

Research Article

Agromorphological Characterization of Biofortified Cassava Genotypes (*Manihot esculenta*)

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Cassava is an important food security crop and millions of people rely on it as a major source of food around the world. Cassava is a main staple in Ghana and an ideal candidate for biofortification to improve its nutritional content to mitigate malnutrition and increase food security. The objective of the study was to assess the genetic diversity of 21 biofortified cassava accessions using agromorphological descriptors to determine significant variations among the genotypes for breeding programs. The trial was carried out in a complete randomized block design with two replications at the University of Ghana, Legon. Data were collected at 3, 6, 9, and 12 months after planting. Significant differences were observed for all quantitative traits that were measured. There was a positive correlation between fresh root weight and the number of storage roots and also the number of leaf lobes and the length of the petiole. The first two principal component analyses (PCAs) explained 53.023% of the total variance. The key traits that influenced PC1 and PC2 included the total weight of commercial storage roots, leaf retention, average weight, number of storage roots, height at first branching, petiole length, and percentage of dry matter, further emphasizing the diverse traits among these genotypes and their breeding potential. Genotypes WC 2 and WC 14 made substantial contributions, while WC 15 signifies exceptional trait diversity and are promising candidates for enhancing genetic diversity in breeding programs. The dendrogram revealed phylogenetic relationships among the cassava germplasms, forming two main groups and subgroups. This study revealed substantial phenotypic diversity, providing a foundation for future breeding programs to improve food and nutrition security.

Keywords: biofortified cassava; genetic diversity; malnutrition; morphological characterization; storage roots

1. Introduction

Hidden hunger is the presence of several micronutrient deficiencies (particularly iron, zinc, iodine, and vitamin A), which can occur as a result of consuming a nutrient-poor diet. It is prevalent in low- and middle-income countries, affecting over a billion people worldwide, who depend majorly on low-cost food staples [1]. Africa is among the continents in the world with serious micronutrient

malnutrition problems that lead to prevalent economic consequences [2]. In recent years, consumers have become more discerning in their food choices, prioritizing qualities such as food safety, nutrition, fair trade, organic production, locally sourced ingredients, free range, traceability, and sustainability. These changing preferences shape consumer attitudes and behaviors toward biofortified foods and impact their acceptance and uptake on the market in many developing countries [3].

Cassava is a major staple in Africa and millions of people rely on starchy roots as a main source of food [4]. Cassava serves as a source of food and income for more than 800 million people around the world [5]. The beneficial part of cassava that serves as a food and for industrial purposes is its roots since it accumulates starch (approximately 30%–60% dry matter), as such, it is considered the second source of starch globally, after maize [6, 7]. Little attention has been paid to cassava over the years, and it is usually referred to as the “poor man’s crop” [8]. Ironically, even though cassava is often called the “poor man’s crop,” it actually plays an important role in contributing to food security, rural industrial development, and job creation [9]. Cassava prominence among small farmers is particularly pronounced in regions characterized by arid soils and challenging climate conditions, due to its resilience and consistently substantial yields compared to other staple crops [10]. Moreover, cassava has rather straightforward cultivation practices and its capacity to remain stored in the ground for extended periods, often spanning several months [10]. Rich in carbohydrates, cassava contributes to the diets of approximately 500 million individuals around the world [11]. Its edible starchy root tuber plays a pivotal role in meeting the calorie needs of more than 800 million people in Asia, sub-Saharan Africa, and Latin America [12].

Characterization is very crucial to facilitate the identification of diversity among plant’s genetic resources, at both genotypic and phenotypic levels, by morphological or molecular characterization, or both. Most plant breeders use morphological characterization, which is the study of morphological variability, as a way of assessing genetic diversity [13]. This process mainly entails assessing and measuring the morphological traits of plants grown in the field and determining the agronomic value of the plants. Identifying morphological traits plays a crucial role in comprehending heritable genetic diversity, although genetic analysis is essential to validate relationships among accessions [14, 15]. The success of a breeding program is based on a deep understanding of genetic variability within the cassava population [16]. The cassava gene pool has demonstrated remarkable genetic variability in terms of characteristics associated with resilience to challenging environments, such as drought [10]. Morphological classifications of cassava are rooted in traits such as plant height, stem color, leaf morphology, apical leaf coloration, central leaflet shape, leaf lobe characteristics, stem growth habits, stipule length, presence of fruit and seeds, and more [17].

