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Phenotypic Characterization of Cassava (*Manihot esculenta* Crantz) Germplasm in Kenya

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Abstract

Cassava (*Manihot esculenta)* is an important cash crop for many small scale farmers in Kenya. The cassava genetic resources in Kenya are often underestimated due to improper characterization of the germplasm available. The objective of this study was to characterize popular cassava landraces and improved varieties grown by small-scale farmers based on their phenotypic traits. The materials were collected from seven major cassava growing counties in Kenya. The survey collected 131 cassava genotypes. These were planted at two experimental sites. Both quantitative and qualitative phenotypic traits data was collected at 3, 6, 9 and 12 months after planting. The data was subjected to Multivariate analysis and dendogram developed at $p < 0.05$. Analyzed phenotypic traits categorized the genotypes into four cluster groups. Cluster 1, 2, 3, and 4 had 72.5%, 16.0%, 3.1% and 8.4% genotypes respectively. Out of the 25 phenotypic characters assessed, a total of 11 principal components (PCs) trait sets accounted for 71.58%cumulative genetic variation at $p<0.05$.A follow up study on genetic characterization should be done to show the correlation between genetic and phenotypic characterization. Results from this study will assist farmers and breeders to optimize utilization of cassava germplasm for food security.

Keywords: Phenotypic characterization, Cassava, cluster analysis, Principal components, Kenya

Introduction

Cassava (*Manihot esculenta* Crantz) is mainly cultivated in tropical countries, particularly in sub-Saharan Africa, South America and Asia as an important staple food (FAOSTAT, 2020). Worldwide, cassava production is estimated to be 277 million tons on approximately 24.5 million hectares and provides food for more than 800 million people (FAOSTAT, 2020). According to Leon-Pacheco *et al.*, (2020), cassava crop rank third in terms of carbohydrate food source in the tropics after rice and maize and provides more than 60% of the daily calorific needs of the populations in tropical Africa and Central America. In Africa, over 90% of cassava produced is consumed as human food with only 6% devoted to livestock feed (Okbenin *et al.* 2013; Adu *et al*., 2018). Cassava production in Africa is estimated at 160 million tons on 18 million hectares and Nigeria being the largest producer country of cassava (FAO, 2018). According to FAO (2018), Eastern Africa production is estimated at 30 million tons on 3 million hectares. Tanzania leads in production with 5 million tons, followed by Uganda, Burundi, Rwanda, Kenya and South Sudan. According to the Kenya Ministry of Agriculture Annual Report (MOA, 2022), the country currently produces one million metric tons annually and has the potential to produce 3 million tons. Cassava production in Kenya takes

place mainly in the low altitude areas of the coastal region, mid-altitude zones in central and eastern regions and in Nyanza and western regions (Mware *et al*., 2009). The area under cassava in western, Nyanza and central/eastern regions is estimated at 49,000, 34,000 and 19,000 ha respectively, representing nearly all the country's total area under this crop.

In Kenya, some of the challenges in domestication of cassava are attributed to the need of possession of a great part of the biological diversity and traditional knowledge associated with this species (Masinde *et al*, 2018). Farmers partly use morphological characteristics and other attributes to distinguish, manage and conserve varieties they grow on farm. An obstacle to the reliable identification of cultivars is the existence of considerable linguistic polymorphism. Each region or farmer community has its own unique series of names for different or same cultivars with specific meaning. This informal naming of varieties, however, can lead to overestimation or underestimation of crop diversity because the same variety can take different names between regions and communities. Smallholder farmers are important guardians of crop genetic diversity beyond the centers of origin. Traditionally, farming communities are known to maintain knowledge of this genetic diversity through vernacular names. Since cassava was introduced in Kenya, farmers have named the varieties according to the source of planting material, the distinguishing phenotypic characteristics or the cyanide content. Thus the same cassava genotype may be given different names in different areas depending on the farmer's perception. For example, the variety *Adhiambo lera* (clean lady) in one area, *Karembo* (beautiful*)*, in another area, or *Kasukali* (sweet) elsewhere. In another scenario Kenya experienced a severe outbreak of Cassava Mosaic Disease (CMD) in the 1980's and 1990's. The Kenya Agricultural Livestock Research Organization (KALRO) in collaboration with the International Institute for Tropical Agriculture (IITA) introduced Tropical Manioc Selection (TMS) cassava varieties. After testing for agronomic adaptability, suitable varieties were released to farmers for growing. The varieties were released to farmers with their original coded numbers such as MM96/4466, MH95/0183, MM96/0067, SS4, KME-4. For failure to memorize these codes, farmers named all these genotypes, "*Agriculture*".

