

African Crop Science Journal by African Crop Science Society is licensed under
a Creative Commons Attribution 3.0 Uganda License.

Based on a work at www.ajol.info/

DOI: <https://dx.doi.org/10.4314/acsj.v32i4.4>



DELIMITATION OF CASSAVA GERMPLOSM CLUSTERS IN KENYA BASED ON PHENOTYPIC TRAITS

C.N. NYAMWAMU, P. JERUTO, E. NJENGA, P.F. ARAMA¹ and R.M. MULWA²

School of Science, Department of Biological Sciences, University of Eldoret, P. O. Box 1125 - 30100,
Eldoret, Kenya

¹School of Science, Agriculture and Environmental Studies, Rongo University,
P. O. Box 103 - 40404, Rongo, Kenya

²Faculty of Agriculture, Department of Crops, Horticulture and Soils, Egerton University,
P. O. Box 536 - 20201, Egerton, Kenya

Corresponding author: nyamwamucharles@gmail.com

(Received 18 October 2024; accepted 30 November 2024)

ABSTRACT

Cassava (*Manihot esculenta* Crantz) is a staple food and more lately, cash crop in Kenya, supporting millions of stakeholders along its value chain. However, the phenotypic variability of the crop in the country is not fully understood. The objective of this study was to delimit clusters within the cassava germplasm in Kenya. The study involved 131 cassava stem cuttings of genotypes collected from seven major cassava growing counties in Kenya. Genotypes cuttings were planted in two experimental sites; namely Rongo University farm and Mawego Technical Training Institute farm. Data were collected on both quantitative and qualitative phenotypic traits, at three monthly intervals, during 3 to 12 months after planting. The data were subjected to Multivariate analysis ($P < 0.05$). The cassava germplasm was categorised into four cluster groups based on phenotypic traits; namely Cluster 1 (72.5%), 2 (16.0%), 3 (3.1%), and 4 (8.1%) 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 ($P < 0.05$). Furthermore, delimitation of these clusters was done based on the 11 assessed phenotypic traits. In Cluster 1, five PCs accounted for 61.7% of total variation among the genotypes. In Cluster 2, four principal components accounted for 69.2% of the variation; while in Cluster 3, two PCs explained 100% of the variation. In Cluster 4, four PCs accounted for 79.1% of the total variation among the genotypes. Delimitation of these clusters will inform targeted breeding strategies and conservation efforts.

Key Words: Genetic diversity, *Manihot esculenta*, phenotypic variability

RÉSUMÉ

Le manioc (*Manihot esculenta* Crantz) est un aliment de base et, plus récemment, une culture commerciale au Kenya, soutenant des millions d'acteurs dans sa chaîne de valeur. Cependant, la variabilité phénotypique de la culture de manioc dans le pays n'est pas entièrement rationalisée. L'objectif de cette étude était de délimiter les groupes au sein du matériel génétique du manioc au Kenya. L'étude a porté sur 131 boutures de tiges de manioc de génotypes collectés dans sept principaux comtés producteurs de manioc au Kenya. Les boutures de génotypes ont été plantées dans deux sites expérimentaux, à savoir la ferme de l'Université de Rongo et la ferme de Mawego Technical Training Institute. Des données ont été collectées sur les traits phénotypiques quantitatifs et qualitatifs, à des intervalles de trois mois, pendant 3 à 12 mois après la plantation. Les données ont été soumises à une analyse multivariée ($P < 0,05$). Le matériel génétique du manioc a été classé en quatre groupes de groupes en fonction des traits phénotypiques ; à savoir les groupes 1 (72,5 %), 2 (16,0 %), 3 (3,1 %) et 4 (8,1 %) génotypes respectivement. Sur les 25 caractères phénotypiques évalués, un total de 11 ensembles de traits des composantes principales (PC) représentaient 71,58 % de la variation génétique cumulée ($P < 0,05$). De plus, la délimitation de ces groupes a été effectuée sur la base des 11 traits phénotypiques évalués. Dans le groupe 1, cinq PC représentaient 61,7 % de la variation totale entre les génotypes. Dans le groupe 2, quatre composantes principales représentaient 69,2 % de la variation ; tandis que dans le groupe 3, deux PC expliquaient 100 % de la variation. Dans le groupe 4, quatre PC représentaient 79,1 % de la variation totale entre les génotypes. La délimitation de ces groupes éclairera les stratégies de sélection ciblées et les efforts de conservation.

Mots Clés: Diversité génétique, *Manihot esculenta*, variabilité phénotypique

INTRODUCTION

Phenotypic trait characterisation of cassava germplasm bears a range of benefits; including supporting breeding research, biodiversity and conservation projects; enables the identification of genetic traits that are important to pre-breeding, breeding and crop improvement efforts; and supporting crop optimisation and improvement efforts (Rabbi *et al.*, 2017; Asante *et al.*, 2020; Ntawuruhunga and Legg, 2022). Different cassava accessions have been distinguished by phenotypic characteristics, such as colour and shape of central leaflet, branching habit, plant height, colour of stem and petiole, root shape and skin colour, time to maturity, yield and the cyanogenic glycosides content in the roots (Fukuda *et al.*, 2010; Saravanan, 2016). However, the genetic diversity and phenotypic variability of the crop in Kenya are not fully understood.

Otherwise, studies elsewhere have analysed genetic diversity of cassava, with

overwhelming outputs. In Brazil, a study focused on the morphological and agronomic traits of cassava and the findings revealed significant diversity within the cassava germplasm, highlighting the potential for selecting superior genotypes for specific agro-ecological zones (da Silva *et al.*, 2019).

In Mexico, a study explored the phenotypic and genetic diversity of local cassava varieties, and the study identified several distinct groups with unique trait combinations, suggesting that targeted breeding strategies could be developed to enhance productivity and adaptability to various environmental conditions (Gómez *et al.*, 2021). In Nigeria, Adebola *et al.* (2018) examined the phenotypic variation among cassava accessions in Nigeria using a range of morphological traits, including leaf shape, stem colour, and root characteristics, to cluster the germplasm.

In Ghana, a comprehensive assessment of cassava germplasm using both qualitative and quantitative phenotypic traits was done to identify distinct clusters associated with

specific agronomic traits such as drought tolerance and starch content (Obeng-Bio *et al.*, 2019). A related study in Burundi focused on the phenotypic characterisation of local cassava varieties which employed multivariate analysis to delineate clusters based on root yield, dry matter content, and disease resistance. The results revealed significant intra- and inter-cluster variability, suggesting that local varieties possess unique traits that could be harnessed for genetic improvement (Nduwimana *et al.*, 2020).

