



Article

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

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Abstract: The dearth of information on the 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 out 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 seeds (PSE) ($r = 0.86$ ***), root yield per plant (RYPP) and number of storage roots (NSR) ($r = 0.76$ ***), RYPP and number of commercial roots (NCR) ($r = 0.68$ ***), length of leaf lobes (LLL) and width of leaf lobes (WLL) ($r = 0.66$ ***), and between NSR and NCR ($r = 0.84$ ***). The cooking time, cooking percentage, texture, mealiness, taste, and aroma varied widely among the accessions. The findings established that the cassava germplasm possesses useful genetic variability that could be exploited through selection for short-term release programs, genetic conservation of the valuable germplasm, and genetic improvement of the crop.

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



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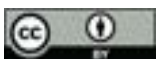
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1. Introduction

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 (such as soil and 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.

The generation of such data involves the use of genetic markers. Genetic markers serve as an effective 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 of the cassava germplasm [6]. Certain morphological traits have proven to accurately reflect the diversity perceived 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 during 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.

Assessing the extent of genetic variation within the breeding population is essential for identifying valuable genetic divergence that is crucial for improving cassava populations [12]. Knowledge regarding the diversity of cassava accessions and their agronomic traits could be useful for breeding programs to develop high-yielding and disease-resistant varieties with improved culinary traits [13]. Therefore, the characterization of the cassava germplasm can help to identify and promote the use of diverse cassava varieties with different agronomic and culinary traits. This can improve the resilience of cassava production systems in Sierra Leone by reducing the risk of crop failure due to pest and disease outbreaks or changes in environmental conditions. The agro-morphological and culinary trait characterization of the cassava germplasm can provide breeders with information on the genetic diversity of cassava varieties in Sierra Leone. This information can be used to identify desirable traits, such as high yield, disease resistance, and culinary qualities, which can be incorporated into new breeding programs. 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 region of the School of Agriculture and Food Sciences experimental site, Njala during May 2020/2021, in the cropping season. Njala is located at an elevation of 50 m above sea level at altitude 8°6' N and longitude 12°6' W of the equator. Njala experiences distinct dry and wet seasons. The rainy season is from April to November and the dry season is from October to May. The mean monthly air temperature ranges from 21 °C to 23 °C for the 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 a 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 Leone and 3 improved released varieties (SLICASS 4, SLICASS 6 and SLICASS 7) were 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 distance between the blocks. The total experimental area utilized was 43 m × 28 m. About 10 stem cuttings per genotype, each measuring 30 cm in length, were planted on 10 m long ridges in a 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 by Fukuda et al. [14]. The harvest index (HI) was calculated at harvest-time as the ratio of fresh root yield to the total fresh biomass (weight of roots and weight of aboveground biomass). Root dry matter content (RDMC) determination was conducted at harvest-time 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, oven dried at 65–70 °C and reweighed after 72 h to obtain a constant weight [14]. The qualitative and quantitative data collected, codes, scoring, and sampling periods 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

Table 1. *Cont.*

Trait	Code	Scoring	Sampling Time (MAP)
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. [14]; numbers in the brackets indicate score codes.

Table 2. Quantitative data and techniques used for scoring.

Trait	Code	Techniques of Measurement	Sampling Time (MAP)
Width of leaf lobe	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 lobes	NLL	Counted on five leaves per plant with consideration of the predominant number of lobes	6
Distance between foliar scars	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 roots with length greater than 20 cm from three plants	12
Number of storage roots	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 roots showing length greater than 20 cm are weighted	12
Root dry matter content	RDMC	Weighed dry roots	12

Source: Fukuda et al. [14]; MAP = months after planting.

2.3.2. Culinary Traits of Selected Cassava Genotypes

Thirty farmers were randomly selected for participatory identification and selection of their five best preferred, five moderately preferred, and five least preferred cassava accessions based on aboveground traits (such as leaves and petioles) 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 roots.

For CT (mins), a 5 cm 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 conducted at 5 min intervals for ease of cooking using a fork and the cooking time was recorded when 6 pieces (50% + 1) no longer resisted penetration with a fork [15]. 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 [16]. Thus, all cassava roots were categorized to reflect their 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); mealiness (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 described by Iwe [17]. 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 $M \geq 3$ 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 a 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 the R software version 3.6.1 program [18]. In the PCA, eigenvalues and load coefficient values were generated from the data sets. The relevance of trait contribution to the variation accounted for by each principal component was based on the absolute eigenvector arbitrary cutoff value of 0.30 [19]. 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 ascending hierarchical clustering (AHC) to plot a dendrogram. Data on culinary traits were subjected to analysis of variance using the R software version 3.6.1 program [18] and the means were compared using Scott–Knott test.