Germplasm characterization is an important aspect of cassava breeding and conservation. It involves the evaluation and documentation of genetic diversity of a collection of cassava genotypes, which is important for the development of improved varieties and for maintaining genetic diversity of crops (KEPHIS, 2016; Tumuhimbise *et al*, 2016). Some of the important parameters that are used for characterization of germplasm in cassava include: Phenotypic/morphological, biochemical, molecular, agronomic, and phonological (Okogbenin *et al*. 2013). Phenotypic identification of plants is commonly based on the morphological traits assessed and recorded in the field (Fukuda *et al.* 2010). Different cultivars have been distinguished by phenotypic characteristics, such as color and shape, branching habit, plant height, color of stem and petiole, root shape and root skin color, time of maturity, yield and the cyanogenic glycosides content in the roots (Fukuda *et al*., 2010; Saravanan, 2016).

The objective of this study was to characterize the existing popular local cassava varieties grown by small scale farmers in Kenya.

Materials and Methods
Map of the Study Area

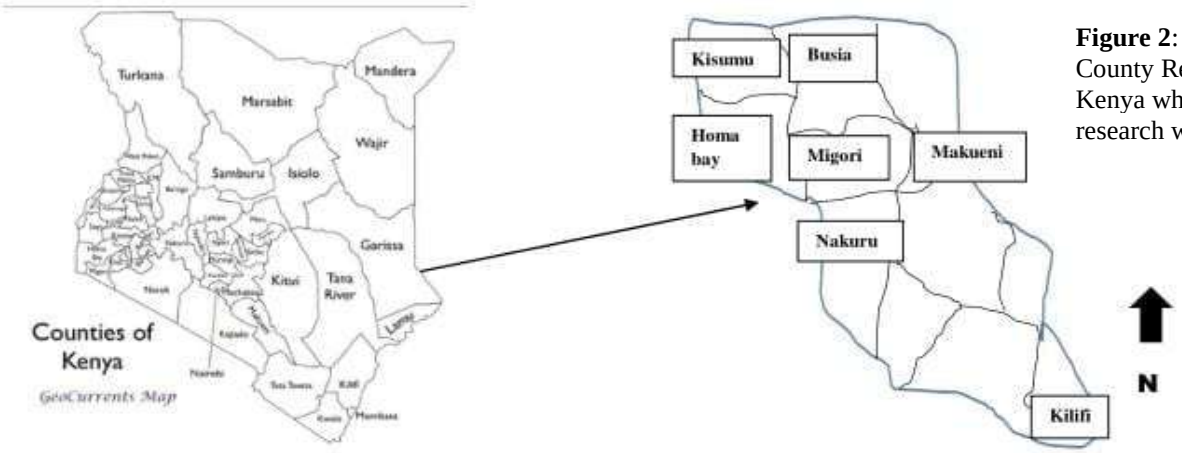

Figure 1: Map of Kenya, where the research was undertaken.
Source: Adopted from Google map (10/6/2023)

Figure 2: Sampled County Regions in Kenya where the research was done.

