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Phenotypic profiles of different accessions of sweet potato (*Ipomoea batatas* L. Lam) in the coastal savanna agro-ecological zone of Ghana

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Twenty accessions of sweet potato (*Ipomoea batatas* L. Lam) cultivated under rain-fed conditions were evaluated based on their agromorphological traits to assess diversity in yield, morphology and other key agronomic characteristics of the accessions under study. The accessions consisted of 13 local and 7 exotic breeding lines grown in the research farm of the Biotechnology and Nuclear Agriculture Research Institute during the rainy and dry seasons of 2011. The Randomised Complete Block Design (RCBD) was used with four replicates. Results indicate high genetic variability among the 20 accessions based on the agromorphological and yield characteristics. The exotic accession (US 020) recorded the highest total root yield and harvest index of 56.32 t/ha and 57.11%, respectively, indicating its superiority over the local accessions. Two accessions (ER 001 and HMA 2) were found to be possible duplicates. This study provides valuable information that can be utilised in a breeding programme to ameliorate local clones of sweet potato in Ghana.

Key words: Sweet potato, accessions, agromorphological characteristics, harvest index, total root yield, percent dry matter, Ghana.

INTRODUCTION

Sweet potato (*Ipomoea batatas* L. Lam), is a hexaploid (2n = 6x = 90), and usually considered the only species of economic significance within the genus *Ipomoea* (Sossah et al., 2014; Zhang et al., 2000). Sweet potato is

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generally cultivated for its tuberous roots and leaves, useful for human consumption, animal feed and for industrial purposes (Lebot, 2009). Sweet potato is the world's seventh most important food crop after wheat, rice, maize, potato, barley and cassava, and second most important tuber crop after cassava with a yearly production of 106 million tonnes (FAOSTATs, 2010; Loebenstein, 2009; Hijmans et al., 2001). It is widely adapted in the tropics, sub-tropical and warm temperate regions and is easily propagated in both high and low input agricultural systems (Kapinga et al., 1995). In Ghana, sweet potato cultivation and consumption are very prominent (Otoo et al., 1995) and rapidly becoming more important attributable to its high yielding ability, high energy and nutrient content, especially vitamin A in orange-fleshed and its capacity to grow on marginal soils (Sossah et al., 2014).

With annual production of 0.13 million tonnes in 2010, Ghana ranks the fourth largest producer of sweet potato in West Africa (Food and Agricultural Organisation (FAO), 2010) with an extensive production at almost all agro-ecological zones in the country, yielding 1.75 t/ha on average per annum. However, low yields are realised by Ghanaian farmers with poor quality of produce occasioned by the paucity of high-yielding varieties, pests and diseases infestation (especially viruses), fluctuating agro-climatic conditions and poor agronomic practices (Sossah et al., 2014; Ndunguru et al., 2009; Otoo et al., 2001). Previous improvement programmes in the country has been limited to evaluation of local and exotic varieties at different agro-ecological regions, which led to the release of 8 varieties (6 white and 2 orange-fleshed) to farmers with enhanced attributes for food quality and marketability (Akoroda, 2009; Otoo et al., 1995, 1998). These locally ameliorated genotypes offers higher yields, but these qualities have declined over the years particularly in the face of change in climate in the local agroecology. Moreover, considerable variation of local names has characterised naming of both local and released genotypes (Sossah et al., 2014).

Agromorphological characterisation is an important first step in the assessment of genetic diversity in crops including sweet potato (Amoatey et al., 2015; Ahiakpa et al., 2013). Major variation has been reported in the vine, leaf, flower and storage root characteristics (Tairo et al., 2008; Tsegaye et al., 2007). Several other researchers have used morphological and agronomic characters to distinguish between and among sweet potato accessions, assess comparative reaction and susceptibility to pests, diseases and other stress factors resulting from change in climate and appraise genetic variability (Elameen et al., 2011; Yada et al., 2010; Tairo et al., 2008; Tsegaye et al., 2007; Veasey et al., 2007). Morphological characters are easy to study, relatively cheap to evaluate and can be visually detected. Agromorphological characterisation is not only useful in describing each accession but potentially useful for clonal identification and estimation of genetic distance (Ahiakpa et al., 2013; Elameen et al., 2011); therefore, the need to characterise existing local and introduced accessions of sweet potato, identify duplicate accessions and evaluate their phenotypic diversity for effective utilisation in breeding programmes.

MATERIALS AND METHODS

Study site

The study was conducted at the research farm of Nuclear Agriculture Research Centre, Biotechnology and Nuclear Agriculture Research Institute (NARC-BNARI) of the Ghana Atomic Energy Commission (GAEC), during the minor and major seasons of 2011. The study site is located at 05°40′ N, 0° 13′ W, 76 m above sea level within the Coastal Savannah agro-ecological zone of Ghana. The soil at the site is the Nyigbenya-Haatso series, which is a typically well-drained savannah Ochrosol (Ferric Acrisol) derived from quartzite Schist (FAO/UNESCO, 1994). The maximum and minimum average temperatures for the period of the study were 30.7 and 23.2°C, respectively, with mean annual rainfall and relative humidity of 220 mm and 40.54%, respectively (Local Weather Station, 2012).

Germplasm assembly

A total of twenty (20) accessions of sweet potato were collected for the study comprising 13 local and 7 new introductions from Cuba, South Africa, United Kingdom, and United States of America (Table 1).

Experimental design and layout

A total land area of 70 m x 39 m was ploughed, harrowed to turn the soil, break the soil clods, and provide a fine tilth. Ridges were made with a ridge size of 0.7 m and 0.8 m distance between ridges. A plot consisted of one row (ridge) of 8 m. The Randomised Complete Block Design (RCBD) was used with four replicates consisting of 20 plants. The planting distances were 0.4 m within rows and 1 m between centres of the ridges. Each replicate was separated by a 2 m path from the other. Cultivation of the plants were done manually. Weed control was done manually by hoe. No fertilisers or pesticides were applied. The study was done under rain fed conditions.

Data collection

Morphological characters of all the 20 accessions were scored using CIP-standard descriptors of sweet potato (Hijmans, 1991). A total of 37 characters (25 aerial and 12 storage root characters) were evaluated for each accession (Table 2) and scored using a scale of 0-9 at 90-120 days after planting.

Data recorded for aerial parts were average expressions of characters of at least 3 leaves, 3 internodes located in the middle portion of the main stem for 3 plants. Storage root descriptors were recorded considering the most representative expression of the character shown in medium-to large sized storage roots of five plants. Agronomic traits recorded include Root Form (RF), degree of Damage of Storage Roots (DaMR), Weevil Damage at First Evaluation (WED1), Percent Dry Matter (%DM), Number of Non-Marketable (small) Roots (NSR), Number of Marketable (large) Roots (NLR), Weight of Non-Marketable (small) Roots (WSR), and

Table 1. Name and collection sites of Sweet potato genotypes used in the study.

Accessions	Source	Type
CR001	Ghana (Central Region)	Local
CR002		
ER 001	Ghana (Eastern Region)	
FREEMA	Ghana (Greater Accra Region)	
HMA1		
HMA2	Ghana (Volta Region)	
HMA3	Ghana (Greater Accra Region)	
LOCAL 1		
LOCAL 2		
UE 007	Ghana (Upper East Region)	
CRI001	Ghana (Ashanti Region)	
CRI027		
CRI 054		
DOAK 08-007	Cuba	Introductions/exotic
CEMSA 74-228		
SA/BNARI	South Africa	
UK/BNARI	UK	
US 004	USA	
US 020		
US 029		

Table 2. Agromorphological characters used for evaluating the 20 accessions of sweet potato.