3. Results

3.1. Correlation Analysis, Principal Component Analysis and Genetic Relationships among Cassava Accessions Based on 25 Qualitative Agro-Morphological Traits

The results of the correlation matrices of 25 qualitative characteristics revealed a significant and positive correlation between color of leaf veins and leaf color ($r = 0.22^*$), color of leaf veins and petiole color ($r = 0.62^{***}$), leaf color and color of apical leaves ($r = 0.39^{***}$), leaf color and petiole color ($r = 0.43^{***}$), leaf color and leaf retention ($r = 0.22^*$), color of apical leaves and leaf retention ($r = 0.23^*$), shape of center leaflet and color of stem epidermis ($r = 0.23^*$), leaf margin and presence of foliar scars ($r = 0.29^{**}$), leaf margin and color of end branches ($r = 0.24^*$), petiole color and leaf retention ($r = 0.24^*$), root taste and presence of 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 presence of fruit ($r = 0.32^{**}$), height at first branching and seed ($r = 0.31^{**}$), plant shape and presence of fruit ($r = 0.47^{***}$), plant shape and seed ($r = 0.44^{***}$), and presence of fruit and seeds ($r = 0.86^{***}$) (Table 3). Conversely, significant and negative correlations were noted between leaf color and the shape of the center leaflet ($r = -0.30^{***}$), leaf color and branching habit ($r = 0.20^*$), the shape of the center leaflet and petiole color ($r = -0.42^{***}$), the shape of the center leaflet and root constriction ($r = -0.29^{**}$), petiole color and color of 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 presence of seeds ($r = -0.24^*$), 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 percentage variations of the principal components are presented in Table 4. Ten principal components (PCs), which accounted for 66.744% of the total variation among the genotypes were identified. The first PC axis, with an 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 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, ninth, 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 was positively associated with root taste, orientation of petiole, branching habit, presence of fruit, and presence of seeds. The second PC, with the second highest loading 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 of petiole, while the fourth PC was associated with leaf margin, root cortex, and color of end branches. Traits that were positively associated with the fifth PC were leaf color, color of apical leaf, color of root cortex, color of stem exterior, and presence of fruit and seeds, while leaf retention, color of end branches, and stipule margin were the traits associated with the sixth PC and the seventh PC was positively associated 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 were associated positively with the tenth PC.

The hierarchical classification of 103 cassava genotypes based on qualitative traits grouped the genotypes into three classes with similar 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 clusters with similarities of 1.4. Clusters I and III have a higher number of genotypes, with 40 and 34, respectively, while 29 individuals were in cluster II (Figure 1).

