis of the first component shows that the relevant quantitative traits to assess variability of cassava cultivated in five agroecological regions of Côte d'Ivoire are similar to those used in previous studies (Agre *et al.,* 2015; Nadjiam *et al.,* 2016). These authors respectively showed agromorhological variability in 116 cassava accessions in Benin and 59 cultivars in Chad. The variability observed in the present study is higher than that observed by Kosh-Komba *et al.* (2017) on 59 cassava accessions from the Central African Republic. Indeed, these authors obtained a variability of 7 % for the first two axes combined with a partial contribution of 10 descriptors out of 45 analysed. This difference would suggest the existence of greater variability in Côte d'Ivoire. This could be explained on the one hand by the cultivation practice based on the use of several cultivars in the same field and on the other hand, by the continuous exchange of plant material with interesting agronomic traits between farmers in different localities (Missihoun *et al.,* 2012). This study results are similar to those of Djaha *et al.* (2017) who obtained a significant morphological variability of 63.84 % within 44 cassava accessions from Côte d'Ivoire. The high variability observed by these authors on the 44 cassava accessions could be justified by the fact that they took into account a large number of qualitative variables whereas ours rather considered quantitative variables in majority. The dendrogram produced by the UPGMA method highlighted three groups of accessions based on the 11 relevant agro-morphological characters out of the 14. These three clusters were generally constituted independently of the agro-ecological zones of collection. Yusuf *et al.* (2016) assessed the morphological diversity of 22 cassava accessions from several regions in Riau province, Indonesia. They obtained three morphological clusters and the 22 accessions were not grouped according to their origin, as is the case in the present study. The class being distributed independently of origins could suggest the presence of duplicates within the 200 accessions collected. These results therefore indicate that cultivated cassava in Côte d'Ivoire consists of three distinct genetic clusters. The same pools are also reported grown in different regions with local names. N'zue *et al.* (2014) detected duplicates in the collection from three zones in Côte d'Ivoire. They attributed the presence of duplicates in the collection to farmer nomenclature. Indeed, Elias *et al.* (2001) reported that different cassava cultivars could have the same name or that several names could be given to a single cultivar on the farm. The relevance of the morphological similarities derived from the bottom-up hierarchical classification was assessed by discriminant factor analysis. The variables that discriminate the three clusters were number of branches, height of first branch, height of principal stem, diameter of principal stem, stipule length, petiole length, root weight and number of lobes per leaf. Our results are similar to those of Agre *et al*. (2015) who through the same quantitative parameters revealed a large variability within 116 cassava genotypes from Benin. Djaha *et al.* (2017) also showed that in their study on 44 cassava accessions, a total variability based on the height of the first branch, plant height, number of lobes and petiole length. These results show the relevance of the choice of the different parameters in our study.

CONCLUSION AND APPLICATION OF RESULTS

This study was conducted to characterise 200 cassava accessions collected in five agro-ecological zones of Côte d'Ivoire. It revealed a high degree of morphological variability within cassava accessions. These accessions were structured into three genetic clusters with the following distinctive characteristics: number of branches, height of the first branch, height of the principal stem, diameter of the principal stem, length of the stipule, length of the petiole, root weight and number of lobes per leaf. This observed genetic variability between groups of accessions is important for varietal selection and the building of core collections.

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