In Uganda, a similar study explored the phenotypic diversity of cassava landraces and improved varieties; and identified key phenotypic traits that differentiate the clusters; which included root size and shape, which are important for both consumption and processing industries (Tumuhimbise *et al.*, 2021). In Zambia, Chikoti *et al.* (2022) investigated the phenotypic traits of cassava germplasm from different agro-ecological zones and revealed significant variability among the germplasm.

The objective of the present study was to delimit clusters within the cassava (*Manihot esculenta* Crantz) germplasm in Kenya based on phenotypic traits.

MATERIALS AND METHODS

A survey was carried out in 2018 (main rainy season) up to 2019 (short rainy season) in the major cassava growing regions in Kenya; including the following counties; Coastal region (Kilifi), Eastern and Central (Makueni and Nakuru), Western (Busia), Nyanza (Migori, Homabay and Kisumu).

A single stem from one plant was collected to represent a cassava accession. This is a standard practice in cassava research to ensure accurate, controlled and resource-efficient study that maintain the genetic fidelity of each variety (Fukuda *et al.*, 2010). The local names of the accessions were obtained from the farmer and/or from the supplier of the planting materials. The stem was cut into pieces, 15 cm long each and placed in a collection

polythene bag. These bags were preferred as they typically provided a protective barrier against moisture loss and physical damage during transportation.

Care was taken to avoid damaging the stems by handling them gently and ensuring that they were not bruised. All the samples collected were quickly planted in single rows, each of 5 plants at the Rongo University farm, located in Migori County. The spacing was 1 m between rows and 1 m within rows.

The experiment was conducted in Ranen farm (Migori county), Mawego Technical Training Institute farm (Homa bay county) and Rongo university farm (Migori county), during the rainy seasons of October-December 2018 (short rains) and March-May 2019 (long rains). A total of 131 cassava accessions were planted each in plots of 25 m by 26 m. The study was laid out in a randomised complete block design (RCBD); replicated three times; and repeated twice. It was hand-weeded twice and irrigated using distilled water whenever necessary, to maintain optimal soil moisture levels.

Data on phenotypic traits were collected from the rows of each accession plot. Phenotypic characterisation was done using the selected morphological and agronomic descriptors for characterisation of cassava as described in Table 1 (Fukuda *et al.*, 2010). The characterisation process separated the 131 cassava accessions into four major clusters based on a similarity index of 0.5.

Data analysis. The genetic variation among the studied genotypes for agro-morphological traits was explored using the Multivariate analysis technique (Karim *et al.*, 2020). Multivariate analysis of each of the four cluster's data matrix, comprising of principal component analysis (PCA), was 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). The PCA and correlation matrices were used to determine the relationships among the traits. The delimitation of cassava accession clusters based on phenotypic traits was carried out by analysing the clustering patterns, which were derived from the agro-morphological data. This involved grouping accessions with similar phenotypic characteristics based on their genetic diversity, and the clustering was validated using hierarchical clustering methods.

RESULTS

Cassava phenotypic Cluster 1. Cassava accessions analysed revealed larger degrees of morphological variations based on the 25 phenotypic qualitative and quantitative descriptors used (Table 1). The process of cassava phenotypic cluster delineation identified four clusters as described below.

Cluster 1 depicted 95 cassava genotypes, which accounted for 72.5% of the accessions (Table 2). The eigenvalues and percentage variations of the PCA are presented in Table 3. Five PCA that accounted for 61.7% of the total variation, were identified among these accessions. Based on these results, the first principal component (PC1) was the colour of the root cortex, with a correlation of rotated component matrix of 0.985; accounting for 15.4% of the total variation. The second PC, was cortex thickness, with a correlation of rotated component matrix of 0.994, accounting for 13.7% of the total variation, among the accessions. The third PC was orientation of petiole with a correlation of rotated component matrix of 0.987; accounting for 12.9% of the total variations. The fourth PC was root taste with correlation of rotated component matrix of 0.986; accounting for 10.2% among the genotypes. The fifth PC was leaf colour, with a correlation of rotated component matrix of 0.989 and a percentage of variance of 9.5 (Table 3).

TABLE 1. Qualitative and quantitative phenotypic descriptors for the characterisation of 131 cassava accessions

SN	Trait descriptor	Score code
1	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-pyramidal; 9 = linear-pandurate; 10 = linear-hostalobalate
2	Leaf colour	3 = light green; 5 = dark green; 7 = purple green; 9 = purple
3	Lobe margins	3 = smooth; 7 = winding
4	Orientation of petiole	1 = inclined upwards; 3 = horizontal; 5 = inclined downwards; 7 = irregular
5	Colour of stem epidermis	1 = cream; 2 = light brown; 3 = dark brown; 4 = orange
6	Colour of stem exterior	3 = orange; 4 = greeny-yellowish; 5 = golden; 6 = light brown; 7 = silver; 8 = grey; 9 = dark brown
7	Extent of root peduncle	0 = sessile; 3 = pedunculate; 5 = mixed
8	Root shape	1 = conical; 2 = conical-cylindrical; 3 = cylindrical; 4 = irregular
9	Colour of root cortex	1 = white or cream; 2 = yellow; 3 = pink; 4 = purple
10	Root taste	1 = sweet; 2 = intermediate; 3 = bitter
11	Cortex thickness	1 = thin; 2 = intermediate; 3 = thick