Horticulturae 2024, 10, x FOR PEER REVIEW

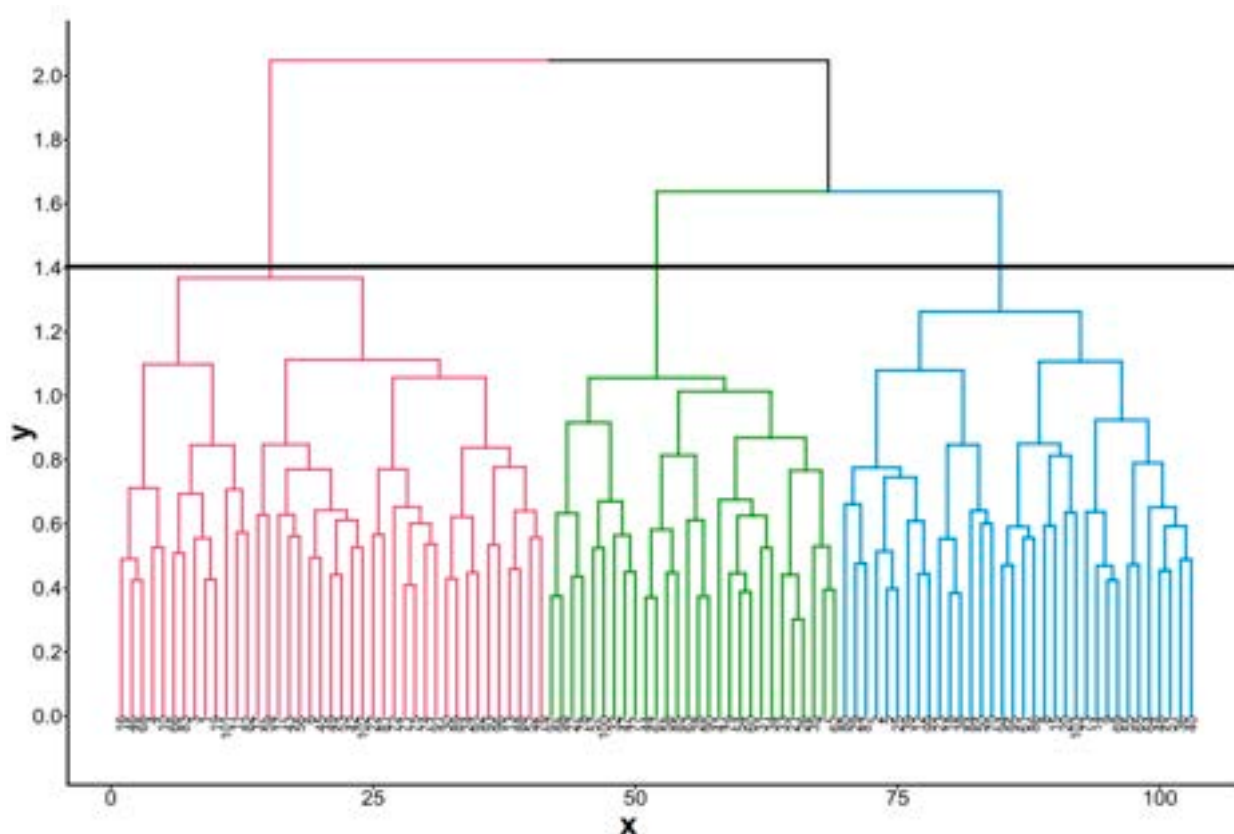


Figure 1. Dendrogram showing relationships among 103 genotypes of cassava classified by the Ward method using 25 qualitative agro-morphological traits. The black horizontal line passing across the main clusters indicates the different heterotic groups represented by red, green and blue.

3.2. Descriptive Statistics, Correlation Analysis, Principal Component Analysis, and Genetic Relationships among Cassava Accessions Based on 14 Quantitative Agro-Morphological Traits

The cassava genotypes showed variability for fourteen quantitative morphological traits assessed (Table 5). The ranges of the values produced were 1.0 to 5.0 cm for distance between leaf scars, 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 21.8 cm for length of leaf lobes, 1.0 cm to 5.0 cm for length of stipule, 1.0 to 24.0 for number of commercial roots, 3.0 to 9.0 for number of leaf lobes, 2.0 to 53.0 for number of storage roots, 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 lobes (Table 5). The

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	−0.10	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	−0.10	−0.06	0.13	0	−0.15	−0.15	0.07	−0.03	−0.02	1		
ECR	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	−0.10
PO	0.10	0.11	0.10	0.15	0.04	0	0.04	−0.03	0.10	0.13	−0.05	−0.14	−0.06	−0.20
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	−0.10
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	−0.10
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	−0.10
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	−0.10
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							

Table 3. Cont.

Trait	LR	OPE	CSE	CEBR	STM	BRH	PS	EXT	RCO	PFRT	PSE
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

*, **, and *** = significant at $p < 0.05$, $p < 0.01$, and $p < 0.001$, respectively; the bold represent qualitative traits with significant correlation coefficients; 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—prominence 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 peduncle; RCO—root constrictions; PFRT—presence of fruit; PSE—presence of seeds.

Table 4. Principal component analysis, eigenvalues, and percentage variation of 25 characteristics 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

Table 4. Cont.

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
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—prominence of foliar scar; CRP—color of root pulp; COX—cortex; CSE—color of stem epidermis; ECSR—external color of storage roots; 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 peduncle; RCO—root constrictions; PFRT—presence of fruit; PSE—presence of seeds; the bold values represent the traits with high (≥ 0.3) contribution to each component.

3.2. Descriptive Statistics, Correlation Analysis, Principal Component Analysis, and Genetic Relationships among Cassava Accessions Based on 14 Quantitative Agro-Morphological Traits

The cassava genotypes showed variability for fourteen quantitative morphological traits assessed (Table 5). The ranges of the values produced were 1.0 to 5.0 cm for distance between leaf scars, 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 21.8 cm for length of leaf lobes, 1.0 cm to 5.0 cm for length of stipule, 1.0 to 24.0 for number of commercial roots, 3.0 to 9.0 for number of leaf lobes, 2.0 to 53.0 for number of storage roots, 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 lobes (Table 5). The coefficients of variation varied from 14.7% (root dry matter content) to 81.2% (level of branching). Based on the 14 quantitative characteristics/traits, 11 had high (CV > 20%) coefficients of variation (Table 5). Only three characteristics had low variation, including the root dry matter content (14.8%), the distance between leaf scars (18.7%), and the number of leaf lobes (17.8%).