Plant organ	Characters scored
Vine	Plant type (PTY), vine internode length (VIL), vine internode diameter (VID), predominant colour of vine (PVC), and secondary colour of vine (SVC).
Leaf	General outline of leaf (GOL), leaf lobe type (LLT), leaf lobe number (LLN), shape of central leaf lobe (SCLL), mature leaf size (MLS), abaxial leaf vein pigmentation (ALVP), mature leaf colour (MLC), immature leaf colour (ILC), petiole pigmentation (PP), and petiole length (PL).
Flower	Flower (FLR), flower colour (FCL), flower length (FL), flower width (FW), shape of limb (SLB), sepal shape (SS), sepal apex (SA), sepal colour (SLL), colour of stigma (CST), colour of style (CSL), stigma exertion (SE).
Storage root	Storage root arrangement (SRA), storage root shape (SRS), storage root defects (SRD), predominant skin colour (PSC), intensity of predominant skin colour (IPC), secondary skin colour (SSC), predominant root flesh colour (PFC), secondary flesh colour (SFC), distribution of secondary flesh colour (DSF).
Agronomic traits	Root form (RF), Damage of storage roots (DaMR), Weevil damage at first evaluation(WED1), percent dry matter (%DM), number of small roots per plant (NSR/P), number of large roots per plant (NLR/P), weight of small roots (WSR), weight of large roots (WLR).

Source: Huamán (1991).

Weight of Marketable (large) Roots (WLR). A number of variables, which are useful in evaluating the performance of clones, were calculated from the raw data of the agronomic traits. These include Percent of Plants without Storage Roots (%PWSR), Large Root Yield (LRY) (t/ha), Small Root Yield (SRY) (t/ha), Total Root Yield (TRY) (t/ha), Foliage Yield (FY) (t/ha), Root Dry Matter Yield (RDMY) (t/ha), Fresh Biomass Yield (t/ha), Number of Large Roots Per Plant (NLR/P), Number of Small Roots Per Plant (NSR/P) and Harvest Index (HI).

Determination of storage root dry matter (DM) content was done according to the method described by Carey and Reynoso (1999) using an oven and a balance with an accuracy of 0.1 g. To avoid post-harvest changes in DM content prior to DM determination, initial steps were done within 24 h after harvest. Medial sections of 3 undamaged market-size roots were chopped into small flakes and mixed thoroughly out of which a 150 g sample was taken for the next step. The samples of 150 g fresh weight were placed in paper bags and dried at 60°C for 72 h to a stable weight. The dried samples were weighed and the resulting value used for estimating dry matter content as

$$\%DM = \frac{Dry\ weight}{Fresh\ weight} \times 100\ \%$$

Table 3. Variability in agromorphological characters and percentage of accessions in each class.

Character	Score	% Accessions	Character	Score	% Accessions	Character	Score	% Accessions	Character	Score	% Accessions
	3	5		1	10		0	10		1	55
	5	25		3	40		1	5		3	45
	7	45		5	35		2	10			
	9	25		7	15		3	5			
PTY			LLN			SRS	4	15	VIL		
							5	30			
							7	5			
							8	10			
							9	10			
	1	20		0	25		1	40		1	5
	2	20		1	5		3	25		2	15
	3	15		3	25		4	10		3	20
SCLL	4	30	SRD	4	10	PVC	6	20	ILC	6	35
	5	15		5	25		8	5		7	5
				6	5					8	5
				7	5					9	15
	0	25		1	15		2	25		0	10
	1	10		3	35		3	5		2	35
SVC	2	25	PP	4	30	ALVP	5	5	PSC	5	5
	5	20		8	10		6	5		6	20
	6	20		9	10		7	15		8	30
							8	45			
	3	45		0	10		1	40		0	10
	4	15		1	10		3	35		1	5
	5	5		2	20		5	10		3	45
GOL	6	35	PFC	4	35	LLT	7	15	SRA	5	40
				6	5						
				7	10						
				8	10						

*Values in the score column represent the scores for each character evaluated. PTY = plant type; LLN = leaf lobe number; SRS = storage root shape; VIL = vine internode length; SCLL = shape of central leaf lobe; SRD = storage root defects; PVC = predominant colour of vine; ILC = Immature leaf colour; SVC = secondary colour of vine; PP = petiole pigmentation; ALVP = abaxial leaf vein pigmentation; PSC = predominant skin colour; GOL = general outline of leaf; PFC = predominant root flesh colour; LLT = leaf lobe type; SRA = storage root arrangement.

Statistical data analyses

Correlation analysis was performed to delineate the degree of association among the accessions. Furthermore, the principal components analysis (PCA) was done to assess the percentage contribution of each trait to total genetic variation among the accessions. Cluster analysis based on similarity matrices (CLA) was also employed to assess the relatedness among the accessions. All the data collected were analysed for variation in each character scored. The General statistical package (Genstat, ver. 9.2), Statgraphics Plus (XV.I) were used for the Analysis of Variance (ANOVA) and Duncan Multiple Range Test (DMRT) for mean separation. Microsoft Excel was used for collation of all data gathered.

RESULTS AND DISCUSSION

Variation in quantitative traits among the 20 sweet potato accessions

Table 3 shows 16 qualitative traits exhibiting most variation in the collection. The accessions exhibited significant variation with respect to 15 characters. Vine internode length (VIL) exhibited the least variability with 55% of the accessions being very short and 45% short. Five characters, plant type (PTY), general leaf outline (GOL), type of leaf lobe (LLT), number of leaf lobes (LLN)

and storage root arrangement (SRA) exhibited four classes of variability in all the 20 accessions studied. The rest of the characters had classes ranging from five to nine. Storage root shape (SRS) displayed the highest number of variation consisting of nine classes in all the accessions. The numbers in the score column represent the scores for each character (Table 3) and the percentages refer to percentages of accessions per score. Thus, high level of genetic diversity was exhibited in the sweet potato accessions. Some morphological characters were highly variable among the accessions studied. The high variability in morphological traits by the 20 sweet potato accessions are consistent with reports by Elameen et al. (2011), Yada et al. (2010), Vimilar and Hariprakash (2010), Tsegaye et al. (2007), Veasey et al. (2007) and Islam et al. (2002) who recorded significant variations in VIL, PTY, GOL, LLT, LLN and SRA in sweet potato.

General leaf outline were cordate (45%), triangular (15%), hastate (5%) and lobed (35%) confirming reports by Yada et al. (2010), Tsegaye et al. (2007) and Veasey et al. (2007). According to Yada et al. (2010), the lobed leaves could perhaps be an adaptation for decreasing insect pest damage. Only 45% of the accessions flowered, with variation in stigma exertion ranging from inserted (stigma shorter than the longest anther), same height as highest anther, slightly exerted, to exerted (stigma longer that the longest anther). Similarly, Veasey et al. (2007) reported that, sweet potato cultivars vary in their ability to flower, and some cultivars may not flower or produce very few flowers, whereas others flower profusely under normal field conditions. The variation in stigma exertion can be ascribed to the occurrence of heterostyly in sweet potato, which probably reinforces the self-incompatibility system within the crop, useful as morphological marker in inheritance studies (Vimilar and Hariprakash, 2010).

The predominant skin colour were cream (35%), brownish orange (5%), pink (20%), and purple red (30%). 10% of the accessions failed to produce storage roots. Similarly, flesh colour also ranged from predominantly white to dark orange with 10% of the accessions unable to produce storage roots. The colour of root skin and flesh colour is determined by pigments such as carotenoids and anthocyanin, the combination of which produces different skin and flesh colour depending on the cultivar (Vimilar and Hariprakash, 2010; Gasura et al., 2008). These traits could be controlled by several genes with epistatic interactions and complementary gene actions as reported by Gasura et al. (2008). On the other hand, 8 classes of storage root shape was detected. 30% of the accessions were obovate, 5% were round, 10% were round elliptic, 5% were elliptic, 15% were ovate, 5% were long oblong, 10% were long elliptic and 10% long irregular or curved; as 10% of the accessions had no storage roots. The presence of numerous intermediate in storage root shape clearly reveals incomplete dominance as well as occurrence of multiple alleles for this trait. This may have accounted for this observation which is consistent with report by Vimilar and Hariprakash (2010).

Variability in quantitative traits among the 20 accessions of sweet potato

Table 4 shows the performance of 20 sweet potato accessions evaluated based on 11 quantitative traits. The accessions revealed significant variation with respect to the 11 traits evaluated. The percent of plants without storage root (%PWSR) was highest in CR 002 (a local accession) followed by the introduced accession CRI 027 with significant difference (Table 4). However, differences in percent of plants without storage roots (%PWSR) for all the other accessions were not statistically significant. The highest large root yield was observed in US020 (an introduced accession) (46.88 t/ha), followed by FREEMA (local accession) (27.90 t/ha) and UK/BNARI (introduced accession) (23.48 t/ha) while the lowest were CR002 (0), CRI027 (1.97 t/ha) and DOAK.08-007 (3.48 t/ha). However, the highest and lowest small root yields were recorded in Local 2 (25 t/ha) (local accessions) and CR002 (0.0t/ha), respectively.

