

Agronomic Characterization of 88 Accessions of the Sweet Potato (*Ipomoea batatas* (L.) Lam.) Collection of Côte d'Ivoire

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Abstract: The characterization of genetic resources is essential for improvement and conservation programs. The objective of this study was to study the morphological and agronomic variability of the sweet potato (*Ipomoea batatas* (L.) Lam.) collection of the Centre National de Recherche Agronomique (CNRA) of Côte d'Ivoire. The work was carried out with 88 accessions on the basis of 12 agronomic characters according to a Fisher design with two replicates. The correlations observed showed the degree of linkage between the traits. Principal component analysis revealed significant variability between individuals in the four groups formed (1.1, 1.2, 1.3, and 1.4). The most discriminating characters of sweet potato accessions were percentage of productive plants (PPPR), total number of storage roots (SRNU), total storage root weight (SRNU), storage root yield (SRYD), mosaic incidence (VIRD), weevil incidence (SRWE), nematode incidence (SRNE) and rodent incidence (SRRO). The hierarchical cluster analysis resulted in the formation of five groups of accessions independently of geographical origin. Discriminant factor analysis revealed that the grouping of accessions is a function of yield characteristics and disease and pest incidence.

Keywords: Characterization, Variability, *Ipomoea batatas*, Accessions, Principal Component Analysis, Hierarchical Cluster Analysis, Discriminant Factor Analysis

Introduction

Sweet potato (*Ipomoea batatas* (L.) Lam.), belonging to the family Convolvulaceae, is a widespread crop in tropical and subtropical regions of the world (Wera et al, 2014). The sweet potato is native to the region between the Yucatán Peninsula in Mexico and the Orinoco River in Venezuela. It was already widely distributed in the Americas before the arrival of Europeans and from there it spread to Europe by different routes (Zhang et al, 2000). Linguistic evidence of the frequency of use of the words *batata*, *tata* and *mbatata* and other names close to sweet potato names in Africa supports the theory of the introduction of sweet potato to Africa by the Portuguese (Gichuki et al, 2003). Cultivated varieties of *I. batatas* show significant polymorphism. And among the species of the genus *Ipomoea* in the Batatas series, 13 are considered to be closely related to sweet potato (Srisuwan et al, 2006).

Sweet potato is the third most important root and tuber crop in the world after potato (*Solanum tuberosum* L.) and cassava (*Manihot esculenta* Crantz) (Naidoo et al, 2016). Its roots and leaves are

used for human and animal consumption (Dibi et al, 2017; Shumbusha et al, 2017). In Côte d'Ivoire, it is cultivated in all regions for consumption and as a source of income (Dibi et al, 2017). The Centre National de Recherche Agronomique (CNRA) in Côte d'Ivoire maintains an important collection of sweet potato consisting of local accessions from different agro-ecological zones of the country and introductions from West, East and Southern Africa.

This crop is very heterozygous and cross-pollinated with many traits showing continuous variation (Mohanty et al, 2016). Thus, it contains a extensive variability that could be exploited by breeders. Quantitative approaches can be used to exploit this genetic variability (Tsegaye et al, 2007).

Multivariate statistical methods are used for the analysis of genetic diversity and the classification of germplasm collections (Mohammadi and Prasanna, 2003). They allow the simultaneous analysis of several statistical variables. Multivariate analyses include several methods such as principal component analysis (PCA), hierarchical cluster analysis (HCA),



discriminant factor analysis (DFA) and Mahalanobis distance (D^2).

Work on different crops has been conducted using multivariate methods (El-Kady, 2015; Chakravorty et al, 2018; Zanklan et al, 2018).

The objective of this work is to analyze the agronomic diversity of the CNRA sweet potato collection in order to provide basic information useful to breeders.

Materials and Methods

Study site

The experiments were carried out at the Station de Recherche sur les Cultures Vivrières (SRCV) of the CNRA in Bouaké located in the center of Côte d'Ivoire (5°41'N-5°02'W), in the region of Gbêkê. This region is a transitional equatorial climate zone

between sub-equatorial and sub-tropical climates called Baouléen climate. The rainfall regime of the region is bimodal, with an annual precipitation of 1,200 mm and an average temperature of 27°C (N'Ganzoua et al, 2018). The study zone is characterized by four seasons, including a large dry season (November to February), a large rainy season (March to June), a small dry season (July to August) and a small rainy season (September to October) (N'Zi et al, 2010). Each of these periods has become less marked in recent years (Brou et al, 2005). The soils belong to the subclass of moderately and slightly desaturated ferrallitic soils (Soro et al, 2007). The vegetation is a transition zone between forest and savannah (N'Zoué et al, 2003).

Figure 1 shows the average rainfall and temperatures recorded during the study period.