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

Traits	Minimum	Maximum	Mean	Standard Deviation	Coefficient of Variance (%)
Distance between leaf scars (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 lobes (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 lobes	3.0	9.0	6.3	1.1	17.8
Number of storage roots	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 lobes (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 roots ($r = 0.24^*$) (Table 6). The root yield per plant is highly significant and positively correlated with the number of storage roots ($r = 0.76^{***}$) and the number of commercial roots ($r = 0.68^{***}$). The petiole length is significantly and positively correlated with the length of leaf lobes ($r = 0.22^*$) and the number of leaf lobes ($r = 0.26^{**}$). The length of leaf lobes is significantly and positively correlated with the width of leaf lobes ($r = 0.66^{***}$) and the number of leaf lobes ($r = 0.41^{***}$); the width of leaf lobes is also positively correlated with plant height ($r = 0.20^*$).

The number of storage roots was significantly and positively correlated with the number of commercial roots ($r = 0.84^{***}$), while the plant height was positively correlated with the number of leaf lobes ($r = 0.24^*$), and the height at first branching was positively correlated with the level of branching ($r = 0.25^*$). Conversely, significant and negative correlations were noted between the harvest index and the distance between leaf scars ($r = 0.20^*$), length of leaf lobes, and level of branching ($r = 0.21^*$), and between the width of leaf lobes and the level of branching ($r = 0.21^*$).

The principal component analysis of quantitative agro-morphological traits revealed that the six main principal components accounted for 67.72% 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 were harvest index (43.0%), root yield per plant (86.0%), number of storage roots (90.0%), and number of commercial roots (85.0%). The

variables that were significantly correlated with axis 2 were petiole length (43.0%), length of leaf lobes (83.0%), width of leaf lobes (70.0%), plant height (40.0%), and number of leaf lobes (53.0%).

Table 6. Correlation coefficients 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	

*, **, and *** = significant at $p < 0.05$, $p < 0.01$, and $p < 0.001$, respectively; the bold represent qualitative traits with significant correlation coefficients; 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 roots; PHT—plant height; HFB—height at first branching; NLL—number of leaflet; DLS—distance between leaf scars; LST—length of stipule; LBR—level of branching; NCR—number of commercial roots.

Table 7. Principal component analysis, eigenvalues, and percentage variation of 14 quantitative characteristics 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 roots	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 leaflets	0.16	0.53	0.23	−0.09	0.44	−0.42
Distance between leaf scars	−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 roots	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

The bold represent the traits with high (≥ 0.3) contribution to each component.

The traits that were significantly related to axis 3 were petiole length (44.0%), height at first branching (35.0%), and level of branching (30.0%). The variables significantly correlated to axis 4 were plant height (30.0%), height at first branching (66.0%), and level of branching (61.0%). The variables significantly related to axis 5 were harvest index (54.0%), number of leaf lobes (44.0%), and length of stipule (32.0%), and the traits that were significantly correlated to axis 6 were 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 into three classes with similar 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 six genotypes, and cluster III contains 44 genotypes.