US 020 produced the highest total tuber yield which was significantly different from those of FREEMA, Local 2 and UK/BNARI. Conversely, FREEMA yielded significantly higher total root yield than UK/BNARI while Local 2 was not statistically significant compared to the rest of the accessions. Two accessions (CR 002 and CRI 027) which gave the lowest total root yield also recorded the highest foliage yield of 157.13 t/ha and 84.19 t/ha, respectively. The foliage yield of FREEMA, Local 1, UE 007, DOAK.08-007, UK/BNARI, US 020 and US 029 were high but not significantly different from one another. The fresh biomass for all the accessions ranged from 29.66 t/ha-57.13 t/ha, with no significant differences among HMA 2, HMA 3, UE 007, US 029, SA/BNAR and US 004. FREEMA produced the highest number of large roots per plant (1.44) followed by Local 2 and UE 007 at 1.38 and 1.19, respectively. There were no significant differences in the number of large roots among most of the accessions. Also, CR 001 had the highest mean score for number of small roots per plant (4.31) followed by HMA 2 (3.44) and UK/BNARI (3.0). There was no significant difference in the number of small roots among most of the accessions under study.

ER 001 recorded the highest dry matter (36.65%) with corresponding increase in root dry matter yield. In contrast, UK/BNARI had the least dry matter content (14.79%) with parallel decrease in root dry matter yield. US 020, UK/BNARI, US 004, FREEMA, SA/BNARI and Local 2 recorded high harvest indices (57.11, 49.47, 46.51, 45.07, 44.37 and 40.29%, respectively). However, there was no significant difference between harvest indices for FREEMA and any of SA/BNARI, Local 2, UE

Table 4. Variability in quantitative traits among 20 accessions of *Ipomoea batatas* L.

Accessions	%PWSR	LRY (t/ha)	SRY(t/ha)	TRY (t/ha)	FY (t/ha)	FB (t/ha)	NLR/P	NSR/P	%DM	RDMY (t/ha)	HI (%)
CR001	6.25^{c}	12.06^{bcde}	12.01^{abc}	24.06^{bcdef}	67.93^{bcd}	91.99^{bc}	0.56^{bcde}	**4.31^{a}**	32.34^{bcde}	7.65^{bcde}	24.08^{cdefg}
CR002	**100.00^{a}**	0.00^{e}	0.00^{c}	0.00^{f}	**157.13^{a}**	**157.13^{a}**	0.00^{e}	0.00^{e}	0.00^{i}	0.00^{e}	0.00^{h}
ER001	12.50^{c}	2.90^{de}	11.92^{abc}	14.82^{ef}	60.43^{bcde}	75.25^{cdef}	0.19^{de}	2.75^{acbd}	**36.65^{a}**	5.46^{de}	18.68^{efgh}
FREEMA	6.25^{c}	27.90^{b}	16.99^{ab}	44.89^{ab}	41.29^{defgh}	86.18^{bcd}	1.44^{a}	1.81^{bcde}	31.99^{bcde}	14.17^{abc}	45.07^{abcd}
HMA 1	6.25^{c}	14.73^{bcde}	13.10^{abc}	27.83^{bcde}	54.24^{bcdef}	82.07^{bcde}	0.63^{abcde}	3.44^{ab}	32.18^{bcde}	9.318^{bcd}	32.92^{bcde}
HMA 2	0.00^{c}	8.93^{cde}	5.16^{bc}	14.09^{ef}	48.66^{cdefg}	62.75^{cdefg}	0.88^{abcd}	1.81^{bcd}	30.70^{cdef}	4.28^{de}	26.56^{bcdef}
HMA 3	6.25^{c}	8.93^{cde}	10.62^{abc}	19.55^{cdef}	54.24^{bcdef}	73.79^{cdefg}	0.94^{abcd}	1.74^{bcde}	34.89^{ab}	6.81^{cde}	23.42^{cdefgh}
LOCAL 1	12.50^{c}	7.37^{cde}	3.14^{bc}	10.51^{ef}	34.49^{defgh}	44.99^{defg}	0.38^{cde}	1.44^{cde}	30.34^{def}	4.62^{de}	19.51^{efgh}
LOCAL 2	18.75^{c}	17.99^{bcde}	**25.00^{a}**	42.98^{abc}	80.73^{bc}	123.72^{ab}	**1.38^{ab}**	1.46^{cde}	34.61^{abc}	15.15^{ab}	40.29^{abcde}
UE007	0.00^{c}	19.74^{bcd}	4.36^{bc}	24.00^{bcdef}	35.76^{defgh}	59.76^{cdefg}	1.19^{abc}	2.38^{abcd}	27.37^{fg}	6.73^{cde}	36.67^{abcde}
CRI001	6.25^{c}	8.57^{cde}	6.80^{bc}	15.38^{def}	20.57^{fgh}	35.94^{fg}	0.50^{cde}	2.13^{bcd}	31.09^{bcdef}	4.74^{de}	39.31^{abcde}
CRI027	75.00^{b}	0.00^{e}	1.97^{bc}	1.97^{f}	84.19^{b}	86.16^{bcd}	0.00^{e}	0.81^{de}	0.00^{i}	0.00^{e}	2.42^{gh}
CRI054	0.00^{c}	2.23^{de}	5.25^{bc}	7.49^{ef}	24.11^{fgh}	31.60^{fg}	0.44^{cde}	2.13^{bcd}	26.03^{g}	1.98^{de}	25.40^{cdefg}
DOAK 08-007	18.75^{c}	0.00^{e}	3.48^{bc}	3.48^{ef}	40.18^{defgh}	43.66^{defg}	0.00^{e}	1.68^{bcde}	32.35^{bcde}	1.02^{e}	7.23^{fgh}
CEMSA 74-228	18.75^{c}	7.37^{cde}	2.65^{bc}	10.00^{ef}	27.99^{efgh}	38.00^{efg}	0.50^{cde}	1.56^{bcde}	33.32^{abcd}	3.42^{de}	26.85^{bcdef}
SA/BNARI	0.00^{c}	9.38^{cde}	6.02^{bc}	15.40^{def}	14.27^{h}	29.66^{g}	0.81^{abcde}	1.81^{bcde}	24.44^{g}	3.81^{de}	44.37^{abcd}
UK/BNARI	0.00^{c}	23.48^{bc}	16.65^{ab}	40.13^{abcd}	41.03^{defgh}	81.16^{bcde}	0.75^{abcde}	3.00^{abc}	14.79^{h}	5.95^{de}	49.47^{ab}
US004	18.75^{c}	10.18^{bcde}	4.56^{bc}	14.73^{ef}	15.40^{gh}	30.13^{g}	0.94^{abcd}	0.88^{de}	34.32^{abcd}	5.26^{de}	46.51^{abc}
US020	0.00^{c}	**46.88^{a}**	9.44^{bc}	**56.32^{a}**	36.16^{defgh}	92.48^{bc}	0.94^{abcd}	1.19^{cde}	33.07^{abcd}	**18.29^{a}**	**57.11^{a}**
US029	0.00^{c}	8.26^{cde}	4.65^{bc}	12.91^{ef}	35.49^{defgh}	48.40^{cdefg}	0.44^{cde}	2.31^{bcd}	28.43^{efg}	3.56^{de}	22.08^{defgh}
Mean	15.30	11.80	8.20	20.00	48.70	68.70	0.644	1.93	27.45	6.11	29.40
P value	***<.001***	***<.001***	***0.048***	***<.001***	***<.001***	***<.001***	***0.004***	***0.015***	***<.001***	***<.001***	***<.001***
STD	26.01	11.27	6.49	15.38	32.13	33.32	0.43	0.96	10.53	4.88	16.85
CV (%)	117.50	40.20	75.20	57.30	15.50	21.60	35.60	30.30	3.20	59.70	38.60

Means in the same column followed by the same letter are not significantly different at P ≤ 0.01. %PWSR = Percent of plant without storage roots; LRY = Large root yield; SRY = Small root yield; TRY = Total root yield; FY = Foliage yield; FB = Fresh Biomass; NLR/P = Number of large roots per plant; NSR/P = Number of small roots per plant; DM = percent dry matter; RDMY = root dry matter yield; HI = Harvest Index.