TABLE 2. Cassava accession name, source, location and county name for cluster 1

Accession	Location collected	County
Nyakanyamkago	Sigiria	Migori
MM96/0039	Chakol	Busia
Nyar-ICIPE	Sigiria	Migori
Mygera	Rongo	Migori
Adhiambo lera-002	Mtwapa	Kilifi
Nyatanga	Rabuor	Kisumu
Nyarkokaro	Rakwaro	Migori
Amakuria	Masaba- Kehancha	Migori
Busia-004	Busia	Busia
Agriculture-019	Maram	Homa bay
Nyatonge-002	Sigiria	Migori
Mygera-002	Sigiria	Migori
Obaro dak-003	Ranen	Migori
Otia	Sigiria	Migori
Agriculture-020	Ranen	Migori
Agriculture-021	Maram	Homa bay
Kanono	Ranen	Migori
Agriculture-022	Pembe	Migori
Agriculture-023	Kitere	Migori
Agriculture-024	Sigiria	Migori
Unknown	Maram	Homa bay
Obaro dak-004	Nyamarere	Migori
Mufutu	Migori	Migori
Nyaodendo	Sigiria	Migori
NyarMaseno	Busia	Busia
MM96/4878	Busia	Busia
Yellow-002	Chakol	Busia
MH95//0183	Chakol	Busia
Magana	Chakol	Busia
MH96/0031	Chakol	Busia
Mygera-003	Chakol	Busia
Bwana Terana	Chakol	Busia
MH95/2480	Kolwa	Kisumu
Agriculture-018	Ranen	Migori
Bwong	Ranen	Migori
Obaro dak-001	Maram	Homa bay
Nyarkanyamkago	Ranen	Migori
Obaro dak-002	Nyamarere	Migori
Agriculture-003	Rapogi	Migori
Katune	Kiboko	Makueni
KME-4	Kiboko	Makueni
Kazanzwara	Kiboko	Makueni
KBK-20	Kiboko	Makueni
Agriculture-004	Busia	Busia

TABLE 2. Contd.

Accession	Location collected	County
Nyaeta	Kehancha	Migori
Wild cassava-001	Ranen	Migori
Kienyeji	Maram	Homa bay
Wild cassava-002	Rusinga island	Homa bay
Unknown accession	Kegonga-Kehancha	Migori
Buria	Maeta, Kehancha	Migori
Nyaogutu Ngalo	Maram	Homa bay
Nyagire	Maram	Homa bay
Agriculture-006	Opago	Migori
Unknown accession-03	Maram	Homa bay
Nyasega	Rakwaro	Migori
Nyasuna	Kokuro	Migori
Nyatanga-003	Opapo	Migori
Nyakakelo	Kanga	Migori
Obiero Abele	Ranen	Migori
Opopo	Urii	Migori
Nyakasamwel	Awendo	Migori
Nyarkagutu	Ngothe	Migori
Agriculture-007	Suba; Kuria	Migori
Agriculture-008	Busia	Busia

TABLE 3. Principal component analysis, eigenvalues and percentage variations of eleven phenotypic traits of 95 cassava genotypes

Principal component (PC)	Initial eigen values			Correlation of rotated component matrix				
	Total	% of variance	Cumulative (%)	PC1	PC2	PC3	PC4	PC5
1. Colour of root cortex	1.697	15.428	15.428	0.985	-0.013	0.005	0.017	0.008
2. Cortex thickness	1.504	13.674	29.101	-0.013	0.994	0.033	-0.011	-0.002
3. Orientation of petiole	1.429	12.94	42.006	0.005	0.034	0.987	-0.027	0.018
4. Root taste	1.21	10.19	52.796	0.017	-0.011	-0.027	0.986	0.074
5. Leaf colour	1.047	9.515	61.711	0.008	-0.002	0.017	0.073	0.989
6. Shape of central leaflet	0.897	8.159	69.87	0.046	0.006	0.109	0.018	0.025
7. Lobe margins	0.845	7.684	77.554	0.123	-0.021	0.043	-0.085	0.006
8. Colour of stem epidermis	0.746	6.778	84.334	-0.07	0.093	-0.047	-0.017	0.032
9. Colour of stem exterior	0.654	5.949	90.281	0.089	0.031	-0.005	0.064	0.08
10. Extent of root puduncle	0.547	4.973	95.253	0.035	0.027	0.007	0.094	-0.082
11. Root shape	0.522	4.747	100	0.03	-0.045	0.092	0.047	-0.043

The data highlighted in yellow are the key PCs (PC1–PC5), which are the primary PCs explaining the variance among the cassava accessions, drawing attention to the most critical traits being analysed. The data in red prints correspond to the correlation values of the rotated component matrix, emphasising the strength of the association between each phenotypic trait and its respective PC (Table 3).

Cassava phenotypic Cluster 2. Cluster 2 had 21 phenotypic clusters (Table 4) representing 16% of the total number of entries. Four PCs that accounted for 69.2% of the total variation among the accessions, were identified (Table 5). Colour of stem exterior was the PCA 1, with a correlation of rotated component matrix of 0.936; accounting for 23.9% of the total variation.

The shape of central leaflet, root taste and extent of root puduncle were the second, third and fourth PCs that showed correlations of rotated component matrices of 0.932, 0.975 and 0.963, respectively (Table 5).

The data shaded in yellow indicates the key PCs (PC1–PC4), which contribute to the major variations among the cassava accessions. The correlation values of the rotated component matrix are represented by the data in red colour, which highlights how strongly each phenotypic characteristic is associated with its corresponding PC (Table 5).

Cassava phenotype Cluster 3. Cluster 3 had 4 phenotypic clusters (3.1%) as shown in Table 6. The second PC which was orientation of leaf petiole, showed a correlation of rotated component matrix of 0.968, and accounted for 38.5% of the total variation. The fourth

TABLE 4. Cassava accession name, source location and county name for Cluster 2

Accession	Location collected	County
Rateng	Pembe	Migori
Agriculture-017	Mtwapa	Kilifi
Odiero	Rongo	Migori
Agriculture-001	Ranen	Migori
Ratena	Nyamarere	Migori
Yellow-001	Rapogi	Migori
Kamgundho	Rapogi	Migori
KBK-4	Kiboko	Makueni
KBK-21	Kiboko	Makueni
Nyarkawuor	Uriri	Migori
Wild cassava-003	Kendu bay	Homa bay
Agriculture-005	Maeta-Kehancha	Migori
Unknown accession-002	Rakwaro	Migori
Adhiambo Lera	Awendo	Migori
Busia-003	Busia	Busia
Nyakasani	Awendo	Migori
Mtwapa-009	Mtwapa	Kilifi
MM96/0067	Mtwapa	Kilifi
Selele rachar	Rapogi	Migori
Mbale-001	Miida Creek	Kilifi
Nyaranen	Ranen	Migori

Source: Nyamwamu *et al.* (2023)

TABLE 5. Principal component analysis, eigenvalues and percentage variations of eleven phenotypic traits of 21 cassava genotypes

