

Agro-Morphological Characterization of Sweet Potato Genotypes Grown in Different Ecological Zones in Kenya

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Abstract. The main characteristic of sweet potato [*Ipomoea batatas* (L.) Lam.] is its high phenotypic and genotypic variability. There is no, or limited, information on the suitability of agro-morphological characteristics for utilization in production and processing. Currently, farmers are growing different sweet potato genotypes characterized with low yield. The aim of the study was to evaluate agro-morphological characteristics of 68 sweet potato genotypes in order to determine the best-performing ones. The sweet potato genotypes were grown at the Kenya Agricultural and Livestock Research Organization and the Embu and Miyare Agriculture Training College. The locations were chosen because they are the main sweet potato producing areas with different climatic and production conditions. Six storage root and five aerial characters were used in the characterization. The genotypes differed in storage root stalk and root length; vine internode length and vine internode growth rate; petiole length and leaf size, and yield at both sites. Genotype Nyautenge was the best performing in terms of storage root yield. There was poor correlation among agro-morphological attributes. The study demonstrates the potential of some sweet potato genotypes such as Nyautenge for high productivity.

Introduction

Sweet potato [*Ipomoea batatas* (L.) Lam.] is grown in many parts of East Africa because it is highly productive and requires little demand for input and labor for its cultivation [1]. Sweet potato is a cheap and valuable source of vitamin A, is a good source of calcium and ascorbic acid (vitamin C), and provides more edible energy than other staple foods. These characteristics make this crop suitable and attractive to farmers with limited resources [2]. The possibility of improvement in any crop is dependent on the available variability. The wider the genetic variability in traits, the better the chances of improvement through selection [3]. Analysis of genotypes at the genetic level provides more information on genetic relationships which, along with agro-morphological traits, will be helpful in guiding breeding for improvement in sweet potato. Characterization of crops is valuable for providing complete information on the characteristics of given germplasm, thereby contributing to optimal management of collections [4].

Variation exists in the skin and flesh color, depth of rooting, storage root shape and size, variations in the resistance to insect pests and diseases, and partitioning of dry matter content in sweet potato [5, 6]. Establishment of appropriate understanding of these variations would contribute to the selection and improvement of the crop. Traditionally, sweet potato characterization has been based on morphological and agronomic traits as they are easy to evaluate, and the methods relatively cheap [7]. Expression of these traits is subject to genetic makeup, environmental factors and their interactions. Most important characters, including yield, are highly influenced by the environment since they are polygenically controlled [8]. However, qualitative characters such as general outline of the leaf and shape of the central leaf lobe have been reported to be important in studying diversity in sweet potato [9] since these characters are not affected by environment. High agro-morphological variability in sweet potato accessions have been reported [4]. The most

informative descriptors were abaxial leaf vein pigmentation, the shape of roots and vine tip pubescence [4].

Morphological variation has been widely used to characterize sweet potato genotypes [9-11] and to eliminate duplicates among genetic accessions [12, 13]. Additionally, [14] and [1], using agro-phenotypic characters, reported wide diversity among sweet potato genotypes. One of the main characteristics of sweet potato is its high phenotypic and genotypic variability [15] that confers adaptability to different climatic conditions. Through characterization, a diversity that exists in a germplasm population can be estimated and studied. Morphological characterization provides information on conserved germplasm, placing it in the most effective form for use, and the value of the germplasm increases as it becomes known and documented [9]. Agro-morphological characterization in sweet potato is done by assessing variations in the vine, leaf, flower and storage root characteristics. This method has been used for identifying sweet potato cultivars, duplicate accessions, detecting unique character traits, and correlation with characteristics of agronomic importance. Morphological and agronomic characters, such as the storage root to vine ratio, have been used to identify and select dual-purpose sweet potato varieties [1]. Currently, sweet potato yield in developing is far below compared with developed countries. It is essential to determine the best performing genotypes to be recommended to farmers for production [10]. This way, it will be possible to estimate the real variability maintained to make conserved germplasm available for effective use by researchers and farmers. Agro-morphological characterization provides information on conserved germplasm, placing it in the most effective form for use, and the value of the germplasm increases as it becomes known and documented. There is no, or limited, information on the suitability of agro-morphological characteristics for utilization in production and processing. The objective of the study was to characterize accessions of sweet potato genotypes based on their agro-morphological descriptors.

Materials and Methods

The experiment was done between October, 2013 and April, 2014 in season one and between March, 2014 to October, 2014, for season two at the Miyare Agriculture Training College farm situated in the Migori County (ACT-Miyare) and Kenya Agricultural and Livestock Research Organization in Embu County (KALRO-Embu). The latter is at an altitude of 1497 m a.s.l., annual rainfall of 1252 mm, and annual temperature of 19.5 °C with humic nitisols soils. The ATC-Miyare is at an altitude of 1460 m a.s.l., annual rainfall of 1700 mm, annual temperature of 16.5 °C and humic acrisols soils.

Sixty-eight sweet potato genotypes, collected as vine cuttings from sites in Kenya and Uganda were used (Table 1). The genotypes included 57 local Kenyan landraces and 11 F1 hybrids from a polycross obtained from the National Crops Resources Research Institute, Uganda. The genotypes collected from Kenya were from the Western, Nyanza and Eastern regions. The criterion for genotype collection was based on genotypes commonly grown by farmers in the Western region of Kenya which have some resistance to weevils (*Cylas* spp.). The 68 sweet potato genotypes were multiplied at KALRO-Embu.

Table 1. List of the sweet potato genotypes collected for agro-morphological characterization.