007 and CRI 001, HMA 2 and CEMSA 74-228, and CR001 and CRI 054. Most of the accessions had harvest indices ranging from 18 to 27%. Similarly, other workers, Tumwegamire et al. (2011) and Laurie (2010) recorded high coefficient of variations (CV). The CV values obtained in this study were however higher than those by Otoo et al. (2001) except percent dry matter (%DM) and fresh biomass (FB). Caliskan et al. (2007), Abidin et al. (2005), Grüneberg et al. (2005) all reported varying CVs and attributed this to high sensitivity of sweet potato to environmental variations as affirmed in this current study. Also, many authors have reported the presence of significant genotype x environment (G X E) interactions in the crop in both yield and quality traits (Caliskan et al., 2007; Abidin et al., 2005; Grüneberg et al., 2005). The implication of high CV or the presence of significant G X E interaction is useful to the plant breeder to develop widely or specifically adapted genotypes and/ or diversify resources for yield and

auxiliary qualities (Grüneberg et al., 2005).

Accession CR 002 had the highest percentage of plants without storage roots. US 020 recorded the highest total root yield (TRY) (56.23 t/ha) followed by FREEMA (44.89 t/ha). A high percentage of plants without storage roots may be attributed to lack of adaptation or lateness of a clone (Carey and Reynoso, 1999). FREEMA also recorded the highest number of large roots per plant (1.44) while CR 001 recorded the highest number of small root per plant (4.31). These results are consistent with those by Ssebuliba et al. (2006) who reported higher number of plants per root for local accessions compared to introduced orange-fleshed varieties. Total root yield for most of the accessions are much higher than those evaluated by Otoo et al. (1995, 2001). Gasura et al. (2008) reported that root yield depends on the number of storage roots per plant. Therefore, tuber number could be useful for estimating yielding potential of given cultivars. In sweet potato, large numbers of small roots may indicate potential for higher yields at later harvests (Carey and Reynoso, 1999). The total root yield for the local accessions were generally higher than the introduced accessions. This may be attributable to the adaptability of the landraces to the local environment.

At large, the local accessions produced higher foliage yield (FY) and fresh biomass (FB) than the introduced accessions. CR 002 recorded the highest foliage yield (FY) and fresh biomass (FB) (157.13 t/ha) but with no storage roots even after 170 days after planting. Similarly, Tairo et al. (2008) and Lebot (1986), recorded high foliage yield (FY) with no storage roots after 180 days post-planting. Generally, accessions with the highest foliage yield (FY) produce lower total root yields (TRY). This may be ascribed to variances in rate of photosynthate translocation to storage roots ensuing in yield differences among the accessions. CR 002, CRI 027 and LOCAL 2 which recorded both high foliage yield (FY) and fresh biomass (FB) may be recommended for fodder production for livestock feed formulation (Otoo et al., 2001).

Again, percent dry matter (%DM) content among the 20 accessions varied from 14.49 to 36.65%. It was generally higher for the white-, cream- and yellow-fleshed accessions compared to the orange-fleshed accessions (SA/BNARI, UK/BNARI and US 029) which are all exotic lines. UK/BNARI nonetheless recorded the lowest %DM content of 14.49%. Brabet et al. (1998) reported that orange-fleshed sweet potato genotypes have lower %DM than the white/cream and yellow-fleshed genotypes which is consistent with findings of this study. In the same vein, high %DM content contributed significantly to root dry matter yield (RDMY) among the accessions. US 020 registered the highest (18.29 t/ha) RDMY while the rest of the accessions ranged from 15.15 to 1.02 t/ha. The local accessions generally produced more RDMY than the introduced accessions, which were comparatively higher than reports by Otoo et al. (2001) in the coastal savannah zone of Ghana however less than what was reported in the forest zone of Ghana (Otoo et al., 1995).

Harvest indices (HI) for the exotic lines were relatively higher than those of the local accessions. The highest HI was recorded by US 020 (57.11%), an introduction from USA. Among the local accessions, FREEMA recorded the highest HI of 45.0.7%. High HI of genotypes could be indicative of the level of tuber photosynthetic efficiency to draw photo-assimilates (Otoo et al., 2001).

Genetic relationship among 20 accessions of *I. batatas* L. using both qualitative and quantitative traits

Figure 1 shows the relatedness among the accessions generated using qualitative and quantitative agromorphological traits. The accessions were separated into two clusters at a genetic similarity index (GSI) of 61.6%, and further regrouped into 6 sub-clusters at levels up to 100% similarity. These accessions are related by presence of flowers, flower colour, sepal shape, sepal colour and colour of style. The clustering pattern of the 20 sweet potato accessions are consistent with reports by Yuan et al. (2011), Li et al. (2009) and Yan et al. (2009) who recorded 6 sub-clusters of genetic similarity among their collections. Characters of sweet potato flowers can serve as tool to detect duplicates among collections (Reynoso et al., 1999). Traits such as general outline of leaf and shape of the central leaf lobe have been recognised as crucial in the study of sweet potato diversity (Karuri et al., 2010, 2009; Tairo et al., 2008; Gichuru et al., 2006), which contrasts findings of this study.

Seven local accessions (CR001, FREEMtableA, HMA 1, ER001, HMA 2, LOCAL 1 and UE 007) were grouped into IIF sub-cluster at 87.8% similarity. The pattern of clustering of these local accessions showed possible relationship to a common geographic origin. With exception of UE 007 from the forest agro-ecological zone, all the other accessions were from the coastal savannah agro-ecological zone of Ghana. This is in consonance with Zhang et al. (2000) and He et al. (1995), who detected clustering of several accessions together based on their geographic origin. In contrast, Karuri et al. (2010), Yada et al. (2010), Tairo et al. (2008) and Veasey et al. (2007) reported no distinct relationships between clusters generated based on their geographic origins. However, for accessions to be considered as possible duplicates, their genetic similarity index should be equal or greater than 95% (Andersson et al., 2007). Accessions ER 001 and HMA 2 exhibited the closest resemblance at a similarity index of 97.1% (possible duplicates). Some workers also identified possible duplicates in their sweet potato collections (Karuri et al., 2010; Yada et al., 2010; Veasey et al., 2007; Huamán et al., 1999a and b). Only one of the duplicates could be used in plant breeding and