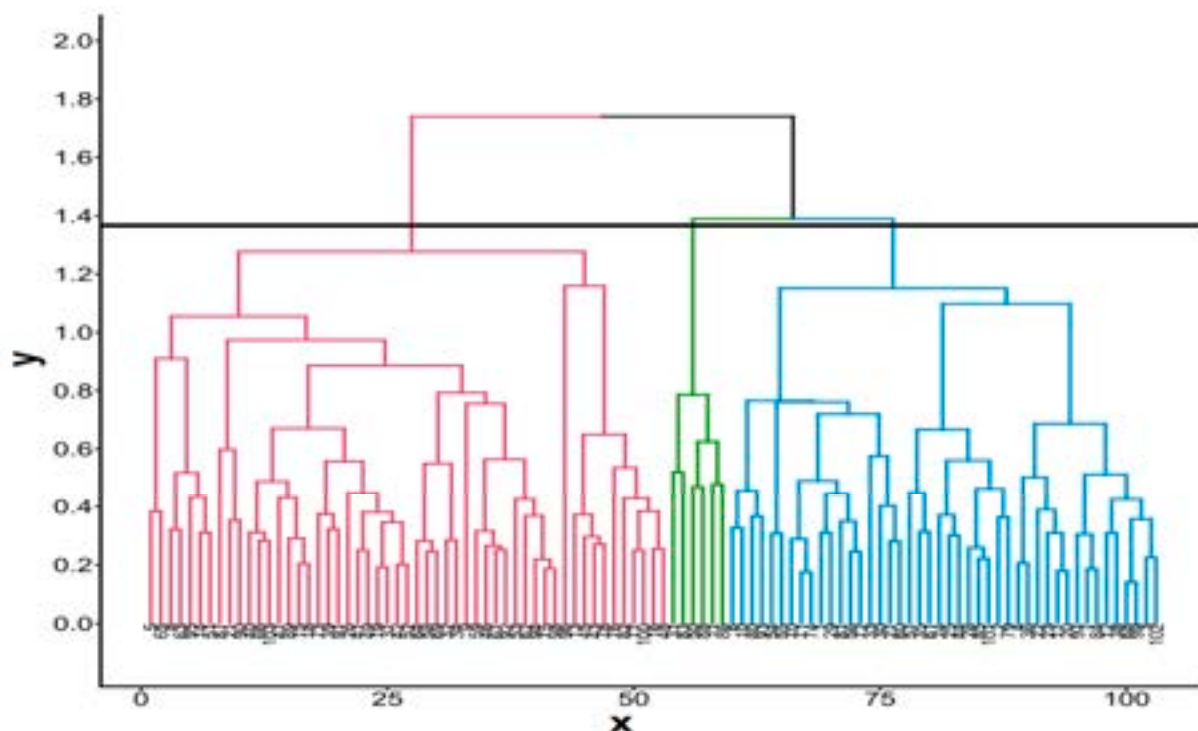


Figure 22. Dendrogram showing relationships among 103 genotypes of cassava classified by the Ward method using 14 significant quantitative morphological traits. The black horizontal line across the main cluster indicates the distance that differentiates the three groups represented by red, green and blue.

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 had shorter and better cooking times were Cookson (15.2 min) and Butter cassava (15.4 min), while those with the longest cooking times were Pink lady (30.0 min), SLICASS 4 (30.0 min), and SLICASS 6 (30 min). The cooking percentage was included 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 percentages were classified into two groups. The group with lowest membership included the genotypes SLICASS 4 (27.9%), SLICASS 6 (30.2%), and SLICASS 7 (58.3%). The means of the other groups of genotypes ranging from 63.2% to 96.4% were Pink lady (63.2%), Soja color (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%), Ndiamongyamalo (88.3%), Butter cassava (95.0%), and Cookson (96.4%).

Mean scores for surface appearance, mealiness, taste, and aroma ranged from 2.0 to 4.75, and for texture, from 2.0 to 4.50, indicating the acceptable mean threshold (Table 8). Comparing the means for sensory characteristics, genotypes that had the highest mean scores for surface appearance were Cookson (4.50 ± 0.50), Butter cassava (4.50 ± 0.58), and Cocoa cassava (4.50 ± 0.50), closely followed by Ndiamongyamalo (4.3 ± 0.50), Nikaneh (4.3 ± 0.58), Tapiyoka (4.3 ± 0.55), 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 these traits, while other genotypes like Kendemeh (3.5 ± 0.58), Pink lady (3.5 ± 0.82), SLICASS 6 (3.5 ± 0.58) and Soja color (3.5 ± 0.50) were fairly acceptable to consumers. SLICASS 4 has the lowest mean score (2.0 ± 0.40) for surface appearance, thus indicating poor acceptability to consumers/farmers (Table 8).

The results for mealiness revealed that Cookson 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), Ndiamongyamalo (4.25 ± 0.48), Cocoa cassava (4.25 ± 0.80), Tangagboi (4.0 ± 0.40), Mende

