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DIVERSITY AND RELATIONSHIPS AMONG MORPHOLOGICAL CHARACTERS IN THE SWEET POTATO COLLECTION OF COTE D'IVOIRE

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ABSTRACT

Collection and characterisation of plant materials is a crucial step in crop improvement programmes. The objective of this study was to characterise a sweet potato (*Ipomoea batatas* [L.] Lam.) collection from the Centre National de Recherche Agronomique (CNRA) in Côte d'Ivoire, based on morphological characters, and to elucidate the relationships among them. The experiment was carried out in a Fisher design with two replications. The descriptive analyses revealed a substantial phenotypic variation within the collection. The multiple correspondence analysis showed that 15 characters out of 27 were the most discriminant to explain the variation. Furthermore, significant relationships were observed between phenotypic traits related to leaves, stems and storage roots. The hierarchical classification placed accessions into three genetic groups regardless of their geographical origin and revealed the existence of duplicate accessions. The results obtained could be used for the selection, improvement and sustainable management of sweet potato genetic resources.

Key Words: Accessions, *Ipomoea batatas*, multiple correspondence analysis

RESUME

La collecte et la caractérisation de matériel végétal est une étape cruciale dans les programmes d'amélioration des cultures. L'objectif de cette étude était de caractériser la collection de patate douce (*Ipomoea batatas* [L.] Lam.) du Centre National de Recherche Agronomique (CNRA) en Côte d'Ivoire, à partir de 27 caractères morphologiques et d'élucider les relations entre eux. Les expérimentations ont été réalisées selon un dispositif de Fisher en deux répétitions. Les analyses descriptives ont révélé une variation phénotypique importante au sein de la collection. L'analyse des correspondances multiples a montré que 15 caractères sur 27 ont été les plus discriminants pour expliquer la variation. De plus, des relations significatives ont été mises en évidence entre les caractères phénotypiques liés

aux feuilles, aux tiges et aux racines tubéreuses. La classification hiérarchique a classé les accessions en trois groupes génétiques indépendamment de leur origine géographique et a révélé l'existence d'accessions en doublons. Les résultats obtenus pourraient être utilisés pour la sélection, l'amélioration et la gestion durable des ressources génétiques de la patate douce.

Mots Clés : Accessions, *Ipomoea batatas*, analyse des correspondances multiples

INTRODUCTION

Sweet potato (*Ipomoea batatas* [L.] Lam.) is an autohexaploid species ($2n = 6x = 90$) belonging to the family Convolvulaceae. It was first domesticated in tropical America. The primary centre of diversity is believed to be in north-western South America (Colombia, Peru and Ecuador) (Huamàn *et al.*, 1999). It is the world's seventh largest food crop after wheat (*Triticum aestivum* (L.)), rice (*Oryza sativa* (L.)), maize (*Zea mays* (L.)), Irish potato (*Solanum tuberosum* (L.)), barley (*Hordeum vulgare* (L.)), and cassava (*Manihot esculenta* Crantz); and the second most important tuber crop after cassava, with an annual world production of 106 million tonnes (Amoatey *et al.*, 2016). The crop is generally propagated asexually (Veasey *et al.*, 2007).

Sweet potato is grown mainly for its storage roots and leaves. Storage roots are consumed raw, boiled or fried; whereas the leaves are used as vegetables or fodder (Glato *et al.*, 2013). Sweet potato contains high levels of carbohydrates, and minerals, and also is an important source of vitamins A and C, especially orange-fleshed varieties (Rodriguez-Bonilla *et al.*, 2014).

In Côte d'Ivoire, sweet potato is grown mainly by small scale farmers, both for consumption and as a source of income for households in rural areas (Dibi *et al.*, 2017). Several varieties of sweet potato are grown in varied agro-climatic growing-regions. The varieties of this species of economic and social importance are the subject of a considerable informal transaction in local markets; and it is expected that the demand for the crop will expand.

Centre National de Recherche Agronomique (CNRA) in Côte d'Ivoire holds an important sweet potato collection. This gene bank includes local and introduced accessions from various parts of Africa and North or South America. Furthermore, surveys and collections indicate that many local names were conferred to the farmers' accessions and introduced sweet potato varieties. However, little or no data are available on the genetic diversity and agronomic performances of local and introduced varieties identified as promising. Because of its better adaptability to local agro-ecological conditions, local germplasm is more sought after than introduced accessions.

Generally, species adapted to various environmental conditions contain an intra-specific variability that provides germplasm of interest for any appropriate conservation and sustainable management programme. Although cultivated under various climatic and ecological conditions in Côte d'Ivoire, a sweet potato diversity map and its organisation are not yet well developed. Understanding this diversity is highly important for the rational management and efficient use of the crop (Koussao *et al.*, 2014).

Morphological characterisation is the first step in the description and classification of germplasm (Smith and Smith, 1989); and is essential for the identification of desirable traits of interest (Shrestha, 2016). It also helps in identification of duplicates among collected materials to reduce the number of conserved accessions. Several works based on vine, leaf, flower and storage root characteristics, revealed significant morphological variability in sweet potato (Karuri *et al.*, 2010; Yada *et al.*, 2010; Fongod *et al.*, 2012). In addition to

its production in ruggedness condition, marginal soils, resistance to pests and diseases and drought tolerance (Jackson *et al.*, 2012; Laurie *et al.*, 2015; Mabhaudhi, 2015; Motsa *et al.*, 2015), the great phenotypic and genotypic variability found in sweet potato is an indispensable asset in the current climate change context. Assessment of germplasm diversity and genetic relationships among genotypes and introduced lines is also essential in conservation and improvement strategies for any crop (Elameen *et al.*, 2008). CNRA sweet potato germplasm collection has neither been characterised nor related to sweet potato genotypes from other countries. For that, a research programme was launched to evaluate the genetic diversity of the collection.

The aim of this research was to use morphological characters to investigate diversity of local and introduced accessions of sweet potato from the CNRA gene bank and identify relationships between characters of interest to enhance conservation strategies and rational exploitation of the germplasm in yield improvement programmes.

MATERIALS AND METHODS

Plant materials. For this research, 88 accessions of sweet potato from the germplasm collection of CNRA of Côte d'Ivoire were used (Table 1). The sample of accessions included 72 landraces and 16 introduced lines. The landraces were collected from different farms in various agro-ecological growing-regions of Côte d'Ivoire. The introduced lines were obtained from Peru (2), United States (2), Uganda (3) and Mozambique (9).