Source: Adopted from Google (10/6/2023)

Cassava genotypes collection and multiplication

Surveys were carried out in 2018 – 2019 main rain season and short rain season in the major cassava growing regions in Kenya. The objective was to collect the popular cassava improved varieties and landraces grown by farmers. The regions were represented by the following counties:Coastal region (Kilifi), Eastern and Central (Makueni and Nakuru), Western (Busia), Nyanza (Migori, Homabay and Kisumu). During collection, a single stem from one plantwas collected to represent the cassava accession. The local name of the variety was obtained from the farmer and also the source of the planting materials. The stem was cut into pieces length 15 cm and placed in a collection bag. The samples collected were planted in single rows for multiplication at the Rongo University farm located in Migori County. Each single row had 5 – 10 plants. The spacing was 1m between rows and 1 m within rows.

Experimental design and plot layout

The accessions were harvested from the multiplication block in January-February, 2021. Two experimental sites were established: Rongo University (-0.826279^{o}, 34.614186^{o}) and Mawego Technical Training Institute (-0.39652^{o}, 34.77068^{o}). The plants harvested from each accession were cut into pieces with each having 4-5 nodes. Each accession was planted three rows, with each row planted 5 plants. The spacing was 1m between rows and 1m between plants. Normal agronomic practices were carried out during the experimental period. No fertilizer or pesticides were applied on the crop.

Data Collection

Phenotypic data was collected on the plants in the middle row of each accession. Phenotypic characterization was done using the selected morphological and agronomic descriptors for the characterization of cassava as described by (Fukuda *et al*., 2010) (Table 1). The observations were made at 3, 6, 9, and 12 months after planting (MAP).

Table 1: Selected qualitative and quantitative phenotypic descriptors for the characterization of 131 cassava genotypes

SN	Trait descriptor	Score code	Sampling time
1	Colour of apical leaves	3 = light green; 5 = dark green; 7 = purplish green; 9 = purple	3 MAP
2	Shape of central leaflet	1 = ovoid; 2 = elliptical-lanceolate; 3 = obovate-lanceolate; 4 = oblong-lanceolate; 5 = lanceolate; 6 = straight or linear; 7 = pandurate; 8 = linear-piramidal; 9 = linear-pandurate; 10 = linear-hostalobalate	6 MAP
3	Petiole colour	1 = yellowish-green; 2 = green; 3 = reddish-green; 5 = greenish-red; 7 = red; 9 = purple	
4	Leaf colour	3 = light green; 5 = dark green; 7 = purple green; 9 = purple	
5	Number of leaf lobes	3 = three lobes; 5 = five lobes; 7 = seven lobes; 9 = nine lobes; 11 = eleven lobes	
6	Length of leaf lobe	Measurement of two middle leaf lobes from three middle plants	
7	Width of leaf lobe	Measure the width of the widest part of the same lobes in SN 6 above	
8	Ratio of lobe length to lobe width of central lobe	Calculation	
9	Lobe margins	3 = smooth; 7 = winding	
10	Petiole length	Measure two leaves per plant	
11	Colour of leaf vein	3 = green; 5 = reddish-green in less than half of the lobe; 7 = reddish-green in more than half of the lobe; 9 = all red	
12	Orientation of petiole	1 = inclined upwards; 3 = horizontal; 5 = inclined downwards; 7 = irregular	
13	Flowering	0 = absent; 1 = present	
14	Pollen	0 = absent; 1 = present	
15	Prominence of foliar scars	3 = semi-prominent; 5 = prominent	9 MAP
16	Colour of stem apex	1 = orange; 2 = light green; 3 = dark green	
17	Colour of stem epidermis	1 = cream; 2 = light brown; 3 = dark brown; 4 = orange	
18	Colour of stem exterior	3 = orange; 4 = greeny-yellowish; 5 = golden; 6 = light brown; 7 = silver; 8 = grey; 9 = dark brown	
19	Distance between leaf scars	3 = short < (8 cm); 5 = medium (8-15 cm); 7 = long > (15 cm)	
20	Growth habit of stem	1 = straight; 2 = zig-zag	
21	Colour of end branches of adult plant	3 = green; 5 = green-purple; 7 = purple	
22	Extent of root peduncle	0 = sessile; 3 = pedunculate; 5 = mixed	12 MAP (at harvest)
23	Root shape	1 = conical; 2 = conical-cylindrical; 3 = cylindrical; 4 = irregular	
24	External colour of storage root	1 = white or cream; 2 = yellow; 3 = light brown; 4 = dark brown	
25	Colour of root pulp (parenchyma)	1 = white; 2 = cream; 3 = yellow; 4 = orange; 5 = pink	
26	Colour of root cortex	1 = white or cream; 2 = yellow; 3 = pink; 4 = purple	
27	Cortex: ease of peeling	1 = easy; 2 = difficult	
28	Texture of root epidermis	3 = smooth; 5 = intermediate; 7 = rough	
29	Root taste	1 = sweet; 2 = intermediate; 3 = bitter	
30	Cortex thickness	1 = thin; 2 = intermediate; 3 = thick	