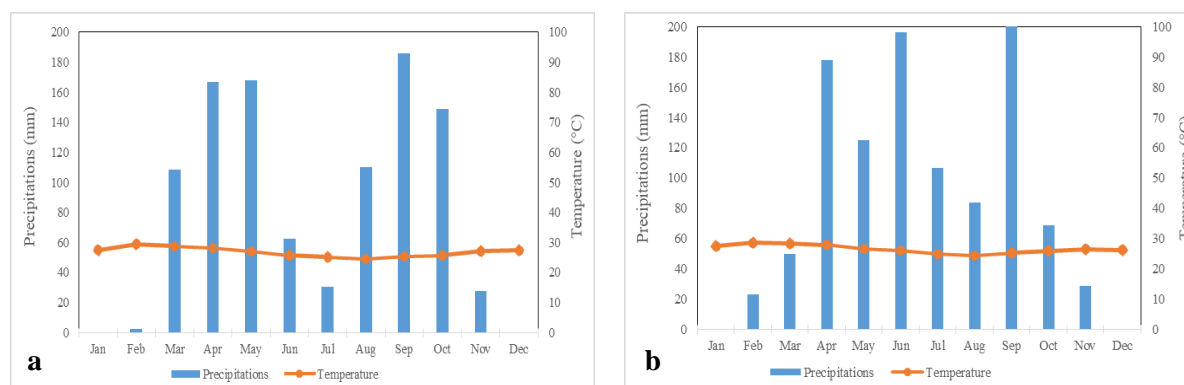


Figure 1. Ombrothermal diagram of the city of Bouaké for the years 2016 (a) and 2017 (b) (GDSME : CNRA)

Plant Material

The plant material used in this study consists of 88 accessions of sweet potato from the collection of the Station de Recherche sur les Cultures Vivrières (SRCV) of the CNRA of Bouaké (Table 1). This material consists of 72 local accessions collected

during the prospection and collecting missions carried out in the different agro-ecological zones of Côte d'Ivoire and 16 varieties with coloured flesh introduced from Peru (2), USA (2), Uganda (3) and Mozambique (9).

Table 1. Origin of the 88 accessions of the evaluated sweet potato collection

N°	Accession	Origin	N°	Accession	Origin
1	TIB-440060	Peru	45	Gbossolom vihiou	CNRA
2	CIP 199062-1	Peru	46	Safo gningne	CNRA
3	Caromex	USA	47	Kokia fiou	CNRA
4	Comensal	USA	48	Wosso gbè	CNRA
5	Tacha-2 Ininda	Mozambique	49	Anonyme1	CNRA
6	SPK004 1616 Kabode	Ouganda	50	Djè wosso1	CNRA
7	Kakamega 7 Irène	Mozambique	51	Wosso wolé	CNRA
8	UW11906 289 Sumaia	Mozambique	52	Safo gnin	CNRA
9	Ejumula	Ouganda	53	Safo figuié1	CNRA
10	SPK004 416 Vita	Ouganda	54	Safo gnian	CNRA
11	UWII 906-79 Bela Bela	Mozambique	55	Safo figuié2	CNRA
12	UWII 906-175 Namanga	Mozambique	56	Gotchin gown1	CNRA
13	UWII 906-284 Erica	Mozambique	57	Gbossolom vihou	CNRA
14	WII 9-15 Melinda	Mozambique	58	Fatôni1	CNRA
15	Ejumula gloria	Mozambique	59	Fatôni2	CNRA
16	MUSG061 Tio Joe	Mozambique	60	Fatôni3	CNRA
17	Camp1	CNRA	61	Gotchin gown2	CNRA

18	Camp2	CNRA	62	Aléda manda1	CNRA
19	Camp4	CNRA	63	Aléda okloè1	CNRA
20	Azag1	CNRA	64	Kondro bouhi5	CNRA
21	Azag2	CNRA	65	Aléda oufoué3	CNRA
22	Azag3	CNRA	66	Aléda okloè3	CNRA
23	Abobo1	CNRA	67	Aléda okloè4	CNRA
24	Tékin sino	CNRA	68	Aléda oufoué4	CNRA
25	Tchéhitan	CNRA	69	Aléda okloè6	CNRA
26	Pangnon sahon	CNRA	70	Wosso bah	CNRA
27	Sino pli pôhò	CNRA	71	Wosso guèman	CNRA
28	Sanhon plou	CNRA	72	Aléda chinois1	CNRA
29	Plou dôhò	CNRA	73	Aléda manda oufoué	CNRA
30	Banlé pou1	CNRA	74	Aléda manda laha	CNRA
31	Libéria	CNRA	75	Aléda manda3	CNRA
32	Féyi banlé	CNRA	76	Toumodi	CNRA
33	Banlé pou3	CNRA	77	Pyaré ciamou	CNRA
34	Banlé	CNRA	78	Pyaré plohoun	CNRA
35	Wessé pou	CNRA	79	Voungo kangalé	CNRA
36	Wessé behizé	CNRA	80	Pola mbla yéra koamidouho	CNRA
37	Man pou	CNRA	81	Samory djorbana douho	CNRA
38	Man louèzin	CNRA	82	Gbossolom pélékaha	CNRA
39	Man zunzi	CNRA	83	Margofi	CNRA
40	Gbossolom1	CNRA	84	Aléda oklè	CNRA
41	Gbossolom2	CNRA	85	Sino bahun	CNRA
42	Gbossolom3	CNRA	86	Anonyme2	CNRA
43	Safo gnihou	CNRA	87	SRCV1	CNRA
44	Safo vihiou	CNRA	88	SRCV2	CNRA

Methods

Experimental design and field management

The trials were carried out over two growing seasons (2016 and 2017) on one of the parcels of the CNRA's SRCV experimental site in Bouaké, using a randomized Fisher block design with two (2) replicates. Each treatment consisted of an accession represented by ten plants planted on two (2) ridges each 4.5 m long, 0.5 m wide and 0.5 m high. The spacing between the ridges was one (1) m apart. Cuttings of 3 or 4 nodes per accession were used and planted obliquely on the ridges. Regular weeding was

done as needed during the growing cycles to avoid competition between sweet potato plants and weeds. No fertilizers or pesticides were used during the work. Harvesting was done four (4) months after planting.