Principal component (PC)	Initial eigen values			Correlation of rotated component matrix			
	Total	% of variance	Cumulative (%)	PC1	PC2	PC3	PC4
1. Colour of stem exterior	2.394	23.94	23.94	0.936	-0.124	0.045	-0.019
2. Shape of central leaflet	1.845	18.453	42.393	-0.124	0.932	-0.129	-0.076
3. Root taste	1.499	14.989	57.383	0.043	-0.116	0.975	-0.054
4. Extent of root puduncle	1.179	11.788	69.171	-0.021	-0.064	-0.056	0.963
5. Leaf colour	0.856	8.561	77.732	-0.01	0.018	-0.09	-0.147
6. Lobe margins	0.732	7.324	85.055	-0.155	-0.098	-0.071	-0.051
7. Orientation of petiole	0.529	5.29	90.345	-0.097	0.127	0.015	-0.077
8. Colour of stem epidermis	0.384	3.835	94.18	0.311	-0.316	0.203	-0.167
9. Root shape	0.361	3.609	97.789	-0.152	-0.121	-0.063	0.169
10. Cortex thickness	0.221	2.211	100	-0.005	-0.021	-0.012	-0.017

TABLE 6. Cassava accession name, source location and county name for Cluster 3

Accession	Location collected	County
Kasukali	Kiboko	Makueni
Toji	Kendu bay	Homa bay
Agriculture-010	Kegonga, Kehancha	Migori
Madam	Opapo	Migori

Source: Nyamwamu *et al.* (2023)

and fifth PCs were root taste and leaf colour with each showing a correlation of rotated component matrix of -0.968; accounting for 0.0% of the total variation among the genotypes. The ninth and tenth PCs were colour of stem epidermis and cortex thickness; which showed correlation of rotated component matrices of -0.713 and -0.964, respectively; accounting for 0.0% of the total variation of the genotypes (Table 7). The primary PCs (PC1–PC2), which contributed to major variation among the cassava accessions, are indicated by the data in yellow. The data in red prints indicates the correlation values of the rotated component matrix,

highlighting the degree to which each phenotypic trait is linked to its respective PC.

Cassava phenotypic Cluster 4. Cluster 4 had 11 phenotypic clusters (8.4%) as presented in Table 8. The four PCs accounted for a total variation of 79.1% among the genotypes identified (Table 9). The data in yellow sheds represent the main PCs (PC1–PC4) that contributed to major variance among the cassava accessions. The degree to which each phenotypic characteristic was connected to its corresponding PC, is indicated by the data in red prints; which represents the correlation values of the rotated component matrix.

TABLE 7. Principal component analysis, eigenvalues and percentage variations of eleven phenotypic traits of 4 cassava genotypes

Principal component (PC)	Initial eigen values			Correlation of rotated component matrix	
	Total	% of variance	Cumulative (%)	PC1	PC2
1. Colour of stem exterior	6.15	61.495	61.495	0.997	0.08
2. Orientation of petiole	3.85	38.505	100.000	0.968	-0.25
3. Shape of central leaflet	0.000	0.000	100.000	0.968	-0.25
4. Root taste	0.000	0.000	100.000	-0.968	0.25
5. Leaf colour	0.000	0.000	100.000	-0.968	0.25
6. Extent of root puduncle	0.000	0.000	100.000	-0.267	0.964
7. Root shape	0.000	0.000	100.000	-0.267	0.964
8. Lobe margins	0.000	0.000	100.000	0.701	0.713
9. Colour of stem epidermis	0.000	0.000	100.000	-0.701	-0.713
10. Cortex thickness	0.000	0.000	100.000	0.267	-0.964

TABLE 8. Cassava accession name, source location and county name for Cluster 4

Variety	Location collected	County
Unknown accession-003	Rakwaro	Migori
Selele-007	Sigiria	Migori
Selele-009	Ranen	Migori
Fumbachai	Chakol	Busia
Selele-002	Rongo	Migori
Selele-003	Maram	Homa bay
Selele-004	Rakwaro	Migori
Nyatanga-002	Uriri	Migori
Selele-005	Maram	Migori
Selele-006	Busia	Busia
Nyasuna	Masaba, Kehancha	Migori

Source: Nyamwamu *et al.* (2023)

DISCUSSION

Cassava phenotypic Cluster 1. The analysis of cassava accessions revealed substantial morphological variation, particularly within Cluster 1, which comprised 95 genotypes, accounting for 72.5% of the total accessions (Table 2). The use of 25 phenotypic qualitative and quantitative descriptors allowed for the identification of key traits that contributed to

this variation, which were further examined using PCA. The PC1, which focused on the colour of the root cortex, was the most influential, accounting for 15.4% of the variation. This is consistent with previous studies, which highlighted the importance of root characteristics, such as colour, as significant phenotypic traits in cassava characterisation (Nweke *et al.*, 2016; Enesi *et al.*, 2022).

TABLE 9. Principal component analysis, eigenvalues and percentage variations of eleven phenotypic traits of 11 cassava genotypes

Principal component (PC)	Initial eigen values			Correlation of rotated component matrix			
	Total	% of variance	Cumulative (%)	PC1	PC2	PC3	PC4
1. Lobe margins	2.521	28.008	28.008	0.919	0.247	-0.041	-0.086
2. Cortex thickness	1.853	20.593	48.601	-0.929	-0.012	0.022	-0.194
3. Colour of stem exterior	1.575	17.499	66.099	0.18	0.92	-0.047	-0.231
4. Leaf colour	1.17	13.003	79.103	-0.133	-0.622	0.516	-0.373
5. Shape of central leaflet	0.949	10.549	89.651	-0.023	-0.08	0.978	-0.037
6. Extent of root puduncle	0.456	5.07	94.722	0.073	-0.122	-0.064	0.972
7. Orientation of petiole	0.413	4.59	99.312	0.12	-0.148	0.035	-0.102
8. Root shape	0.051	0.564	99.876	-0.001	-0.011	-0.04	0.114
9. Colour of stem epidermis	0.011	0.124	100	0.088	-0.096	-0.232	0.095

In addition to root colour, PC2, which described cortex thickness, accounted for 13.7% of the variation and was found to be strongly correlated (0.994) with the phenotypic trait (Table 3). This finding is consistent with the study by Adejumo *et al.* (2019), who also identified cortex thickness as a crucial trait for cassava characterisation, as it can influence both the storage and culinary quality of the roots. Furthermore, the orientation of the petiole (PC3) and root taste (PC4) were significant contributors to the variation observed in Cluster 1. This corroborated earlier findings that emphasised the role of petiole orientation in leaf morphology and root taste in determining consumer preferences and culinary uses of cassava (Agre *et al.*, 2016; Chaengsee *et al.*, 2020).