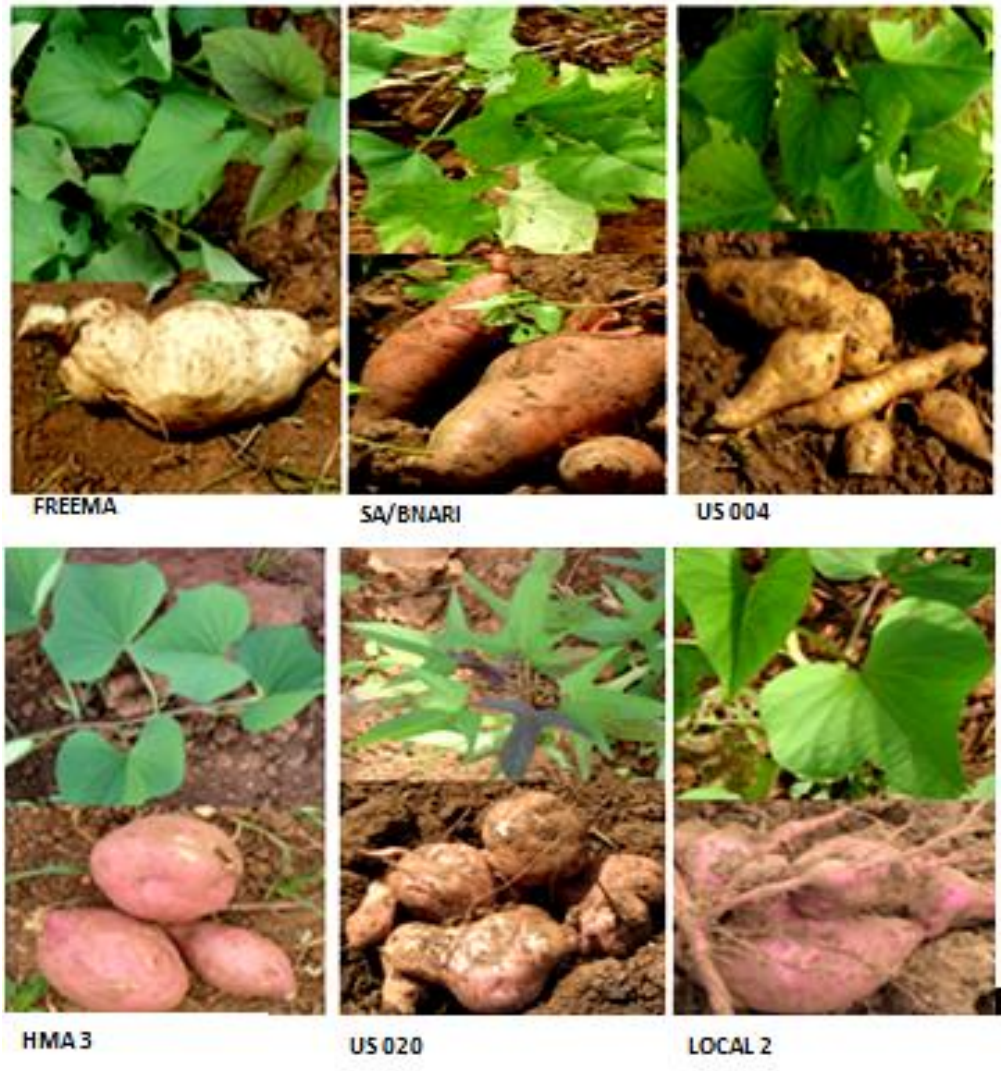

Figure 1. Photographs of leaves and tubers of some accessions on the field.

in germplasm conservation to save cost. CR001 and US 020 were the most diverse accessions.

The second major sub-cluster II (74% genetic distance) contained the highest number of accessions (13) which subsequently regrouped into five sub-sub clusters (1 - 5) at a genetic distance of 71.4%. Sub-cluster 5 contained CRI 027 and CR 002 at a genetic distance of 89% and were clustered based on similar foliar characters (plant type, vine internode diameter, mature leaf size, mature leaf colour and petiole length) and storage root characters (thus, absence of storage roots). Sub-cluster 4 housed four accessions namely, SA/BNARI, CEMSA 74 - 228, CRI 054 and DOAK 08-007 all grouped at a genetic distance of 83.3% (Figure 2). SA/BNARI and CEMSA 74-228 were regrouped at a genetic distance of 89.1% based on vine internode length and damage by weevils on first evaluation. CRI 054 and DOAK 08-007 were individually grouped at a genetic distance of 83.3 and 83%, respectively. CRI 054 was separated based plant type and secondary flesh colour with erect plant type and orange secondary flesh colour as unique traits.

Principal components analysis for 18 quantitative traits of *Ipomoea batatas* L.

Table 5 shows the eigenvalues, percentage variation and cumulative percent variations of 5 principal components of 18 quantitative traits scored among 20 sweet potato accessions. The first five principal component axes (PC_1, PC_2, PC_3, PC_4 and PC_5) in the PCA analysis had eigenvalues greater than 1.0, with cumulative variance of 84.29%. Principal component one (PC_1), with eigenvalue of 6.72, contributed 37.35% to total genetic variability,

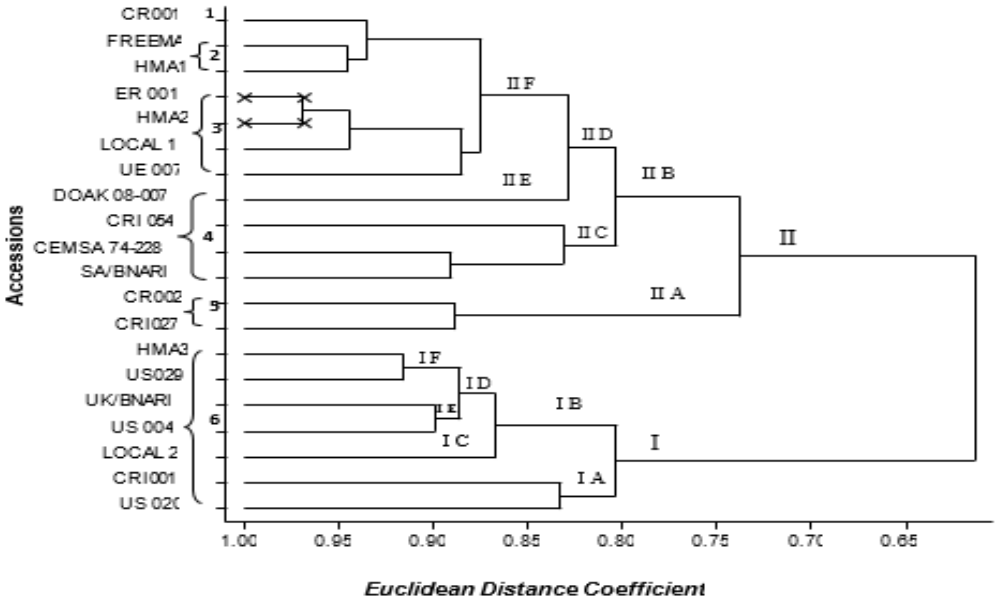

Figure 2. Average-linked dendrogram based on Euclidean distance coefficient of 20 accessions of *I. batatas* L. generated by qualitative and quantitative traits.

Table 5. Principal components analysis of 18 quantitative traits for 20 Accessions of *I. batatas* L.

Traits	PC_1	PC_2	PC_3	PC_4	PC_5
PTY	-0.151	0.260	0.347	0.282	0.247
VID	0.043	0.355	0.163	-0.421	0.051
VIL	-0.041	-0.004	0.444	0.378	0.406
MLS	0.142	0.169	0.252	0.040	-0.478
PL	-0.038	0.248	0.394	-0.292	0.210
FW	0.270	0.104	-0.045	-0.396	0.231
FL	0.276	0.099	-0.036	-0.375	0.218
%PWSR	-0.283	0.267	-0.263	0.031	0.020
LRY(t/ha)	0.314	0.136	-0.049	0.218	0.259
SRY(t/ha)	0.268	0.238	-0.007	0.009	-0.298
TRY(t/ha)	0.342	0.181	-0.055	0.177	0.056
FY(t/ha)	-0.187	0.423	-0.133	0.098	-0.142
FB (t/ha)	-0.022	**0.491**	-0.154	0.176	-0.111
NLR/P	0.316	-0.005	-0.185	0.147	-0.010
NSR/P	0.151	-0.043	**0.493**	***0.000***	-0.400
%DM	0.244	-0.234	0.160	0.014	-0.146
RDMY(t/ha)	0.331	0.162	-0.074	0.245	0.025
HI	0.328	-0.117	-0.098	0.118	0.158
Eigenvalue	**6.723**	3.504	1.965	1.584	1.398
% Variance	**37.352**	19.467	10.915	8.798	7.765
% CV	37.352	**56.819**	**67.734**	**76.532**	**84.297**

% CV = Percent cumulative variance; Values bolded made substantial contribution to total genetic variance.

while PC2, with eigenvalue of 3.50, accounted for 19.47% of total variability among the 20 sweet potato accessions. PC_3, PC_4 and PC_5 had eigenvalues of 1.97, 1.58 and 1.40 contributing 10.92, 8.80 and 7.77% to the

total genetic variance, respectively.