Data Analysis

The genetic variation among the studied genotypes for agro-morphological traits was explored using multivariate analysis technique (Karim *et al*. 2020). Multivariate analysis of the 131 data matrix comprising of principal component analysis (PCA) processed using IBM SPSS statistics software version

25. In the PCA, Eigenvalues and load coefficient values were generated from the data set. The relevance of trait contribution to the variation accounted by each principal component was based on the absolute eigenvector arbitrary cutoff value of 0.30 (Richman, 1988). Structure of morphological changeability was visualized using ascending hierarchical clustering (AHC) based on data and Ward's Method to plot a dendrogram (Karim *et al*., 2020). The principal component analysis and correlation matrices were used to determine the relationships among the traits.

Results

Principal component analysis of phenotypic characters

The eigenvalues and percentage variations of the principal component analysis are presented in Table 2. Eigenvalues are the special set of scalar values that is associated with the set of linear equations most probably in the matrix equations. Eleven principal components that accounted for 71.58% of the total variation among the genotypes were identified. The first PC axis with eigenvalue of 3.27 accounted for 13.07% of the total variation whereas the second, third, fourth and the fifth PC axes with eigenvalues of 2.39, 2.04, 1.74 and 1.54 accounted for9.55%, 8.15%, 6.97% and 6.15% of the total variation, respectively. The sixth, seventh, eighth, ninth, tenth and eleventh PC axes with eigenvalues of 1.41, 1.27, 1.16, 1.11, 0.99 and 0.98 accounted for 5.64%, 5.08%, 4.65%, 4.45%, 3.95%and 3.93% of the total variation, respectively (Table 2).

Table 2. Principal component analysis, eigenvalues and percentage variations of twenty five phenotypic traits of 131 cassava genotypes

Principal Component	**Characteristics**	Initial Eigenvalues		
		Total	% of variance	Cumulative %
1	Shape of central leaflet	3.27	13.07	13.07
2	Lobe margins	2.39	9.55	22.62
3	Colour of stem epidermis	2.04	8.15	30.76
4	Colour of stem exterior	1.74	6.97	37.73
5	Leaf colour	1.54	6.15	43.88
6	Orientation of petiole	1.41	5.64	49.53
7	Extent of root puduncle	1.27	5.08	54.61
8	Colour of root cortex	1.16	4.65	59.26
9	Root shape	1.11	4.45	63.70
10	Root taste	0.99	3.95	67.65
11	Cortex thickness	0.98	3.93	71.58
12	Distance between leaf scars	0.88	3.50	75.09
13	Colour of root pulp (parenchyma)	0.82	3.27	78.36
14	Texture of root epidermis	0.77	3.08	81.43
15	Average petiole length	0.66	2.64	84.07
16	Color of apical leaves	0.62	2.49	86.57
17	Cortex ease of peeling	0.57	2.26	88.82
18	Colour of end branches of adult plant	0.51	2.02	90.84
19	Flowering	0.46	1.83	92.67
20	Colour of stem cortex	0.42	1.66	94.35
21	Number of leaf lobes	0.35	1.40	95.74
22	Colour of leaf vein	0.34	1.35	97.09
23	Petiole colour	0.30	1.20	98.29
24	External colour of storage root	0.24	0.98	99.27
25	Average ratio of lobe length to lobe width	0.18	0.73	100.00