The fifth principal component (PC5), leaf colour, accounted for 9.5% of the variance, which is supported by findings from previous studies, suggesting that leaf colour is a reliable phenotypic marker for distinguishing cassava genotypes (Elias *et al.*, 2001; Rimoldi *et al.*, 2010). The correlations between these morphological traits and their respective PCs affirmed the strength of certain phenotypic features in determining genetic diversity and their potential applications in breeding

programmes aimed at improving cassava productivity and quality.

The variation in this Cluster, as reflected in the PCA, highlighted the critical phenotypic traits of cassava, particularly those related to root characteristics and leaf morphology, which have been widely discussed in previous studies (Nweke *et al.*, 2016; Adejumo *et al.*, 2019; Enesi *et al.*, 2022). Thus, these findings provide valuable insights for the selection and development of improved cassava varieties with enhanced quality and adaptability.

Cassava phenotypic Cluster 2. Cluster 2's phenotypic diversity can be attributed to four key PCs, which accounted for 69.2% of the total variation among the cassava accessions (Table 5). Principal component one (PC1), which primarily captured the colour of the stem exterior, had the highest correlation with the data, reflecting 23.9% of the total variation. The strong correlation of 0.936 between stem colour and PC1 aligns with previous studies emphasising the importance of stem colour as a morphological trait in cassava. This is often linked to specific biochemical properties such as anthocyanin content, which can influence drought tolerance and disease resistance (Tao *et al.*, 2020). This characteristic, therefore,

plays a central role in understanding genetic diversity in cassava. PC2 focused on the shape of the central leaflet, which exhibited a correlation of 0.932 (Table 5). The shape of the central leaflet is a well-documented morphological trait used to classify and distinguish cassava varieties.

As noted by Ridwan *et al.* (2022), leaf morphology has significant implications for photosynthetic efficiency and overall plant vigor. Leaf shape variability in this study highlights the potential for leaf morphology to serve as a reliable phenotypic marker for cassava breeding programs aimed at improving yield and resilience.

Root taste, represented as PC3 with a correlation of 0.975 (Table 5), is a prominent phenotypic trait which contributed to the variability within this cluster. The correlation affirmed the significant role of root characteristics, particularly taste, in cassava consumer preference and acceptability, which are crucial for cassava's marketability (Okonkwo *et al.*, 2021). Previous studies have shown that root taste directly influences the selection of cassava varieties for both local consumption and international trade, reinforcing the relevance of this trait in cassava breeding (Kengkanna *et al.*, 2019).

The fourth PC, related to the extent of the root peduncle, demonstrated a correlation of 0.963 (Table 5). The root peduncle, while often overlooked in many cassava studies, plays a role in the overall architecture of the plant and can affect harvesting efficiency and yield potential. Another study by Rattanasopa *et al.* (2022) noted that the extent of the root peduncle may influence the transport of nutrients from the soil, further linking this morphological feature to plant performance.

Data from the rotated component matrix (Table 5) further highlighted the strong association between these phenotypic characteristics and their respective PCs, reinforcing the importance of each trait in explaining the genetic diversity observed in

cassava accessions. These findings are consistent with studies that utilise principal component analysis to capture the main sources of phenotypic variation and provide a clearer understanding of the interrelationships among various traits (Afonso *et al.*, 2014).

Cassava phenotypic Cluster 3. Cluster 3 suggested that the two primary phenotypic characteristics, the colour of the stem exterior and the orientation of the leaf petiole, were the main contributors to the total variation among the genotypes in this Cluster. PC1, associated with the colour of the stem exterior, accounted for 61.5% of the variation, showing a high correlation of 0.997 in the rotated component matrix (Table 7). This suggested that stem colour is a key distinguishing trait within this cluster, which is consistent with previous studies that have highlighted the importance of stem colouration in cassava genotypic variation (Ogbonna *et al.*, 2021).

Principal component 2, related to the orientation of the leaf petiole and accounted for 38.5% of the variation with a correlation of 0.968 (Table 7). This high correlation further emphasised the relevance of leaf morphology, particularly the petiole's orientation, in characterising variation within cassava genotypes (Karim *et al.*, 2020).

Interestingly, the PC4 and PC5 (root taste and leaf colour), showed a correlation of -0.968, but accounted for 0.0% of the total variation (Table 7). This suggested that these traits were not significant in differentiating the genotypes within this cluster. This finding contrasted with previous studies in which root taste was identified as an important trait in cassava breeding and characterisation (Agre *et al.*, 2016). However, the absence of variation attributed to these traits in this specific cluster could indicate that root taste and leaf colour may not be as influential in determining the genetic diversity of this group, or that these traits were less variable within the analysed genotypes.

PC9 and PC10 which were associated with the colour of the stem epidermis and cortex thickness, also showed low correlations of -0.713 and -0.964, respectively, and accounted for non-significant variation (Table 7). The non-significant variation from these components suggested that these phenotypic traits were not useful in distinguishing between the genotypes in this Cluster; thus, reinforcing the idea that not all morphological traits contribute equally to the total phenotypic variation in cassava (Asare *et al.*, 2011). Related studies on cassava morphological traits similarly highlighted that some traits, such as epidermal colour or cortex thickness, may exhibit limited variability across certain genotypes (Ceballos *et al.*, 2016).

These findings provide valuable insights into the phenotypic traits driving variation within this cluster, with colour of the stem exterior and leaf petiole orientation emerging as the most significant characteristics. This conforms to earlier studies that emphasised the importance of stem and leaf morphology in cassava genotypic classification (Oliveira *et al.*, 2015; Karim *et al.*, 2020).

Cassava phenotypic Cluster 4. Cluster 4, consisted of 11 genotypes (8.4%); exhibited significant variation among cassava accessions based on principal component analysis (Table 8). Principal component 1, related to lobe margins, contributed 28% to the total variation, making it the most significant factor in distinguishing genotypes within this Cluster (Table 9). Lobe margin variation is known to be an important trait in cassava, as it can be linked to both genetic and environmental factors (Chavarriaga-Aguirre *et al.*, 1998). The prominence of this trait is consistent with studies that have found morphological traits related to leaf shape and margins as key indicators of genetic diversity in cassava (Alves *et al.*, 2019).