Data collection

Observations and measurements were made on twelve (12) agronomic traits including two (2) related to the whole plant and ten (10) to storage roots (Table 2) from Afuape et al (2011) and Dibi et al (2017).

Table 2. List of descriptors used for the agronomic characterization of sweet potato accessions

Observed traits	Codes	Type of observation and period
Percentage of productive plants	PPPR	Ratio of the number of plants that produced storage roots in each plot to the number of plants planted. It is expressed as a percentage and was estimated at harvest time
Total number of storage roots	SRNU	It was obtained after counting the total number of storage roots harvested in each elementary plot
Total storage roots weight	SRWG	It is the weight of storage roots harvested per plot obtained after weighing
Yield	SRYD	It is expressed in t/ha and was estimated from the weight of fresh storage roots on the area of the harvested plot
Mosaic incidence	VIRD	Ratio of the number of plants showing mosaic symptoms on the leaves to the total number of plants per plot. It allows to determine the severity of mosaic disease on the plants which is estimated according to the scale from 1 to 9 (1: no symptoms, 2: virus symptoms not very visible, 3: - 5% of attacked plants, 4: 6 to 15% of attacked plants, 5: 16 to 33% of attacked plants, 6: 34 to 66% of attacked plants, 7: 67 to 99% of attacked plants, 8: all attacked plants, 9: all attacked plants with slowed growth). It was determined 4 to 6 weeks after planting and 1 month before harvest
weevil incidence	SRWE	Ratio of number of storage roots attacked by weevils to total number of storage roots
Nematode incidence	SRNE	Ratio of number of storage roots attacked by nematodes to total number of storage roots
rodent incidence	SRRO	Ratio of number of storage roots attacked by rodents to total number of storage roots
Appearance	APPE	Determined after cooking and tasting tests of peeled and boiled storage roots. Acceptability tests were carried out with three tasters who were given three cards of green, yellow and red color to express their preference with the

Cooking	COOK	following values (green : good, yellow : average and red : bad) It's determined after cooking and tasting tests of peeled and boiled storage roots. Acceptability tests were carried out with three tasters who were given three cards of green, yellow and red color to express their preference with the following values (green : good, yellow : average and red : bad)
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Table 2 (continued). List of descriptors used for the agronomic characterization of sweet potato accessions

Observed traits	Codes	Type of observation and period
Taste	TAST	Determined after cooking and tasting tests of peeled and boiled storage roots. Acceptability tests were carried out with three tasters who were given three cards of green, yellow and red color to express their preference with the following values (green : good, yellow : average and red : bad)
Dry matter content	DM	It was determined by placing 200 g of fresh storage roots from each accession, cut into thin slices and placed in an oven at 100°C for 24 hours. The dry weight obtained at the exit of the oven was recorded and the DM was determined according to the following formula : $\% \text{ DM} = \frac{\text{Fresh weight}}{\text{Dry weight}} \times 100 \%$

Statistical analysis of the data

Apart from descriptive statistics (means, standard deviation), multivariate analyses were used to analyze the collected data.

These are Principal Component Analysis (PCA), Hierarchical Cluster Analysis (HCA) and Discriminant Factor Analysis (DFA). These methods have made it possible to elucidate the nature and structure of the agronomic variability of accessions.

PCA is a method that consists in transforming interrelated or "correlated" variables into new variables that are decorrelated from each other. These new variables are called "principal components" or principal axes. It has made it possible to assess the degree of similarity between the units analyzed and the identification of the variables that contributed most to the differentiation of the units. It aimed to elucidate the nature and structure of morphological and agronomic variability.

HCA is a method whose goal is to successively aggregate objects that have a sufficient degree of similarity to be joined together in a single class. It has made it possible to aggregate homogeneous groups, to appreciate the degree of similarity between the different factors to be gathered in the same class and to appreciate the phylogenetic relations existing between the factors. It tends to minimize intra-class

variance and allows smaller homogeneous groups to be formed. HCA has led to the creation of trees, also called dendrograms.

The purpose of the DFA is to describe the differences related to predefined categories of objects. It resulted in the description of the differences observed between the different groups formed. The importance of the DFA lies in the calculation of the Mahalanobis distance (D^2), which makes it possible to separate the different factors considered. It was followed by the test of significance of these distances. The distance D^2 made it possible to assess the level of remoteness of the units considered.

The statistical analyses were carried out with the Statistica software, version 7.1 (Statistica 2005).

Results

Comparative study of accessions

The analyzes of variance (ANOVA) indicates the traits which help to differentiate accessions. The ANOVA using the traits taken individually made it possible to highlight the traits which discriminate the accessions. These are percentage of productive plants, total number, total weight and storage roots yield, incidence of weevils and nematodes, cooking of boiling storage roots and dry matter content of storage roots (Table 3).