Decades of dedicated research efforts and intervention programs and projects focused on enhancing cassava through breeding programs have resulted in the development and introduction of more than 25 cassava varieties in Ghana [18]. However, only 40% of these variants have found adoption among farmers, potentially due to mismatches between certain varieties and the specific nutritional needs of end-users [19]. Despite cassava integration into traditional farming systems, limited progress has been made in genetic improvement. This can be attributed in part to the historical selection and distribution of planting materials by subsistence farmers. The selection process has been influenced

by various ethnic groups, resulting in the existence of multiple vernacular names for identical cassava varieties, predicated on ethnic distinctions. Consequently, numerous traditional varieties have proliferated [19]. To address these challenges and advance cassava breeding programs, it becomes crucial to evaluate the phenotypic and agronomic characteristics of diverse biofortified cassava genotypes [19]. Significant progress has already been made in the breeding of biofortified cassava varieties [20]. The biofortified varieties developed are not only nutritional in content but also strengthen yield and resistance to diseases, with the potential to significantly increase agricultural productivity and raise the incomes of smallholder farmers [21]. This study aims to characterize and analyze morphological variability among 21 biofortified cassava genotypes.

2. Materials and Methods

2.1. Experiment Location. The experiment was carried out at the School of Agriculture farm of the University of Ghana. This field is located in the Coastal Savannah agroecological zone with an altitude of approximately 97 m above sea level. The research field has a 5°38N lat. and is 00°11E long.

2.2. Experimental Materials and Field Establishment. Twenty-one cassava accessions (Table 1) collected from the International Institute of Tropical Agriculture (IITA) and the Sierra Leone Agricultural Research Institute (SLARI) were grown in a randomized complete block design (RCBD) with two replications. Each genotype was replicated twice due to the limited availability of planting materials. Two locally adapted varieties were used as border plants. The field trial was established for one cropping season. The planting distance used was 1 × 1 m, in 7 hills per row, with each row representing a single genotype. Cassava cuttings of about 20–30 cm were used. Agronomic practices such as manual weeding, irrigation, and pest control were carried out in the field. The 21 genotypes were selected based on their high nutritional contents such as high total carotenoid content, protein, zinc, and iron. Data were collected at 3-month intervals, and the mature cassava tubers were harvested after 12 months.

2.3. Data Collection. Data were collected using the IITA descriptor [22]. Data were collected on 5 plants as per genotype in each block. Data collected include color of apical leaf (CAL), presence of pubescence (PP), leaf retention (LR), leaf color (LC), petiole length (PL), petiole vein color (CLV), orientation of petiole (OP), number of leaf lobe (NLL), length of leaf lobe (LLL), width of leaf lobe (WLL), color of stem epidermis (CSE), color of stem cortex (CSC), color of the exterior of the stem (CSE), height at the first branch (HFB), plant height (PH), number of storage root (NSR), weight of commercial storage root (WgtCSR), average WgtCSR (Av. weight), external color of storage root (ECSR), color of root pulp (CRP), and percentage of total solids (dry matter) (X. total. Solids). Data were

TABLE 1: List of genotypes and their sources.

Genotype code	Germplasm source
WC 1	SLARI, Sierra Leone
WC 2	SLARI, Sierra Leone
WC 3	SLARI, Sierra Leone
WC 4	SLARI, Sierra Leone
WC 5	SLARI, Sierra Leone
WC 6	SLARI, Sierra Leone
WC 7	SLARI, Sierra Leone
WC 8	SLARI, Sierra Leone
WC 9	IITA, Nigeria
WC 10	IITA, Nigeria
WC 11	IITA, Nigeria
WC 12	IITA, Nigeria
WC 13	SLARI, Sierra Leone
WC 14	SLARI, Sierra Leone
WC 15	SLARI, Sierra Leone
WC 16	SLARI, Sierra Leone
WC 17	SLARI, Sierra Leone
WC 18	SLARI, Sierra Leone
WC 19	SLARI, Sierra Leone
WC 20	SLARI, Sierra Leone
WC 21	SLARI, Sierra Leone

collected at 3-month intervals. The mature cassava tubers were harvested after 12 months.