Study site. The experiment was carried out at the Food Crops Research Station of CNRA at Bouaké (5°41'N-5°02'W), in the Gbêkê region in central Côte d'Ivoire. This area is characterised by equatorial climate of moderate transition or baoulean climate (Noufé *et al.*, 2011). The rainfall regime is bimodal, with two rainy seasons (March to June and September

to October) spaced by two dry seasons (November to February and July to August). These periods have become less marked in recent years (Brou *et al.*, 2005). The average annual rainfall is between 1100 and 1200 mm (N'Gbesso *et al.*, 2010). The average annual temperature is 28 °C (Akassimadou and Yao-Kouamé 2014). The soils are of the gravellery ferrallitic type, rearranged, shallow and derived from a granitic alteration material (N'Gbesso *et al.*, 2013). Vegetation is a transition zone between forest and savannah (N'Zoué *et al.*, 2003).

Experimental procedure. The field trial was conducted over two growing seasons, using a randomised Fisher block design with two blocks covering an area of 1032 m². Each block was divided into 2 plots of 473 m² (43 m × 11 m), spaced 1 m apart. Each sub-plot consisted of 44 tilled ridges, 4.5 m long, 0.5 m wide and 0.5 m high each. One ridge had a row of 10 equidistant seedling points, 0.5 m apart. The spacing between the ridges was 1 m. Each ridge of a plot was allocated an accession, and vine cuttings of 3 or 4 nodes were planted obliquely on the sowing points, at a depth of 3 cm. This corresponds to 20 plants per accession, depending on the availability of cuttings. The harvests were carried out in January 2017 (first season) and October 2017 (second season), respectively. Regular weeding was carried out during the growing cycles to minimise competition between sweet potato plants and weeds. No inputs (fertilisers and pesticides) were applied.

Data collection. Morphological characterisation was achieved using the sweet potato standard descriptors from the International Potato Center, the Asian Vegetable Research and Development Center and the International Board for Plant Genetic Resources (CIP, AVRDC, IBPGR, 1991). A total of 27 characters (18 aerial, 1 flowering and 8 storage root) were evaluated (Table 2). Characters were scored on five plants,

TABLE 1. Description of the 88 sweet potato accessions used for this study

N°	Accession	Origin	Skin colour	Flesh colour
1	TIB-440060	Perou	Orange	Pale yellow
2	CIP 199062-1	Perou	Orange	Pale yellow
3	Caromex	USA	Pink	Dark yellow
4	Comensal	USA	Pink	Pale yellow
5	Tacha-2 Ininda	Mozambique	Brownish orange	Dark orange
6	SPK004 1616 Kabode	Ouganda	Pink	Intermediate orange
7	Kakamega 7 Irène	Mozambique	Pink	Dark orange
8	UW11906 289 Sumaia	Mozambique	Orange	Intermediate orange
9	Ejumula	Ouganda	Orange	Dark orange
10	SPK004 416 Vita	Ouganda	Pink	Intermediate orange
11	UWII 906-79 Bela Bela	Mozambique	Brownish orange	Pale yellow
12	UWII 906-175 Namanga	Mozambique	Cream	Dark orange
13	UWII 906-284 Erica	Mozambique	Orange	Dark orange
14	WII 9-15 Melinda	Mozambique	Orange	Dark orange
15	Ejumula gloria	Mozambique	Orange	Dark orange
16	MUSG061 Tio Joe	Mozambique	Brownish orange	Dark orange
17	Camp1	CNRA	Pink	White
18	Camp2	CNRA	Pink	Cream
19	Camp4	CNRA	Pink	Dark yellow
20	Azag1	CNRA	Orange	Cream
21	Azag2	CNRA	Pink	White
22	Azag3	CNRA	Pink	Dark yellow
23	Abobo1	CNRA	Cream	Pale yellow
24	Tékin sino	CNRA	Pink	Cream
25	Tchéhitan	CNRA	White	Cream
26	Pangnon sahon	CNRA	Pink	Cream
27	Sino pli pôhò	CNRA	Cream	Cream
28	Sanhon plou	CNRA	Pink	Pale yellow
29	Plou dôhò	CNRA	Cream	Cream
30	Banlé pou1	CNRA	Cream	Cream
31	Libéria	CNRA	Orange	Pale yellow
32	Féyi banlé	CNRA	Pink	Pale yellow
33	Banlé pou3	CNRA	Cream	Dark cream
34	Banlé	CNRA	Pink	Pale yellow
35	Wessé pou	CNRA	Cream	Cream
36	Wessé behizé	CNRA	Cream	Cream
37	Man pou	CNRA	Pink	Cream
38	Man louêzin	CNRA	Pink	Dark orange
39	Man zunzi	CNRA	Pink	Pale yellow
40	Gbossolom1	CNRA	Pink	Cream
41	Gbossolom2	CNRA	Pink	Cream
42	Gbossolom3	CNRA	Pink	Cream
43	Safo gnihou	CNRA	Pink	Cream
44	Safo vihiou	CNRA	Cream	Cream
45	Gbossolom vihiou	CNRA	Cream	Cream

TABLE 1. Contd.