Phenotypic characterization

Cassava landraces analyzed revealed larger degree of morphological variations based on 25phenotypic qualitative and quantitative descriptors used (Table 1).The dendrogram obtained (Fig 3)using phenotypic characters separated the 131cassava genotypes into four major clusters (1, 2, 3 and 4) at similarity index of 0.5. Results presented in Table3 showed that 95cassava genotypes accounting for 72.5% of the accessions were grouped in cluster #1 (Table 3). Cluster #2had 21phenotypes representing 16% of the total number of entries. Cluster #3 and 4 had 4 genotypes (3.1%) and 11 genotypes (8.4%) respectively (Table 3).

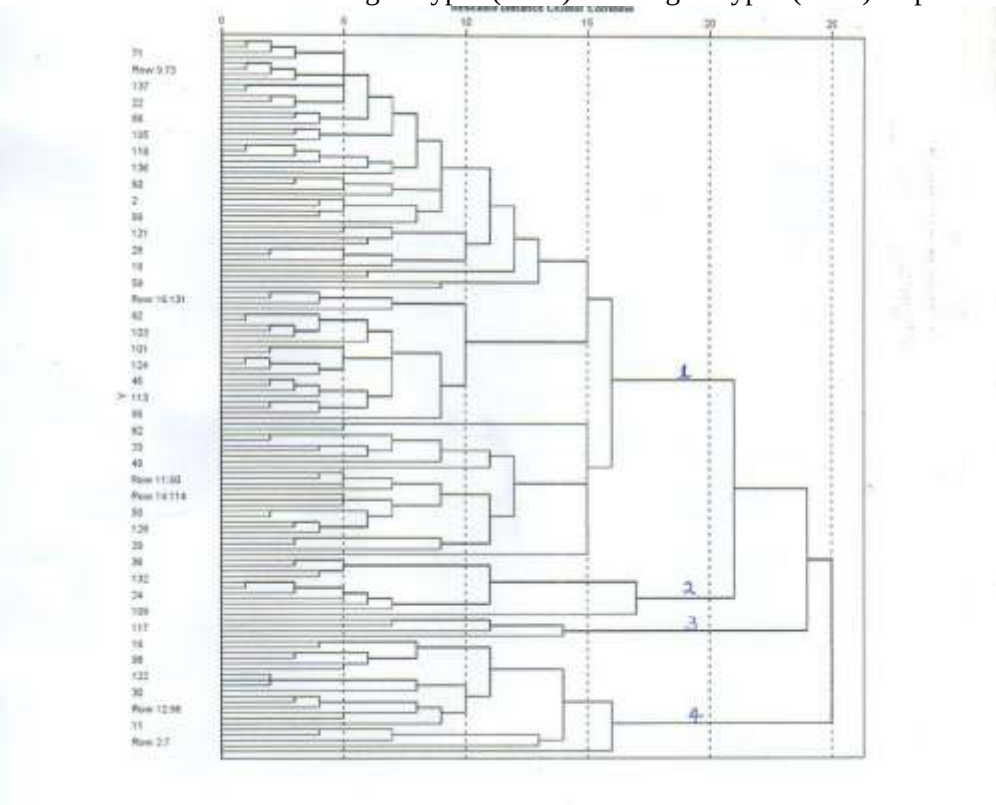

Figure 3: Dendrogramillustrating131Cassava genotypes based on average linkage (between groups) cluster analysis

Table 3: Names of cassava varieties, locations and the counties they were collected