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

Genotypes	Cooking Time	Cooking Percent	Surface Appearance	Mealiness	Taste	Aroma	Texture
	Mean \pm SE	Mean \pm SE	Mean \pm SE	Mean \pm SE	Mean \pm SE	Mean \pm SE	Mean \pm SE
Cookson	15.2 \pm 1.2	96.4 \pm 2.4	4.5 \pm 0.50	4.75 \pm 0.80	4.8 \pm 0.50	4.8 \pm 0.50	4.5 \pm 0.58
Butter cassava	15.4 \pm 1.2	95.0 \pm 1.8	4.5 \pm 0.58	4.50 \pm 0.50	4.9 \pm 0.43	4.8 \pm 0.50	4.5 \pm 0.50
Ndiamonyamalo	21.0 \pm 1.4	83.3 \pm 1.6	4.3 \pm 0.50	4.25 \pm 0.48	4.5 \pm 0.50	4.3 \pm 0.50	4.3 \pm 0.50
Cocoa cassava	20.0 \pm 1.7	88.2 \pm 2.1	4.5 \pm 0.50	4.25 \pm 0.80	4.5 \pm 0.58	4.5 \pm 0.58	4.3 \pm 0.58
Tangagboi	28.7 \pm 1.8	76.2 \pm 2.3	4.3 \pm 0.58	4.0 \pm 0.40	4.5 \pm 0.50	4.3 \pm 0.58	4.3 \pm 0.58
Mende Tangai	28.6 \pm 1.5	78.4 \pm 2.0	4.0 \pm 0.65	4.0 \pm 0.65	4.0 \pm 0.65	4.0 \pm 0.65	4.0 \pm 0.65
Nikaneh	27.0 \pm 1.5	80.2 \pm 2.5	4.3 \pm 0.58	4.3 \pm 0.58	4.3 \pm 0.58	4.3 \pm 0.50	4.0 \pm 0.50
Yaa Kanu	27.0 \pm 1.7	80.2 \pm 3.0	4.0 \pm 0.50	4.0 \pm 0.60	4.3 \pm 0.50	4.3 \pm 0.82	3.5 \pm 0.58
Kendemeh	28.6 \pm 1.6	73.4 \pm 1.9	3.5 \pm 0.58	4.0 \pm 0.63	4.3 \pm 0.50	4.0 \pm 0.58	3.5 \pm 0.50
Tapiyoka	25.7 \pm 1.4	82.0 \pm 3.2	4.3 \pm 0.55	4.3 \pm 0.50	4.5 \pm 0.80	4.3 \pm 0.50	4.0 \pm 0.60
Soja color	29.8 \pm 1.5	70.3 \pm 2.8	3.0 \pm 0.50	3.0 \pm 0.58	2.0 \pm 0.50	3.0 \pm 0.65	2.0 \pm 0.82
Pink lady	30.0 \pm 1.5	63.2 \pm 2.6	3.5 \pm 0.82	3.0 \pm 0.80	3.5 \pm 0.65	3.0 \pm 0.50	3.0 \pm 0.58
SLICASS 7	29.8 \pm 1.8	58.3 \pm 1.7	4.0 \pm 0.50	3.5 \pm 0.40	3.0 \pm 0.45	4.0 \pm 0.60	3.0 \pm 0.50
SLICASS 6	30.0 \pm 1.7	30.2 \pm 3.1	3.5 \pm 0.58	3.0 \pm 0.55	2.0 \pm 0.50	3.0 \pm 0.50	3.0 \pm 0.50
SLICASS 4	30.0 \pm 1.3	27.9 \pm 1.8	2.0 \pm 0.40	2.0 \pm 0.82	2.0 \pm 0.50	2.0 \pm 0.82	2.0 \pm 0.82