Genotype	Origin ^a	Flesh color
Kenspot 1	Eastern (Kenya)	Yellow
Saly boro	Nyanza (Kenya)	Orange
91/2187	Western (Kenya)	Yellow
Oduogo jodongo	Nyanza (Kenya)	White
5 Nyandere	Western (Kenya)	Cream-Yellow
Odinga	Nyanza (Kenya)	Yellow
Naspot 1	Western (Kenya)	Yellow
Kenspot 3	Eastern (Kenya)	Orange
Naspot × New Kawogo 2	NaCCRI (Uganda)	Cream
Nyamuguta	Western (Kenya)	Cream-white
Nyautenge	Western (Kenya)	Cream

Ejumula × New Kawogo 4	NaCCRI (Uganda)	Yellow-orange
Nyarambe	Western (Kenya)	Cream
Nyakagwa	Western (Kenya)	Cream
Naspot × New Kawogo 3	NaCCRI (Uganda)	Yellow-orange
Ejumula × New Kawogo 2	NaCCRI (Uganda)	Cream
Nangili	Western (Kenya)	Yellow-orange
Kenspot 2	Eastern (Kenya)	White
SPK 013	Nyanza (Kenya)	White
Mugande × New Kawogo 4	NaCCRI (Uganda)	Yellow-orange
Alupe-or	Western (Kenya)	Orange
12 Marooko	Western (Kenya)	Cream
Kenspot 5	Eastern (Kenya)	Orange
36 Kalamb Nyerere	Nyanza (Kenya)	Cream-yellow
K/KA/2004/215	Western (Kenya)	Yellow
Ejumula × New Kawogo 3	NaCCRI (Uganda)	Yellow
292-H-12	Western (Kenya)	Yellow-cream
Mogesi Gikenja	Western (Kenya)	White
Lungabure	Western (Kenya)	Cream-white
Kenspot 4	Eastern (Kenya)	Orange
Vitaa	Nyanza (Kenya)	Cream
9 Nduma	Western (Kenya)	Purple-cream
24 Kampala	Western (Kenya)	Yellow-orange
Obugi	Western (Kenya)	Yellow-orange
56682-03	Western (Kenya)	Cream
Nyawo Nyathiodiewo	Nyanza (Kenya)	Orange
Gachaka	Western (Kenya)	Yellow-orange
Mugande	Western (Kenya)	White
Amina	Nyanza (Kenya)	Orange
Fumbara jikoni	Western (Kenya)	Cream
Ejumula	Western (Kenya)	Orange
Karunde	Nyanza (Kenya)	Cream
SPK 004	Nyanza (Kenya)	Orange
Kuny kibuojo	Nyanza (Kenya)	Cream-white
K/KA/2002/12	Western (Kenya)	White
55 Nganyomba	Western (Kenya)	Cream
1 Ujili	Western (Kenya)	Yellow
Santo Amaro	Rift valley (Kenya)	Cream
Mugande × New kawogo 2	NaCCRI (Uganda)	Cream
Wera	Nyanza (Kenya)	Yellow
Kemb 10	Nyanza (Kenya)	Yellow
Mbita	Western (Kenya)	Yellow
Naspot × New Kawogo 1	NaCCRI (Uganda)	Cream
Kibuonjo	Nyanza (Kenya)	Cream-white
29 Kuny kibuojo	Nyanza (Kenya)	Yellow
62 Odhiogo	Western (Kenya)	Yellow
52 Nyakisumu	Nyanza (Kenya)	Yellow-orange
Ejumula × New kawogo 1	NaCCRI (Uganda)	Cream
Bungoma	Nyanza (Kenya)	Cream
K117	Nyanza (Kenya)	White
Fundukhusia	Western (Kenya)	Yellow-orange
SPK 031	Western (Kenya)	Orange
Mugande × New kawogo 1	NaCCRI (Uganda)	Yellow
Mwavuli	Nyanza (Kenya)	Cream
Polo yiengo	Nyanza (Kenya)	Yellow
Mugande × New kawogo 3	NaCCRI (Uganda)	Cream
Sinia	Nyanza (Kenya)	Yellow
Tainung	Eastern (Kenya)	Orange

^a All crosses in the study are F1 hybrids from a polycross obtained from National Crops Resources Research Institute, Uganda.

The sweet potato genotypes were planted in a randomized complete block design replicated three times at ATC-Miyare and KALRO-Embu. Each plot was 1.5×3.75 m with a plant spacing of 30×75 cm having 25 plants per plot. Sweet potato cuttings measuring 30 cm long from each genotype were planted in 5 rows. Weeding was at both sites 6 weeks after planting. Experimental fields were rain fed. No fertilizer was applied as a common practice done by sweet potato farmers. Harvesting was 160 days after planting.

Agro-morphological characterization of above and below ground parts was with the International Potato Center (CIP) guide [16] at 100 and 160 days after planting, respectively. The evaluation was on 9 plants of each genotype excluding border plants of each plot. Key agro-morphological characters for sweet potato genotypes such as vine growth rate, vine internode length, vine internode diameter, storage root cortex thickness, storage root stalk, mature leaf size, storage root length, storage root diameter, petiole length, the weight of largest tuber and yield were evaluated (Table 2).

Analysis of variance of agro-morphological data was in SAS (ver. 10, SAS Institute Inc, Cary, NC). Data were classified according to genotypes, locations, blocks and replications. Variation between sites was in SAS. If interactions were significant they were used to explain the results. If interactions were not significant means were separated using LSD. Cluster analysis was done on standardized agro-morphological data based on Euclidian distance coefficient and the Un-weighted Pair Group Method with Arithmetic means (UPGMA) using NCSS-pc (ver. 11, Tarragona, Spain). The hierarchical program in Number cruncher statistical systems (NCSS-pc) was used to generate dendrograms. Data points with smaller distances between them were grouped together. The Pearson correlation matrix was done using DARwin, ver. 6.