The relative discriminating power of the principal axes as indicated by the eigenvalues was high (6.72) for axis 1 and low (1.40) for axis 5. In PC_1, traits that accounted for most of the observed variability among the 20 accessions include flower width (FW) with vector loading of 0.270, flower length (FL) (0.276), large root yield (LRY) (0.314), small root yield (SRY) (0.268), total root yield (TRY) (0.342), number of large root per plant (NLR/P) (0.316), number of small root per plant (NSR/P) (0.151), percent dry matter (%DM) (0.244), root dry matter yield (RDMY) (0.331), and harvest index (HI) (0.328).

PC_2, PC_3, PC_4 and PC_5 were positively correlated with plant type (PTY). Characters that were mostly correlated with the PC_2 were fresh biomass yield (FB), foliage yield (FY) and vine internode diameter (VID). Number of small roots per plant (NSR/P), vine internode length (VIL) and petiole length (PL), vine internode length (VIL) and root dry matter yield (RDMY), vine internode length (VIL) and large root yield (LRY) correlated with PC_3, PC_4 and PC_5, respectively. In PC_4 and PC_5, PTY, VIL and LRY contributed substantially to total genetic variation. These results confirm the results of studies of the association between root yield and other agromorphological traits (Easwari et al., 1999). The current study reveals that root yield is significantly correlated with plant type, petiole length and number of roots per plant. Plant type in turn is highly correlated with petiole length and number of roots per plant. Vine internode length and vine internode diameter showed significant association as shown in PC_2, PC_3, PC_4 and PC_5. In addition, root yield and petiole length are highly correlated with number of roots per plant as shown in PC_3 and PC_5.

The total contribution of the five principal component axes of this study was higher (84.3%) than those detected by other workers (Amoatey et al., 2015; Ahiakpa et al., 2013; Afuape et al., 2011; Tairo et al., 2008) where the principal component axes contributed 76, 52.5 and 70.09% to total variation, respectively. In the present study, all the eigenvalues except that for PC_1 were higher than observed by Afuape et al. (2011). Hence, based on the factor scores of the 18 characters, accessions which recorded high scores for the component traits in PC_1 could be selected as parents in any future hybridisation programme.

Pearson correlation analysis of 18 quantitative traits in 20 accessions of *Ipomoea batatas* L.

Table 6 displays association among eighteen (18) quantitative traits of the various accessions of sweet potato. Vine internode length (VIL) and petiole length (PL) showed a poor to very low positive/negative correlations among all the traits. Similarly, five traits; plant type (PT), vine internode diameter (VID), mature leaf size (MLS), fresh biomass (FB) and number of small root per plant (NSR/P) showed poor to low positive and negative correlations among all traits except plant type (PT) and vine internode length (VIL), vine internode diameter (VID) and petiole length (PL), mature leaf size (MLS) and number of small root per plant (NSR/P) which showed moderate positive correlations (r = 0.59; 0.63 and 0.56), respectively. Interestingly, flower width (FW) and flower length (FL) recorded poor to very low positive/negative correlations to all other traits except storage yield determinants and flower length where low to moderate and perfect positive correlations were recorded, respectively.

Also, very low to high negative correlation was observed between foliage yield (FY) and percent of plants without storage root (%PWSR) with all other traits except fresh biomass (FB) and foliage yield (FY) which recorded high positive correlation. Finally, all the storage root traits showed very low to very high positive correlations among all other traits except foliage yield for which there was very low negative correlation. The correlation matrix generally showed a markedly low and negligibly positive/negative (±0.00 - ±0.10) correlation to low positive/negative (±0.30 - ±0.50) correlation between storage root traits and shoot traits (plant type (PTY), vine internode diameter (VID), vine internode length (VIL), mature leaf size (MLS), petiole length (PL), flower width (FW), and flower length (FL)). This result is consistent with those reported by Afuape et al. (2011) and Yada et al. (2010) but contrasts report of Tsegaye et al. (2007) who recorded moderate positive correlation in shoot traits to root traits. Many economically important traits of plants are usually related to one another in one or several ways. Correlations are measures of the degree of associations between these traits (Steel and Torrie, 1984). Selection for one trait results in progress for all characters that are positively correlated but reduces for traits that are negatively correlated. Therefore correlation analysis enables the breeder to understand the mutual component characters on which selection can be based for genetic improvement.

All the root traits were low to highly negative correlations with percentage of plants without storage roots (%PWSR); thus, increase in %PWSR automatically reduces storage root yield. Foliage yield (FY) and fresh biomass (FB) showed moderate to highly positive correlations (r = 0.57 and r = 0.81) with %PWSR. Also, the root traits were poorly correlated to FY and FB. According to Lewthwaite and Triggs (2000), storage root yield depends on leaf photosynthesis. Hence, canopy type might have influenced the net assimilation rate (Sasaki et al., 2005). The transport of photo-assimilates from the leaves to the root stalk is prejudiced by storage root growth, as storage root cell must be formed and expanded prior to storage of assimilates. Therefore, increased foliage yield without considerable storage root cells development would spontaneously induce reduction in tuber yield, hence the negative correlation between

Table 6. Pearson correlation coefficients between 18 quantitative traits of 20 *I. batatas* L. accessions evaluated at NARC in Ghana.

Traits	PTY	VID	VIL	MLS	PL	FW	FL	%PWSR	LRY(t/ha)	SRY(t/ha)	TRY(t/ha)	FY(t/ha)	FB (t/ha)	NLR/P	NSR/P	%DM	RDMY(t/ha)
PTY																	
VID	0.21																
VIL	**0.59***	-0.14															
MLS	0.05	0.13	-0.10														
PL	0.39	**0.63****	0.20	0.21													
FW	-0.27	0.34	-0.14	0.17	0.12												
FL	-0.26	0.32	-0.13	0.21	0.10	**1.00*****											
%PWSR	0.37	0.09	-0.10	-0.15	0.09	-0.37	-0.38										
LRY(t/ha)	-0.08	0.13	0.07	0.24	0.05	**0.52***	**0.53***	-0.43									
SRY(t/ha)	-0.13	0.44	-0.18	0.41	-0.06	0.46	0.47	-0.32	0.49								
TRY(t/ha)	-0.14	0.25	-0.04	0.34	-0.03	**0.55***	**0.57***	-0.46	**0.94*****	**0.76****							
FY(t/ha)	0.47	0.30	-0.05	0.08	0.20	-0.22	-0.24	**0.81****	-0.23	0.07	-0.16						
FB (t/ha)	0.39	0.40	-0.06	0.23	0.18	0.04	0.03	**0.57***	0.21	0.42	0.31	**0.89*****					
NLR/P	-0.38	-0.08	-0.18	0.23	-0.18	0.46	0.47	**-0.53***	**0.68****	**0.57***	**0.75****	-0.32	0.04				
NSR/P	-0.01	0.10	0.19	**0.56***	0.10	0.13	0.15	**-0.61****	0.12	0.40	0.26	-0.28	-0.15	0.11			
%DM	-0.37	-0.20	0.03	0.19	-0.17	0.31	0.32	**-0.77****	0.27	0.36	0.35	**-0.60****	-0.42	0.46	0.39		
RDMY(t/ha)	-0.15	0.12	0.01	0.38	-0.07	0.51	**0.52***	-0.42	**0.88*****	**0.73****	**0.94*****	-0.12	0.32	**0.74****	0.17	0.48	
HI	-0.38	-0.12	-0.09	0.16	-0.24	0.49	**0.52***	**-0.65****	**0.79****	0.37	**0.76****	**-0.61****	-0.24	**0.75****	0.21	0.44	**0.68****

* = significant (P<0.05); ** = very significant (P<0.001); *** = highly significant (P<0.0001) computed using standard linear Pearson *correlation*. PTY = Plant type; VID = vine internode diameter; VIL = vine internode length; MLS = mature leaf size; PL = petiole length; FW = flower width; FL = flower length; %PWSR = percent plant without storage root; LRY = large root yield; SRY = storage root yield; TRY = total root yield; FY = foliage yield; FB = fresh biomass; NLR/P = number large root per plant; NSR/P = number of small root per plant; %DM = percent dry matter; RDMY = root dry matter yield; HI = harvest index.; NARC = Nuclear Agriculture Research Centre.

foliage yield (FY) and fresh biomass (FB) to storage root traits. The low positive to moderate positive correlations between flower width (FW) and flower length (FL) and storage yield determinants could be attributed to *MADS-box genes* found in sweet potato flowers and storage roots (Ravi et al., 2009; Ku et al., 2008; Kim et al., 2002, 2005). These *MADS-box genes* are expressed in relation with anthocyanin accumulation in both flowers and pigmented root periderm and cortex tissue (Lalusin et al., 2006) or may impact the different stages of storage root development (Ku et al., 2008; Kim et al., 2005).