N°	Accession	Origin	Skin colour	Flesh colour
46	Safo gningne	CNRA	Cream	Cream
47	Kokia fiou	CNRA	Cream	Cream
48	Wosso gbè	CNRA	Pink	Cream
49	Anonyme1	CNRA	Pink	Dark cream
50	Djè wosso1	CNRA	Cream	Cream
51	Wosso wolé	CNRA	Pink	Cream
52	Safo gnin	CNRA	Cream	Cream
53	Safo figuié1	CNRA	Cream	Cream
54	Safo gnian	CNRA	Pink	Cream
55	Safo figuié2	CNRA	Cream	Cream
56	Gotchin gown1	CNRA	Orange	Pale orange
57	Gbossolom vihou	CNRA	Cream	Intermediate orange
58	Fatôni1	CNRA	Pink	Pale orange
59	Fatôni2	CNRA	Pink	Pale yellow
60	Fatôni3	CNRA	Pink	Pale yellow
61	Gotchin gown2	CNRA	Orange	Pale yellow
62	Aléda manda1	CNRA	Yellow	Dark yellow
63	Aléda okloè1	CNRA	Pink	Dark yellow
64	Kondro bouhi5	CNRA	Pink	Pale yellow
65	Aléda oufoué3	CNRA	Pink	Cream
66	Aléda okloè3	CNRA	Pink	Dark yellow
67	Aléda okloè4	CNRA	Pink	Pale orange
68	Aléda oufoué4	CNRA	Pink	Dark cream
69	Aléda okloè6	CNRA	Cream	Dark yellow
70	Wosso bah	CNRA	Pink	Pale yellow
71	Wosso guèman	CNRA	Yellow	Pale orange
72	Aléda chinois1	CNRA	Yellow	Pale yellow
73	Aléda manda oufoué	CNRA	Cream	Cream
74	Aléda manda laha	CNRA	Cream	Cream
75	Aléda manda3	CNRA	Orange	Pale yellow
76	Toumodi	CNRA	Pink	Cream
77	Pyaré ciamou	CNRA	Pink	Cream
78	Pyaré plohou	CNRA	Cream	Cream
79	Voungo kangalé	CNRA	Cream	Cream
80	Pola mbla yéra koamidouho	CNRA	Cream	Cream
81	Samory djobana douho	CNRA	Cream	Cream
82	Gbossolom pélékaha	CNRA	Cream	Cream
83	Margofi	CNRA	Pink	Cream
84	Aléda oklê	CNRA	Pink	Pale yellow
85	Sino bahon	CNRA	Pink	Dark orange
86	Anonyme2	CNRA	Pink	Pale yellow
87	SRCV1	CNRA	Pink	Cream
88	SRCV2	CNRA	Pink	Dark yellow

TABLE 2. Morphological characters used to evaluate the 88 sweet potato accessions

Characters	Phenotypes
Twining (TNNG)	1-non-twining, 2-slightly twining, 3-moderately twining, 4-twining, 5-very twining
Plant type (PTYP)	1-erect (< 75cm), 2-semi-compact (75-150 cm), 3-spreading (151-250 cm), 4-extremely spreading (> 250)
Ground cover (GCOV)	1-weak (< 50%), 2-medium (50-74%), 3-strong (75-90%), 4-total (> 90%)
Internode length (ILEN)	1-very short (<3 cm), 2-short (3-5 cm), 3-long (10-12 cm), 4-very long (> 12cm)
Internode diameter (IDMT)	1-very thin (<4mm), 2-thin (4-6 mm), 3-intermediate (7-9 mm), 4-thick (10-12 mm), 5-very thick (> 12 mm)
Predominant vine colour (PVIC)	1-green, 2-green with few purple spots, 3-green with many purple spots, 4-green with many dark spots, 5-mostly purple, 6-mostly dark purple, 7-totally purple, 8-totally dark purple
Secondary vine colour (SVIC)	1-absent, 2-green base, 3-green tip, 4-green nodes, 5-purple base, 6-purple tip, 7-purple nodes, 8-other
Vine tip pubescence (VTIP)	1-none, 2-sparse, 3-moderate, 4-heavy
General leaf outline (GLOL)	1-rounded, 2-reniform, 3-cordate, 4-triangular, 5-hastate, 6-lobed, 7-almost divided
Mature leaf size (MLES)	1-small (< 8 cm), 2-medium (8-15 cm), 3-large (16-25 cm), 4-very large (> 25 cm)
Leaf lobe type (LTYP)	1-no lateral lobes, 2-very slight, 3-slight, 4-moderate, 5-deep, 6-very deep
Leaf lobes number (LLON)	1-none, 2-1 lobe, 3-3 lobes, 4-5 lobes, 5-7 lobes, 6-9 lobes
Central leaf lobe shape (CLLO)	1-absent, 2-teeth, 3-triangular, 4-semi-circular, 5-semi-elliptic, 6-elliptic, 7-lanceolate, 8-oblongate, 9-linear
Mature leaf colour (MLCO)	1-yellow-green, 2-green, 3-green with purple edge, 4-greyish, 5-green with purple veins on upper surface, 6-slightly purple, 7-mostly purple, 8-green upper purple lower, 9-purple on both surfaces
Immature leaf colour (ILCO)	1-yellow-green, 2-green, 3-green with purple edge, 4-greyish, 5-green with purple veins on upper surface, 6-slightly purple, 7-mostly purple, 8-green upper purple lower, 9-purple on both surfaces
Abaxial leaf vein pigmentation (APIG)	1-yellow, 2-green, 3-purple spot at base of main rib, 4-purple spot in several veins, 5-main rib partially purple, 6-main rib mostly or totally purple, 7-all veins partially purple, 8-all veins mostly or totally purple, 9-lower surface and totally purple

TABLE 2. Contd.

Characters	Phenotypes
Petiole pigmentation (PPIG)	1-green, 2-green with purple near leaf, 3-green with purple near stem, 4-green with purple at both ends, 5-green with purple spots throughout petiole, 6-green with purple stripes, 7-purple with green near leaf, 8-some petiole purple others green, 9-totally or mostly purple
Petiole length (PLGT)	1-very short (< 10 cm), 2-short (10-20 cm), 3-intermediate (21-30 cm), 4-long (31-40 cm), 5-very long (> 40 cm)
Flowering ability (FLAT)	1-none, 2-sparse, 3-moderate, 4-profuse
Storage root shape (STOR)	1-round, 2-round elliptic, 3-elliptic, 4-obovate, 5-ovate, 6-oblong, 7-long oblong, 8-long elliptic, 9-long irregular or curved
Storage root defects (STOD)	1-absent, 2-alligator's like skin, 3-veins, 4-shallow horizontal constrictions, 5-deep horizontal constrictions, 6-shallow longitudinal grooves, 7-deep longitudinal grooves, 8-deep constrictions and deep grooves
Predominant skin colour (PSCO)	1-white, 2-cream, 3-yellow, 4-orange, 5-brownish orange, 6-pink, 7-red, 8-purple-red, 9-dark purple
Intensity of predominant skin colour (ISCO)	1-pale, 2-intermediate, 3-dark
Secondary skin colour (SSCO)	1-absent, 2-white, 3-cream, 4-yellow, 5-orange, 6-brownish orange, 7-pink, 8-red, 9-purple-red, 10-dark purple
Predominant flesh colour (PFCO)	1-white, 2-cream, 3-dark cream, 4-pale yellow, 5-dark yellow, 6-pale orange, 7-intermediate orange, 8-dark orange, 9-strongly pigmented with anthocyanins
Secondary flesh colour (SFCO)	1-absent, 2-white, 3-cream, 4-yellow, 5-orange, 6-pink, 7-red, 8-purple-red, 9-purple, 10-dark purple
Distribution of secondary flesh colour (DFCO)	1-absent, 2-narrow ring in cortex, 3-broad ring in cortex, 4-scattered spots, 5-narrow ring in flesh, 6-broad ring in flesh, 7-ring and other areas in flesh, 8-in longitudinal sections, 9-covering most of the flesh, 10-covering all flesh

randomly selected from each accession and in each block, based on a scale of 1 to 10 from the vegetative phase to the harvest (90 to 120 days after planting).