Table 3. Mean values and standard deviation of the quantitative traits analyzed in accessions of the sweet potato collection

Caractères	Valeur minimale	Valeur maximale	Moyenne ± écart type	F	p
PPPR	0	100	57,44 ± 27,08	11,4	< 0,001
SRNU	1	70	15,29 ± 12,47	13,2	< 0,001
SRWG	0	13,8	2,00 ± 2,41	19,8	< 0,001
SRYP	0,04	63,71	10,82 ± 11,84	26,2	< 0,001
VIRD	0	9	6,26 ± 2,39	1,29	0,257
SRWE	0	28	2,28 ± 4,28	67,9	< 0,001
SRNE	0	14	1,46 ± 2,25	13,2	< 0,001
SRRO	0	4	0,34 ± 0,72	1,61	0,207
APPE	0	3	1,88 ± 0,40	0,01	0,914
TAST	0	3	1,77 ± 0,40	3,52	0,062
COOK	0	3	1,60 ± 0,41	11,3	< 0,001
DM	0	50,48	29,46 ± 14,16	21,3	< 0,001

Correlations between quantitative traits

The Pearson correlation coefficient matrix (r) is summarized in Table 4. In the analysis, only correlations greater than 0.5 were retained. Thus, the percentage of productive plants was positively related to the number of storage roots (r = 0.53). The number of storage roots was positively correlated with weight (r = 0.78), storage root yield (r = 0.69), incidence of

weevils (r = 0.58) and incidence of nematodes (r = 0.65). Storage root weights were positively related to yield (r = 0.93), incidence of weevils (r = 0.64) and incidence of nematodes (r = 0.55). The yield of storage roots was positively correlated with the incidence of weevils (r = 0.60) and the incidence of nematodes (r = 0.53).

Table 4. Pearson correlation matrix (r) of the variables used in this study

	PPPR	SRNU	SRWG	SRYP	VIRD	SRWE	SRNE	SRRO	APPE	TAST	COOK	DM
PPPR	1.00	0.53	0.48	0.48	-0.30	0.36	0.30	0.30	-0.14	-0.25	-0.20	0.32
SRNU		1.00	0.78	0.69	-0.39	0.58	0.65	0.31	-0.09	-0.27	-0.13	0.18
SRWG			1.00	0.93	-0.45	0.64	0.55	0.24	-0.10	-0.22	-0.13	0.08
SRYP				1.00	-0.47	0.60	0.53	0.20	-0.15	-0.25	-0.19	0.11
VIRD					1.00	-0.28	-0.35	-0.27	0.17	0.31	0.11	-0.26
SRWE						1.00	0.37	0.21	0.05	-0.14	-0.10	0.15
SRNE							1.00	0.22	-0.16	-0.21	-0.07	0.06
SRRO								1.00	-0.10	-0.18	-0.06	0.09
APPE									1.00	0.21	0.29	-0.08
TAST										1.00	0.36	-0.22
COOK											1.00	-0.26
DM												1.00

PPPR : percentage of productive plants ; SRNU : total number of storage roots ; SRWG : total storage roots weight ; SRYP : storage roots yield ; VIRD : mosaic incidence ; SRWE : incidence of weevils ; SRNE : incidence of nematodes ; SRRO : incidence of rodents ; APPE : appearance of boiling storage roots ; TAST : taste of boiling storage roots ; COOK : cooking of boiling storage roots ; DM : dry matter content of storage roots.

Characterization on the basis of agronomic traits

In the analysis, only axes with eigenvalues greater than 1 were used. Thus, the first two axes accounted for 38.07% (axis 1) and 13.26% (axis 2) of the total variability, respectively, for a cumulative variance of 51.32% (Table 5). These first two PCA axes were used in this analysis.

The first component (axis 1) which explained 38.07% of the total variability was characterized by the eight variables which are the percentage of productive plants, the total number, the total weight and the yield of storage roots. It was also defined by the incidence of weevils, nematodes and rodents positively correlated with this axis and the incidence of mosaic negatively correlated with this axis. The second

component (axis 2), with 13.26% of the total variability, was defined by the appearance, cooking and taste of boiled storage roots negatively correlated with this axis and the dry matter content of the storage roots correlated positively to this axis.

The projection of variables (Figure 2) and individuals (Figure 3) on the first two axes made it possible to analyze the agronomic variability of accessions. The representation of individuals (Figure 3) showed two groups relative to axis 1 and two groups relative to axis 2.

Group 1.1, located on the positive side of axis 1, consists of accessions with good yield traits and high dry matter content. On the other hand, group 1.2

located on the negative side of this axis is represented by accessions sensitive to mosaic but with good culinary and organoleptic characteristics.

Group 2.1 located on the positive side of axis 2 is grouped accessions which had a high dry matter

content but good culinary and organoleptic characteristics. Group 2.2 located on the negative side of this axis was characterized by good yield, culinary and organoleptic characteristics and the high incidences of weevils and nematodes.