Table 2. List of agro-morphological descriptors for characterizing sweet potato genotypes.

Aboveground characters	Description
Vine growth length	Description of the relative speed of growth of the main vines based on average length reached at about 60 days after planting
Vine internode length	Length of the vines in cm
Vine internode diameter	Thickness of the vines in cm
Mature leaf size	Measured vertically from the apex
Petiole length	Average petiole length of leaves located between 8th and 10th node from the apical shoots
Underground characters	Description
Storage root cortex thickness	Thickness of the root cortex
Storage root stalk	Description of the length of the stalk joining the storage roots to the stems
Storage root length	Length of the roots in cm
Largest storage root diameter	Average of largest diameter of 10 storage roots in cm
Weight of largest root	Weight of largest root in kg
Root yield	Weight of the roots in $\text{Mt}\cdot\text{ha}^{-1}$

Results

The ANOVA analysis indicated that the main effects of site and genotype affected all agro-morphological variables except vine internode length (VIL), vine internode diameter (VID), storage root cortex thickness (SRCT), mature leaf size (MLS), petiole length and weight of the largest root (WLR) which not significant between sites (Table 3), and there was no significant interaction between sites and genotype. There were differences in vine growth rate (VGR) due to genotype and site (Table 4). Genotypes that had the least VGR were Ejumula \times New Kawogo 4, Kenspot 2, Alupe or, 24 Kampala, Mugande, and Bungoma, and were regarded as having a slow VGR. Genotypes Kenspot 1, Kenspot 3, Kenspot 5, Nyautenge and Ejumula had the fastest VGR. Genotypes from ACT-Miyare had longer VGR compared with KALRO-Embu. There were

differences on vine internode length (VIL) of genotypes (Table 4). The VIL of all genotypes ranged from very short to short. No genotype exhibited intermediate, long or very long VIL. Genotypes that had the lowest VIL were Saly boro, Ejumula × New Kawogo 4, Ejumula × New Kawogo 2, Naspot × New Kawogo 3, 24 Kampala, Mugande, 55 Nganyomba, 1-Ujili and Mugande × New Kawogo 2. Genotypes Fundukhusia and Mwavuli were rated as having short VIL; genotype Mvaluli had the longest VIL compared with other. There was no difference in VIL between sites.

Analysis of variance indicated differences in vine internode diameter (VID) of genotypes (Table 4). The VID of all genotypes ranged from very thin to thin. There were no genotypes that exhibited intermediate, long or very long VID. Genotypes that had the least VID were Fundukhusia and SPK 031. Genotypes 36 Kalamb Nyerere, Mogesi Gikenja, Ejumula × New Kawogo 1 and Polo yiengo had a thin VID. There was no difference in VID between sites. Analysis of variance indicated differences on storage root cortex thickness (SRCT) for genotypes (Table 4). The SRCT of genotypes ranged from thin to intermediate. There were no genotypes that exhibited very thin, thick or very thick SRCT. Genotypes that had the largest SRCT were Nyakagwa and Kuny kibunjo and were regarded as having intermediate SRCT. Genotypes 91/2187, Naspot × New Kawogo 2, Naspot × New Kawogo 3, 12 Marooko, Lungabure, 56682-03, 29 Kuny kibunjo and Bungoma were rated as having thin SRCT. There was no difference in SRCT between sites.

Table 3. Analysis of variance results for the agro-morphological characteristics of sweet potato genotypes at ATC-Miyare and KALRO-Embu sites.

Source	DF	Mean Square										
		VGR ^a	VIL	VID	SRCT	SRS	MLS	SRL	LSRD	PL	WLR	RY
Block (B)	2											
Site (S)	1	3620.5*	510.1*	121.4ns	120.8ns	133.6*	254.3ns	332.8*	198.6*	200.7ns	105.7ns	110.4*
Genotype (G)	67	32.6*	44.8ns	3.4*	4.6*	4.5*	4.5*	14.5*	3.0*	3.0*	3.8*	3.5*
Interaction (S × G)	67	58.6ns	50.8*	3.5ns	2.0ns	2.0ns	4.2ns	4.4ns	1.7ns	1.6ns	3.0ns	2.3ns

ns, *, not significant or significant at $p < 0.05$, ANOVA.

^a VGR = vine growth length; VIL = vine internode length; VID = vine internode diameter; SRCT = storage root cortex thickness; SRS = storage root stalk; MLS = mature leaf size; SRL = storage root length; LSRD = largest storage root diameter; PL = petiole length; WLR = weight of largest root; RY = root yield.

Table 4. Means for vine and root character(s) recorded on the sweet potato genotypes at ATC-Miyare and KALRO-Embu sites.