Statistical analysis. Data collected were subjected to descriptive statistics. Phenotypic frequencies for all traits were computed and their distribution was analysed using all accessions. To assess the structure of the genetic diversity within the collection, two approaches were implemented. Multiple correspondence analysis (MCA) was performed to reveal the most discriminant characters, relationships between characters and the distribution pattern of the accessions in a two-dimensional space. Inertias Adjustment procedure was applied to improve the MCA's results (Abdi and Valentin, 2007; Moschidis, 2009). To examine the relationships between accessions, the hierarchical cluster analysis (HCA) was carried out based on the most discriminant characters of the MCA using Ward method with Euclidean distances. The similarity/dissimilarity matrix allowed to identify duplicates within each cluster. All analyses were carried out with XLSTAT software version 2016.2 (Addinsoft, 2016).

RESULTS

Phenotypic diversity. The value of each phenotypic frequency for all examined traits are presented in Table 3. The number of phenotypic classes for each character ranged from three to nine with a predominance of some phenotypic classes. A total of 138 phenotypic classes were identified within the germplasm analysed. The most remarkable range of phenotypic variation was achieved with regard to five traits, which showed seven to nine patterns among accessions studied. These were petiole pigmentation (7), predominant vine colour (8), storage root defects (8), predominant flesh colour (8) and storage root

shape (9) with their respective number of phenotypic classes (Table 3).

Among the accessions, the different predominant vine colours and their proportions were: green with many purple spots (27.27%), green with many dark purple spots (21.59%), green (17.04%), mostly purple (14.77%), green with few purple spots (7.96%), totally dark purple (4.55%), mostly dark purple (4.55%), and totally purple (2.27%). Concerning the secondary colour of the vines, three phenotypic classes were recorded. Vines with purple nodes as secondary colour were the most observed among accessions (55.68%); followed by vines without secondary colour (35.23%); while vines with a green tip (9.09%) were observed in a few accessions.

The variation in the petiole pigmentation was also noticeable. The proportion of the different phenotypic classes for this trait was: 45.45% (green with purple at both ends), 10.23% (green with purple near stem), 10.23% (totally or mostly purple), 9.09% (green), 9.09% (green with purple spots throughout petiole), 9.09% (green with purple stripes) and 6.82% (some petiole purple others green).

The most common storage root shapes among accessions were long irregular or curved (34.09%), long elliptic (22.73%) and obovate (18.18%). Ovate storage roots (9.09%) were observed in very few accessions as well as round elliptic (7.95%), round (3.41%), elliptic (2.27%), oblong (1.14%) and long oblong (1.14%) accessions.

Regarding the storage root defects, accessions with storage roots without defect (60.20%) were the most represented. The other patterns of storage roots defects were represented with the following proportions: shallow horizontal constrictions (10.23%), shallow longitudinal grooves (9.09%), alligator's like skin (7.95%), deep horizontal constrictions (7.95%), veins (2.27%), deep longitudinal grooves (1.14%), deep constrictions and deep grooves (1.14%). Eight

TABLE 3. Distribution of sweet potato phenotypic percentages of the 27 morphological characters examined in the study

Characters	1	2	3	4	5	6	7	8	9	10
Twining	14.80	12.50	29.50	29.50	13.60					
Plant type	7.96	34.10	14.80	43.20						
Ground cover	3.41	28.40	27.30	40.90						
Internode length	20.50	48.90	27.30	3.41	0					
Internode diameter	12.50	75.0	12.50	0	0					
Predominant vine colour	17.0	7.96	27.30	21.60	14.80	4.55	2.27	4.55		
Secondary vine colour	35.20	0	9.09	0	0	0	55.70			
Vine tip pubescence	17.0	38.60	13.60	30.70						
General leaf outline	0	2.27	0	25.0	5.68	64.80	2.27			
Mature leaf size	7.95	88.60	3.41	0						
Leaf lobe type	6.82	34.10	3.41	15.90	35.20	4.54				
Leaf lobes number	0	6.82	36.40	53.40	2.27	1.14				
Central leaf lobe shape	0	0	40.90	0	13.60	4.54	35.20	2.27	3.41	
Mature leaf colour	0	50.00	0	0	48.90	0	0	1.11	0	
Immature leaf colour	4.54	2.27	83.0	4.54	0	0	0	0	5.00	
Abaxial leaf vein pigmentation	0	13.60	2.27	7.95	0	0	7.95	67.00	1.14	
Petiole pigmentation	9.09	0	10.20	45.50	9.09	9.09	0	6.82	10.20	
Petiole length	15.90	80.70	3.41	0	0					
Flowering ability	42.05	36.36	9.09	12.50						
Storage root shape	3.41	7.95	2.27	9.09	18.20	1.14	1.14	22.70	34.10	
Storage root defects	60.20	7.95	2.27	10.20	7.95	9.09	1.14	1.14		
Predominant skin colour	1.14	28.40	3.41	13.60	3.41	50.0	0	0	0	
Intensity of predominant skin colour	10.20	61.40	28.40							
Secondary skin colour	93.20	3.41	1.14	1.14	1.14	0	0	0	0	0
Predominant flesh colour	2.27	43.20	3.41	21.60	9.09	4.54	3.41	12.50	0	
Secondary flesh colour	62.50	0	2.27	14.77	7.95	12.50	0	0	0	0
Distribution of secondary flesh colour	63.64	1.14	23.86	1.14	5.68	0	0	4.54	0	0

Diversity and phenotypic relationships in the sweet potato collection

phenotypic classes were observed for flesh colour of the storage roots. Among them, the predominant flesh colour was cream (43.18%) followed by pale yellow (21.59%), dark orange (12.50%), dark yellow (9.09%), pale orange (4.54%), intermediate orange (3.41%), dark cream (3.41%) and white (2.27%) flesh.