CLUSTER #1			
Accession No.	**Variety**	**Location collected**	**County**
Row 14:114	Nyakanyamkago	Sigiria	Migori
Row 16:131	MM96/0039	Chakol	Busia
Row 13:104	Nyar-ICIPE	Sigiria	Migori
Row 10:83	Mygera	Rongo	Migori
Row 11:90	Adhiambo lera-002	Mtwapa	Kilifi
Row 4:23	Nyatanga	Rabuor	Kisumu
Row 5:33	Nyarkokaro	Rakwaro	Migori
Row 7:53	Amakuria	Masaba- Kehancha	Migori
Row 9:73	Busia-004	Busia	Busia
106	Agriculture-019	Maram	Homa bay
107	Nyatonge-002	Sigiria	Migori
108	Mygera-002	Sigiria	Migori

110	Obayo dak-003	Ranen	Migori
111	Otia	Sigiria	Migori
112	Agriculture-020	Ranen	Migori
113	Agriculture-021	Maram	Homa bay
115	Konono	Ranen	Migori
116	Agriculture-022	Pembe	Migori
118	Agriculture-23	Kitere	Migori
119	Agriculture-024	Sigiria	Migori
120	Unknown	Maram	Homa bay
121	Obaro dak-004	Nyamarere	Migori
124	Mufutu	Migori	Migori
126	Nyaodendo	Sigiria	Migori
127	NyarMaseno	Busia	Busia
128	MM96/4878	Busia	Busia
129	Yellow - 002	Chakol	Busia
130	MH95/0183	Chakol	Busia
134	Magana	Chakol	Busia
135	MH96/0031	Chakol	Busia
136	Migyera - 003	Chakol	Busia
137	Bwana Terana	Chakol	Busia
138	MH95/2480	Kolwa	Kisumu
100	Agriculture-018	Ranen	Migori
101	Bwong	Ranen	Migori
102	Obaro dak-001	Maram	Homa bay
103	Nyarkanyamkago	Ranen	Migori
105	Obar dak-002	Nyamarere	Migori
12	Agriculture-003	Rapogi	Migori
18	Katune	Kiboko	Makueni
19	KME-4	Kiboko	Makueni
20	Kazanzwara	Kiboko	Makueni
21	KBK-20	Kiboko	Makueni
22	Agriculture-004	Busia	Busia
25	Nyaeta	Kehancha	Migori
26	Wild cassava-001	Ranen	Migori
28	Kienyeji	Maram	Homa bay
29	Wild cassava -002	Rusinga island	Homa bay
34	Unknown variety	Kegonga-Kehancha	Migori
37	Buria	Maeta, Kehancha	Migori
38	NyaogutuNgalo	Maram	Homa bay
40	Nyagire	Maram	Homa bay
41	Agriculture 006	Opago	Migori
44	Unknown variety-003	Maram	Homa bay
45	Nyasega	Rakwaro	Migori
46	Nyasuna	Kokuro	Migori
47	Nyatanga-003	Opapo	Migori
48	Nyakakelo	Kanga	Migori
49	Obiero Abele	Ranen	Migori
50	Opoto	Uriri	Migori
51	Nyakasamwel	Awendo	Migori
52	Nyarkagutu	Ngothe	Migori
54	Agriculture-007	Suba; Kuria	Migori

