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Characterization of Cassava (*Manihot esculenta*) Germplasm from Sierra Leone Based on Agro-Morphological and Culinary Traits

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Abstract: Dearth of information on extent of genetic variability in cassava limits the genetic improvement of cassava in Sierra Leone. This study aimed at assessing the genetic variability and relationships within 103 cassava genotypes using agro-morphological and culinary markers. A field trial was conducted in the School of Agriculture and Food Sciences research site. The experiment was laid in an augmented randomized block design. Morphological classification based on qualitative and quantitative traits categorized the germplasm into three different groups. A total of ten principal components (PCs) in the qualitative and six PCs in the quantitative trait sets accounted for 66.74% and 67.27% of the total genetic variation, respectively. Traits with significantly strong and positive correlations included presence of fruit (PFRT) and presence of seed (PSE)($r = 0.86^{***}$),root yield per plant (RYPP) and number of storage root (NSR) ($r = 0.76^{***}$), RYPP and number of commercial root (NCR) ($r = 0.68^{***}$), length of leaf lobe (LLL) and width of leaf lobe (WLL) ($r = 0.66^{***}$),and between NSR and NCR (0.84^{***}). Cooking time, cooking percentage, texture, mealiness, taste and aroma varied widely among the accessions. Findings established that the cassava germplasm possess useful genetic variability that could be exploited through selection for short term release programme, genetic conservation of valuable germplasm and genetic improvement of the crop.

Keywords: Cassava; germplasm; genetic variability; morpho-culinary markers; phenotypic relationship

1. Introduction

Cassava (*Manihot esculenta* Crantz) is a highly significant root crop, widely utilized for human consumption, animal feed, and industrial applications [1]. The starchy storage roots of cassava have emerged as a crucial source of dietary energy in sub-Saharan Africa (SSA), offering higher returns per unit of input compared to other staple crops [1,2]. Cassava exhibits exceptional resilience, thriving in nutrient-poor soils and displaying superior yield performance in comparison to other root and tuber crops [2,3]. Nevertheless, the response of cassava genotypes to diverse environmental factors (soil, climate) and biotic stresses can vary significantly [3,4].

In Sierra Leone, the lack of comprehensive data regarding the genetic variation within the cassava breeding population hampers the development of superior cassava genotypes. Assessing the extent of genetic variation within the breeding population is essential for identifying valuable genetic divergence that is crucial for improving cassava populations. Genetic markers serve as an effective

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tool for evaluating genetic divergence within the breeding population [5]. Preliminary studies often utilize genetic markers, including agro-morphological markers, due to their efficiency and simplicity in assessing the diversity among germplasm [6]. Certain morphological traits have proven to accurately reflect the perceived diversity by farmers [7,8]. Additionally, Elias et al. [9] reported that morphological traits exhibit heritable genetic variation. Morphological traits, both quantitative and qualitative, have been widely employed in the systematic identification of genotypes, species, and genera in various crops [10]. Qualitative traits are typically governed by a few major genes, resulting in distinct observable differences that facilitate genotype differentiation and identification. On the other hand, quantitative traits are influenced by numerous minor genes with complex inheritance patterns. These traits are more susceptible to environmental effects and the developmental stage of the crop. Genetic diversity studies based solely on morphological traits can be constrained by environmental factors and genotype-environment interactions [11]. These limitations may hinder the accurate identification of duplicate genotypes through morphological classification techniques alone. To overcome these challenges, Collard et al. [11] highlighted the use of molecular markers, which enable the detection of genetic distinctions among closely related genotypes. This study assessed the genetic variability and relationships within 103 cassava genotypes using agro-morphological and culinary markers

2. Materials and Methods

2.1. Description of the study area

A field experiment was carried out in the upland ecology of the School of Agriculture and Food Sciences experimental site, Njala during May 2020/2021 cropping season. Njala is located on an elevation of 50 m above sea level on latitude 8°6N and longitude 12°6W of the equator. Njala experiences distinct dry and wet seasons. The rainy season starts from April to November and the dry season starts from October to May. The mean monthly air temperature ranges from 21°C to 23°C for greater part of the day and night especially during the rainy season. The land cover of the experimental site is predominantly secondary bush and consists of well-balanced mixture of sand, clay, and humus.

2.2. Plant material, experimental design and layout

The experimental materials included stem cuttings of 103 cassava genotypes, of which, 100 accessions were collected from all districts of Sierra Leoneand3 improved released varieties (SLICASS 4, SLICASS 6 and SLICASS 7) utilized as checks. The experiment was laid out in an Augmented Randomized Design with four blocks, each block measuring 28 m × 10 m with 1 m apart between two blocks. The total experimental area utilized was 43 m × 28 m. About 10 stem cuttings per genotype each measuring 30cm long were planted on a 10 m long ridges at 1 m × 1 m spatial arrangement

2.3. Data collection

2.3.1. Agro-morphological traits

Agro-morphological traits comprising both quantitative and qualitative traits were evaluated based on the agro-morphological descriptor of cassava described by Fukuda et al. [12]. Harvest index (HI) was calculated at harvest as the ratio of fresh root yield to the total fresh biomass (weight of roots and weight of above ground biomass). Root dry matter content (RDMC) determination was done at harvest by selecting three representative roots from the bulk of roots harvested from 5 plants. Cassava roots were washed and shredded into pieces. A standard measure of 100 g weight of the fresh samples was taken and oven dried at 65–70°C and reweighed to obtain a constant weight after 72 h [12]. The qualitative and quantitative data collected, codes, scoring and sampling period are presented in Tables 1 and 2.

Table 1. Qualitative data and techniques used for scoring.

Trait	Code	Scoring	Sampling time (MAP)
Color of apical leaves	CAL	(3) Light green; (5) Dark green; (7) Purplish green; (9) Purple	3
Leaf color	LC	3 = light green; 5 = dark green; 7 = purple green; 9 = purple	6
Presence of fruit	PFRT	(0) Absent; (1) Presence	6
Presence of seeds	PSE	(0) Absent; (1) Presence	9
Lobe margins	LM	(3) Smooth; (7) Winding	6
Color of leaf vein	CLV	(3) Green; (5) Green-reddish; (7) Red	6
Petiole color	PEC	(1) Yellowish-green; (2) Green; (3) Reddish-green; (5) Greenish-red; (7) Red; (9) Purple	6
Shape of central leaflet	SCL	(1) Ovoid; (2) Elliptic-lanceolate; (3) Obovate-lanceolate; (4) Oblong-lanceolate; (5) Lanceolate; (6) Straight or linear; (7) Pandurate; (8) Linera-piramidal; (9) Linear-pandurate; (10) Linear-hostatilobalate	6
Orientation of petiole	OPE	(1) Inclined-upwards; (3) Horizontal; (5) inclined-downwards; (7) Irregular	6
Leaf retention	LRE	(1) Very poor retention; (2) Less than average retention; (3) Average; (4) Better than average retention	6
Stipule margin	STM	(1) Entire; (2) Split	9
Color of stem epidermis	CSTE	(1) Creme; (2) Light brown; (3) Dark brown; (4) Orange	9
Color of end branches	CEBR	(3) Green; (5) Green-purple; (7) purple	9
Color of stem cortex	CSC	(1) Orange; (2) Light green; (3) Green	9
Color of stem exterior	CSE	(3) Orange; (4) Greeny-yellowish (5) Golden; (6) Light brown; (7) Silver; (8) Gray; (9) Dark brown.	9
Prominence of foliar scar	PFS	(3) Semi-prominent; (5) Prominent	9
Branching habit	BRH	(1) Erect; (2) Dichotomous; (3) Trichotomous; (4) Tetrachomotous	12
Root constrictions	RCO	(1) Few to none; (2) Some; (3) Many	12
Color of root cortex	CRC	(1) White or cream; (2) Yellow; (3) Pink; (4) Purple	12
Color of root pulp	CRP	(1) White; (2) Cream; (3) Yellow; (4) Orange; (5) Pink	12
External color of storage root	ECSR	(1) White or cream; (2) Yellow; (3) Light brown; (4) Dark brown	12
Extent of root peduncle	ERP	(0) Sessile; (3) Pedunculate; (5) Mixed	12
Root taste	RT	(1) Sweet; (2) Intermediate; (3) Bitter	12
Root shape	RS	(1) Conical; (2) Conical-cylindrical; (3) Cylindrical; (4) Irregular	12
Plant shape	PLNS	(1) Compact; (2) Open; (3) Umbrella; (4) Cylindrical	12