The range of variation for most morphological traits (16 out of 27) varied from four to six phenotypic classes. In ascending order of phenotypic classes, these traits were: plant type (4), ground cover (4), internode length (4), vine tip pubescence (4), flowering ability (4), twining (5), general leaf outline (5), leaf lobes number (5), immature leaf colour (5), secondary skin colour (5), and secondary flesh colour (5). The other phenotypic classes are: leaf lobe type (6), central leaf lobe shape (6), abaxial leaf vein pigmentation (6), predominant skin colour (6), and distribution of secondary flesh color (6). The frequency distribution of the various phenotypic classes of these traits also differed among accessions studied (Table 3). For example, accessions had five patterns of twining in the following proportions: non-twining (14.80%), slightly twining (12.50%), moderately twining (29.50%), twining (29.50) and very twining (13.60%). Frequencies of the accessions with leaf lobe types showed the following trend: no lateral lobes (6.82%), very slight lobes (34.10%), slight lobes (3.41%), moderate (15.90%), deep (35.20%), and very deep (4.54%).

The lowest variations in the sample was found in five traits, namely, internode diameter, mature leaf size, immature leaf colour, petiole length, and intensity of predominant skin colour. These traits presented only three phenotypic classes (Table 3). Accessions producing thin diameters (4-6 mm) were the most frequent (75%); followed by those with intermediate diameters (7-9 mm; 12.5%) and very thin diameter (< 4 mm; 12.5%).

With regard to mature leaf size, a large proportion (88.60%) of the accessions exhibited a medium size (8-15 cm); while 7.95% of accessions had a small size (< 8 cm).

Only 3.41% of the accessions showed a large size (16-25 cm). Among accessions, the phenotypic variations expressed in mature leaf colour were green (50%), green with purple veins on upper surface (48.90%) and green upper purple lower (1.14%).

Most of the accessions (80.70%) produced a short petiole (10-20 cm); followed by the accessions (15.90%) with a very short petiole (< 10 cm). Only 3.41% of the accessions had intermediate petiole (21-30 cm). Concerning the intensity of predominant skin colour, the majority of the accessions expressed intermediate predominant skin (61.40%); followed by accessions with dark predominant skin (28.40%); while accessions with pale predominant skin were poorly represented (10.20%).

Multiple correspondence analysis. The magnitude of phenotypic diversity and the specific weight of the phenotypic traits, most closely linked to the first three factorial axes of the multiple correspondence analysis (MCA), are presented in the Table 4. It is clear from the scree plot of singular values (Fig. 1), the first three factors of MCA were the most appropriate for interpreting the variance explained. These factors together accounted for 36.71% of the total variance (Table 4).

Of the 138 phenotypic traits identified within the sample, 28 phenotypic traits derived from 16 characters contributed heavily to the determination of these first three factors. For multifactorial scaling solutions, usually two or three factors are interpreted. Thus, based on the first two factors accounting for 29.38% of the total variance, 22 phenotypic traits (Table 4) derived from 15 characters were the most relevant for describing the phenotypic diversity.

Hierarchically, the most discriminant phenotypic traits are listed for these two factors as follows for the first (17.32%), non-twining (for twining), 7 lobes (leaf lobes number), cream (predominant flesh colour), very short (for internode length), absent (secondary vine colour), yellow (secondary

TABLE 4. Adjusted inertia and loading of sweet potato phenotypic traits in squared cosine for the first three factors of the multiple correspondence analysis (MCA). The values in bold indicate the most discriminant phenotypic traits

	F1	F2	F3
Adjusted inertia (%)	17.316	12.063	7.332
% cumulative inertia	17.316	29.379	36.712
TNNG-1	0.466	0.001	0.001
GCOV-4	0.012	0.020	0.213
ILEN-1	0.344	0.071	0.012
PVIC-1	0.116	0.095	0.234
PVIC-6	0.057	0.211	0.083
PVIC-8	0.041	0.315	0.025
SVIC-1	0.335	0.012	0.012
SVIC-3	0.015	0.220	0.108
SVIC-7	0.236	0.141	0.087
GLOL-5	0.037	0.230	0.063
GLOL-6	0.092	0.000	0.319
LTYP-1	0.014	0.104	0.302
LTYP-2	0.208	0.022	0.028
LTYP-4	0.013	0.208	0.047
LLON-2	0.014	0.104	0.302
LLON-4	0.001	0.019	0.264
LLON-5	0.394	0.002	0.021
CLLO-3	0.255	0.100	0.018
CLLO-5	0.007	0.302	0.015
ILCO-4	0.235	0.000	0.002
ILCO-9	0.002	0.259	0.013
PPIG-9	0.000	0.528	0.080
PLGT-3	0.002	0.246	0.015
PSCO-6	0.017	0.182	0.011
PFCO-2	0.353	0.008	0.036
SFCO-1	0.273	0.005	0.101
SFCO-4	0.288	0.010	0.004
DFCO-1	0.287	0.005	0.085

TNNG = Twining (1-non-twining); GCOV = Ground cover (4-total); ILEN = Internode length (1-very short); PVIC = Predominant vine colour (1-Green, 6-mostly dark purple, 8-totally dark purple); SVIC = Secondary vine colour (1-absent, 3-green tip, 7-purple nodes); GLOL = General leaf outline (2-reniform, 5-hastate, 6-lobed, 7-almost divided); LTYP = Leaf lobe type (1-no lateral lobes, 2-very slight, 4-moderate, 6-very deep); LLON = Leaf lobes number (2-1 lobe, 4-5 lobes, 5-7 lobes); CLLO = Central leaf lobe shape (3-triangular, 5-semi-elliptic, 8-oblongate, 9-linear); ILCO = Immature leaf colour (2-green, 4-greyish, 9-purple on both surfaces); PPIG = Petiole pigmentation (3-green with purple near stem, 9-totally or mostly purple); PLG = Petiole length (3-intermediate); PSCO = Predominant skin colour (6-pink); PFCO = Predominant flesh colour (2-cream); SFCO = Secondary flesh colour (1-absent, 4-yellow); DFCO = Distribution of secondary flesh colour (1-absent, 3-broad ring in cortex)