55	Agriculture-008	Busia	Busia
56	Agriculture-009	Masaba; Kehancha	Migori
57	MM96/4466	Subukia	Nakuru
59	Busia-001	Busia	Busia
60	Busia-002	Busia	Busia
61	Machoberi	Kegonga;Kehancha	Migori
66	Agriculture-011	Kegonga; Kehancha	Migori
67	Agriculture -012	Awendo	Migori
71	Agriculture -013	Dede	Migori
74	Nyarkogutu-002	Ngothe	Migori
75	Nyarkadera	Kadera	Migori
76	Agriculrure-014	Uriri	Migori
78	Unknown variety-004	Kehancha	Migori
80	Agriculture-015	Busia	Busia
81	Agriculture-016	Rongo	Migori
82	Waite-002	Kegonga; Kehancha	Migori
85	Achuth	Uriri	Migori
86	Nyanchama	Rongo	Migori
87	Nyatanga-004	Rongo	Migori
88	F-19	Mtwapa	Kilifi
91	Katsuhanzala	Mtwapa	Kilifi
92	Kasukari	Mtwapa	Kilifi
93	Karembo	Mtwapa	Kilifi
94	Mtwapa-002	Mtwapa	Kilifi
95	Tajirika	Mtwapa	Kilifi
97	Kibanda meno-003	Mtwapa	Kilifi
99	MM96/0067	Mtwapa	Kilifi
10	Agriculture-001	Ranen	Migori
2	Mzungu	Mida Creek	Kilifi
3	Miida	Mida Creek	Kilifi
6	Mbale-002	Mida Creek	Kilifi
9	Mary Kaluorore	Ranen	Migori
CLUSTER #2			
Row 15:123	Rateng	Pembe	Migori
Row 12:96	Agriculture-017	Mtwapa	Kilifi
Row 6:43	Odiero	Rongo	Migori
Row 2:7	Agriculture-001	Ranen	Migori
122	Ratena	Nyamarere	Migori
13	Yellow-001	Rapogi	Migori
14	Kamgundho	Rapogi	Migori
16	KBK-4	Kiboko	Makueni
17	KBK-21	Kiboko	Makueni
30	Nyarkawuor	Uriri	Migori
31	Wild cassava-003	Kendu bay	Homa bay
32	Agriculture-005	Maeta-Kehancha	Migori
42	Unknown variety-002	Rakwaro	Migori
62	AdhiamboLera	Awendo	Migori
72	Busia-003	Busia	Busia
77	Nyakasani	Awendo	Migori
89	Mtwapa-009	Mtwapa	Kilifi
98	MM96/0067	Mtwapa	Kilifi

11	Selele rachar	Rapogi	Migori
4	Mbale-001	Miida Creek	Kilifi
8	Nyaranen	Ranen	Migori
CLUSTER #3			
Row 3:15	Kasukali	Kiboko	Makueni
117	Toji	Kendu bay	Homa bay
58	Agriculture-010	Kegonga, Kehancha	Migori
68	Madam	Opapo	Migori
CLUSTER #4			
Row 8:63	Unknown variety-003	Rakwaro	Migori
109	Selele-007	Sigiria	Migori
125	Selele-009	Ranen	Migori
132	Fumbachai	Chakol	Busia
24	Selele-002	Rongo	Migori
27	Selele-003	Maram	Homa bay
35	Selele-004	Rakwaro	Migori
36	Nyatanga-002	Uriri	Migori
39	Selele-005	Maram	Migori
64	Selele-006	Busia	Busia
84	Nyasuna	Masaba, Kehancha	Migori

Discussion

Numerical taxonomic studies are important for discovering and documenting new character and character states (Rahman, 2013). Cluster analysis (CA) and principal component analysis (PCA) are two techniques commonly used in numerical classification (Sonibare *et al*., 2004). PCA is usually used as an exploratory tool in systematic. There are as many components as original variables, and these components are linear combinations of the original variables. Most of the variance is usually summarized by the first few components, and PCA thus reduces a larger number of variables to fewer variables, which are often easier to interpret and is thus described as a dimension reducing method (Rahman, 2013). Cluster analysis (CA) is an exploratory tool for classifying objects with no statistical assumptions about the data. Cluster analysis produces a hierarchical classification of entities (taxa) based on the similarity matrix. Results are usually presented in the form of trees or dendrograms (Henderson, 2006).