Genotype	VGR ^b (cm)	VIL (cm)	VID (mm)	SRCT (mm)	SRS (cm)	MLS (cm)	SRL (cm)	LSRD (cm)	PL (cm)	WLR (kg)	RY (Mt·ha ⁻¹)
Kenspot 1	5.7a ^a	2.7b	2.7b	4.7bc	5.0d ^a	5.3a	13.3c	8.0b	3.0cd ^a	0.6b	8.1d
Saly boro	4.3bc	1.4c	3.0ab	4.7bc	4.3e	5.3a	15.2b	6.3d	3.0cd	0.4c	6.8e
91/2187	5.4ab	2.7b	3.0ab	3.0e	5.0d	5.3a	12.3d	7.2bc	3.0cd	0.4c	3.9fg
Oduogo jodongo	4.3bc	1.7bc	3.0ab	4.3c	4.3e	5.3a	15.5b	7.0bc	4.3ab	0.5bc	9.1cd
5 Nyandere	4.7bc	2.0bc	3.0ab	3.7d	4.7de	5.3a	13.1c	8.3b	3.7bc	0.5bc	8.2d
Odinga	4.7bc	1.7bc	2.7b	3.3de	5.0d	5.3a	12.1d	6.2d	3.7bc	0.4c	7.7de
Naspot 1	4.7bc	2.7b	3.0ab	3.7d	5.0d	5.0a	13.3c	5.9d	3.7bc	0.6b	9.0cd
Kenspot 3	5.7a	2.7b	3.0ab	3.7d	4.3e	5.3a	12.3d	10.1a	4.0b	0.5bc	6.4ef
Naspot × New Kawogo 2	5.0ab	2.3bc	3.0ab	3.0e	4.3e	5.3a	11.4de	7.2c	3.0cd	0.5bc	7.1de
Nyamuguta	4.7bc	2.7b	2.7b	4.7bc	5.3cd	5.3a	14.8bc	7.3c	3.0cd	0.5bc	5.8ef
Nyautenge	5.7a	2.7b	2.3bc	4.3c	4.3e	5.3a	17.5a	7.4bc	4.0b	0.6b	16.0a
Ejumula × New Kawogo 4	4.0c	1.3c	3.0ab	4.0cd	6.0bc	5.3a	13.5bc	6.4cd	4.0b	0.4c	2.8g
Nyarambe	4.7bc	2.0bc	2.3bc	3.7d	4.7de	5.0a	9.9e	5.6d	4.0b	0.3d	4.9f
Nyakagwa	4.7bc	2.0bc	2.7b	6.0a	4.3e	5.3a	14.2bc	6.1d	3.3c	0.3d	7.8de
Naspot × New Kawogo 3	4.0c	1.3c	2.7b	3.0e	4.7de	5.0a	12.6cd	7.2c	3.7bc	0.5bc	5.1f