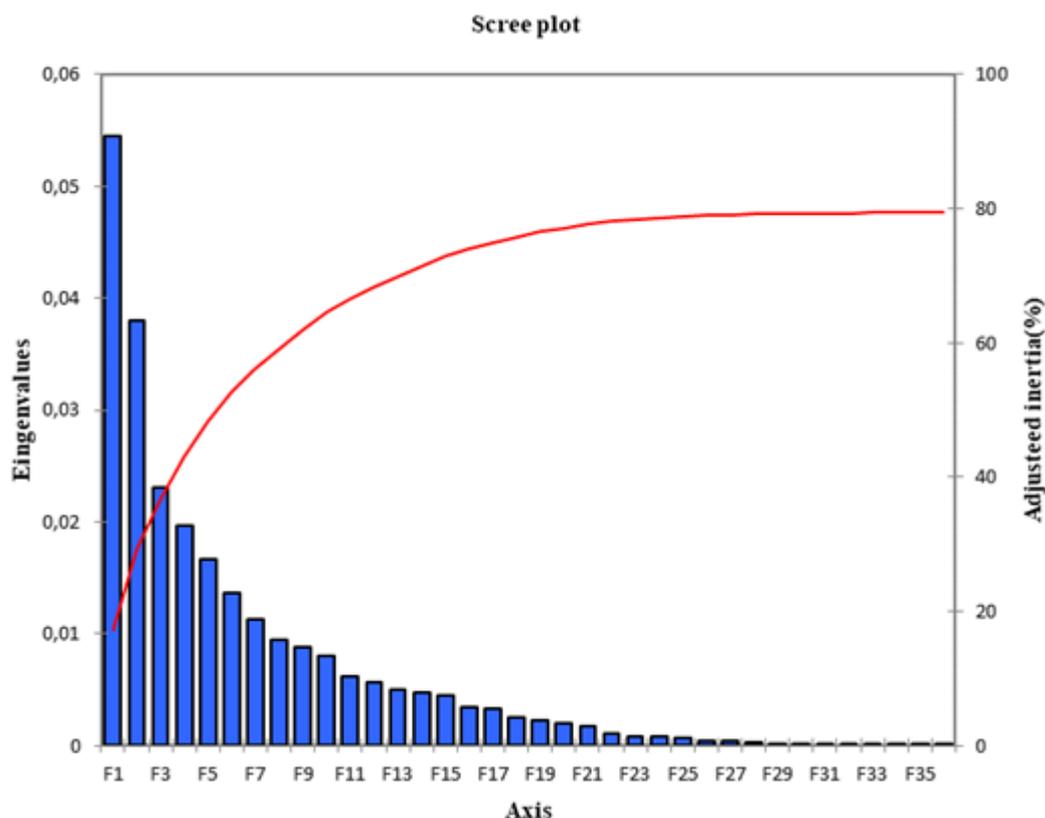


Figure 1. Scree plot of singular values for all extracted factors of sweet potato.

flesh colour). Then, absent (distribution of secondary flesh colour), absent (secondary flesh colour), triangular (central leaf lobe shape), purple nodes (secondary vine colour), greyish (immature leaf colour) and very slight (leaf lobe type) were the major phenotypic traits that were associated. For the second factor (12.06%), totally or mostly purple (petiole pigmentation), totally dark purple (for predominant vine colour), semi-elliptic (central leaf lobe shape), purple on both surfaces (immature leaf colour), intermediate (petiole length), and hastate (general leaf outline). Then, green tip (secondary vine colour), mostly dark purple (predominant vine colour), moderate (leaf lobe type), and pink (predominant skin colour) were the predominant phenotypic traits that were associated.

Hierarchical cluster analysis. Only the characters most closely linked to the MCA's were subjected to hierarchical cluster analysis. The 88 accessions were clustered regardless of their areas of origin into three clusters at dissimilarity level 150 (Fig. 2). Cluster I was the largest, comprising of 49 accessions, with 46 from Côte d'Ivoire and three introduced accessions. It consisted of 65% accessions presenting stems with purple nodes vines, 73% presenting lobed leaves, 16% with triangular leaves shape, 10% with hastate leaves shape, 65% with 5-lobed leaves, 33% with 3-lobed leaves, 55% with pink skin, 29% with cream-coloured skin and 53% with cream-coloured flesh.

Cluster II contained 13 accessions, all originating from Côte d'Ivoire. It included 92% of accessions with purple nodes vines, 77%