In this study eigenvalues and percentage variations of the principal component analysis were evaluated. Eleven principal components accounting for 71.58% of the total variation among the genotypes were identified. The PCs were: Shape of central leaflet, lobe margins, colour of stem epidermis, colour of stem exterior, leaf colour, orientation of petiole, extent of root puduncle, colour of root cortex, root shape, root taste and cortex thickness. Similar studies have been carried out in other regions. Studies carried out in Sierra Leone (Karim *et al* 2020) identified a total of seven principal components (PCs) in the qualitative and four PCs in the quantitative trait sets accounted for 79.03%and 72.30% of the total genetic variation in 102 cassava genotypes, respectively. In the same study five cluster groups were identified based on the qualitative agronomic traits. The estimation of descriptive statistics of 25 different morphological traits studied in the present study revealed the existence of morphological diversity among cassava landraces. From the small sample of 131 genotypes it was possible to characterize them into four clusters with a majority (72.5%) falling into one cluster. This signifies that a large population of cassava grown in Kenya have similar characteristics as only 27.5% are characterized in the other three clusters. This makes it difficult for farmers to select the distinctive planting materials. These results are similar with those obtained in Brazil (Tiago *et al*, 2020). Among the 45 cassava ethno-varieties studied, they presented 97.35% polymorphism, which showed that there were morphological divergence between the evaluated samples (Tiago *et al*., 2020).

The three wild cassava accessions included in this study were characterized in clusters where cultivated cassava were identified. Wild cassava – 003 (entry 31) was classified in cluster #2 while Wild cassava – 002 (entry 29) and Wild cassava – 001 (entry26) were classified in cluster #1. These results differed with the findings of Dissanayake *et al*., (2019) in Sri Lanka who carried out morphological assessment of cassava cultivars and established that the leaf morphology of wild-accessions and landrace cultivars were significantly different from the rest of the cultivars. Stem morphology among the cultivars was significantly different mainly by the mean inter-nodal length of the stems whereas wild-accession cultivars were significantly different from the rest by the diameter of the stems. In this study, it was expected that the wild cassava genotypes would be clustered in a distinct group. In Indonesia, details of 14 morphological characteristics for 29 cassava genotypes were used in cassava landrace characterization. It was established that almost all genotypes had purple petiole color and horizontal orientation, smooth lobe margin, and seven lobes (Ridwan *et al*., 2022). In Burundi, Niyonzima *et al*., (2021) assessed landrace cassava morphological traits and noted that stem, root and leaf traits distribution differed among cassava landraces.

The TMS cassava varieties released by KALRO and named *Agriculture* by farmers were coded Agriculture – 001 – Agriculture 021. The genotypes appeared in clusters 1, 2 and 3; signifying that the varieties that were in different clusters were different varieties. This is a first step in the identification of these genotypes. There were also varieties whose names the farmers did not know (*Unknown variety*). This is a common occurrence especially for farmers who are planting cassava for the first time or who are recently introduced to cassava farming. For them the name of the variety is not important. This observation also applied to the genotypes collected from Mtwapa (Kilifi County). It was expected that this study would shed light on their identities. Further genetic studies need to be carried out to correlate the phenotypic and genotypic traits for proper characterization.

Conclusion

This study highlighted the phenotypic variability within the cassava genotypes collected. Despite the variability found within the germplasm, it is concluded that cassava phenotype base in Kenya is narrow as it was revealed that 72.5% phenotypes were clustered in one group. Genotypes with very close morphological characteristics such as Adhiambo lera in Migori (cluster #1) and Adhiambo lera (cluster #2) in Mtwapa should be considered as putative duplicates, hence, need to be pooled together as one cultivar.

Recommendations

Future studies on phenotypic characterization should focus on the 11 phenotypic traits that accounted for 71% cumulative variation. The application of phenotypic descriptors in identification of cassava landrace germplasm should be backed by the use of molecular markers (genetic characterization), since the former alone does not reveal much diversity due to the effects of the environment on quantitative traits.

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Conflict of Interest

"The author(s) declare(s) that there is no conflict of interest." There was no role of the funding sponsors in the design of the study; in the collection, analyses or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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