Source: Fukuda et al. [12].

Table 2. Quantitative data and techniques used for scoring.

Trait	Code	Techniques of measurement	Sampling time (MAP)
Width of leaf robe	WLL	Two leaves from the middle of the plant measured from the widest part of the middle lobe	6

Length of leaf lobe	LLL	Measured from the intersection of all lobes to the end of the middle lobe	6
Petiole length	PLEN	Measured on two leaves per plant	6
Number of leaf robes	NLL	Counted on five leaves per plant with consideration of the predominant number of lobes	6
Distance between foliar scar	DSL	Measuring the distance between two foliar scars	6
Length of stipule	LST	Measured using meter rule.	9
Height at first branching	HFB	Measured vertically from ground to first primary branch	12
Level of branching	LBR	Number of branching points or levels	12
Plant height	PHT	Measured vertically from the ground to the top of the canopy	12
Number of commercial roots	NCR	Recorded on root with length greater than 20 cm from three plants	12
Number of storage root	NSR	Number of roots with length greater than 20 cm from three plant	12
Harvest index	HI	Measured as ratio of fresh root yield to the total fresh biomass	12
Root yield per plant	RYPP	All the root showing length greater than 20 cm are weighted	12
Root dry matter content	RDMC	Weighed the dry roots	12

Source: Fukuda et al. [12]; MAP=months after planting.

2.3.2. Culinary traits of selected cassava genotypes

Thirty farmers were randomly selected for participatory identification and selection of five best preferred, five moderately preferred and five least preferred cassava accessions based on above ground (leaf, petiole) traits for marketability and consumption. The selected 15 cassava accessions were tagged for further culinary evaluation after harvest. The culinary traits measured included time of cooking (CT), cooking percentage (CP), surface appearance of the cooked storage root, mealiness, aroma, texture and taste of the cooked cassava root.

For CT (min), a 5cm long piece was removed from the central region of each of the 10 fresh storage roots per genotype. The 10 pieces were peeled, washed in fresh water and placed in 1.5 l of boiling water. Checking was done at 5 min intervals for ease of cooking using a folk and the cooking time was recorded when 6 pieces (50% + 1) no longer resisted penetration with a fork [13]. The roots continued to cook for a maximum of 30 min in total and after this period, the number of tender cooked pieces was recorded. The CP (%) was calculated by dividing the number of tender cooked pieces by the total number of the roots placed in the boiling water.

Mealiness of the root is an attribute used in describing cassava roots which when boiled become soft and chewable [14]. Thus, all cassava roots were categorized to reflect the degrees of mealiness. The cooked samples were divided into small pieces and placed randomly on labeled plates. Each panelist was given a glass of water to rinse his or her mouth before the next sample. Each of the samples was rated for surface appearance (surface color); mealy (floury); taste (mouth feel and after taste); texture (feel of the tongue before chewing) and aroma (smell). Sensory evaluation was carried out according to a method by Iwe [15]. A five-point hedonic scale (5 = very good, 4 = good, 3 = fair, 2

= poor, 1 = worst) was utilized. A product with a mean score of M≥3 for a given attribute was considered acceptable and each accepted variety was further sampled for its culinary aspects by six trained panelists.

2.4. Data analysis

The data were first entered into an Excel spreadsheet in the form of an ″accessions / morphological characters ″ matrix. The genetic variation among the studied genotypes for agro-morphological traits was explored using multivariate analysis technique. Multivariate analysis of the 103 × 25 qualitative data and 103 × 14 quantitative data matrices were separately subjected to principal component analysis (PCA) and descriptive statistics was performed for the quantitative data using R software program [16]. In the PCA, eigen-values and load coefficient values were generated from the data sets. 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 [17]. The PCA and correlation matrices were used to determine the relationships among the traits. The organization and structure of the morphological variability was visualized using the Ascending Hierarchical Clustering (AHC) to plot a dendrogram. Data on culinary traits were subjected to analysis of variance using the R software program [16] and the means were compared using Scott-Knott test.

3. Results

3.1. Correlation analysis, principal component analysisand genetic relationshipsamong cassava assessions based on 25 qualitative agro-morphological traits

The results on the correlation matrices of 25 qualitative characters revealed a significant and positive correlation between color of leaf vein and leaf color (r= 0.22*), color of leaf vein and petiole color (r= 0.62***), leaf color and color of apical leaf (r= 0.39***), leaf color and petiole color (r= 0.43***), leaf color and leaf retention (r= 0.22*), color of apical leaf and leaf retention (r= 0.23*), shape of center leaflet and color stem epidermis (r=0.23*), leaf margin and presence of foliar scar (r= 0.29**), leaf margin and color of end branches (r= 0.24*), petiole color and leaf retention (r=0.24*), root taste and fruit (r= 0.25*), color of stem epidermis and plant shape(r = 0.21*), leaf retention and stipule margin (r= 0.24*), height at first branching and fruit(r= 0.32**), height at first branching and seed (r= 0.31**), plant shape and fruit (r= 0.47***), plant shape and seed (r= 0.44***), fruits and seeds (r= 0.86***) (Table 3). Conversely, significant and negative correlation were noted between leaf color and shape of center leaflet(r= -0.30***), leaf color and branching habit (r= 0.20*), shape of center leaflet and petiole color (r= -0.42***), shape of center leaflet and root constriction (r= -0.29**), petiole color and color stem exterior (r= -0.25*), root shape and color of root cortex (r= -0.24*), color of stem cortex and leaf retention (r= -0.27**), color of stem exterior and seed (r= -0.24*), orientation of petiole and plant shape (r= -0.23*), stipule margin and root constriction (r= -0.19*), and branching habit and plant shape (r= -0.53***).