Table 5. Matrix of eigenvalues and correlations between the variables and the main axes of the PCA of the 88 accessions of sweet potato

	Axis 1	Axis 2
Eigenvalue	4.568	1.591
% Total	38.065	13.255
Cumul	4.568	6.158
% Cumul	38.065	51.320
PPPR	0.655	0.142
SRNU	0.859	-0.195
SRWG	0.884	-0.280
SRYD	0.867	-0.198
VIRD	-0.603	-0.150
SRWE	0.687	-0.298
SRNE	0.679	-0.175
SRRO	0.404	0.087
APPE	-0.227	-0.535
COOK	-0.430	-0.541
TAST	-0.286	-0.664
DM	0.299	0.495

Values in bold show the most discriminating characteristics of accessions.

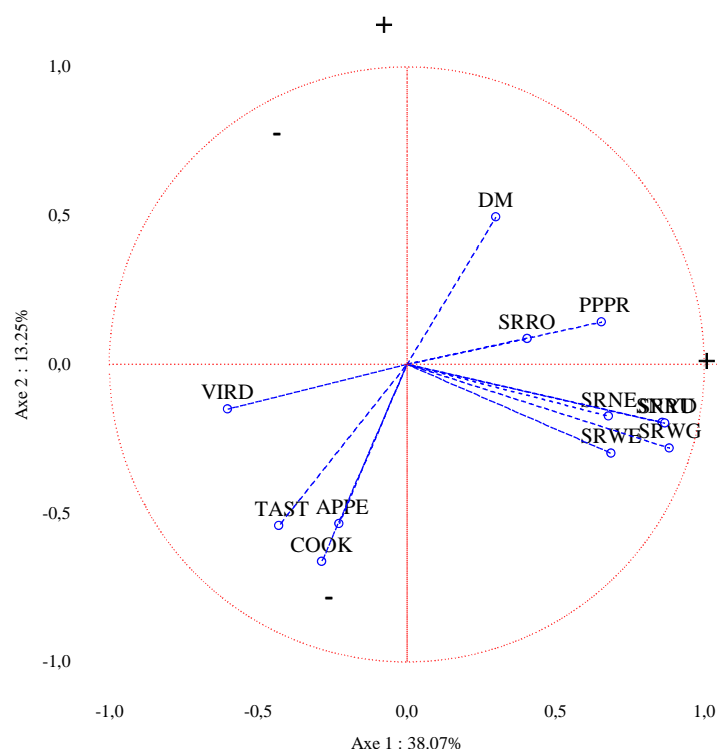


Figure 2. Projection of the 12 quantitative variables across the two principal components of sweet potato accessions

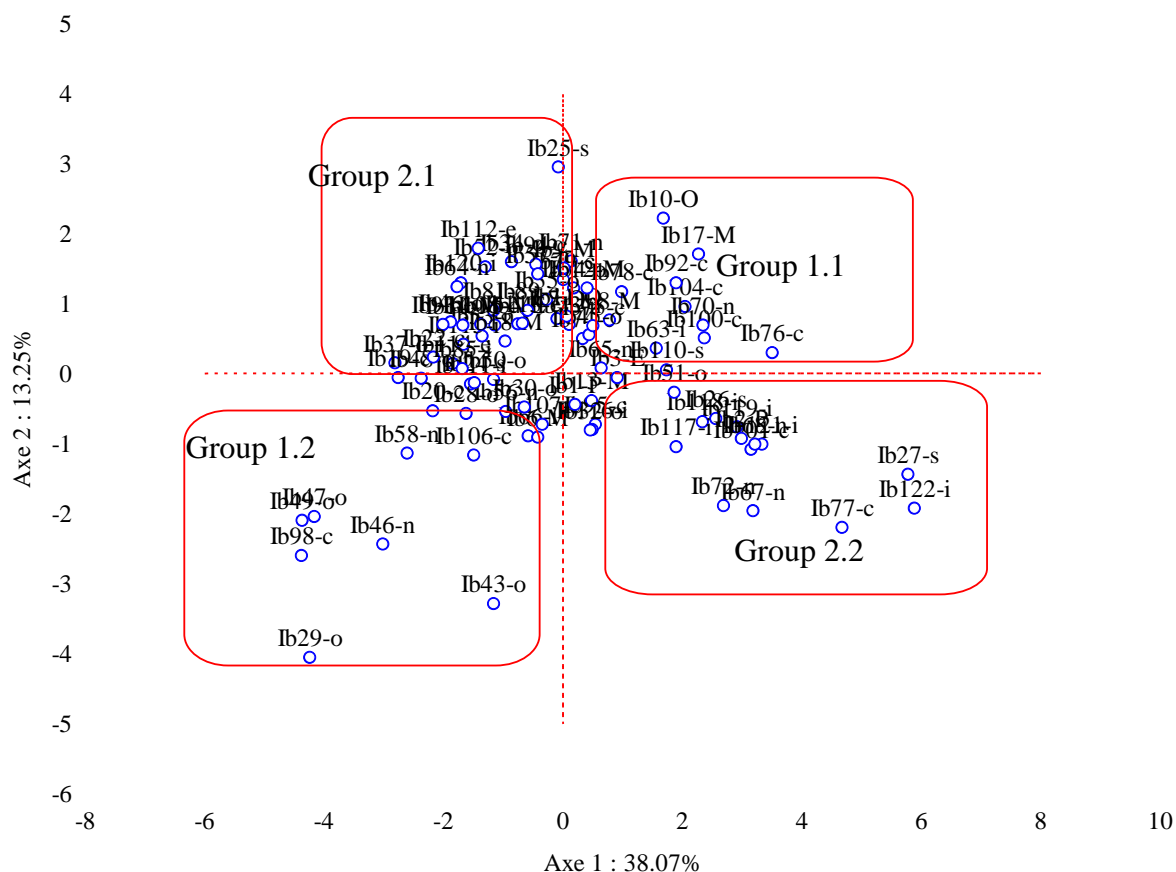


Figure 3. Graphical representation of accessions across the two principal components