There was moderate to high positive correlations between total root yield and large root yield (LRY) and small root yield (SRY) and also positive correlations between total root yield and number or large roots per plant (NLR/P) and number of small roots per plant (NSR/P). These results corroborate that of Afuape et al. (2011), but contrast the results of Islam et al. (2002) and Tsegaye et al. (2007) who reported negative correlations between total root yields (TRY) and, number of large roots per plant (NLR/P) and number of small roots per plant (NSR/P). Root dry matter yield (RDMY) and harvest index (HI) had moderate to very high positive correlations with total root yield (TRY), large root yield (LRY), small root yield (SRY), and number of large root per plant (NLR/P). This is consistent with results by Felenji et al. (2011). There was low positive correlation between percent dry matter (%DM) and total root yield (TRY), large root yield (LRY), small root yield (SRY), number of large roots per plant (NLR/P) and number of small root per plant (NSR/P). These results are consistent with findings made by Felenji et al. (2011) but inconsistent with those by Tairo et al. (2008). These results therefore suggest that total root yield in sweet

potato is a composite character with contributions from a number of traits. Thus, total root yield trait can be improved by simultaneous selection for other traits positively correlated to it.

Conclusion

There were significant genetic variability among the 20 accessions of sweet potato studied based on the agromorphological characters evaluated. Hierarchical cluster analysis grouped accessions into two clusters at a genetic similarity index of 61.6%. Accessions, ER 001 and HMA 2 were found to be possible duplicates. Accession US 020 recorded the highest total root yield and harvest index of 56.32 t/ha and 57.11%, respectively. The PCA showed characters contributing differently to the 84.29% of total genetic variability with only PC_1 contributing 37.35% to the total variability. Key component traits contributing to total root yield (TRY) include large root yield (LRY), number of large root per plant (NLR/P), percent dry matter (%DM), root dry matter yield (RDMY) and Harvest index (HI). This study provides valuable information that can be utilised in a breeding programme to ameliorate local clones of *I. batatas* L in Ghana. Further studies using molecular markers are needed to delineate useful genetic information at the molecular level.

Conflict of Interests

The authors have not declared any conflict of interest.

REFERENCES

Abidin PE, van Eeuwijk FA, Stam P, Struik PC, Malosetti M, Mwanga ROM, Odongo B, Hermann M, Carey EE (2005). Adaptation and stability analysis of sweet potato varieties for low-input systems in Uganda. Plant Breed. 124:491-497.

Afuape SO, Okocha PI, Njoku D (2011). Multivariate assessment of the agromorphological variability and yield components among sweet potato (*Ipomoea batatas* (L.) Lam) landraces. Afr. J. Plant Sci. 5(2):123-132.

Ahiakpa JK, Kaledzi PD, Adi EB, Peprah S, Dapaah HK (2013). Genetic diversity, correlation and path analyses of okra (*Abelmoschus* spp L. Moench) germplasm collected in Ghana. Int. J. Dev. Sustain. 2(2):1396-1415.

Akoroda M (2009). Sweet potato in West Africa. In: The Sweet potato. Loebenstein G, Thotthappilly G (Eds.). Springer Sciences Business Media BV, Dordrecht, the Netherlands. pp. 441-468.

Amoatey HM, Klu GYP, Quartey EK, Doku HA, Sossah FL, Segbefia MM, Ahiakpa JK (2015). Genetic Diversity Studies in 29 Accessions of Okra (*Abelmoschus* spp L.) Using 13 Quantitative Traits. Am. J. Exp. Agric. 5(3):217-225.

Andersson MS, Schultze KR, Peters M, Duque MC, Gallego G (2007). Extent and structure of genetic diversity in a collection of the tropical multipurpose shrub legume Cratylia argentea (Desv.) O. Kuntze as revealed by RAPD markers. Electronic J. Biotechnol. 10(3):1-9.

Brabet C, Reynoso D, Dufour D, Mestres C, Arredondo J, Scott G (1998). Starch content and properties of 106 sweet potato clones from the world germplasm collection held at CIP, Peru. International Potato Centre Program Report (1997-1998). pp. 279-285.

Caliskan ME, Erturk E, Sogut T, Boydak E, Arioglu H (2007): Genotype × environment interaction and stability analysis of sweet potato (Ipomoea batatas) genotypes. New Zealand J. Crop Hortic. Sci. 35(1):87-99.

Carey EE, Reynoso D (1999). Procedures for the evaluation of pathogen tested sweet potato clones In: Sweet potato Germplasm Management (*Ipomoea batatas*) Training manual. International Potato Centre, Lima, Peru. pp. 170-186.

Easwari CS, Naskar SK, Sheela MN, Nair SG (1999). *Ipomoea batatas* Genetic Resources in India. In: International training Course on Maintenance, Characterisation and Duplicate Identification of *Ipomoea batatas* Collections. Central Tuber Crops Research Institute, Sreekariyam, India and International potato Centre, Lima. P 5.

Elameen A, Larsen A, Klemsdal SS, Fjellheim S, Sundheim L, Msolla S, Masumba E, Rognli OA (2011). Phenotypic diversity of plant morphological and root descriptor traits within a sweet potato, Ipomoea batatas L. Lam., germplasm collection from Tanzania. Genet. Resour. Crop Evol. 58:397-407.

FAOSTATs (2010). Food and Agriculture Organisation, (FAO) statistical database. Available at: http://faostat.fao.org/site/567/desktopDefault.aspx?PageID=567

FAO/UNESCO (1994). FAO/UNESCO Soil Map of the world, revised legend, world resources report 60. FAO, Rome, Italy. 146 p.

Felenji H, Saeed A, Gholam RA, Mostafa A (2011). Evaluating Correlation and Factor Analysis of Morphological Traits in Potato Cultivars in Fall Cultivation of Jiroft Area American-Eurasian. J. Agric. Environ. Sci. 11(5):679-684.

Gasura E, Mashingaidze AB , Mukasa SB (2008). Genetic variability for tuber yield, quality, and virus disease complex traits in Uganda sweet potato germplasm. Afr. Crop Sci. J. 16(2):147-160.

Gichuru V, Aritua V, Lubega GW, Edema R, Adipula E, Rubaihayo PR (2006). A preliminary analysis of diversity among East African sweet potato landraces using morphological and simple sequence repeats (SSR) markers. Acta Hortic. 703:159-164.

Grüneberg WJ, Manrique K, Zhang D, Hermann M (2005). Genotype × environment interactions for a diverse set of sweet potato clones evaluated across varying eco-geographic conditions in Peru. Crop Sci. 45:2160-2171.

He G, Prakash CS, Jarret RL (1995). Analysis of genetic diversity in a sweet potato (*Ipomoea batatas*) germplasm collection using DNA amplification fingerprinting. Genome 38(5):938-945.

Hijmans R, Low J, Walker T (2001). The potential impact of orange-flavoured sweet potatoes on vitamin A intake in sub-Saharan Africa. Paper presented at a Regional Workshop on Food-based Approaches to Human Nutritional Deficiencies-A CIP Project. pp. 1-6.

Huamán Z (1991). Descriptors for sweet potato. Descriptores de la batata (No. 583.79 H874). Centro Internacional de la Papa, Lima (Perú). International Board for Plant Genetic Resources, Roma (Italia).Rome, Italy. pp. 6-48.

Huamán Z, Aguilar C, Ortiz R (1999a). Selecting a Peruvian sweet potato core collection on the basis of morphological, eco-geographical, disease and pest reaction data. Theor. Appl. Genet. 98:840-844.

Huamán Z, Aguilar C, Ortiz R (1999b). Systematic botany and morphology of the sweet potato plant. In: Sweet potato Germplasm Management (*Ipomoea batatas*) Training manual. International Potato Centre, Lima, Peru. pp. 18-26.