The results for mealiness revealed that Cookson has the highest mean score (4.75 \pm 0.80), followed by Butter cassava (4.50 \pm 0.50), Tapiyoka (4.3 \pm 0.50), Nikaneh (4.3 \pm 0.58), Ndiamonyamalo (4.25 \pm 0.48), Cocoa cassava (4.25 \pm 0.80), Tangagboi (4.0 \pm 0.40), Mende tangai (4.0 \pm 0.65), Yaa kanu (4.0 \pm 0.60) and Kendemeh (4.0 \pm 0.63), thus indicating good acceptability of the genotypes by consumers/farmers for mealiness. Pink lady (3.5 \pm 0.82), SLICASS 6 (3.5 \pm 0.58), and Soja color (3.0 \pm 0.50) were fairly acceptable to farmers. The genotype that recorded the lowest mean score in terms of mealiness was SLICASS 4 (2.0 \pm 0.82), indicating poor acceptability by consumers of the genotype for this trait. Cookson was highly rated for its taste and thus records the highest mean score (4.75 \pm 0.50), closely followed by Butter cassava (4.50 \pm 0.43), Ndiamonyamalo (4.50 \pm 0.50), Cocoa cassava (4.50 \pm 0.58), Tapiyoka (4.50 \pm 0.80), Tangagboi (4.50 \pm 0.50), Nikaneh (4.3 \pm 0.58), Yaa kanu (4.25 \pm 0.50), Kendemeh (4.25 \pm 0.50), and Mende tangai (4.0 \pm 0.65), indicating good acceptability to farmers, while Pink lady (0.5 \pm 0.65) and SLICASS 7 (3.0 \pm 0.45) were fairly acceptable to farmers for this trait. However, SLICASS 4 (2.0 \pm 0.50), SLICASS 6 (2.0 \pm 0.50), and Soja color (2.0 \pm 0.50) were rated poorly for taste quality. Sensory evaluation on the aroma of the cooked roots of the genotypes revealed that Cookson (4.75 \pm 0.50) and Butter cassava (4.75 \pm 0.50) scored the highest mean followed by Ndiamonyamalo (4.3 \pm 0.50), Tapiyoka (4.3 \pm 0.50), Cocoa cassava (4.25 \pm 0.58), Tangagboi (4.25 \pm 0.58), Nikaneh (4.25 \pm 0.50), Yaa kanu (4.25 \pm 0.82), Mende tangai (4.0 \pm 0.65), Kendemeh (4.0 \pm 0.58), and SLICASS 7 (4.0 \pm 0.60), which indicate good acceptability by consumers, while Soja color (3.0 \pm 0.65), Pink lady (3.0 \pm 0.50), and SLICASS 6 (3.0 \pm 0.50) were fairly acceptable to consumers in terms of aroma. However, SLICASS 4 was poorly accepted by consumers, with a mean score of 2.0 \pm 0.82. Cookson and Butter cassava scored the highest means of 4.50 \pm 0.58 and 4.50 \pm 0.50, respectively, in terms their texture, followed by Ndiamonyamalo (4.3 \pm 0.50), Cocoa cassava (4.25 \pm 0.58), Tangagboi (4.25 \pm 0.58), Mende Tangai (4.0 \pm 0.65), Nikaneh (4.0 \pm 0.50) and Tapiyoka (4.0 \pm 0.60), which indicate good acceptability to consumers. Other genotypes like Yaa kanu (3.5 \pm 0.58), Kendemeh (3.5 \pm 0.50), Pink lady (3.0 \pm 0.58), SLICASS 7 (3.0 \pm 0.50), and SLICASS 6 (3.0 \pm 0.50) were fairly acceptable to consumers. SLICASS 4 (2.0 \pm 0.82) and Soja color (2.0 \pm 0.82) were poorly accepted.

3.4. Marketable Leaf Assessment

The five elite varieties selected by farmers based on the desired leaf traits for selling and consumption included Tangagboi, Coco cassava, Cookson, Butter cassava, and Ndiamonyamalo, followed by the moderately preferred varieties Tapiyoka, Yaa kanu, Nikaneh,

Mende tangai, and Kendemeh (Table 9). However, the leaves of the varieties SLICASS 4, SLICASS 6, SLICASS 7, Pink lady, and Soja color are 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 color	Not good

4. Discussion

Significant variation was noted from the analysis of the qualitative morphological traits (root taste, external color of storage roots, color of root pulp, ease of peeling, color of leaf veins, lobe margins, leaf color, color of apical leaves, shape of central leaflets, 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, and 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 genotypes exhibited white root pulp and dark brown external storage roots. The aboveground leaf traits of the studied genotypes were green leaf veins, light green leaves, light green apical leaves, smooth lobe margins, and elliptic-lanceolate center leaflets. The leaf attributes play significant roles in cultivar identification and, more significantly, in cassava selection by farmers for leafy vegetable markets. The findings agree with the work of Karim et al. [13], who reported that leaf attributes are important for cassava identification and selection for leafy vegetable markets in Sierra Leone, where cassava leaves are widely consumed. The findings also agree with Agre et al. [20], who reported that farmers use the color of the leaves and stems to identify their cassava cultivars.

Principal component analysis is a powerful data reduction technique utilized to reduce large numbers of correlated variables to a small number that is independent and very useful. The PCA revealed the traits that contributed most to the variation present in the cassava germplasm. Qualitative traits with the highest positive contribution to the first PCA included root shape, orientation of petioles, branching habits, and presence of fruit and seeds. The findings of the study revealed the usefulness of these traits for genotype identification and genetic diversity studies in cassava. The high positive values of phenotypic correlations indicate that the positive selection of one of these traits results in increases in the other trait, whereas the reverse is also true. Traits with high correlation coefficients are among the key traits often considered relevant for the selection of varieties for the genetic improvement of the crop. The findings concur with the view that PCA results reveal a trend towards higher genetic values for some traits with significant strong positive or negative contributions to the observed genetic variability compared to the contributions of those with weak correlation coefficients [21]. Thus, the PCA results of the present study demonstrated a pattern of higher phenotypic values for some traits with significant strong positive or negative contributions to the observed phenotypic variability compared to the

contributions of those with weak correlation coefficients. The trait variations reflected among the genotypes could be attributable to their different genetic backgrounds.