Adjusting the classification of accessions by hierarchical cluster analysis

The Hierarchical cluster analysis (HCA) was used to group the accessions in the collection into homogeneous groups. It led to a dendrogram with five diversity groups based on Ward's method (Figure 4). The agronomic characteristics of the accession groups are as follow :

- group 1 : this group is composed of 17 accessions of various geographical origins : North, South, Center and West of Côte d'Ivoire. Individuals in this group are characterized by a low percentage of productive plants and low values of yield parameters. However, they have the highest dry matter content. They are less affected by pest (weevils, nematodes and rodents) damage ;
- group 2 : this group consists of 24 accessions from the North, South, Center, East, West of Côte d'Ivoire and Mozambique. This group is characterized by a low percentage of productive plants and low dry matter content and very low yield parameters. Individuals in this group also suffered less pest damages ;
- group 3 : This group had the largest number with 27 accessions. It is made up of accessions of various origins : North, Center, West of Côte

d'Ivoire, Uganda, Mozambique, United States and Peru. Individuals in this group have a high percentage of productive plants and high value of yield parameters. The dry matter content was low. The pest damages was significant ;

- group 4 : this group had the lowest number with 5 accessions collected in the North, Center and West of Côte d'Ivoire. Individuals in this group presented the percentages of productive plants and yield parameters with the lowest values. Pest damage was less severe in the accessions of this group, but with significant mosaic symptoms. The dry matter content could not be determined for this group because the number of storage roots recorded was very low ;
- group 5 : this group consists of 15 accessions from the North, Center, South of Côte d'Ivoire and Peru. Individuals in this group exhibited high percentages of productive plants and high yield parameters. However, the dry matter content was low and pest damage was very severe.