The eigenvalues and percent variations of the principal components are presented in Table 4. Ten principal components (PC) that accounted for 66.744% of the total variation among the genotypes were identified. The first PC axis with eigenvalue of 2.971 accounted for 11.885% of the total variation, while the second, third and fourth PCs with eigenvalues of 2.611, 1.774 and 1.651 accounted for 10.444%, 7.098% and 6.604% of the total variation, respectively. The fifth, sixth and the seventh PCs with eigenvalues of 1.577, 1.501 and 1.177 accounted for 6.309%, 6.004% and 4.707% of the total variation, respectively, while the eighth, nineth and tenth PCs with eigenvalues of 1.167, 1.156 and 1.1 accounted for 4.669%, 4.625% and 4.4% of the total variation, respectively. The first principal component positively associated with root taste, orientation petiole, branching habit, presence of fruits and presence of seeds. The second PC with second highest loadings factor was positively associated with color of leaf vein, leaf color, color of apical leaf and petiole color. The third PC was associated with root taste, color of apical leaf, leaf retention and orientation petiole, while fourth PC was associated with leaf margin, root cortex and color of end branches. Traits that were positively associated with fifth PC are leaf color, color of apical leaf, color of root cortex, color of stem exterior, presence of fruit and Seeds while leaf retention, color of end branches and stipule margin were the traits was associated with the sixth PC and the Seventh PC was positively associated with mainly with storage root characteristics (root taste and external color of storage). The eighth and ninth PCs were positively associated with root taste, root shape, external color of storage and leaf margin, color of root cortex and leaf retention, respectively, while petiole color and prominence of foliar scale were the only traits that associated positively with the tenth PC.

Table 3. Correlation coefficient among 25 qualitative traits of 103 cassava genotypes.

Trait	RT	CLV	LC	CAL	SCL	LM	PEC	RS	PFS	CRP	CSC	CSE	ECR	CRC
RT	1													
CLV	-0.08	1												
LC	0.03	**0.22***	1											
CAL	0.11	0.03	**0.39*** **	1										
SCL	0.1	-0.14	**-0.30*** *	-0.1	1									
LM	0.14	-0.08	-0.1	0.06	-0.16	1								
PEC	0.08	**0.62*** **	**0.43*** **	0.04	**-0.42*** **	0.02	1							
RS	-0.13	-0.09	-0.02	0.02	0	0.06	0.01	1						
PFS	0.13	-0.14	-0.11	0.09	0.03	**0.29** **	-0.18	0	1					
CRP	0.10	0.05	-0.03	-0.01	0.02	0.08	-0.06	0.03	-0.09	1				
CSC	0.01	-0.07	-0.03	-0.03	-0.05	0.12	-0.05	0.10	0	-0.09	1			
CSE	0.11	-0.12	-0.1	-0.06	0.13	0	-0.15	-0.15	0.07	-0.03	-0.02	1		
ECSR	0.12	-0.04	-0.05	-0.18	0.08	-0.14	0.02	0.07	-0.01	0.11	-0.05	-0.05	1	

CRC	-0.17	0.01	0.05	-0.14	-0.06	-0.06	-0.01	**-0.24***	**-0.24***	-0.05	0.12	0.08	0.07	1
LR	0.07	0.03	**0.22***	**0.23***	-0.12	0.13	**0.24***	-0.01	-0.05	0.06	**-0.27****	-0.19	-0.14	-0.1
PO	0.10	0.11	0.1	0.15	0.04	0	0.04	-0.03	0.10	0.13	-0.05	-0.14	-0.06	-0.2
CSE	0.04	-0.13	-0.01	-0.02	**0.23***	-0.11	**-0.25***	-0.01	0.12	**-0.21***	-0.08	0.18	-0.03	0.15
CEBR	0.04	0.06	-0.07	-0.03	-0.16	**0.24***	0.16	0.07	-0.17	0.02	0.09	-0.12	-0.03	-0.04
STM	-0.01	0.03	-0.08	-0.10	0.06	-0.03	0.04	-0.05	-0.12	-0.05	-0.12	0.06	0.04	0.09
BRH	-0.03	-0.08	**-0.20***	0	0.07	0.10	-0.14	0.10	0.04	-0.11	0.03	-0.02	0.01	-0.1
PLNS	-0.03	0	0.16	0.05	0.01	-0.12	0.09	-0.13	-0.10	-0.12	-0.09	**0.21***	-0.06	0.12
ERP	-0.02	0	-0.18	-0.07	0.09	-0.10	-0.07	0	0.04	0.08	-0.12	-0.10	0.10	-0.1
RCO	-0.04	0.08	0.11	-0.15	**-0.29****	0.02	0.13	0.16	-0.01	0.13	0.01	-0.04	0.05	0.07
PFRT	0.02	-0.11	-0.04	0.16	0.01	0.06	-0.03	**0.25***	-0.03	-0.03	0.03	-0.18	0.03	-0.1
PSE	0	-0.05	-0.07	0.14	0.05	0.03	0	0.14	0.01	-0.08	0.01	**-0.24***	0.04	-0.1

Table 3. Continues.

Trait	LR	OPE	CSE	CEBR	STM	BRH	PS	EXT	RCO	PFRT	PSE
LR	1										
PO	0.19	1									
CSE	-0.08	-0.22*	1								

CEBR	-0.05	-0.12	-0.19	1							
STM	**0.24***	-0.07	-0.04	0.11	1						
BRH	0.06	0.18	-0.05	0.07	-0.06	1					
PLNS	-0.03	**-0.23***	0.05	-0.04	0.16	**-0.53*****	1				
ERP	0.06	0.06	-0.08	-0.18	-0.09	0.06	-0.18	1			
RCO	-0.05	-0.05	-0.08	-0.11	**-0.19***	0	-0.11	0.09	1		
PFRT	0.14	0.17	0	0.01	-0.14	**0.32****	**0.47*****	0.08	0.07	1	
PSE	0.09	0.14	0.07	-0.01	-0.17	**0.31****	**0.44*****	0.13	0.04	**0.86*****	1

RT=root taste, CLV=color of leaf vein, LC=leaf color, CAL=color of apical leaf, SCL= shape of center leaflet, LM=lobe margin, PEC=petiole color, RS=root shape, PFS=prominent of foliar scar, CRP=color of root pulp, CSC=color of stem cortex, CSE=color of stem epidermis, ECSR= external color of storage root, CRC=color of root cortex, LR=leaf retention, PO= petiole orientation, CSE=color of stem exterior, CEBR=color of end branches, STM=stipule margin, BRH=branching habit, PLNS=plant shape, ERP=extent of root penduncle, RCO=root constrictions, PFRT=presence of fruits, PSE=presence of seeds.

Table 4. Principal component analysis, eigen value and percentage variation of 25 characters of 103 cassava genotypes.