2.4. Data Analysis. Descriptive statistics was used for the traits in Excel. Analysis of variance (ANOVA) was conducted to test for significant differences among genotypes using *R* software Version 4.0.1. Principal component analysis (PCA) was used to identify and explain variance between genotypes using *R* software Version 4.0.1. Cluster analysis was used to group genotypes based on similarities and dissimilarities using *R* software vRsrion 4.0.1. The associations between the traits and parameters were visualized using a heat plot, which depicts the strength and direction of the correlations using *R* software Version 4.0.1.

3. Results

3.1. Morphological Qualitative Traits. The predominant apical LC recorded among the genotypes was the purplish green color, which was recorded by 43% of them, followed by dark green (33%), light green (19%), and purple (5%) (Figure 1(a)). The pubescence on the apical leaf was only present in 19% of the genotypes (Figure 1(b)). 85% of the genotypes exhibited a LR range between average LR and outstanding LR, with average LR defined as a plant with leaves covering about half of the plant (Figure 1(c)). Most genotypes scored better than average retention. The most common shapes were central leaflet lanceolate (52%) and elliptic lanceolate (43%). The most notable LC among the genotypes was dark green, recorded in 81% of the genotypes, and light green, recorded in 19% of the genotypes (Figure 1(d)). The most prominent petiole color exhibited among the genotypes was the yellowish green recorded in 38% of the genotypes (Figure 1(e)), with 43% of the genotypes exhibiting horizontal orientation (Figure 1(g)). A

notable number of genotypes recorded the gray color of the stem exterior. However, about 23% of the genotypes had a golden stem exterior which could be an indicator of high beta-carotene content (Figure 1(h)). The root shapes of more than 50% of the genotypes were cylindrical or irregular (Figure 1(i)).

3.2. PCA. The eigenvalues with their corresponding variance and cumulative variance are represented in Figure 2. The first dimension (Dim. 1) explains the most variance (28.138%), followed by the second dimension (Dim. 2) with 24.886%. These two components together explain 53.023% of the total variance. The first four components explained 74.448% of the total variation in the 21 genotypes. The scree plot shows the eigenvalues of each principal component, assessing the relative importance of each principal component in explaining the variance. The elbow point where the eigenvalues start to level off starts at PC 3. This is an indication of the diminishing returns in terms of the amount of variance explained. PC1 and PC2 before the elbow point significantly contributed to the total variance (Figure 2).

The traits that had the most significant contribution to the main components were highlighted (Table 2). The correlation (*R*-squared) measures the strength and direction of the relationship between the traits and the principal components. It has a range of 0–1, where 0 indicates no linear relationship and 1 represents a perfect linear relationship, with the *p* values indicating the significance of the relationship. The results suggest that “WgtCSR” has a strong positive linear relationship with the variables, as indicated by a high *R*-squared (0.8016) and a low *p* value (2.143793e–05). This suggests that the variables measured are good predictors of “WgtCSR” (Table 2). Similarly, LR, Av. weight, NSR HFB, PL, and X. total. Soilds also exhibited statistically significant positive linear relationships with the variables measured, as their *R*-squared values are relatively high and their *p* values are below the significance threshold (Table 2). Characteristics such as LLL, PL, WgtCSR, LR, and Av. weight significantly contributed the most to Dim. 1 and Dim.2 (Figure 3). The PCA-biplot analysis revealed that traits such as WgtCSR, NSR, Av. weight, LR, and PL had longer vectors, an indication of greater variability and their influence on Dim. 1 and Dim. 2 (Figure 4). Genotypes such as WC 19, WC 17, WC 13, and WC 14 that were clustered together on the biplot have similar trait patterns, and hence share common characteristics or trait combinations (Figure 4). There was a positive correlation between NSR, WgtCSR, Av. weight, HFB, and PH and also between NLL, LLL, WLL, and LR (Figure 4).