Principal component 2, representing cortex thickness, accounted for 20.6% of the variation (Table 9). This trait is particularly

important for cassava's processing qualities, as thicker cortex can impact the tuber's overall yield and suitability for various uses (Noerwijati *et al.*, 2014). The variation in cortex thickness in this Cluster, could have practical implications for cassava breeding programmes focused on improving the crop's performance, particularly in terms of root quality for both consumption and industrial uses.

Principal component 3, representing stem exterior colour, explained 17.5% of the total variation (Table 9). Stem colour, although less frequently studied, has been noted as an important phenotypic trait in cassava, potentially affecting resistance to pests and diseases (Hillocks *et al.*, 2012). The variation in this trait within this Cluster could reflect underlying genetic diversity that may influence cassava's adaptability to different agro-ecological conditions.

Principal component 4, related to leaf colour, accounted for 13% of the variation (Table 9). Leaf colour in cassava has been linked to physiological traits such as photosynthetic efficiency and resistance to biotic stressors (De Souza and Long, 2018). The contribution of leaf colour to the total variation suggests that this trait plays an important role in differentiating the genotypes within this cluster, which may have implications for cassava cultivation under varying environmental conditions.

The correlation values in the rotated component matrix, provide deeper insights into how these traits interrelate, and they are essential for understanding the genetic structure of cassava accessions within this cluster. Thus, the PCA results have revealed that lobe margins, cortex thickness, stem exterior colour, and leaf colour are key traits contributing to genetic differentiation among cassava genotypes. The findings conform to those of previous studies that have emphasised the importance of these phenotypic characteristics in cassava's genetic diversity and breeding potential (Chavarriaga-Aguirre *et al.*, 1998; Oliveira *et al.*, 2015).

This study has established a reduction of phenotypic characters from 25 to 11 in some clusters (Cluster 1, Table 3) and even fewer in others (Cluster 4, Table 5). This provides breeders with a more streamlined approach to identifying important phenotypic traits, which can be tailored according to environmental factors. Thus, breeders do not need to study all the 25 phenotypic characters, but can prioritise the ones that contribute significantly to phenotypic variation, as evidenced by this present study.

This approach offers a more targeted strategy for breeding programmes, as fewer characters simplify the selection process; while still capturing significant genetic diversity (Oliveira *et al.*, 2015). The environment and specific phenotypic traits may influence the selection of characters, so flexibility is required in defining the key traits for different cassava accessions (Shirima *et al.*, 2022).

This study provides a significant distinction from the analysis of the Correlation of the Rotated Component Matrix which is different from most studies on cassava accession characterisation, which hitherto focus on unrotated components. The rotated matrix helps achieve clearer and more interpretable factor loadings by minimising the complexity of factor structures (Jolliffe and Cadima, 2016). This rotation ensures that the resulting components are better aligned with distinct phenotypic characters, enhancing the identification of meaningful clusters. For example, in the present study, the rotated matrix revealed that PC1 was primarily associated with root cortex colour (correlation of 0.985); while other PCs highlighted cortex thickness, petiole orientation, root taste, and leaf colour (Table 3). These results are of great significance since they allow for clearer distinctions between clusters, contributing to cumulative variance by aligning specific phenotypic traits to the most significant principal components.

The decrease in number of phenotypic characters from 11 in Cluster 1 (Table 3) to 9 in Cluster 4, (Table 9) highlights how

phenotypic traits are influenced and grouped by both environmental and genetic factors. As the cumulative percentage variance among clusters reaches 70% or more, the importance of certain characters decreases (Jolliffe, 2002). For instance, in Cluster 4, phenotypic traits such as stem exterior colour and root taste, with correlations of 0.936 and 0.975, respectively; played significant roles in explaining the variation among accessions, but the reduction to nine characters suggests that some phenotypic traits became redundant or contributed minimally to variation (Joaqui *et al.*, 2016).

This phenomenon is common in PCA, where only a few PCs explain the bulk of variance, allowing for the exclusion of less influential characters while still capturing essential genetic diversity (Sánchez *et al.*, 2018). Therefore, this study provides an insight into optimising phenotypic trait selection while maintaining high levels of explained variance, which could serve as a model for future cassava breeding research. Related studies have observed that the site effect, likely influences the phenotypic variation observed in cassava variety clusters, as environmental factors can impact traits such as root colour, leaf morphology, and stem characteristics (Adejumo *et al.*, 2019; Malik *et al.*, 2020). Therefore, differences in agro-ecological conditions across selected sites may have contributed to the genetic diversity and variability in cassava accessions within the Kenyan germplasm.

All clusters demonstrated the importance of root characteristics, leaf morphology, and stem color in defining phenotypic diversity in cassava. This conforms with previous studies highlighting these traits as key determinants in cassava characterisation (Fukuda *et al.*, 2010). However, the relative importance of these traits varies significantly across clusters. For example, root cortex colour is crucial in Cluster 1, while stem exterior colour dominated in Clusters 2 and 3. Cluster 4 uniquely emphasises lobe margins. These findings provide valuable insights for cassava

breeding programmes. Focusing on the key traits identified within each cluster, breeders can develop more targeted and efficient breeding strategies for specific objectives, such as improving root quality, enhancing disease resistance, or increasing yield potential.

CONCLUSION

This study has identified 11 phenotypic cassava clusters out of the original 25 phenotypic traits of the cassava germplasm in Kenya. This implies that breeders can streamline their selection process; while still capturing significant genetic diversity. This tailored approach to phenotypic trait selection, allows for flexibility depending on the specific environmental conditions and genotype characteristics. Importantly, the ability to focus on traits that contribute the most to cumulative variation, enhances breeding efficiency and allows for more targeted strategies in breeding programmes.

The analysis of the Correlation of the Rotated Component Matrix in this study offers a key advantage over unrotated components used in previous research, the latter providing clearer associations between phenotypic traits and clusters. This clearer distinction allows for more precise identification of meaningful phenotypic characters that define each cluster, further aiding breeders in the selection of critical traits for cassava improvement.

The findings from this study offer breeders a valuable methodology for optimising phenotypic characterisation, emphasising the importance of using PCA to identify the most impactful traits. This approach not only enhances the efficiency of cassava breeding programmes, but also provides a foundation for future research in cassava phenotypic diversity, offering insights into optimising trait selection based on environmental and genetic factors.