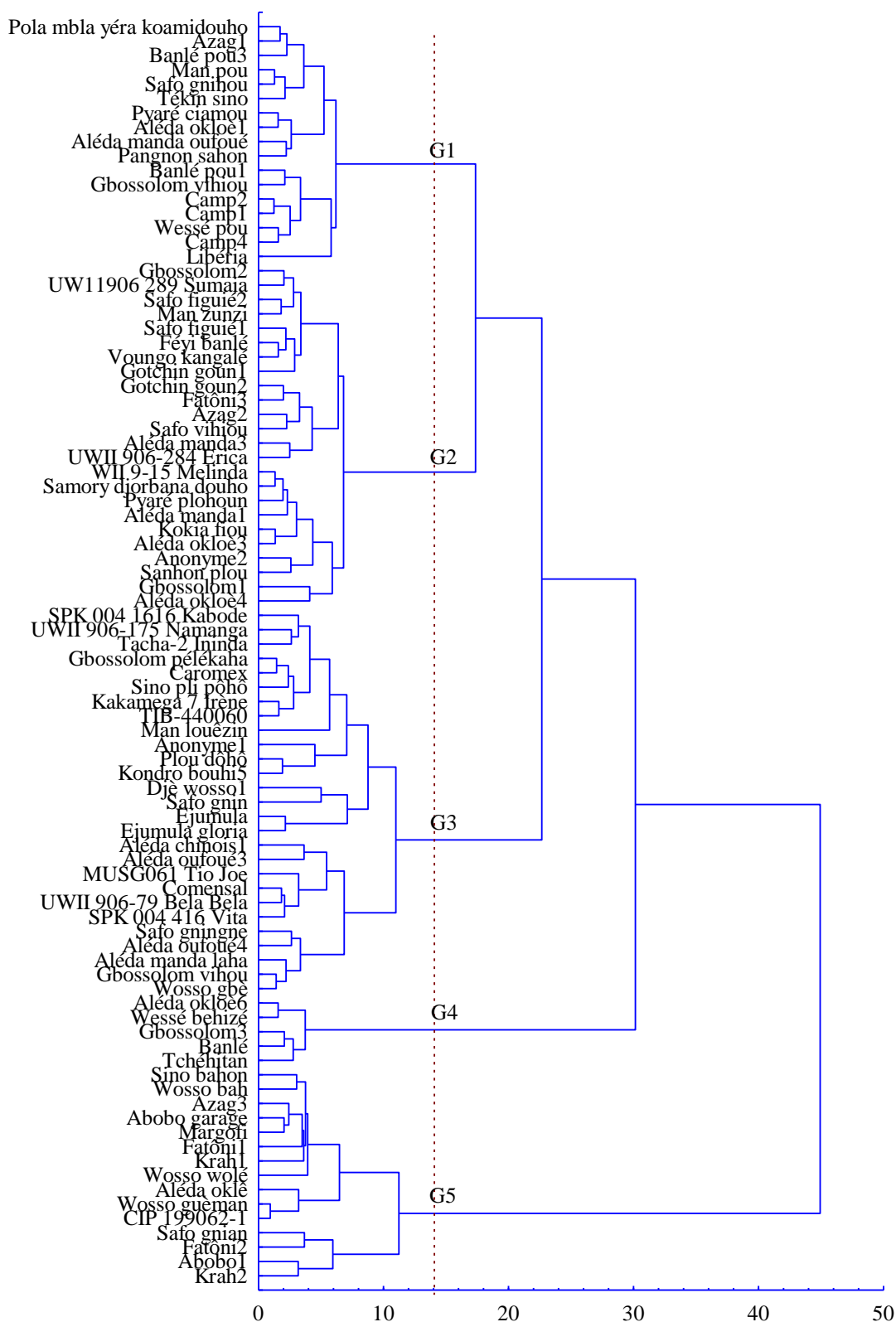


Figure 4. Hierarchical cluster analysis of sweetpotato accessions according to Ward's method

Selection of discriminant traits by DFA

Discriminant factor analysis (DFA) was performed for the selection of discriminant traits. The first

function (axis 1) represented 71.88% of the total variability. It is represented by the weight of storage roots and the incidence of nematodes negatively

correlated with this axis. The second discriminant function (axis 2) accumulated 25.20% of the total variability. It was characterized by the incidence of mosaic and weevils negatively correlated with this axis and the incidence of rodents positively correlated with this axis (Table 6).

The graphic representation of DFA in the factorial plane 1-2 showed a structuring of individuals into five groups. Group 1 located in the negative part of axis 1 is characterized by a high weight of storage roots and a high incidence of nematodes. It is the same for groups 2 and 4 located in the same part of this axis 1. Group 3 located in the positive part of

axis 2 is characterized by a high incidence of mosaic and weevils. Group 5 located in the negative part of axis 2 is characterized by a high incidence of rodents. DFA has shown a structuring of accessions independently of their geographical origin (Figure 5).

The Mahalanobis distances (D^2) measuring the separation between the five groups were calculated (Table 7). The pair-wise distances was significant for all groups ($p < 0.001$). The maximum value ($D^2 = 61.2$) was observed between group 4 and group 5. The smallest distance ($D^2 = 1.7$) was recorded between group 1 and group 2.

Table 6. Contribution of the canonical axes and the factorial weight of the variables

	Axis 1	Axis 2
Eigenvalue	5.117	1.794
% Total	5.117	6.911
Cumul	71.884	25.200
% Cumul	71.884	97.083
SRRO	-0.010	0.041
SRWE	-0.031	0.035
APPE	-0.340	-0.089
COOK	0.017	0.040
TAST	0.279	-0.459
DM	-0.193	-0.247

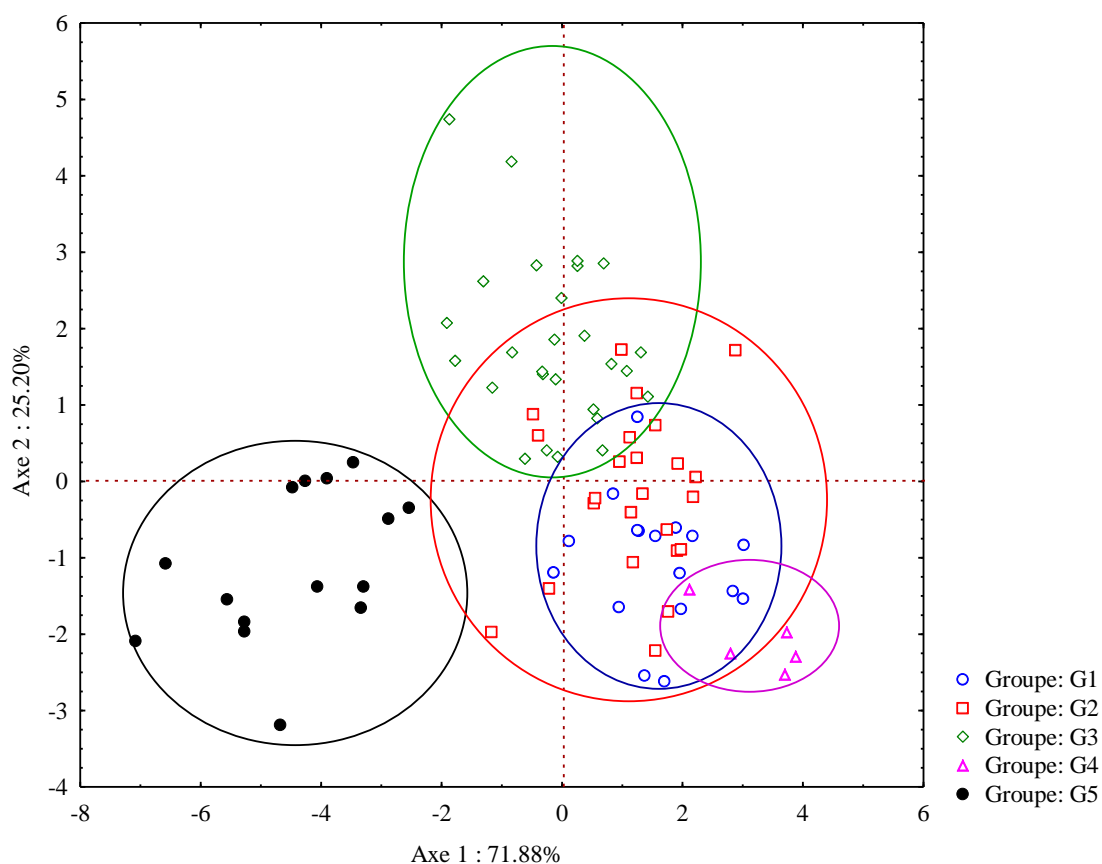


Figure 5. Distribution of sweet potato accessions's groups across the two factorial axes 1-2 of the discriminant factor analysis