Figure 5 shows the influence of genotypes on Dimensions 1 and 2. The height of the bar corresponds to the contribution of that genotype to Dim. 1 and Dim. 2 and the average line (red line) serves as a reference point to compare individual genotype contributions. Genotypes below the red line contributed less to the dimensions. Genotypes WC 2 and WC 14 made a substantial contribution to Dim. 1 and Dim. 2 and the genotypes WC 15 and WC 6 had a moderate influence on Dim. 1 and Dim. 2.

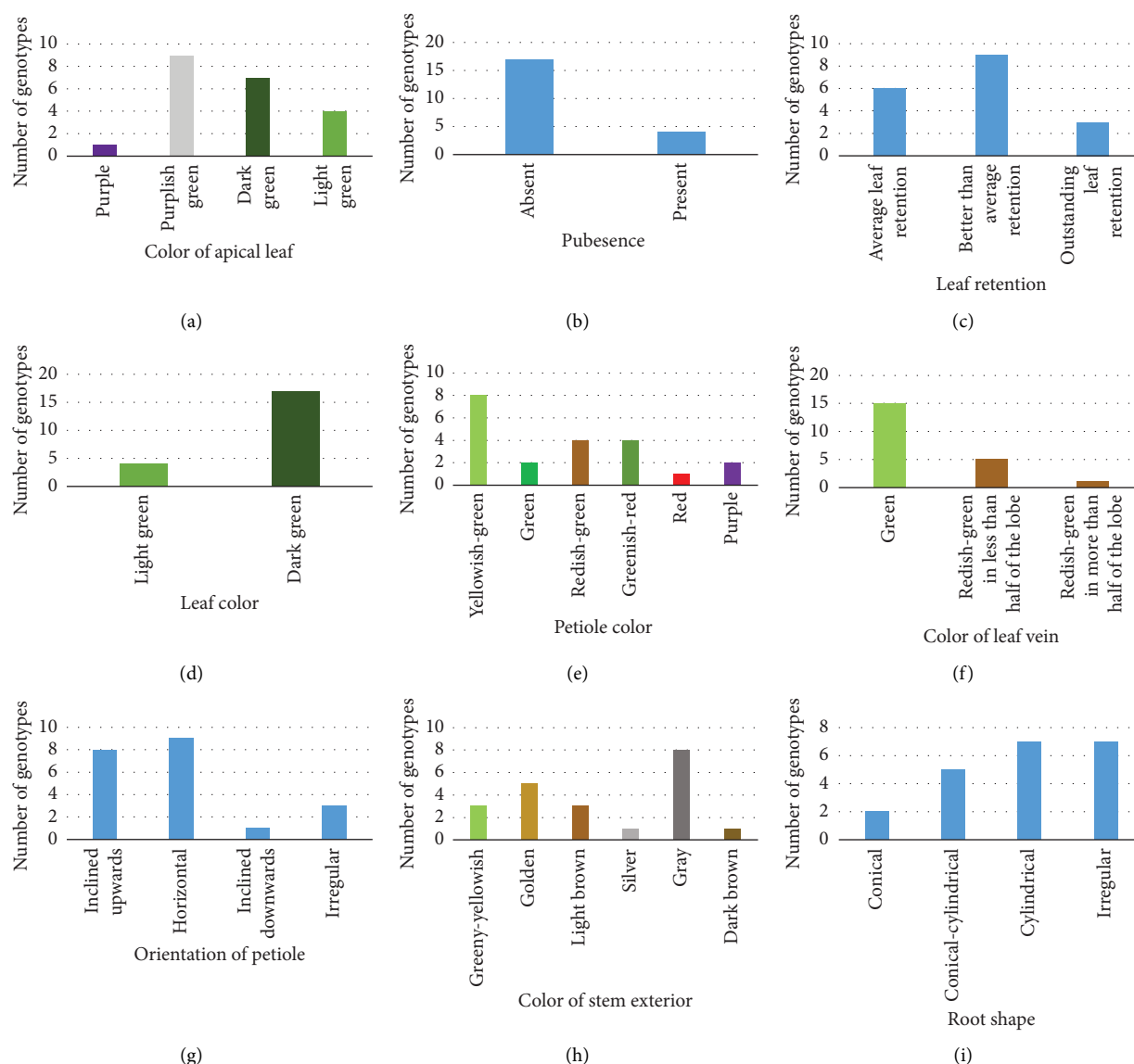


FIGURE 1: Qualitative traits of the 21 genotypes: (a) color of apical leaf, (b) presence of apical pubescence, (c) leaf retention, (d) leaf color, (e) petiole color, (f) color of leaf vein, (g) orientation of petiole, (h) color of stem exterior, and (i) root shape.

3.3. Cluster Analysis. The cluster analysis grouped the genotypes into two main groups, of which most were clustered in the first group with 5 subgroups and the second group has 2 subgroups (Figure 6). The dissimilarity matrix is the dissimilarity or distance between pairs of genotypes. The values in the matrix are an indication of how different or similar the corresponding genotypes are based on the measured traits. In the pairwise matrix, zero is used as an indication for genotypes that are identical in the measured traits (Table 3). As the values increase, the dissimilarity between the genotypes increases. Larger values indicate a greater difference in the measured morphological traits. The hierarchical classification based on the measured morphological traits was to highlight the variations and the relationship between the cassava genotypes. Similarities between genotypes mean that the genotypes have a close relationship.