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
RT	0.053	-0.003	**0.384**	0.184	-0.230	-0.115	**0.574**	**0.402**	-0.007	0.052
CLV	-0.150	**0.581**	-0.149	-0.185	-0.111	0.002	0.246	-0.293	-0.083	**0.356**
LC	-0.181	**0.628**	0.230	-0.141	**0.339**	-0.228	0.077	0.105	-0.085	-0.129
CAL	0.144	**0.327**	**0.573**	0.048	**0.301**	-0.081	-0.032	0.025	-0.212	-0.243
SCL	0.057	**-0.594**	0.206	-0.266	-0.134	0.199	0.137	-0.025	-0.314	-0.003
LM	0.188	0.081	0.135	**0.704**	-0.114	-0.021	-0.061	0.108	**0.340**	0.010
PEC	-0.143	**0.805**	-0.124	-0.032	-0.004	0.02	0.197	0.049	0.012	**0.347**
RT	**0.327**	0.036	-0.222	0.113	0.079	-0.082	**-0.482**	**0.349**	**-0.385**	0.117
PFS	0.168	-0.237	0.401	0.295	-0.084	**-0.418**	-0.080	-0.042	0.158	**0.369**
CRP	0.056	0.095	-0.046	-0.031	**-0.568**	-0.159	0.032	0.216	-0.039	**-0.536**
COX	0.055	-0.089	**-0.313**	**0.440**	0.248	-0.144	0.216	-0.211	-0.236	-0.216
CSE	**-0.331**	**-0.374**	0.167	0.096	0.055	-0.112	0.210	0.019	0.222	0.047
ECSR	0.037	-0.115	-0.292	-0.248	-0.262	-0.054	**0.323**	**0.488**	-0.110	0.123
CRC	**-0.315**	-0.057	**-0.338**	-0.152	**0.316**	0.135	0.230	-0.040	**0.441**	**-0.372**
LR	0.142	**0.429**	**0.424**	-0.152	-0.090	**0.336**	-0.250	0.168	**0.350**	-0.104
PO	**0.354**	0.228	**0.336**	-0.124	-0.296	-0.050	0.146	**-0.371**	-0.093	-0.177
CSE	-0.089	**-0.419**	0.182	-0.207	**0.487**	-0.053	0.083	0.206	0.130	0.212
CEBR	0.008	0.204	-0.264	**0.550**	-0.070	**0.438**	0.090	0.118	-0.169	0.033
STM	-0.273	0.010	0.073	-0.032	-0.165	**0.651**	-0.122	0.177	0.157	0.097
BRH	**0.594**	-0.130	-0.070	0.099	-0.016	0.218	0.098	-0.257	0.193	0.112
PLNS	**-0.749**	0.018	0.171	-0.025	0.120	0.002	-0.169	0.145	-0.161	-0.012

ERP	0.248	-0.099	-0.066	-0.394	**-0.374**	-0.158	-0.181	-0.105	0.124	0.118
RCO	0.099	0.212	-0.409	-0.071	-0.025	-0.540	-0.148	0.190	0.341	-0.034
PFRT	**0.804**	0.073	-0.048	-0.128	**0.305**	0.128	0.094	0.187	0.034	-0.079
PSE	**0.788**	0.047	-0.039	-0.182	**0.307**	0.119	0.128	0.126	0.003	0.040
Eigenvalue	2.97	2.61	1.77	1.65	1.58	1.50	1.18	1.17	1.16	1.10
Proportion of variance (%)	11.88	10.44	7.1	6.6	6.31	6.00	4.71	4.67	4.63	4.4
Cumulative variance (%)	11.88	22.33	29.43	36.03	42.34	48.34	53.05	57.72	62.34	66.74

RT=root taste, CLV=color of leaf vein, LC=leaf color, CAL=color of apical leaf, SCL= shape of center leaflet, LM=lobe margin, PEC=petiole color, RT=root taste, PFS=prominent of foliar scar, CRP=color of root pulp, COX= cortex, CSE=color of stem epidermis, ECSR= external color of storage root, CRC=color of root cortex, LR=leaf retention, PO=petiole orientation, CSE=color of stem exterior, CEBR=color of end branches, STM=stipule margin, BRH=branching habit, PLNS=plant shape, ERP=extent of root penduncle, RCO=root constrictions, PFRT=presence of fruits, PSE=presence of seeds.

The hierarchical classification of 103 cassava genotypes based on qualitative traits grouped the genotypes into three classes almost with the same characteristics as a function of the variable. The genetic similarity for the 25 qualitative traits ranged from zero to two with a mean similarity of 2.0. The cassava genotypes were grouped into three distinct cluster at 1.4 similarities. Clusters I and III have a higher number of genotypes with 40 and 34, respectively, while 29 individuals were in cluster II (Figure 1).

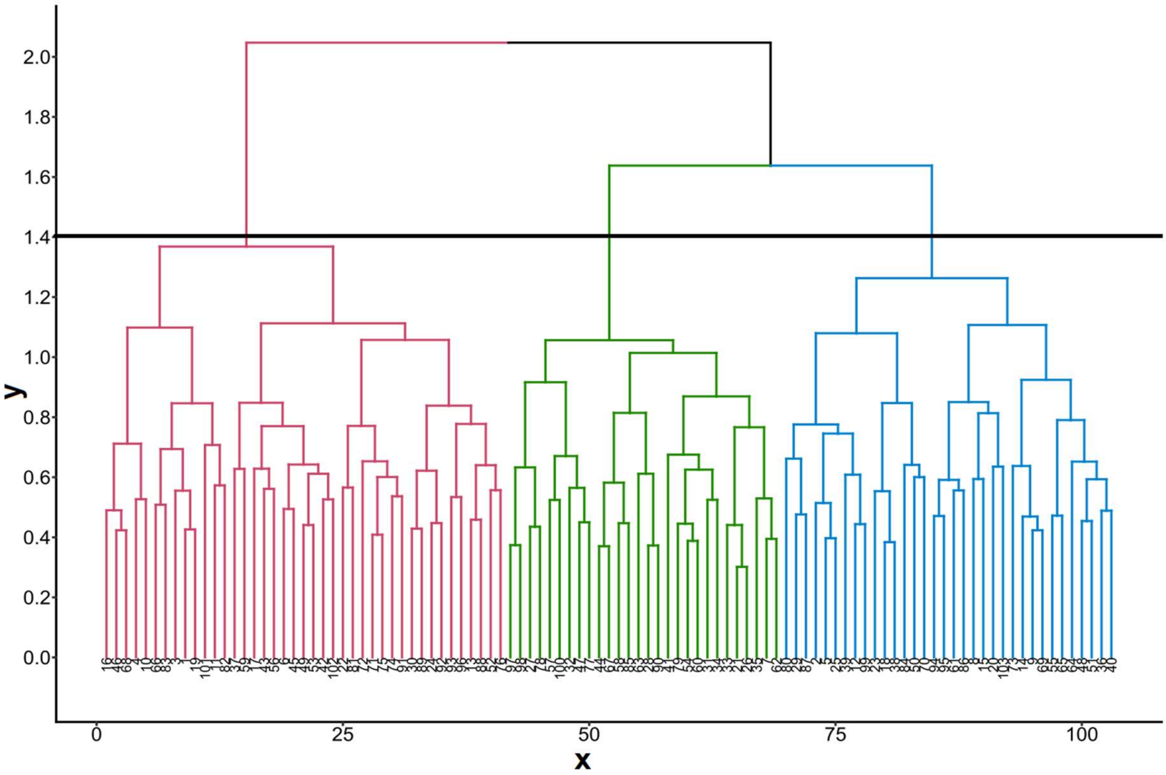

Figure 1. Dendrogram showing relationships among 103 genotypes of cassava classified by Ward method using twenty-five 25 qualitative agro-morphological traits.