Ejumula × New											
Kawogo 2	4.3bc	1.3c	2.7b	3.3de	5.3cd	5.0a	13.2c	6.1d	4.7a	0.2e	2.6g
Nangili	4.7bc	2.7b	2.3bc	3.0e	4.0ef	5.3a	13.2c	7.1c	3.0cd	0.4c	6.9e
Kenspot 2	4.0c	1.3c	2.7b	3.7d	5.0d	5.3a	14.0bc	5.4d	3.3c	0.5bc	5.9ef
SPK 013	5.3ab	2.7b	3.0ab	5.3b	6.0bc	5.3a	14.8bc	9.2b	3.7bc	0.5bc	8.4d
Mugande × New											
Kawogo 4	4.3bc	2.3bc	2.7b	4.7bc	4.7de	5.0a	12.9cd	5.9d	3.3c	0.4c	5.8ef
Alupe or	3.7c	2.3bc	3.0ab	5.0b	4.3e	5.0a	11.8bc	5.5d	2.7d	0.4c	9.8cd
12 Marooko	5.0ab	1.7bc	3.0ab	3.0e	4.0ef	5.3a	13.6bc	7.1c	3.0cd	0.6b	4.7f
Kenspot 5	5.7a	3.0b	2.7b	4.7bc	7.0a	5.0a	10.1e	7.7bc	4.0b	0.6b	5.9ef
36 Kalamb Nyerere	5.3ab	2.7b	3.3a	4.0cd	5.3cd	5.0a	14.5bc	10.0a	3.7bc	0.6b	7.0e
K/KA/2004/215	4.3bc	2.3bc	3.0ab	4.3c	5.3cd	5.3a	13.8bc	5.4d	3.3c	0.3d	2.7g
Ejumula × New											
Kawogo 3	4.7bc	2.3bc	3.0ab	3.3de	4.7de	5.3a	12.3d	6.4cd	3.3c	0.4c	5.6ef
292-H-12	4.7bc	2.7b	3.0ab	4.3c	5.0d	5.0a	13.9bc	6.5cd	3.3c	0.4c	4.6f
Mogesi Gikenja	5.0ab	2.0bc	3.3a	3.3de	6.7ab	5.3a	12.6cd	8.9b	3.7bc	0.6b	6.0ef
Lungabure	4.0c	1.7bc	3.0ab	3.0e	5.0d	5.0a	14.7bc	6.6c	4.0b	0.6b	6.4ef
Kenspot 4	5.0ab	2.7b	2.7b	4.7bc	3.7g	5.3a	11.2de	6.7c	3.7bc	0.4c	6.3ef
Vitaa	5.0ab	2.3bc	3.0ab	3.7d	5.0d	5.0a	13.6bc	7.1c	3.3c	0.5bc	4.1fg
9 Nduma	4.3bc	2.3bc	2.3bc	4.7bc	6.3b	5.0a	12.7cd	5.8d	3.0cd	0.4c	5.8ef
24 Kampala	4.0c	1.0c	2.7b	3.3de	6.3b	5.0a	13.3c	5.5d	2.7d	0.5bc	2.6g
Obugi	5.0ab	2.0bc	2.7b	4.7bc	4.3e	5.3a	15.2b	7.5bc	4.0b	0.7ab	9.4cd
56682-03	5.0ab	3.0b	3.0ab	3.0e	5.7c	5.0a	12.0d	6.3cd	3.0cd	0.5bc	2.9g
Nyawo Nyathiodiewo	4.0c	2.0bc	3.0ab	3.7d	4.7de	5.3a	9.2f	5.1d	4.0b	0.4c	9.0cd
Gachaka	5.3ab	1.7bc	3.0ab	3.7d	3.7g	5.3a	15.5b	5.5d	3.7bc	0.5bc	7.9de
Mugande	4.0c	1.0c	2.7b	3.7d	5.3cd	5.0a	15.3b	5.7d	4.3ab	0.5bc	7.5de
Amina	4.3bc	2.7b	2.7b	5.0b	5.0d	5.0a	14.5bc	6.7c	4.0b	0.6b	10.7c
Fumbara jikoni	4.7bc	2.0bc	2.7b	3.7d	3.7g	5.3a	12.4d	7.4bc	4.0b	0.6b	4.1fg
Ejumula	5.7a	2.0bc	2.7b	3.7d	4.0ef	5.3a	14.4bc	9.1b	3.7bc	0.5bc	7.0e
Karunde	5.0ab	1.7bc	2.7b	3.3de	5.3cd	5.3a	13.9bc	6.8c	4.3ab	0.4c	4.1fg
SPK 004	5.0ab	2.3bc	2.3bc	4.3c	5.3cd	5.3a	11.9d	5.1d	3.0cd	0.3d	4.1fg
Kunyibuonjo	5.0ab	1.7bc	3.0ab	6.3a	5.0d	5.0a	13.5bc	6.5cd	4.3ab	0.3d	2.2h
K/KA/2002/12	4.7bc	2.0bc	3.0ab	4.7bc	4.7de	5.3a	13.8bc	6.7c	3.7bc	0.4c	6.6ef
55 Nganyomba	4.7bc	1.3c	2.7b	4.0cd	4.7de	5.7a	13.2c	6.9c	3.3c	0.5bc	6.1ef
1-Ujili	4.3bc	1.3c	2.3bc	3.7d	5.0d	5.0a	14.9bc	5.8d	3.0cd	0.3d	3.0g
Santo Amaro	5.3ab	2.7b	2.7b	4.3c	4.3e	5.3a	13.1c	6.4cd	3.7bc	0.4c	7.3de
Mugande × New											
Kawogo 2	4.7bc	1.3c	2.7b	4.3c	5.3cd	5.0a	10.5e	4.6e	2.3e	0.4c	3.6fg
Wera	5.3ab	2.0bc	3.0ab	3.7d	5.7c	5.3a	13.3c	7.2c	4.3ab	0.7ab	7.0e
Kemb 10	4.3bc	2.3bc	3.0ab	4.0cd	5.7c	5.0a	12.9cd	7.8bc	3.7bc	0.6b	13.1b
Mbita	5.0ab	2.7b	3.0ab	5.0b	3.7g	5.0a	14.1bc	6.7c	3.0cd	0.8a	7.5de
Naspot × New Kawogo											
1	4.7bc	2.0bc	2.7b	4.0cd	5.7c	5.3a	11.7d	6.4cd	3.3c	0.4c	2.9g
Kibuonjo	4.7bc	1.7bc	3.0ab	4.0cd	2.7h	5.3a	11.8d	10.0a	3.3c	0.4c	5.8ef
29 Kunyibuonjo	5.0ab	2.0bc	3.0ab	3.0e	4.0ef	5.3a	14.3bc	5.0d	4.0b	0.4c	5.8ef
62 Odhiogo	5.0ab	2.3bc	2.7b	4.3c	5.3cd	5.3a	12.3d	8.2b	3.7bc	0.5bc	7.6de
52 Nyakisumu	5.0ab	2.3bc	2.7b	3.7d	5.0d	5.3a	13.0c	8.7b	3.0cd	0.5bc	3.6fg
Ejumula × New											
Kawogo 1	4.7bc	2.7b	3.3a	3.3de	4.7de	5.0a	12.0d	6.3cd	3.0cd	0.4c	6.4ef
Bungoma	4.0c	1.7bc	3.0ab	3.0e	4.7de	5.3a	12.6cd	7.3bc	4.0b	0.5bc	6.1ef
K 117	4.3bc	2.0bc	3.0ab	3.7d	6.0bc	5.3a	13.0c	6.8c	3.3c	0.4c	9.2cd
Fundukhusia	5.7a	3.0b	2.0c	5.7ab	4.0ef	5.0a	12.8cd	8.6b	2.7d	0.5bc	9.2cd
SPK 031	5.0ab	1.7bc	2.0c	3.3de	4.3e	5.3a	11.1de	6.9c	3.3c	0.4c	4.9f
Mugande × New											
Kawogo 1	4.3bc	2.0bc	2.3bc	3.7d	4.7de	5.0a	12.4d	8.4b	3.7bc	0.4c	9.1cd
Mwavuli	5.7a	3.7a	3.0ab	4.0cd	5.0d	5.0a	13.3c	6.9c	4.0b	0.5bc	5.1f
Polo yiengo	5.0ab	2.0bc	3.3a	4.0cd	4.3e	5.3a	11.5de	8.7b	4.0b	0.6b	4.0fg
Mugande × New											
Kawogo 3	4.3bc	2.0bc	2.7b	3.7d	4.3e	5.3a	13.2c	5.9d	3.7bc	0.4c	3.3fg
Sinia	5.0ab	2.7b	3.0ab	3.7d	5.3cd	5.3a	15.5b	8.6b	3.3c	0.5bc	8.7d
Tainung	4.7bc	2.0bc	2.3bc	3.7d	4.3e	5.3a	13.4c	5.6d	2.7d	0.5bc	3.6fg
<i>Location means</i>											
ATC-Miyare	5.4a	2.4a	3.0a	4.3a	6.3a	5.0a	10.8b	6.5b	3.7a	0.5a	5.1b
KALRO-Embu	4.1b	1.9a	2.6a	3.7a	3.4b	5.5a	15.5a	7.3a	3.4a	0.5a	7.5a

^a values in columns with the same letter are not significantly different, LSD test, $p < 0.05$. ^b VGR = vine growth length; VIL = vine internode length; VID = vine internode diameter; SRCT = storage root cortex thickness; SRS = storage root stalk; MLS = mature leaf size; SRL = storage root length; LSRD = largest storage root diameter; PL = petiole length; WLR = weight of largest root; RY = root yield.