3.4. Correlation Heatmap. Positive correlations were present between LR and X. total. Soilds, LR and PL, LR and WgtCSR, and LR and PH (Figure 7). A negative correlation was also recorded between LLL and Av. weight in Figure 7.

4. Discussion

Cassava plays a critical role in Africa's food security, making extensive research crucial. Exploring the various cassava varieties holds immense potential to increase their production globally. This study highlights the importance of agromorphological characterization as the initial step for characterization. By examining morphological and agronomic traits, we assessed the degree of diversity among the 21 cassava genotypes, paving the way for further studies and targeted breeding programs to enhance food security across the continent. To optimize a breeding program, it is

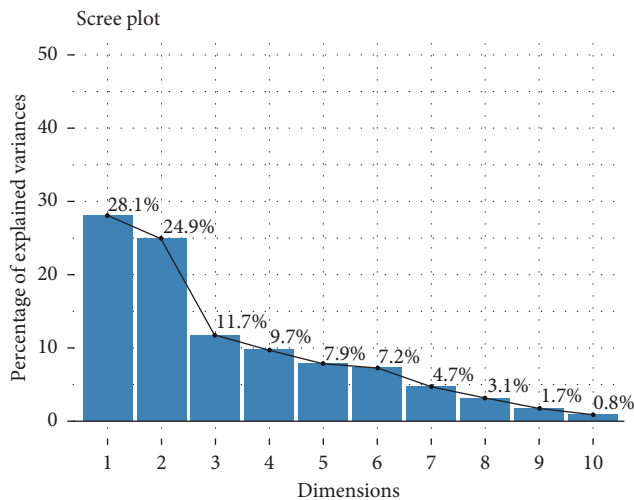


FIGURE 2: Scree plot detailing the variance in the traits measured among the 21 different genotypes.

TABLE 2: R-squared and p values of most significant associated variables within Principal component 1.

	Correlation (R-squared)	p value
WgtCSR	0.8016295	0.00002143793
LR	0.7446738	0.0001657692
Av. weight	0.6963150	0.6963150
NSR	0.5905692	0.0060114110
HFB	0.5786754	0.007514379
PL	0.5422518	0.01351142
X. total. Soilds	0.5266606	0.01704490

important to characterize the genetic diversity within the germplasm to determine the breeding potential of cultivars [23].