3.2. Descriptive statistics, correlation analysis, principal component analysis and genetic relationships among cassava assessions based on 14 quantitative agro-morphological traits

The cassava genotypes showed variability for fourteen quantitative morphological traits assessed (Table 5). The range of the values produced were 1.0 to 5.0 cm for distance between leaf scar, 0.0 to 165.9 cm for height at first branching, 0.16 to 0.68 for harvest index, 0.0 to 20.0 for level of branching, 5.7 cm to 21.8cm for length of leaf lobe, 1.0 cm to 5.0 cm for length of stipule, 1.0 to 24.0 for number of commercial root, 3.0 to 9.0 for number of leaf lobe, 2.0 to 53.0 for number of storage root, 41.0 cm to 346 cm for plant height, 4.7 cm to 37.3 cm for petiole length, 15.0% to 36.0% for root dry matter content, 1.0 kg to 19.0 kg for root yield per plant and 1.5 cm to 6.0 cm for width of leaf lobe(Table 5). The coefficient of variation varied from 14.7% (root dry matter content) to 81.2% (level of branching). Based on the 14 quantitative characters/traits, 11 had high (CV>20%) coefficient of variation (Table 5). Only three characters had low variation including root dry matter content (14.8%), distance between leaf scar (18.7%) and number of leaf lobe (17.8%).

Table 5. Descriptive statistics of 14 quantitative characters of 103 cassava genotypes.

Traits	Minimum	Maximum	Mean	Standard deviation	Coefficient of variance (%)
Distance between leaf scar (cm)	1.0	5.0	3.0	0.5	18.7
Height at first branching (cm)	0.0	165.9	78.8	45.4	57.6
Harvest index	0.2	0.6	0.4	0.1	23.9
Level of branching	0.0	20.0	2.8	2.3	81.2
Length of leaf lobe (cm)	5.7	21.8	14.2	2.8	20.1
Length of stipule (cm)	1.0	5.0	3.3	1.1	34.8
Number of commercial roots	1.0	24.0	8.8	5.1	57.9
Number of leaf lobe	3.0	9.0	6.3	1.1	17.8
Number of storage root	2.0	53.0	15.9	9.7	61.1
Plant height (cm)	41.0	346.0	178.1	43.1	24.2
Petiole length (cm)	4.7	37.3	20.9	6.1	29.2
Roots dry matter content (%)	15.0	36.0	27.8	4.1	14.8
Root yield per plant (kg)	1.0	19.0	6.4	4.2	65.0
Width of leaf lobe (cm)	1.5	6.0	3.3	0.8	24.9

Phenotypic correlations among 14 quantitative traits revealed that harvest index is the principal trait that is significantly and positively correlated with root yield per plant (r= 0.40***) and number of storage root (r= 0.24*) (Table 6). Root yield per plant is highly significant and positively correlated with number of storage root (r= 0.76***) and number of commercial root (r= 0.68***). Petiole length significantly and positively correlated with length of leaf lobe (r= 0.22*) and number of leaf lobe (r= 0.26**). The length of leaf lobe is significantly and positively correlated with the width of leaf lobe (r= 0.66***) and number of leaf lobe (r= 0.41***); the width of leaf lobe also positively correlated with plant height (r= 0.20*).

Number of storage root was significantly and positively correlated with number of commercial roots (r= 0.84***), while plant height was positively correlated with number of leaf lobe (r= 0.24*), and height at first branching positively correlating with level of branching (r= 0.25*). Conversely, significant and negative correlation were noted between harvest index and distance between leaf scar (r= 0.20*), length of leaf lobe and level of branching (r= 0.21*), and between width of leaf lobe and level of branching (r=0.21*).

Table 6. Correlation coefficient among 14 quantitative traits of 103 cassava genotypes.

	HI	RYPP	PLEN	LLL	WLL	RDMC	NSR	PHT	HFB	NLL	DLS	LST	LBR	NCR
HI	1													
RYPP	**0.40*****	1												
PLEN	-0.06	-0.12	1											
LLL	0.02	0.02	**0.22***	1										
WLL	-0.05	0.08	0.05	**0.66*****	1									
RDMC	0.01	0.07	0.11	0.05	0.05	1								
NSR	**0.24***	**0.76*****	-0.03	0.09	0.12	-0.08	1							
PHT	0.03	0.09	0.09	0.17	**0.20***	0.08	0.08	1						
HFB	0.08	0.04	0.04	0.11	0.04	0.08	-0.02	0.11	1					
NLL	0.06	0	**0.26****	**0.41*****	0.14	0.02	0.08	**0.24***	-0.12	1				
DLS	**-0.20***	-0.01	0.19	0.03	-0.04	0.07	0.02	0.06	0.16	-0.05	1			
LST	0.16	0.08	0	0.13	0.06	0.02	0.11	0.09	0	0.01	-0.07	1		
LBR	0.08	0.08	0.02	**-0.21***	**-0.21***	-0.05	0.06	0.04	**0.25***	0.09	0.02	-0.05	1	
NCR	0.17	**0.68*****	-0.09	0.02	0.08	-0.05	**0.84*****	0.04	0.01	0.05	0.01	0.06	0.04	1

Significant at alpha = 0.05, HI=harvest index, RYPP=root yield per plant, PLEN=petiole length, LLL=length of leaflet, WLL=width of leaflet, RDMC=root dry matter content, NSR=number of storage root, PHT=plant height, HFB=height at first branching, NLL=number of leaflet, DLS=distance between leaf scar, LST=length of stipule, LBR=level of branching, NCR=number of commercial root.

The principal component analysis of quantitative agro-morphological traits revealed that the six main principal components accounted for 67.723% of the total variation among the genotypes (Table

7). The first factorial plane contains 18.34% of the variance. The traits that significantly correlated with axis 1 are: harvest index (43.0%), root yield per plant (86.0%), number of storage root (90.0%) and number of commercial root (85.0%). The variables that were significantly correlated with axis 2 are: petiole length (43.0%), length of leaf lobe (83.0%), width of leaf lobe (70.0%), plant height (40.0%) and number of leaf lobe (53.0%).

The traits that were significantly related to axis 3 are: petiole length (44.0%), height at first branching (35.0%) and level of branching (30.0%), the variables significantly correlated to axis 4 are: plant height (30.0%), height at first branching (66.0%) and level of branching (61.0%). The variables significantly related to axis 5 are: harvest index (54.0%), number of leaf lobe (44.0%) and length of stipule (32.0%) and the traits that are significantly correlated to axis 6 are: root dry matter content (54.0%) and length of stipule (44.0%) (Table 7).