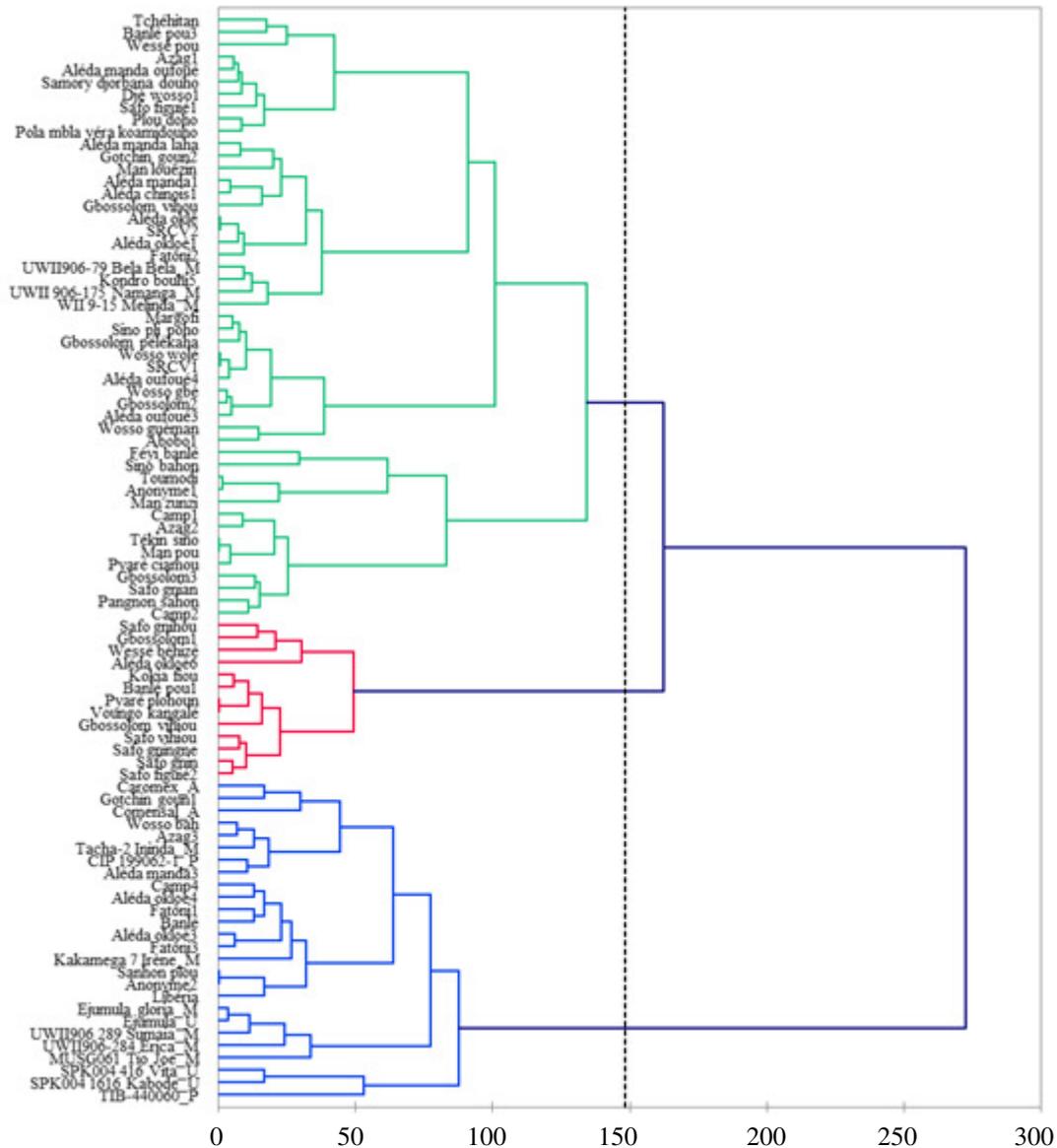


Figure 2. Dendrogram of the 88 sweet potato accessions generated by Ward clustering method using euclidean distance. Introduced accessions are followed by capital letters, M: Mozambique; A: United States of America; U: Uganda; P: Peru.

with triangular leaves, 85% with cream as predominant skin colour and 92% with cream-coloured flesh. Cluster III consists of 26 accessions including 13 from Côte d'Ivoire and 13 introduced. It contained 73% of accessions defined by stems without secondary colour, 77% comprising lobed

leaves shape, 15% with triangular leaves shape, 58% with pink skin, 35% with orange skin, 38% with pale yellow flesh, 27% with dark orange flesh. Otherwise, the similarity / dissimilarity matrix highlighted duplicates across the examined characters. For example, the accessions *Man pou* and *Tékin sino*,

Voungo kangalé and *Pyaré plohou*, *Sanhon plou* and *Anonyme2* were duplicates.

DISCUSSION

Characters evaluated can be grouped into three categories according to their degree of variation; namely strongly, moderately and weakly varied traits; with seven to nine, four to six and three phenotypic classes, respectively. Data, thus collected indicated a total of 138 phenotypic classes. Overall, the nature and number of phenotypic classes found indicate the presence of a wide range of phenotypic variation within the collection studied. For most of the characters, phenotypic variances suggest variabilities among the studied population (Dudley and Moll, 1969) and consequently, a high degree of plasticity of the species.

That would indicate great genotypic heterogeneity of the collection. Similar works have revealed considerable morphological variations within various sweet potato collections (Karuri *et al.*, 2010; Yada *et al.*, 2010; Vimala and Hariprakash, 2011; Fongod *et al.*, 2012; Su *et al.*, 2016). For an asexually-propagated species such as sweet potato, the variation observed would be the result of somatic mutation (Karuri *et al.*, 2010); or both farmers and natural selection. Despite genetic factors, the variability in cultivated species may result from artificial selection under diverse environments such as edaphic factors and geographical origins (Geleta and Labuschagne, 2005; Lule *et al.*, 2012).

The results obtained showed for each examined trait, an irregular distribution of phenotypic frequencies with a high occurrence of some phenotypic traits among accessions. The highest frequencies came mainly from 17 phenotypic traits, namely short (internode length), thin (internode diameter), purple nodes (secondary vine colour), lobed (general leaf outline), medium (mature leaf size), five lobes (leaf lobes number), green (mature leaf colour), green with purple edge (immature leaf

colour), and all veins mostly or totally purple (abaxial leaf vein pigmentation). Also, short (petiole length), absent (storage root defects), pink (predominant skin colour), intermediate (intensity of predominant skin colour), absent (secondary skin colour), cream (predominant flesh colour), absent (secondary flesh colour) and absent (distribution of secondary flesh colour). Among them, the preponderance of five-lobed leaves, green leaves and pink skin accessions was in complete agreement with previous studies (Daros *et al.*, 2002; Veasey *et al.*, 2007; Moulin *et al.*, 2012). The wide distribution of all these remarkable phenotypic traits, suggests a preponderance of genetically closer accessions in the CNRA collection.

Leaf shape and colour, as well as the storage root skin colour, are easily perceptible to farmers and could be the main criterion to distinguish the varieties under cultivation. The large number of accessions presenting these remarkable phenotypic traits, indicates that these are the most widespread in Côte d'Ivoire. Indeed, lobed-leafed varieties are mainly valued for their leaves that are eaten as leaf vegetable. Consumers' preferences would have spanned their widest distribution across the country. Thus, the predominant phenotypic traits recorded in the collection may result from deliberate selections by local farmers.

Storage roots are the most important part of the sweet potato. The accessions showed a high phenotypic variation with respect to shape, storage root defects, and skin and flesh colours, among accessions studied (Table 3). These results suggest that the phenotypic traits of the storage roots can also be good markers of varietal selection. However, smooth storage roots are preferred over those that are cracked, rough and wrinkled because they are easy to peel and wash (Nwankwo *et al.*, 2015).

Creamy flesh accessions, with high dry matter (Yada *et al.*, 2010) were abundant, unlike yellow or orange flesh accessions, which were nutritionally richer. This situation could be explained again by the constant selection made by the farmers for these

varieties. Indeed, according to Tairo *et al.* (2008), leaf outlines and colours of the storage and flesh roots are criteria of farmers' choice. Furthermore, the predominant phenotypic traits (absence of secondary skin colour) found in sample would probably result from the propagation of a limited number of varieties. That would be the case of an introduced variety such as Ejumula, for example. Traditionally, exchanges of plant materials between farmers is done according to their needs and choice; and this process of gene flow is easier with the seeds than vine cuttings. Propagation of common sweet potato varieties across the country could be due to farmers or national agencies responsible for the distribution of food crop seeds.