The results of the qualitative traits showed a variation among the measured traits. The apical LC recorded among the genotypes was the purplish green color. The other colors recorded among the genotypes were purple, dark green, and light green. The pubescence on the apical leaf was only present in 19% of the genotypes. The majority of genotypes had better than average LR, a very crucial trait in breeding. Lenis et al. [24] revealed correlations between LR and root dry matter yield (0.46) and fresh root production (0.43). LR is a critical trait to improve cassava yield, drought tolerance, and adaptation to local conditions [25]. By incorporating LR into breeding programs and using various germplasm resources, cassava varieties that are more productive, resilient, and contribute to improved food security can be developed. The LC among the genotypes was dark green and light green, with the most common being dark green. The most prominent petiole color exhibited among genotypes was yellowish green, with most exhibiting horizontal orientation. The root shapes of more than 50% of the genotypes were cylindrical or irregular. The results of qualitative traits such as LC, central leaflet shape, and petiole orientation in this study showed a limited variation among cassava genotypes. Benassi [26] and Kawuki et al. [25] observed similar results in which

qualitative traits did not uniquely classify cassava accessions. Most accessions had light green and dark brown stem cortex and stem *epidermis*, respectively, with light brown and gray stem exteriors. Similar results were reported by Kosh-Komba et al. [27], who examined the diversity distinguished by stems in shades of light brown and gray.

The majority of cassava genotypes had a light or dark brown color of external storage roots. In some cassava genotypes, the intensity of yellow pigment in roots is strongly associated with beta-carotene [28]. These genotypes can be crucial in plant breeding programs to improve the beta-carotene content and the overall nutritional value of cassava. Beta-carotene biofortification has been the focus of a lot of breeding programs to release lines that are rich in beta-carotene as compared to other micronutrients such as zinc, iron, and proteins.

PCA was used to uncover underlying patterns and structures within the dataset. For phenotypic diversity and trait contribution, the Principal components 1 and 2 explained 53.02% of the total variance, indicating substantial phenotypic diversity among the 21 genotypes. The weight of the commercial storage root showed the strongest positive linear relationship with the measured variables, suggesting that it is a good predictor of the overall phenotype. However, the complexity in yield traits stems from the interaction of several factors [29]. Genotypes WC 2 and WC 14 made substantial contributions to PC1 and PC2, indicating a strong influence on overall diversity. Biplot analysis allows for visualization of the relationships between objects and variables [30]. Genotypes and the measured traits can be grouped based on their proximity to each other and to the main components [31]. Traits such as The weight of commercial storage roots, the number of commercial storage roots, the average weight, LR, and PL exhibited high variability and influence on PC1 and PC2. This result is similar to the finding from [32] who found that PC1 captured the majority of variation in root yield potential, root weight per plant, root number per plant, dry matter yield potential, and starch yield potential, and PC2 was primarily associated with specific gravity, dry matter content, and starch content. A positive correlation was observed between the NSRs, WgtCSR, average weight, HFB, and PH, and between the NLLs, LLL, WLL, and LR. Overall, PCA analysis revealed significant phenotypic diversity among the 21 genotypes. Key traits contributing to the diversity included WgtCSR, LR, Av. weight, and NSRs. The analyses also showed the relationships between different traits and genotypes, which is valuable for further studies on cassava breeding and improvement programs. Breeding programs can focus on genotypes such as WC 2 and WC 14, with high values for these traits to enhance yield and overall performance alongside the nutritional content. The genotypes clustered together share a similar trait pattern and can guide breeding decisions by leveraging the diversity within the clusters for breeding programs. The high-performing yellow-fleshed varieties can be selected as parents for breeding programs. It is, however, important to consider environmental influences, which was a limiting factor by conducting a multilocation trial.