Hierarchical classification of 14 quantitative agro-morphological traits grouped the genotypes in three classes almost with same characteristics as a function of the variable (Figure 2). The genetic similarity for the even quantitative traits ranged from zero to two with a mean similarity of 1.8. Cluster I contains 53 genotypes, cluster II contains 6 genotypes and cluster III contains 44 genotypes.

Table 7. Principal component analysis, eigen value and percentage variation of 14quantitative characters of cassava genotypes.

Variable	Prin1	Prin2	Prin3	Prin4	Prin5	Prin6
Harvest index	**0.43**	-0.13	0.07	0.24	**0.54**	0.27
Root yield per plant	**0.86**	-0.20	0.06	-0.01	-0.05	0.08
Petiole length	-0.08	**0.43**	**0.44**	-0.11	0.05	-0.13
Length of leaflet	0.23	**0.83**	0.01	-0.06	0.01	0.07
Width of leaflet	0.23	**0.70**	-0.48	0.13	**-0.30**	-0.01
Root dry matter content	-0.01	0.17	0.21	0.12	-0.09	**0.54**
Number of storage root	**0.90**	-0.13	0.07	-0.18	-0.11	-0.09
Plant height	0.19	**0.40**	0.15	**0.30**	0.04	-0.09
Height at first branching	0.05	0.05	**0.35**	**0.66**	**-0.32**	0.16
Number of leaflet	0.16	**0.53**	0.23	-0.09	**0.44**	**-0.42**
Distance between leaf scar	-0.06	0.08	0.55	-0.15	**-0.56**	0.05
Length of stipule	0.20	0.12	-0.11	0.15	**0.32**	**0.44**
Level of branching	0.06	-0.26	**0.30**	**0.61**	0.06	**-0.49**
Number of commercial root	**0.85**	-0.19	0.05	-0.18	-0.18	-0.09
Eigenvalue	2.75	2.09	1.73	1.24	1.22	1.11
Proportion of variance (%)	18.34	13.94	11.53	8.30	8.18	7.40
Cumulative variance (%)	18.34	32.29	43.83	52.13	60.31	67.72

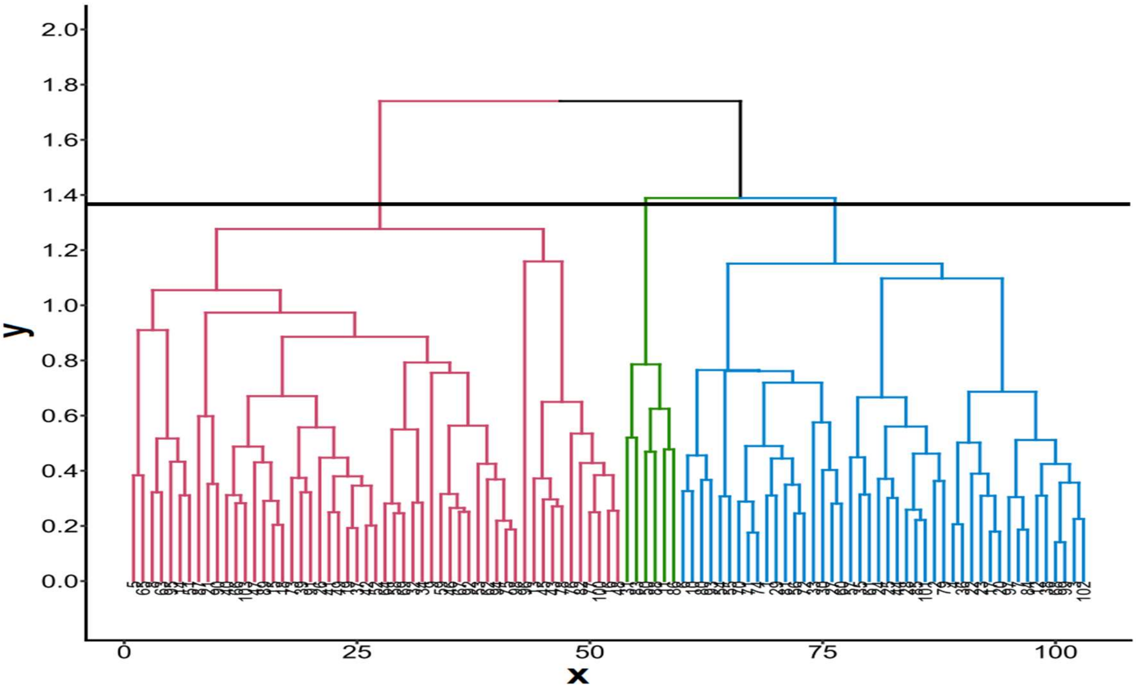

Figure 2. Dendrogram showing relationships among 103 genotypes of cassava classified by Ward method using 14 quantitative agro-morphological traits.

3.3. Culinary traits and marketable leaf assessment of 15 selected cassava genotypes

The mean cooking time (CT) ranged from 15.2 to 30.0 min (Table 8). The genotypes that have short and better cooking time were Cookson (15.2 min) and Butter cassava (15.4 min), those with longest cooking time were pink lady(30.0min), SLICASS 4(30.0 min) and SLICASS 6(30min).The cooking percentage was incorporated as an important culinary trait due to the large variation that is normally observed between the cooking time of cassava varieties. The mean cooking percentage (CP) ranged from 27.9% to 96.4%. The mean percentage were classified into two groups.The group with lowest membership had genotypes SLICASS 4(27.9%), SLICASS 6(30.2%) and SLICASS 7(58.3%). The mean of the other groups of genotypes ranging from 63.2% to 96.4% are pink lady (63.2%), Soja colour (70.3%), Kendemeh (73.4%), Tangagboi (76.2%), Mende tangai (78.4%), Yaa kanu (80.2%), Nikaneh (80.2%), Tapiyoka (82.0%), Cocoa cassada (83.2%), Ndiamonyamalo (88.3%), Butter cassava (95.0%) and Cookson (96.4%).

Mean score for surface appearance, mealiness, taste, and aroma ranged from 2.0 to 4.75 and for texture,from 2.0 to 4.50,indicatingthe acceptable mean threshold (Table 8). Comparing the mean for sensory characteristics, genotypes that had the highest mean scores for surface appearance were cook soon (4.50±0.50), Butter cassava (4.50±0.58) and Cocoa cassada (4.50±0.50), closely followed by Ndiamonyamalo (4.3±0.50), Nikaneh (4.3±0.58), Tapiyoka (4.3±0.55) and Tangagboi (4.25±0.58), Mende Tangai (4.0±0.65), Yaa kanu(4.0±0.50) and SLICASS 7 (4.0±0.50) which clearly indicate good acceptability by consumers for this traits, while other genotypes like Kendemeh(3.5±0.58), Pink lady(3.5±0.82),SLICASS 6 (3.5±0.58) and Soja colour(3.5±0.50) were fairly accepted by consumers. SLICASS 4 has the lowest mean score (2.0±0.40) for surface appearance thus indicating poor acceptability by consumers/farmers (Table 8).