The clustering based on the 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 leaves, green leaf veins, yellowish-green petioles, umbrella plant shapes, and average leaf retention. Cluster II included accessions with elliptic-lanceolate shaped leaflets, light brown stem epidermises, light brown stem exteriors, ease of peeling, and sweet root taste. Cluster III included accessions based on the absence of fruit, absence of seeds, dichotomous branching habits, horizontal petiole orientation, dark brown external storage roots, light green leaves, and ease of peeling. A similar study conducted by Karim et al. [13] using 102 cassava accessions identified five distinct groups. 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. [13] and Afonso et al. [22], 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 characteristics used in the analysis and focuses on the first principal components.

The 103 cassava accessions also showed variability for the 14 quantitative morphological traits assessed. In order 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 coefficients of variation for most of the studied traits, which indicated the presence of high heterogeneity within the characterized population, which could be exploited for future breeding. These results are similar to those reported by Agre et al. [23] and Karim [24]. Agre et al. [23] found higher coefficients of variation for 75% of the traits studied.

The analysis of the first six principal components explained 67.72% of the overall variability in the quantitative analysis. Principal component I presented yield and yield attribute traits such as harvest index, root yield per plant, number of storage roots, and number of commercial roots, while principal components II, III, and IV presented growth attribute traits such as petiole length, length of leaflets, width of leaflets, plant height, height at first branching, and level of branching. Principal components V and VI presented both yield and growth attribute traits such as harvest index, root dry matter content, and length of stipule. The quantitative traits with the highest positive contribution to the distinguishing accessions in the first PCA included harvest index, root yield per plant, number of storage roots, and number of commercial roots. These traits are among the key traits often considered for selection of varieties for the genetic improvement of cassava. This study agreed with the work of Karim et al. [13], who observed that the first principal component presented yields and attribute traits such as harvest index, average yield per plant, number of storage roots, root dry matter content, and starch content, and they were the highest positive contributors to the principal component analysis. The cluster analysis of the 14 quantitative agro-morphological traits also grouped the accessions into three groups. Cluster I comprised accessions with high numbers of storage roots, numbers of commercial roots, root yields per plant, harvest indexes, and numbers of leaf lobes; cluster II included accessions based on high petiole length and root dry matter content; while cluster III accessions exhibited high numbers of commercial roots, numbers of storage roots, root yields per plant, width of leaf lobes, and harvest indexes. The results of this study demonstrate the relevance of aboveground and root attributes in characterizing cassava accessions. This study also demonstrated the usefulness of Fukuda et al.'s [14] agro-morphological descriptor in identifying variability and reducing dimensionality in the trait 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 the

Cookson and butter cassava accessions recorded cooking times below 20 min, which is considered acceptable for cassava according to the work of De Pedri et al. [25]. 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 to the importance of cooking sweet cassava and the variations in 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, Cookson and butter cassava had higher and better cooking percentages than other accessions. This result implied that the shorter the cooking time, the higher the cooking percentage. Thus, Cookson and butter cassava had shorter cooking times and higher cooking percentages than other accessions. SLICASS 4 and SLICASS 6 had low cooking percentages during the 30 min maximum cooking time set. This result confirms the work of Santos et al. [26], who reported wide variations in the cooking percentages of 11 cassava clones evaluated at different harvesting times. The sensory evaluation results indicated that 60% of the total accessions evaluated had good acceptable cooking qualities (surface appearance, mealiness, 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 the Sierra Leone Agricultural Institute (SLARI). The variety is high yielding but lacks acceptable cooking qualities (mealiness, taste, and texture). The findings imply the significance of the incorporation of desired end-user traits in cassava breeding programs. Similar research conducted by Mugalavai et al. [27] 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 the cassava germplasm of Sierra Leone using morphological markers. It also provides vital information to help cassava scientists to make informed decisions for parental selection for morphological and culinary traits based on genetic diversity. The useful genetic variability in root dry matter content, number of storage roots, number of commercial roots, root yield per plant, harvest index, length of leaflets, width of leaflets, height at first branching, distance between leaf scars, 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 fruit and seeds, and color attributes of various qualitative traits studied contributed most to the differentiation of the 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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