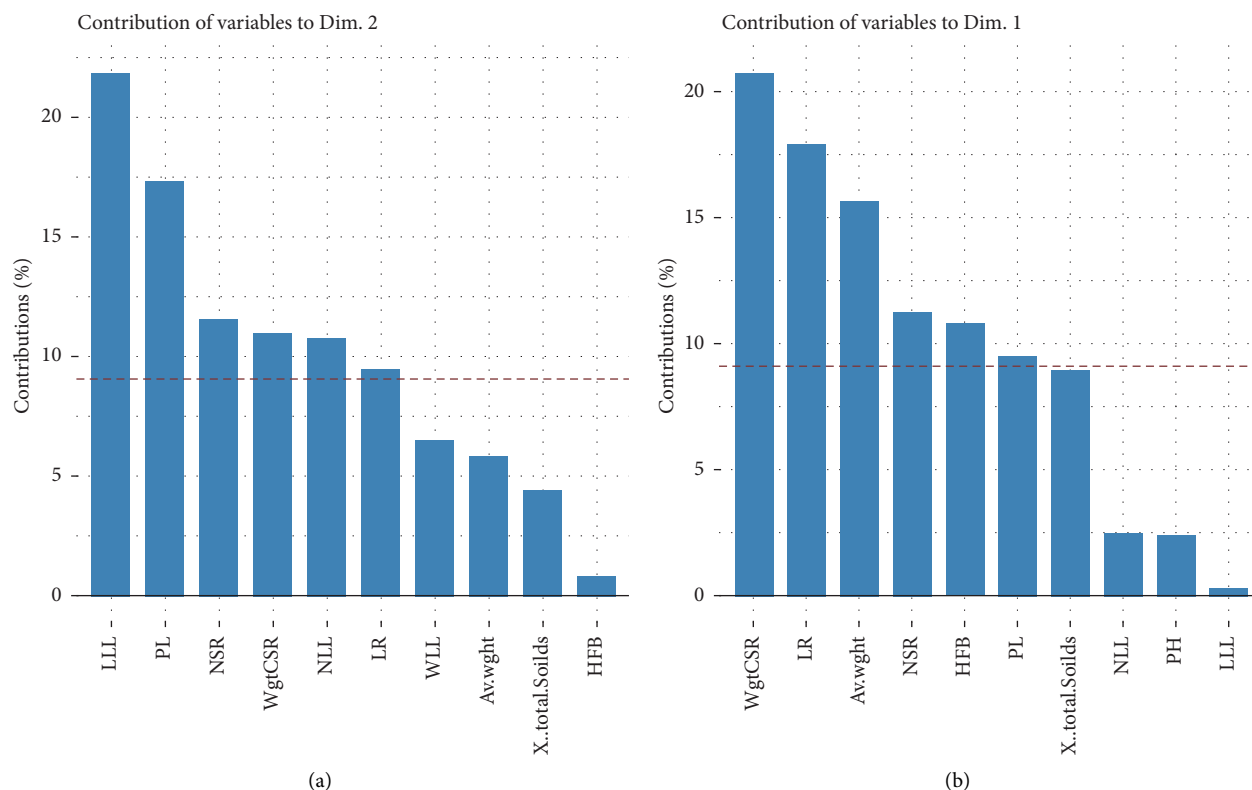


FIGURE 3: Contribution of traits measured to the first two principal components: (a) Dim. 2 and (b) Dim. 1.

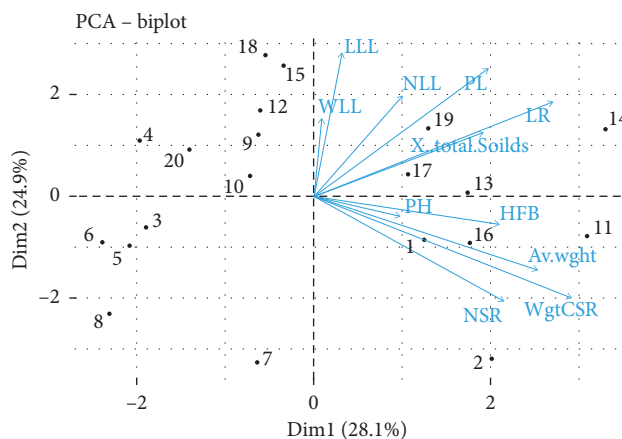
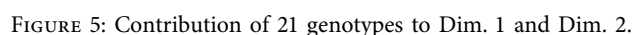


FIGURE 4: Biplot analysis of 21 genotypes: color of apical leaf (CAL), presence of pubescence (PP), leaf retention (LR), leaf color (LC), petiole length (PL), petiole vein color (CLV), orientation of petiole (OP), number of leaf lobe (NLL), length of leaf lobe (LLL), width of leaf lobe (WLL), color of stem epidermis (CSE), color of stem cortex (CSC), color of stem exterior (CSE), height at first branch (HFB), plant height (PH), number of storage root (NSR), weight of commercial storage root (WgtCSR), average weight of commercial storage root (Av. weight), external color of storage root (ECSR), color of root pulp (CRP), and percentage of total solids (X. total. Solids).