In most angiosperms, flower and flowering are respectively an organ and a physiological state extremely useful in selection schemes. Considerable differences were also recorded between accessions studied; with regard to the intensity of flowering. Some accessions did not produce flowers. Some had sparse flowering; while others had moderate or profuse flowering. These observations also agree with the findings of Mok and Schmiediche (1999) and Yada *et al.* (2010), who reported divergences of sweet potato accessions in their flowering ability. This ability may be related to genotype or environmental conditions (Huamàn *et al.*, 1999), or genotype-environment interactions. According to Amoatey *et al.* (2016), the ability to flower could be an excellent indicator for identifying different varieties and duplicates in a given collection. Thus, this ability offers opportunities for sexual hybridisation in conventional breeding programmes (Ngailo *et al.*, 2013).

Kitahara *et al.* (2007) reported that sweet potato breeding is limited by its sterility and cross-incompatibility. Moreover, the presence of flowering accessions in the three genetic groups would allow to make a quick identification of parents, which may be included in the artificial crossings in order to

breed superior varieties with desirable traits. The heterozygotic botanical seeds that could result from both artificial and natural crossing could be used for other purposes such as conservation, distribution and documentation. Trinh *et al.* (1999) reported that they can be considered as an acceptable way of long-term genetic conservation.

The physiological and morphological variations expressed in this study, demonstrate that local climatic conditions should be taken account in all conservation and improvement strategies involving sweet potato landraces.

Elucidation of discriminant characters in a basic collection is a crucial step for breeders to start any breeding and conservation programme. Multiple correspondence analysis (MCA) is a useful tool to identify discriminant variables and uncovering the relationships among categorical variables (Sourial *et al.*, 2010); like those analysed in this study. According to the first three factors of MCA, 15 characters out of the 27 examined were the most discriminant; and as a result allowed a clear description of the phenotypic diversity of the investigated collection. Moreover, considering the first two factors, only 22 phenotypic traits derived from 15 characters were the most relevant elucidating phenotypic diversity. This implies that future characterisation of local germplasm should be limited to a reduced number of characters.

In this research, we observed that leaves had discriminant phenotypic traits relevant in according to the first two principle components, followed by vines and storage roots. Indeed, the leaf shape and colour as well as the vine colour and the storage root skin colour were the most remarkable phenotypes. It was also reported that leaf shape was one of the mainly markers of differentiation in sweet potato diversity (Karuri *et al.*, 2010).

The existence of wider phenotypic variation within the material investigated was further confirmed by the MCA (Table 4). The first two MCA's factors explained 29.37% of the total phenotypic variability. According to Lule

et al. (2012), the degree of genetic diversity among cultivated crops depends on their reproductive mode. For a vegetative-propagated crop like sweet potato, the magnitude of variability observed shows that the current collection has high potential for developing new varieties.

Therefore, determining the relationships between plant traits for a given collection is an important strategy for ensuring efficient and sustainable breeding programmes. Indeed, many economically important plant traits are generally related to each other, in one or various ways (Chakravorty *et al.*, 2013). Another advantage of the MCA is that it helps to describe patterns of relationships distinctively between analysed characters.

Associations observed between these phenotypic traits may be useful for varietal improvement in the species. However, breeding programmes must result in genotypes providing high yields, with qualitative traits acceptable to consumers (Kays and Wang, 2002). A strong heritability of the qualitative characters that showed significant relationships would be interesting in the future breeding programmes. Although a particular plant accession or variety can be distinguished from qualitative traits easily, quantitative traits are the most interesting given their importance in improving yields. For selection purposes, additional studies need to be performed to confirm whether these associated qualitative characters show significant relationships with those related to yield, especially in terms of quality and number of storage roots. In this context, identifying groups of genotypes with complementary characters of interest would be helpful. Thereafter, cluster analysis allows to distinguish clearly groups within the germplasm studied. Accessions were clustered into three genetic groups and a number of subgroups (Fig. 2), indicating the presence of numerous genetically distinct accessions in the local collections. These groups of accessions within collection could be useful for ensuring

efficient breeding programmes (Bozokalfa *et al.*, 2009).

In addition, the distribution of accessions from different origins into the three groups regardless of their geographical origin, suggests not only that genetic diversity was not related to geographical origin, but also high exchanges of plant materials between different growing regions of sweet potato were important. Nevertheless, the most common accessions in the collection were clustered into group I which is mainly composed of local accessions from various growing-regions, suggesting that the local varieties are widely grown in the country. In the first and third groups, local accessions and some introduced lines were grouped together. That confirms the presence of genetically distinct local accessions, which are closely similar to the introduced varieties in their morphological traits. The affinity of local accessions with introduced varieties, could be explained by the equal high agronomic potential of local accessions or the degeneration of the introduced varieties (Adikini *et al.*, 2015; Gibson and Kreuze, 2015) due to their long cultivation under local environmental conditions. Local accessions of sweet potato with these remarkable agronomic performances could be useful in breeding programmes and various phytotechnical routes to improve yields.

The dendrogram in Figure 2 shows that accessions with similar local names differed in their morphological characteristics. Conversely, accessions with different names appeared morphologically very close suggesting the presence of duplicates in the sample collection. According to Trinh *et al.* (1999), collection of duplicate samples occurs when a variety is grown for a long time simultaneously in several places. The presence of duplicates with different names in the collection could also be attributed to the socio-cultural or ethnolinguistic diversity or culinary preferences of farmers from whom the

accessions were collected. Also, the farmers' perception of local sweet potato diversity is not always linked to phenotypic traits.

Thus, the HCA may be an effective first step for solving problems of similar local naming and duplicates that could occur during collecting trips, as reported by Tairo *et al.* (2008). Identifying duplicates in a collection is essential to maintain a reasonable size of germplasm to manage over the long-term. Hence, expanded collecting trips and reliable phenotypic selections resulting from trials in multiple locations and over several years would be supplemented with adequate molecular markers. This could help to maintain a useful core collection for the breeding programmes.

CONCLUSION

The results obtained reveal a wide range of phenotypic variability within the Centre National de Recherche Agronomique's sweet potato collection, and consequently, notable differences among most traits studied. Multiple correspondence analysis showed a relatively high level of phenotypic diversity and highlighted important relation between characters that can help to design breeding schemes. Cluster analysis enabled to distinguish three specific genetic groups showing phenotypic differences based mainly on twining, leaves shape, vine and storage roots colour. In addition, the presence of genetically distinct native accessions that are morphologically close with introduced accessions were observed. Although, morphological characterisation allowed to identify duplicates, local sweet potato germplasm constitute an important source of genetic variation for future breeding programmes. Findings are expected to have direct implications to improve national collection and conservation strategies. For that molecular studies must supplement morphological characterisation due to the genetic complexity of this plant.

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