Table 7. Mahalanobis distances (D^2) calculated between the sweet potato accessions from the hierarchical ascending classification and the significance (p) of the distances

	Group 1		Group 2		Group 3		Group 4		Group 5	
	D^2	p	D^2	p	D^2	p	D^2	p	D^2	p
Group 1	0		1,7	0,063	11,5	< 0,001	5,7	< 0,001	36,7	< 0,001
Group 2			0		6,1	< 0,001	10,2	0,000	32,6	< 0,001
Group 3					0		27,6	< 0,001	27,1	< 0,001
Group 4							0		61,2	< 0,001
Group 5									0	< 0,001

Discussion

The identification of the traits of interest characterizing a species is a prerequisite in plant improvement processes. Thus, the study of agronomic diversity focused on 88 sweet potato accessions made up of 72 local and 16 introduced accessions from the CNRA collection revealed a significant diversity of the species. The high diversity recorded would probably be due to the diversity of agro-ecological zones and the dispersion of the sites where accessions were collected. This diversity reflects the expression of a strong genotypic heterogeneity of the plant material used in this work.

This study found that the yield parameters were highly correlated with each other. Correlations have the advantage of facilitating indirect improvement in the various variables involved in yield. Thus, improvement in one trait leads to improvement in others. Such results have also been reported by Bassey (2017) who showed a correlation between yield parameters. On the other hand, the positive correlation between yield parameters and pest incidence are not useful relationships in a varietal selection context for high yield. Such results were observed by Stathers et al (2003) with the infestation of the weevil *Cylas* spp. and Osunlola and Fawole (2015) with the infestation of *Meloidogyne incognita*, a nematode pest of sweet potato. Based on the results of these correlations and principal component analysis, crossing schemes can be undertaken to create new high-yielding sweet potato varieties with good organoleptic and technological characteristics.

The principal component analysis made it possible to establish the relationships between the variables evaluated and the differences between accessions. The variables that contributed to the variability between accessions are : percentage of productive plants (PPPR), total number of storage roots (SRNU), total storage root weight (SRNU), storage root yield (SRYD), mosaic incidence (VIRD), weevil incidence

(SRWE), nematode incidence (SRNE) and rodent incidence (SRRO).

This result suggests that the study of the diversity of locally grown plant material should be limited to a number of traits. These results also demonstrate that in a crop such as sweet potato, the agromorphological differences are often based on agronomic traits related to yield or the incidence of diseases and pests. Such results suggest that these variables can serve as a selection index for a crop improvement program. Based on the correlation and PCA results, breeding schemes should be undertaken for the creation of new performing sweet potato cultivars with good organoleptic and technological characteristics.

The dendrogram revealed that the accessions were structured independently of their geographic origin. These results suggest that there could be a possibility of frequent exchange of planting material between producers in different areas. These exchanges would be carried out through the migration of populations or during informal transactions on the markets of the country's major cities. It is also likely that the mode of vegetative propagation of the crop and the continuous selection of certain traits by producers would have contributed to the great variability observed within the collection. In groups 1 and 2, local accessions and introductions were grouped together. There would therefore be the presence of genetically distinct local accessions similar to the introduced varieties.

The discriminant factor analysis (DFA) resulted in a clear structuring of the accessions in five different groups. Agronomic variability was also evaluated by the Mahalanobis distance which made it possible to obtain a quantitative estimate of the agronomic divergence of the different groups of accessions. It was translated by very significant Mahalanobis distances between these groups. The genetic diversity recorded in this study has been reported in previous

work on sweet potatoes (Karuri et al 2010 ; da Silva et al 2013 ; Bhadauriya et al 2018). The great variability recorded within the collection demonstrates the possibility of exploiting this potential for a possible improvement in this culture.

Conclusion

Agronomic variability focused on 88 sweet potato accessions from the CNRA collection in Bouaké with a view to selecting morphotypes with interesting agronomic characteristics. Multivariate analysis based on 12 agronomic traits showed strong agronomic differentiation between the accessions assessed. The correlations made it possible to appreciate the links between the different agronomic characters. They make it possible to orient the selection of the traits of interest. The PCA demonstrated significant agronomic variability between the genotypes of the different groups formed. It revealed that the most relevant traits to explain the observed variability are the percentage of productive plants, the total number, the total weight and the yield of storage roots, the incidence of mosaic, weevils, nematodes and rodents. The HCA made it possible to group the accessions into five diversity groups independently of their geographical origin. In addition, DFA provides details on the closeness of the various groups formed. It also specifies that accessions are not grouped together according to their geographical origin. The very significant Mahalanobis distances between the different groups indicate a clear differentiation between the accessions groups.

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Conflict of interest

Authors declare no conflict of interest.

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