Analysis of variance indicated differences in storage root stalk (SRS) of genotypes and sites (Table 4). The SRS of all genotypes ranged from short to very long. There were no genotypes that exhibited very short SRS. Genotypes that had the shortest SRS were Kibuonjo; genotypes Naspot 1 and Mogesi Gikenja had the longest SRS. The ACT-Miyare site had longer SRS than the KALRO-Embu site.

Analysis of variance indicated no difference in mature leaf size (MLS) of sweet potato genotypes (Table 4). The MLS of all genotypes in ACT-Miyare were regarded as small. There was no difference in MLS between sites.

Analysis of variance indicated differences on storage root length (SRL) of sweet potato genotypes and sites (Table 4). The SRL of genotypes ranged from short to long. Genotypes with the shortest SRL were Nyawo Nyathiodiewo. The genotype that recorded the longest SRL was Nyautenge. Genotypes at KALRO-Embu had the longest SRL compared to those at ACT-Miyare.

Analysis of variance indicated differences in storage root diameter (SRD) of sweet potato genotypes and sites (Table 4). Genotypes with the shortest SRD was Mugande × New Kawogo 2. Genotypes with the longest SRD were Kenspot 3 Kenspot 5 and Kibuonjo. Genotypes at KALRO-Embu had longer SRD than at ACT-Miyare.

Analysis of variance indicated significant differences on petiole length of sweet potato genotypes (Table 6). All genotypes had very short petioles. Genotypes that had the shortest petioles were Mugande × New Kawogo 2 while genotypes Ejumula × New Kawogo 2 had the longest petiole length. The sites did not differ in petiole length.

Analysis of variance indicated differences in weight of the largest storage root (WLSR) of sweet potato genotypes (Table 4). Genotypes that had the least weights were Ejumula × New Kawogo 2; the heaviest WLSR was from genotype Mbita. The sites did not differ.

Analysis of variance indicated differences in storage root yield of genotypes and sites (Table 4). The genotype Kunyibuonjo had the lowest root yield and genotype Nyautenge the highest yield. KALRO-Embu had the highest yield compared with ACT-Miyare.

Quantitative characters used to generate the dendrograms were: vine growth rate, vine internode length, vine internode diameter, storage root cortex thickness, storage root stalk, mature leaf size, storage root length, storage root diameter, petiole length, weight of largest tuber and yield (Figs. 1, 2). From the hierarchical cluster analysis, quantitative characters indicated polymorphism of about 2.5 among the genotypes at ATC-Miyare (Fig. 1). The tree obtained separated genotypes into 2 major clusters (A and B) at about 2.5 Euclidean distance. Cluster A contained 36 genotypes and consisted of 2 sub-clusters. Cluster B contained 32 genotypes and formed 3 sub-clusters. Both cluster A and B did not exhibit any distinguishable relationship or pattern. From the hierarchical cluster analysis, quantitative characters showed a polymorphism of about 2.8 among the 68 sweet potato genotypes at KALRO-Embu (Fig. 2). The tree obtained separated genotypes into 2 major clusters (A and B) at about 2.7 Euclidean distance. Cluster A contained 22 genotypes and consisted of 2 sub-clusters. Cluster B contained 46 genotypes and formed 3 sub-clusters (Fig. 2). Clusters A and B did not show any distinguishable relationship or pattern.

Significant correlations occurred among quantitative agro-morphological characters of the genotypes in ATC-Miyare (Table 5). Positive significant correlations occurred between vine growth rate and vine internode length, vine growth rate and mature leaf size, storage root stalk and root yield, and root yield and largest storage root diameter. Similarly, significant correlations occurred among the quantitative agro-morphological characters of the sweet potato genotypes in KALRO-Embu (Table 6). Positive significant correlations occurred between vine growth rate and vine internode length, largest storage root diameter and weight of largest root, storage root length and weight of largest root. Root yield was significantly, and positively, correlated with the weight of largest root.