Thus, the differences in cluster size and diversity affirm the complex interactions between genetic variation, environmental conditions, and selective pressures in cassava

accessions. These findings provide insights into the optimisation of breeding strategies that focus on specific phenotypic traits that are most relevant for enhancing cassava productivity and adaptability.

ACKNOWLEDGEMENT

The Biological Sciences Department of University of Eldoret, Rongo University provided the required human and institutional resources towards the success of this study.

REFERENCES

- Adebola, P.O., Ilona, P., Ogbonna, M.C. and Dixon, A.G.O. 2018. Phenotypic diversity and relationships among cassava accessions in Nigeria using morphological descriptors. *African Journal of Biotechnology* 17(25): 787-796.
- Adejumo, O.O, Balogun, F.A. and Dawodu, M.O. 2019. Investigating cassava root cortex peels as a potential source of toxic contaminant. *EC Nutrition* 14(2): 153-157.
- Afonso, S.D.J., da Silva Ledo, C.A., Moreira, R.F.C., de Oliveira e Silva, S., de Jesus Leal, V.D., da Silva Conceição, A.L. and Iluebbey, P. 2014. Selection of descriptors in a morphological characteristic considered in cassava accessions by means of multivariate techniques. *IOSR Journal of Agriculture and Veterinary Science* 7:13-20. <https://www.researchgate.net/publication/269965886>.
- Agre, A.P., Badara, G., Adjatin, A., Dansi, A., Bathacharjee, R., Rabbi, I.Y., Dansi, M. and Gedil, M. 2016. Folk taxonomy and traditional management of cassava (*Manihot esculenta* Crantz) diversity in southern and central Benin. *International Journal of Innovation Science and Research* 20:500-551.
- Asante, I.K., Offei, S.K. and Ofori, K. 2020. Phenotypic diversity and genetic parameters for agronomic traits in cassava (*Manihot esculenta* Crantz) germplasm collections in Ghana. *Agriculture & Food*

- Security* 9(1):1-10. <https://doi.org/10.1186/s40066-020-00256-y>.
- Alves, A.A.C., Guedes, M.L. and Mühlen, M.R. 2019. Morphological and molecular characterisation of cassava accessions in Brazil. *Genetic Resources and Crop Evolution* 66(3):641-653.
- Asare, P. A. Galyuon, I. K. A. Sarfo, J. K. and Tetteh, J. P. 2011. Morphological and molecular based diversity studies of some cassava (*Manihot esculenta* crantz) germplasm in Ghana. *African Journal of Biotechnology* 10(63):13900–13908.
- Ceballos, H., Perez, J., Barandica, O., Lenis, J.I., Morante, N., Calle, F., Pino, L. and Hershey, C. 2016. Cassava breeding I: The value of breeding value. *Frontiers in Plant Science* 7: 1227. <https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2016.01227/full>.
- Chaengsee, P., Kongsil, P., Siriwong, N., Kittipadakul, P., Piyachomkwan, K. and Petchpoung, K. 2020. Potential yield and cyanogenic glucoside content of cassava root and pasting properties of starch and flour from cassava Hanatee var. and breeding lines grown under rain-fed condition. *Agricultural and Natural Resources* 54:237-244. <https://li01.tci-thaijo.org/index.php/anres/article/view/245653>
- Chavarriaga-Aguirre, P., Maya, M.M., Bonierbale, M.W. 1998. Microsatellites in cassava (*Manihot esculenta* Crantz): discovery, inheritance and variability. *Theory of Applied Genetics* 97:493-501. <https://link.springer.com/article/10.1007/s001220050922>.
- Chikoti, P.C., Tembo, B., Mwansa, K. and Sichilima, S. 2022. Phenotypic traits of cassava germplasm from different agro-ecological zones in Zambia. *Agricultural Sciences* 13(2):78-90.
- da Silva, M.J., Oliveira, E.J., Santos, V.S., Costa, J.L. and Santana, F.A. 2019. Morphological and agronomic characterisation of cassava (*Manihot esculenta* Crantz) germplasm in Brazil. *Agronomy Journal* 111(4):1891-1901.
- De Souza, A.P. and Long, S.P. 2018. Toward improving photosynthesis in cassava: Characterizing photosynthetic limitations in four current African cultivars. *Food Energy Security* 7: e00130. <https://onlinelibrary.wiley.com/doi/full/10.1002/fes3.130>.
- Elias, M., McKey, D., Panaud, O., Anstett, M. C. and Robert, T. 2001. Traditional management of cassava morphological and genetic diversity by the Makushi Amerindians (Guyana, South America): perspectives for on-farm conservation of crop. *Euphytica* 120:143-157.
- Enesi, R.O., Hauser, S., Pypers, P., Kreye, C., Tariku, M. and Six, J. 2022. Understanding changes in cassava root dry matter yield by different planting dates, crop ages at harvest, fertilizer application and varieties. *European Journal of Agronomy* 133: 126448. 10.1016/j.eja.2021.126448.
- Fukuda, W.M.G., Guevara, C.L., Kawuki, R. and Ferguson, M.E. 2010. Selected morphological and agronomic descriptors for the characterisation of cassava. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, 1st edition. 19pp; <https://www.iita.org/wp-content/uploads/2020/07/Selected-morphological-and-agronomic-descriptors-for-the-characterisation-of-cassava.pdf>.
- Gómez, R. O., Chávez, A. L., Sánchez, T. and Roca, W. M. 2021. Phenotypic and genetic diversity of local cassava (*Manihot esculenta* Crantz) varieties in Mexico. *Genetic Resources and Crop Evolution* 68(5):1039-1053.
- Hillocks, R.J., Thresh, J.M. and Bellotti, A.C. 2012. Cassava: Biology, production, and utilization. CABI Publishing. <https://www.cabidigitallibrary.org/doi/book/10.1079/9780851995243.0000>.
- Joaqui, B.O., Lenis, J.I., Calle, F., Morante, N., Pérez, J.C., Hershey, C., Ceballos, H. 2016. Cassava breeding II: Phenotypic