Islam MJ, Haque MZ, Majunder UK, Haque MM, Hossain MF (2002). Growth and yield potential of nine genotypes of sweet potato. Pak. J. Biol. Sci. 5(5):537-538.

Kapinga RE, Ewell PT, Jeremiah SC, Kileo R (1995). Sweet potato in Tanzanian Farming and Food Systems: Implications for Research. CIP, Sub-Saharan Africa Region, Nairobi, and Kenya/Ministry of Agriculture, Dar-es-Salaam, Tanzania. p. 47.

Karuri HW, Ateka EM, Amata R, Nyende AB, Muigai AWT (2009). Morphological markers cannot reliably identify and classify sweet potato genotypes based on resistance to sweet potato virus disease and dry matter content. J. Appl. Biol. Sci. 15:820-828.

Karuri HW, Ateka EM, Amata R, Nyende AB, Muigai AWT, Mwasame E, Gichuki ST (2010). Evaluating diversity among Kenyan sweet potato genotypes using morphological and SSR markers. Int. J. Agric. Biol.

12:33-38.
Kim SH, Hamada T, Otani M, Shimada T (2005). Isolation and characterization of MADS-box genes possibly related to root development in sweet potato (*Ipomoea batatas* L. Lam.). J. Plant Biol. 48:387-393.
Kim SH, Mizuno K, Fujimura T (2002). Isolation of MADS-box genes from sweet potato (*Ipomoea batatas* L.) Lam.) expressed specifically in vegetative tissues. Plant Cell Phys. 43:314-322.
Ku AT, Huang YS, Wang YS, Ma D, Yeh KW (2008). IbMADS1 (*Ipomoea batatas* MADS-box 1 gene) is involved in tuberous root initiation in sweet potato (*Ipomoea batatas*). Ann. Bot. 102:57-67.
Lalusin AG, Nishita K, Kim SH, Ohta M, Fujimora T (2006). MADS-box gene (IbMADS 10) from sweet potato (*Ipomoea batatas* (L.) Lam.) involved in the accumulation of anthocyanin. Mol. Genet. Genom. 275:44-54.
Laurie SM (2010). Agronomic performance, consumer acceptability and nutrient content of new sweet potato varieties in South Africa. PhD Thesis. pp. 91-97.
Lebot V (2009). Tropical root and tuber crops: Cassava, sweet potato, yams, and aroids Oxfordshire: CABI. pp. 91-274.
Lebot V (1986). Evaluation of local and introduced cultivars of Sweet Potato (*Ipomoea batatas* (L.) Lam.) in Vanuatu. J. South Pac. Agric. 11(3):25-31.
Li M, Hou XL, Hao RM (2009). Analysis of genetic relationships of Osmanthus fragrans based on SRAP markers. Acta Hortic. Sin. 36(11):1667-1675. Loebenstein G (2009). Origin, distribution and economic importance. In: The Sweet potato. Loebenstein G, Thotthappilly G (Eds.). Springer Sciences Business Media BV, Dordrecht, the Netherlands. pp. 9-12.
Local Weather Station (2012). Nuclear Agriculture Research Centre, Biotechnology & Nuclear Agriculture Research Institute, Ghana Atomic Energy Commission, Ghana.
Ndunguru J, Kapinga R, Sseruwagi P, Sayi B, Mwanga R, Tumwegamire S, Rugutu C (2009). Assessing the sweet potato virus disease and its associated vectors in northwestern Tanzania and central Uganda. Afr. J. Agric. Res. 4(4):334-343.
Otoo JA, Missah A, Adu-Mensah J, Kissiedu AFK, Afuakwa JJ, Okai E, Asare-Bediako A, Sagoe R (1995). Performance in Ghana (West Africa) of sweet potato bred and selected in East and Southern Africa environments. In: Proceedings of the 6th Triennial Symposium of ISTRC-AB, Lilongwe, 28 October, 1995. pp. 542-545.
Otoo JA, Missah A, Osei C, Carson AG, Okai E, Sagoe R, Dixon AGO (1998). Statistical analysis of sweet potato trials in different agro-ecological zones in Ghana using the Additive Main Effects and Multiplicative Interaction (AMMI) Model. In: Proceedings of the 7th Triennial Symposium of ISTRC-AB, Cotonou, Republic of Benin, 11-17 October, 1998. pp. 368-377.
Otoo JA, Missah A, Carson AG (2001). Evaluation of Sweet potato for Early Maturity across Different Agro-Ecological Zones in Ghana. Afr. Crop Sci. J. 9(1):25-31.
Ssebuliba JM, Muyonga JM, Ekere W (2006). Performance and acceptability of Orange-fleshed sweet potato cultivars in Eastern Uganda. Afr. Crop Sci. J. 14(3):231-240.
Ravi V, Naskar SK, Makeshkumar T, Babu B, Prakash KBS (2009). Molecular Physiology of Storage Root Formation and Development in Sweet Potato (*Ipomoea batatas* L. Lam.). J. Root Crops 35(1):1-27.
Reynoso D, Huamán Z, Aguilar C (1999). Methods to induce flowering in sweet potato. In: Sweet potato Germplasm Mgt. (*Ipomoea batatas*) Training manual. International Potato Centre, Lima, Peru. 126 p.
Sasaki O, Moriyama H, Yoshida K, Tedaka J (2005). The morphology of the sweet potato canopy and its varietal differences. Bulletin of the Faculty of Agriculture, Kagoshima University 55:1-6.
Sossah FL, Oduro V, Amoatey HM, Appiah AS, Nunekpeku W, Ossae FA, Owusu GK, Amiteye S, Ahiakpa JK (2014). Biochemical Characterisation of 18 Accessions of Sweet Potato (*Ipomoea batatas* L. Lam.) Using Total Leaf and Tuberous Root Protein by SDS-PAGE. J. Nat. Sci. Res. 4(11):48-55.
Steel RG, Torrie RH (1984). Principles and procedure of statistics. 2nd edition McGraw-Hill, Inc. New York. P 87.
Tairo F, Mneney E, Kullaya A (2008). Morphological and agronomical characterization of sweet potato germplasm from Tanzania. Afr. J. Plant Sci. 2:77-85.
Tsegaye E, Sastry D, Dechassa N (2007). Genetic variability for the yield and other agronomic traits in sweet potato. Indian J. Hortic. 64:237-240.
Tumwegamire S, Kapinga R, Rubaihayo PR, LaBonte DR, Gruneberg WJ, Mwanga ROM (2011). Evaluation of Dry Matter, Protein, Starch, s-carotene, Iron, Zinc, Calcium and Magnesium in East African Sweet potato (*Ipomoea batatas* (L.) Lam) Germplasm. HortScience 46(3):348-357.
Veasey EA, Silva JSD, Rosa MS, Borges A, Bressan ED, Peroni N (2007). Phenology and morphological diversity of sweet potato (*Ipomoea batatas*) landraces of the Vale do Ribeira. Sci. Agric. 64:416-427.
Vimilar B, Hariprakash B (2010). Variability of Morphological Characters and Dry matter content in the hybrid progenies of Sweet potato (*Ipomoea batatas* L. Lam.). Gene Conserve 10(39):65-86.
Yada B, Tukamuhabwa P, Wanjala B, Dong-Jin K, Skilton RA, Alajo A, Mwanga ROM (2010). Characterization of Ugandan Sweet potato Germplasm Using Fluorescent Labelled Simple Sequence Repeat Markers. HortScience 45(2):225-230.
Yan XY, Xiao BL, Han YJ, Yuan WJ, Shang FD (2009). AFLP analysis of genetic relationships and diversity of some Chinese Osmanthus fragrans cultivars. Life Sci. J. 6(2):11-16.
Yuan WJ, Han YJ, Dong MF, Shang FD (2011). Assessment of genetic diversity and relationships among Osmanthus fragrans cultivars using AFLP markers. Electronic J. Biotechnol. 14:1-9.
Zhang DP, Cervantes JC, Huamàn Z, Carey EE, Ghislain M (2000). Assessing genetic diversity of sweet potato (*Ipomoea batatas* L.) Lam.) cultivars from Tropical America using AFLP. Genet. Resour. Crop Evol. 47:659-665.