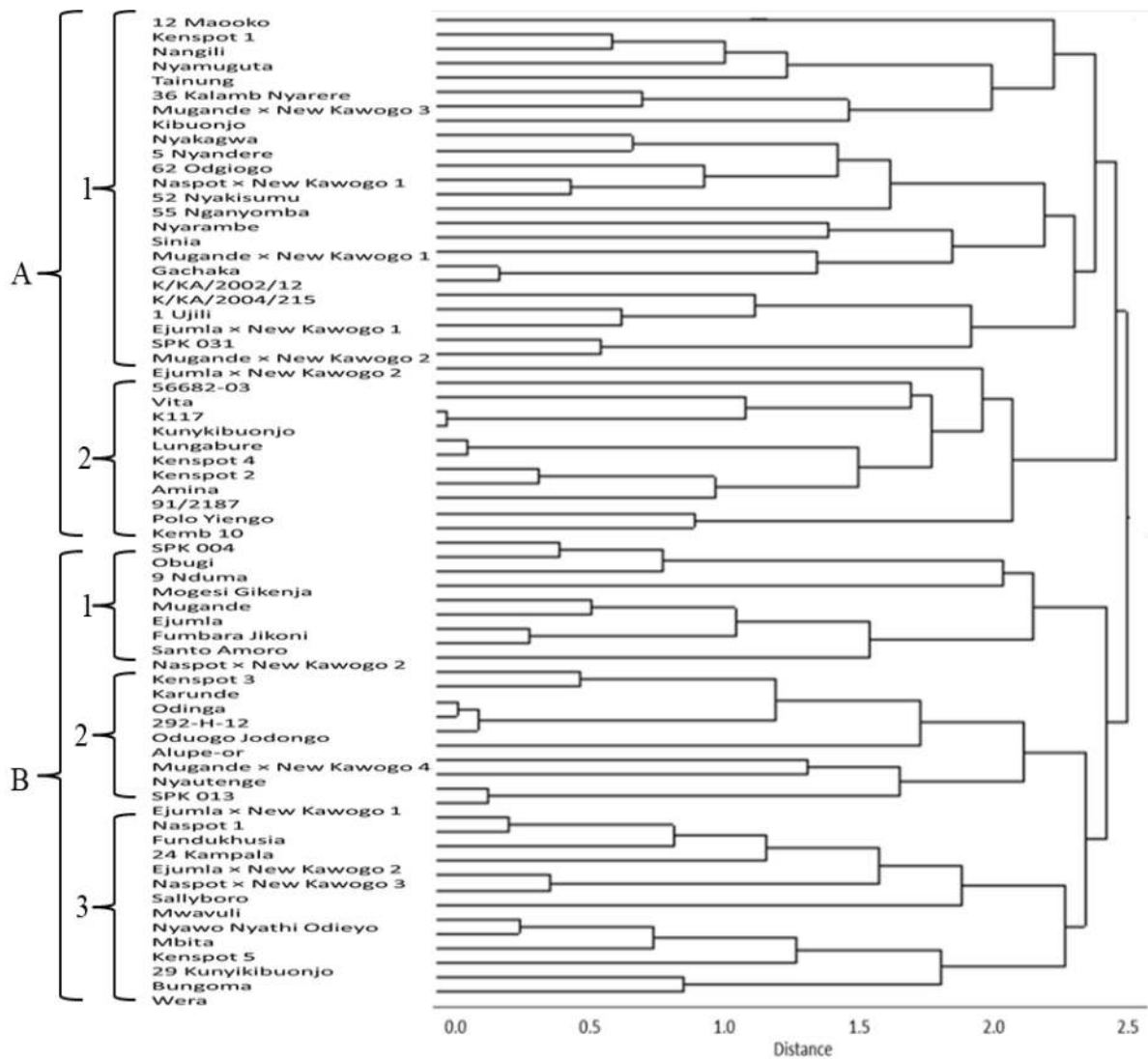


Figure 1. The dendrogram (based on Euclidean distance coefficient) of sweet potato genotypes generated from quantitative data at ATC-Miyare. Genotypes connected by portions of the dendrogram are highly related. As the dendrogram couplets coalesce the genotypes are fit into groups that are related based on vine growth rate, vine internode length, vine internode diameter, storage root cortex thickness, storage root stalk, mature leaf size, storage root length, storage root diameter, petiole length, the weight of largest tuber and yield. Letters (A, B) and numbers (1, 2, 3) represent clusters and sub-clusters respectively.