- correlations through the different stages of selection. *Frontier Plant Science* 7:1649. <https://doi.org/10.3389/fpls.2016.01649>.
- Jolliffe, I. T. 2002. Principal component analysis. 2nd ed. Springer Series in Statistics. <https://doi.org/10.1007/b98835>.
- Jolliffe, I.T. and Cadima, J. 2016. Principal component analysis: A review and recent developments. *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences* 374(2065): 20150202.
- Karim, K.Y., Ifie, B., Dzidzienyo, D., Danquah, E.Y., Blay, E.T., Whyte, J. B. and Norman, P. E. 2020. Genetic characterisation of cassava (*Manihot esculenta* Crantz) genotypes using agro-morphological and single nucleotide polymorphism markers. *Physiology and Molecular Biology of Plants* 26(2):317-330.
- Kengkanna, J., Jakaew, P., Amawan, S., Busener, N., Bucksch, A. and Saengwilai, P. 2019. Phenotypic variation of cassava root traits and their responses to drought. *Applied Plant Science* 7: e1238. <https://pmc.ncbi.nlm.nih.gov/articles/PMC6476172/>.
- Malik, A.I., Kongsil, P., Nguy n, V.A., Ou, W., Sholihin, S.P., Sheela, M., Becerra L pez-Lavalle, L.A., Utsumi, Y., Lu, C. and Kittipadakul, P. 2020. Cassava breeding and agronomy in Asia: 50 years of history and future directions. *Breeding Science* 70:145-166. <https://pubmed.ncbi.nlm.nih.gov/32523397/>.
- Nduwimana, F., Niyongere, C., Ndikumana, C. and Ndayiragije, A. 2020. Phenotypic variability of cassava landraces in Burundi. *Journal of Agricultural Science and Technology* 22(1):45-56.
- Noerwijati, K., Nasrullah, T. and Prajitno, D. 2014. Fresh tuber yield stability analysis of fifteen cassava genotypes across five environments in East Java (Indonesia) using GGE biplot. 2014. *Energy Procedia* 47:156-165. doi: 10.1016/j.egypro.2014.01.209.
- Ntawuruhunga, P. and Legg, J. P. 2022. Cassava germplasm conservation and the genetic improvement of resistance to pests and diseases. *Plant Genetic Resources* 20(3):1-14. <https://doi.org/10.1017/S1479262121000485>.
- Nweke, F.I., Sani, A.G. and Ferris, R.S.B. 2016. Cassava: A critical review of its potential and challenges for food security in sub-Saharan Africa. *Agricultural Systems* 148:109-119. <https://doi.org/10.1016/j.agsy.2016.07.010>.
- Nyamwamu, N.C., Jeruto, P., Njenga, E., Arama, P.F. and Mulwa, R. M. 2023. Phenotypic characterisation of cassava (*Manihot esculenta* Crantz) germplasm in Kenya. *ASRIC Journal on Agricultural Sciences* 4 (1):152-162.
- Obeng-Bio, E., Osei, K., Ofori, E. and Danquah, E.Y. 2019. Phenotypic characterisation of cassava (*Manihot esculenta* Crantz) germplasm in Ghana. *Journal of Plant Breeding and Crop Science* 11(6):112-120.
- Ogbonna, A.C., Braatz de Andrade, L.R. Mueller, L.A. de Oliveira, E.J. and Bauchet, G.J. 2021. Comprehensive genotyping of a Brazilian cassava (*Manihot esculenta* Crantz) germplasm bank: Insights into diversification and domestication. *Theory and Applied Genetics* 134:1343-1362.
- Okonkwo, C.J., Egesi, C.N., Mbanaso, E.N. A., Onyeka, J. and Dixon, A.G.O. 2021. Root quality attributes influencing consumer preference and market acceptability of cassava (*Manihot esculenta* Crantz) varieties in sub-Saharan Africa. *International Journal of Agronomy*. pp. 1-10. <https://doi.org/10.1155/2021/6690152>.
- Oliveira, E.J., Oliveira, O.S., Oliveira, F., Santos, V.S. 2015. Classification of cassava genotypes based on qualitative and quantitative data. *Genetics and Molecular Research* 14(1):906-924.
- Rabbi, I.Y., Kayondo, S.I., Ikpan, A.S., Kulakow, P. and Onyegbule, O. 2017.

- Genomic selection in cassava breeding: Advances, challenges, and prospects. *Frontiers in Plant Science* 8:2332. <https://doi.org/10.3389/fpls.2017.02332>.
- Rattanasopa, K., Saengprachatanarug, K., Wongpichet, S., Posom, J., Saikaew, K., Ungsathittavorn, K., Pilawut, S., Chinapas, A. and Taira, E. 2022. UAV-Based multispectral imagery for estimating cassava tuber yields. *Engineering, Agriculture, Environ and Food* 15:1=12. https://www.academia.edu/92686466/UAV_
- Richman, M.B. 1988. A cautionary note concerning a commonly applied eigen analysis procedure. *Tellus* 40B:50-58.
- Ridwan, D., Suwanto, Santosa, E., Hartono, A., Pramuhadi, G., Nuryartono, N., Yusfiandayani, R. and Prartono, T. 2022. Morphological and physiological characterisation of cassava genotypes on dry land of ultisol soil in Indonesia. *International Journal of Agronomy*. Article ID 3599272, <https://doi.org/10.1155/2022/3599272>.
- Rimoldi, F., Vidigal, Filho, P.S., Kvitschal, M.V., Gonçalves-Vidigal, M.C., Prioli, A.J., Prioli, S.M.A.P. and Costa, T. R. 2010. Genetic divergence in sweet cassava cultivars using morphological agronomic traits and RAPD molecular markers. *Brazilian Archives of Biology and Technology* 53(6):1477-1486.
- Sánchez, R., García, M. and López, D. 2018. Analysis of cassava germplasm using phenotypic traits and PCA in Colombia. *Journal of Crop Science* 28(3):110-125.
- Saravanan, R., Ravi, V., Stephen, R., Thajudhin, S. and George, J. 2016. Post-harvest physiological deterioration of cassava (*Manihot esculenta* Crantz). A review. *Indian Journal of Agricultural Sciences* 86:1383–1390.
- Shirima, R.R., Nuwamanya, E. and Tumuhimbise, R. 2022. Impact of genotype × environment interaction on cassava starch quality in Tanzania. *Journal of Plant Breeding and Genetics* 41(2): 102-112.
- Tao, Z., Zhang, L. and Wu, Z. 2020. The role of stem color in cassava genetic diversity and stress resistance. *Journal of Root Crops* 46(2):135-142.
- Tumuhimbise, R., Melis, R., Shanahan, P. and Kawuki, R. S. 2021. Phenotypic diversity of cassava landraces and improved varieties in Uganda. *Plant Genetic Resources: Characterisation and Utilization* 19(3): 213-224.