The result on the mealiness revealed that cook soon has the highest mean score (4.75±0.80) followed by Butter cassava (4.50±0.50), Tapiyoka (4.3±0.50), Nikaneh (4.3±0.58), Ndiamonyamalo (4.25±0.48), Cocoa cassada (4.25±0.80), Tangagboi (4.0±0.40), Mende tangai (4.0±0.65), Yaa kanu (4.0±0.60) and Kendemeh (4.0±0.63) thus indicating good acceptable of the genotypes by consumers/farmers for mealiness. Pink lady (3.5±0.82), SLICASS 6 (3.5±0.58) and Soja colour (3.0±0.50) were fairly accepted by farmers. The genotype that recorded the lowest mean score in terms of mealiness was SLICASS 4(2.0±0.82) indicating poor acceptability by consumers of the genotype for this trait. Cook soon was highly rated for its taste and thus records the highest mean score (4.75±0.50), closely followed by Butter cassava (4.50±0.43), Ndiamonyamalo (4.50±0.50), Cocoa cassada (4.50±0.58), Tapiyoka (4.50±0.80) and Tangagboi (4.50±0.50), Nikaneh (4.3±0.58), Yaa kanu (4.25±0.50), Kendemeh (4.25±0.50) and Mende tangai (4.0±0.65) indicating good acceptability by farmers while Pink lady(.5±0.65) and SLICASS 7(3.0±0.45) were fairly accepted for this trait by farmers. However, SLICASS 4 (2.0±0.50), SLICASS 6 (2.0±0.50) and Soja colour (2.0±0.50) were rated poorly for taste quality. Sensory evaluation on the aroma of the cooked root of the genotypes revealed that Cook soon (4.75±0.50) and Butter cassava (4.75±0.50) scored the highest mean followed by Ndiamonyamalo (4.3±0.50), Tapiyoka(4.3±0.50), Cocoa cassada(4.25±0.58), Tangagboi(4.25±0.58), Nikaneh(4.25±0.50), Yaa kanu(4.25±0.82), Mende tangai (4.0±0.65), Kendemeh(4.0±0.58) and SLICASS 7(4.0±0.60) which indicate good acceptability by consumers while Soja colour(3.0±0.65), Pink lady(3.0±0.50) and SLICASS 6(3.0±0.50) was fair accepted by consumers in terms aroma. However, SLICASS 4 was poorly accepted by consumers being a mean score of 2.0±0.82. Cook soon and Butter cassava scored the highest means of 4.50±0.58 and 4.50±0.50, respectively, in terms their texture, followed by Ndiamonyamalo (4.3±0.50), Cocoa cassada (4.25±0.58), Tangagboi (4.25±0.58), Mende Tangai (4.0±0.65), Nikaneh (4.0±0.50) and Tapiyoka (4.0±0.60), which indicate good acceptability by consumers. Other genotypes like Yaa kanu (3.5±0.58), Kendemeh (3.5±0.50), pink lady (3.0±0.58), SLICASS 7(3.0±0.50) and SLICASS 6 (3.0±0.50) were fairly accepted by consumers. SLICASS 4 (2.0±0.82) and Soja color (2.0±0.82) were poorly accepted.

Table 8. Culinary traits evaluation of 15 selected cassava accessions in 2020 cropping season.

Genotypes	Cooking time	Cooking percent	Surface appearance	Mealiness	Taste	Aroma	Texture
	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE	Mean± SE	Mean± SE	Mean± SE
Cook soon	15.2±1.2	96.4±2.4	4.5±0.50	4.75±0.80	4.8±0.50	4.8±0.50	4.5±0.58
Butter cassava	15.4±1.2	95.0±1.8	4.5±0.58	4.50±0.50	4.9±0.43	4.8±0.50	4.5±0.50
Ndiamonyamalo	21.0±1.4	83.3±1.6	4.3±0.50	4.25±0.48	4.5±0.50	4.3±0.50	4.3±0.50
Cocoa cassada	20.0±1.7	88.2±2.1	4.5±0.50	4.25±0.80	4.5±0.58	4.5±0.58	4.3±0.58
Tangagboi	28.7±1.8	76.2±2.3	4.3±0.58	4.0±0.40	4.5±0.50	4.3±0.58	4.3±0.58
Mende Tangai	28.6±1.5	78.4±2.0	4.0±0.65	4.0±0.65	4.0±0.65	4.0±0.65	4.0±0.65
Nikaneh	27.0±1.5	80.2±2.5	4.3±0.58	4.3±0.58	4.3±0.58	4.3±0.50	4.0±0.50
Yaa Kanu	27.0±1.7	80.2±3.0	4.0±0.50	4.0±0.60	4.3±0.50	4.3±0.82	3.5±0.58
Kendemeh	28.6±1.6	73.4±1.9	3.5±0.58	4.0±0.63	4.3±0.50	4.0±0.58	3.5±0.50
Tapiyoka	25.7±1.4	82.0±3.2	4.3±0.55	4.3±0.50	4.5±0.80	4.3±0.50	4.0±0.60

Soja color	29.8±1.5	70.3±2.8	3.0±0.50	3.0±0.58	2.0±0.50	3.0±0.65	2.0±0.82
Pink lady	30.0±1.5	63.2±2.6	3.5±0.82	3.0±0.80	3.5±0.65	3.0±0.50	3.0±0.58
SLICASS 7	29.8±1.8	58.3±1.7	4.0±0.50	3.5±0.40	3.0±0.45	4.0±0.60	3.0±0.50
SLICASS 6	30.0±1.7	30.2±3.1	3.5±0.58	3.0±0.55	2.0±0.50	3.0±0.50	3.0±0.50
SLICASS 4	30.0±1.3	27.9±1.8	2.0±0.40	2.0±0.82	2.0±0.50	2.0±0.82	2.0±0.82

3.3. Marketable leaf assessment

The five elite varieties selected by farmers based on desired leaf traits for selling and consumption included Tangaigboi Coco cassada, Cooksoon, Butter cassava and Ndiamonyamalo, followed by moderately preferred varieties. Tapiyoka, Yaa kanu, Nikaneh, Mende tangai, and Kendemeh (Table 9).However, the leaves of varieties SLICASS 4, SLICASS 6, SLICASS 7, Pink lady, and Sojarcolourare not usually consumed and sold.

Table 9. List of 15 varieties selected by farmers for marketability and consumption.