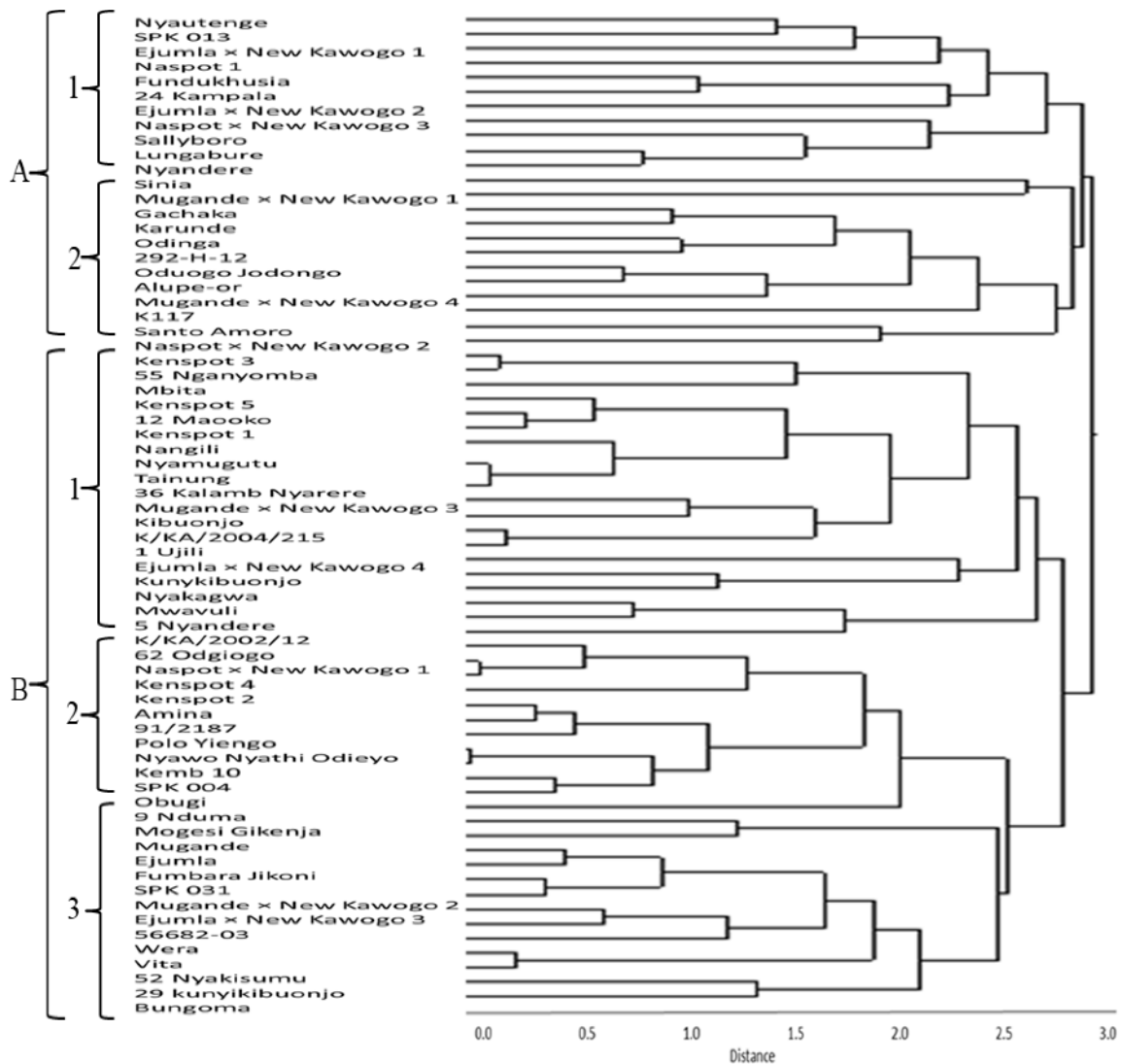


Figure 2. The dendrogram (based on Euclidean distance coefficient) of sweet potato genotypes generated from quantitative data at KALRO-Embu. Genotypes connected by portions of the dendrogram are highly related. As the dendrogram couplets coalesce the genotypes are fit into groups that are related based on vine growth rate, vine internode length, vine internode diameter, storage root cortex thickness, storage root stalk, mature leaf size, storage root length, storage root diameter, petiole length, the weight of largest tuber and yield. Letters (A, B) and numbers (1, 2, 3) represent clusters and sub-clusters respectively.

Table 5. Correlations among selected quantitative agro-morphological traits recorded on the sweet potato genotypes at ATC-Miyare.

	Vine growth rate	Storage root stalk	Largest storage root diameter
Vine internode length	$r = 0.6^*$		
Mature leaf size	$r = 0.7^*$	$r = -0.2$	
Root yield	$r = 0.2$	$r = -0.2^*$	$r = 0.5^*$

*Significant at $p < 0.05$.

Table 6. Correlations among selected quantitative agro-morphological traits recorded on the 68 sweet potato genotypes at KALRO-Embu.

	Vine growth rate	Storage root length	Largest storage root diameter	Weight of largest root
Vine internode length	$r = 0.7^*$			
Weight of largest root	$r = 0.3$	$r = 0.6^*$	$r = 0.6^*$	
Root yield	$r = 0.0$	$r = 0.4$	$r = 0.2$	$r = 0.5^*$

*Significant at $p < 0.05$.

Discussion

Assessment of agro-morphological diversity and relationships among sweet potato varieties is important for germplasm conservation, and for breeding, especially during selection of varieties having superior qualities [17]. Among genotypes, most agro-morphological characters were highly variable. Genotypes in KALRO, Embu had better performance on agro-morphological characters such as storage root length, largest storage root diameter, and root yield compared with ATC, Miyare. Genotypes in ATC, Miyare were superior in vine growth length and storage root stalk compared with KALRO, Embu. This could be attributed to changes in agro-morphological conditions in both locations. The high variability in sweet potato genotypes is caused by natural mutations [18]. No single genotype was superior in all agro-morphological traits, due to unique genetic constitutions. Genotypes exhibiting intermediate, or fast, growth rate can be suitable for animal feed since the vines of sweet potato usually form an excellent source of green fodder [19]. However, most genotypes were not ideal in terms of root yield stability except for genotype Nyautenge. High yield is a product of genetic make up of individual genotypes [5,17], increased weight of roots, or increased number of roots, per plant [20]. There was a potential of some genotypes to yield more if all roots harvested from each plot would be equal to the largest root. Some genotypes exhibited long storage root stalks at both sites. A long root stalk increases rooting depth. Deep rooting can act as an escape mechanism to weevil infestation. Deep rooting and early maturing genotypes are less susceptible to insect pest infestations than shallow rooting and late maturing genotypes [21].

The dendrograms trees could only indicate general germplasm relatedness and diversity. There was high polymorphism of 2.5 and 2.8 in ATC, Miyare and KALRO, Embu respectively. This there indicates high genetic variability among the studied sweet potato genotypes. The probable reason as to why clustering of genotypes was not uniform across the dendrograms is that expression of agro-morphological characters is environment dependency. Similar results were obtained by [22] when studying sweet potato genotypes in Tanzania. That genotypes sharing a common name did not express genetic similarities underlines that artificial naming of biological organisms has no bearing on genetic makeup. This was more pronounced in the F₁ clones. It is possible that the F₁ clones clustered in different groups because they are not genetically stable. The high variability of vegetative characters among varieties can be attributed to high polyploidy level in sweet potato [20].

In ATC, Miyare, there was a significant correlation between vine growth rate with vine internode length and mature leaf size, storage root stalk with root yield and largest root diameter with root yield. In KALRO, Embu there was a significant correlation between vine growth rate with vine internode length, storage root length with weight of the largest root, largest root diameter with weight of the largest root and weight of the largest root diameter with root yield. These correlations indicate the importance of sink-source relationships in plants. M.J. Mbithe et al. [20] observed a similar relationship on sweet potato genotypes in Uganda.

Conclusion

Agro-morphological characters were used to characterize the selected sweet potato germplasm. Findings of the present study reveal that sweet potato germplasm presented high diversity based on the agro-morphological assessment. There was also a significant correlation among the variables of the studied genotypes. The study also revealed that the agro-morphological characters used in this study could effectively discriminate the different genotypes as seen from the dendrograms. Genotype Nyautenge was the best performing in terms of storage root yield.

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