Varieties/Genotypes	Rating
Tangaigboi	Highly preferred
Coco cassada	Highly preferred
Cooksoon	Highly preferred
Butter cassava	Highly preferred
Ndiamonyamalo	Highly preferred
Tapiyoka	Moderately preferred
Yaa kanu	Moderately preferred
Nikaneh	Moderately preferred
Mende tangai	Moderately preferred
Kendemeh	Moderately preferred
SLICASS 4	Not good
SLICASS 6	Not good
SLICASS 7	Not good
Pink lady	Not good
Soja colour	Not good

4. Discussion

Significant variation was noted from the analysis of the qualitative morphological traits (root taste, external color of storage root, color of root pulp, ease of peeling, color of leaf vein, lobe margins, leaf color, color of apical leaves, shape of central leaflet leaf color, color of root cortex, petiole color, root cortex, color of stem exterior, presence of fruit and seeds, leaf retention, color of end branches and stipule margin, external color of storage) among the studied genotypes. The most representative and distinctive trait was color possibly due to the fact that most of the exhibited white root pulp and dark brown external storage root. The above- ground leaf attributed of the studied genotypes were green leaf vein, light green leaf, light green apical leaf, smooth lobe margin, and elliptic-lanceolate center leaflet. The leaf attribute plays significant role in cultivar identification and more significant in

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cassava selection for leafy vegetable market for farmers. The findings agree with work of Karim et al. [18] who reported that leaf attribute is important for cassava identification and selection for leaf vegetable market in Sierra Leone where cassava leaves are widely consumed. Findings also agree with Agre et al. [19], who reported that farmers use color of the leaves and stem to identify their cassava cultivars.

The principal component analysis is a powerful data reduction technique utilized to reduce large number of correlated variables to a small number that is independent and very useful. The PCA unraveled traits that contributed most to the variation present in the cassava germplasm. Qualitative traits with highest positive contribution to the first PCA include root shape, orientation of petiole, branching habit, presence of fruits and seeds. The findings of the study revealed the usefulness of these traits for genotype identification and genetic diversity studies in cassava. Hence these traits are among key traits often considered relevant for selection of varieties for genetic improvement of the crop.

The clustering based on similarity index of the qualitative traits in this study grouped the 103 cassava accessions into three clusters**.** Cluster I contained the accessions characterized by green apical leaves, light green leaf, green leaf vein, yellowish-green petiole, umbrella plant shape and average leaf retention. Cluster II grouped accessions having elliptic-lanceolate shape leaflets, light brown stem epidermis, light brown stem exterior, ease of peeling, sweet root taste. Cluster III characterized accessions based on absence of fruits, absence of seeds, dichotomous branching habit, horizontal petiole orientation, dark brown external storage roots, light green leaves and ease of peeling. Similar study conducted by Karim et al. [18] identified five distinct groups using 102 cassava accessions. In this research, the first two principal components explained 22.33% of the total cumulative variance for the qualitative traits. This result underscored the findings of Karim et al. [18] and Afonso et al. [20] who found 31.18% and 32.56% of the genetic variance in the first factorial plane, respectively. It can also be explained by the fact that the variance distribution is associated with the nature and number of characters used in the analysis and focuses on the first principal components.

The 103 cassava accessions also showed variability for 14 quantitative morphological traits assessed. In other to appreciate the variability of each trait, all the quantitative traits recorded were subjected to descriptive statistical analysis (minimum, maximum, mean, variance, standard deviation and coefficient of variation). This study revealed high variability and higher coefficient of variation for most of the studied traits which indicated the presence of high heterogeneity within the population characterized that could be exploited for future breeding. These results are similar to those reported by Agre et al. [21] and Kumba [22]. Agre et al. [21] found higher coefficient of variation for 75% of the traits studied.

The first six principal components analysis explained 67.72% of the overall variability in the quantitative analysis. Principal component I obtained from the quantitative traits presents yield and yield attribute traits such as harvest index, root yield per plant, number of storage root and number of commercial root, while principal components II, III, and IV present growth attribute traits such as petiole length, length of leaflet, width of leaflet, plant height, height at first branching, level of branching. Principal components V and VI present both yield and growth attribute traits such as harvest index, root dry matter content and length of stipule. The quantitative traits with highest positive contribution to the distinguishing accessions in the first PCA include harvest index, root yield per plant, number of storage root and number of commercial roots. These traits are among the key traits often considered for selection of varieties and genetic improvement of cassava. This study agreed with work of Karim et al. [18], who observed that the first principal component present yield and yields and attribute traits such as d harvest index, average yield per plant, number of storage roots, root dry matter content and starch content and they were the highest contributors positively the principal component. The cluster analysis of the 14 quantitative agro-morphological trails also grouped the accessions into three groups. Cluster I characterized accessions with high number of storage root, number of commercial roots, root yield per plant, harvest index and number of leaf lobe, cluster II characterized accessions based on high petiole length and root dry matter content and cluster III accessions exhibited high number of commercial roots, number of storage root, root yield per plant, width of leaf lobe and harvest index. It can be seen from the result of this study the relevance of above ground and root attribute traits in characterizing the cassava accessions. This study also pointed out the usefulness of the agro-morphological descriptor by Fukuda et al. [12] in identifying variability and reducing dimensionality in the traits set. In this study, the 25 qualitative and 14 quantitative trait sets sufficiently discriminated the 103 genotypes into distinct cluster groups.

Root tenderness after cooking is a relevant attribute for cassava since dry matter content in cassava sometimes plays an important role. The results revealed that only cooksoon and butter cassava accessions recorded cooking time below 20 min, which is considered acceptable for cassava according the work of De Pedri et al. [23]. These authors further reported that the easier the cooking, the better the taste of the cooked product, indicating the relevance of dry matter content for acceptable cassava taste. Due the importance of cooking sweet cassava and the variation of the time of cooking that usually exist between cassava accessions, it is important to consider the cooking percentage of each accession. Among all the accessions evaluated for this trait, cooksoon and butter cassava had highest and better cooking percentage than other accessions. The result implied that the shorter the cooking time, the higher the cooking percentage. Thus, cooksoon and butter cassava had shorter cooking time and higher cooking percentage than other accessions. SLICASS 4 and SLICASS 6 had low cooking percentage during the 30 min maximum cooking time set. This study confirms the work of Santos et al. [24] who reported wide variation in the cooking percentage of 11 cassava clones evaluated at different harvesting time. The sensory evaluation results indicate that 60% of the total accessions evaluated had good acceptable cooking qualities (surface appearance, meliness, taste, aroma and texture). Only one accession (SLICASS 4) was poorly rated by farmers for all the culinary traits. This variety is an improved variety that was developed by Sierra Leone Agricultural Institute (SLARI). The variety is high yielding, but lacks the acceptable cooking qualities (mealiness, taste and texture). The findings imply the significance of incorporation of desired end-user traits in cassava breeding programs. Similar research conducted by Mugalavai et al. [25] revealed that 18.0% of the 51 accessions evaluated had acceptable cooking qualities such as texture, taste and mealiness.

5. Conclusions

This study successfully determined the extent of genetic divergence within cassava germplasm of Sierra Leone using morphological markers. It also provides vital information for cassava scientists to make informed decision for parental selection based on genetic diversity for morphological and culinary traits. The useful genetic variability for root dry matter content, number of storage root, number of commercial root, root yield per plant, harvest index, length of leaflet, width of leaflet, height at first branching, distance between leaf scar, and level of branching that were identified could be exploited for the genetic improvement of the crop and its conservation. The root shape, orientation of petiole, branching habit, presence of fruits and seeds and color attribute of various qualitative traits studied contributed most to the differentiation of genotypes. The agro-morphological and culinary traits were useful in distinguishing and selecting cassava genotypes, respectively. Both approaches should therefore be used for genetic diversity studies of cassava.

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