The dendrogram is a visual representation of cluster relationships, and it reveals how closely related the varieties are based on their characteristics where closely related varieties are grouped together with shorter lines, while more distant varieties form separate clusters with lines further to the right [33]. The presence of clusters is an indication of

morphological variations between genotypes. The cluster analysis grouped the genotypes into two main groups of which the majority were clustered in the first group with 5 subgroups, and the second group has 2 subgroups. It is important to note that the first group had most of the yellow-fleshed cassava varieties. Choosing parents from the

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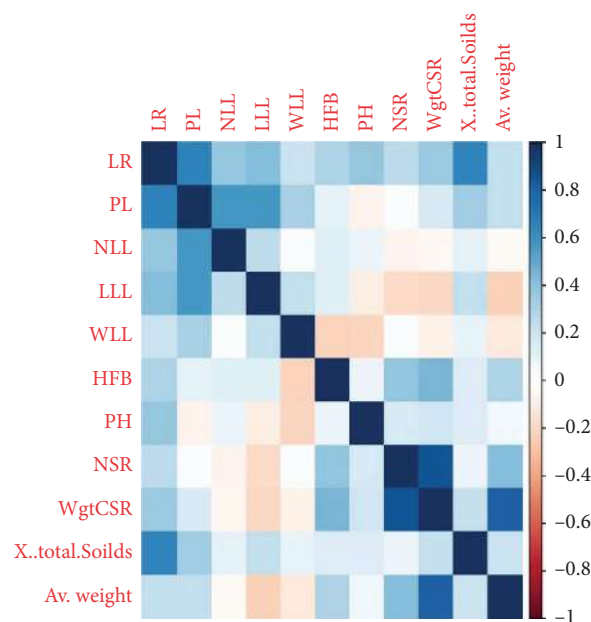


FIGURE 7: Traits correlation heatmap. LR = leaf retention, PL = petiole length, NLL = number of leaf lobe, LLL = length of leaf lobe, WLL = width of leaf lobe, HFB = height at first branch, PH = plant height, NSR = number of storage root, WgtCSR = weight of commercial storage root, Av. weight = average weight of commercial storage root, CRP = color of root pulp, and X. total. Solids = percentage of total solids.

different clusters, that is, the yellow-fleshed cassava varieties and high-performing genotypes, can be used in breeding programs for the development of high-performing hybrids.

5. Conclusions

The agromorphological characterization of the 21 cassava genotypes revealed substantial phenotypic diversity, providing a foundation for further breeding programs to improve food security on the continent. The results of qualitative traits, including LC and LR, highlighted the importance of incorporating diverse germplasm resources into breeding initiatives. The PCA explained significant phenotypic diversity and trait contributions, forming targeted breeding efforts. The dendrogram further illustrated morphological variations among genotypes, with potential implications for cassava breeding and improvement programs. In general, this preliminary assessment further sets the groundwork for advancing cassava research and breeding strategies for improved productivity and nutritional content.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Conflicts of Interest

The authors declare no conflicts of interest.

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References

- [1] J. W. Low, M. Arimond, N. Osman, B. Cunguara, F. Zano, and D. Tschirley, "A Food-Based Approach Introducing Orange-Fleshed Sweet Potatoes Increased Vitamin A Intake and Serum Retinol Concentrations in Young Children in Rural Mozambique," *The Journal of Nutrition* 137, no. 5 (2007): 1320–1327, <https://doi.org/10.1093/jn/137.5.1320>.
- [2] N. M. Agwu, "Patterns and Determinants of Fruit and Vegetable Consumption in Urban and Rural Areas of Enugu State" (2015).
- [3] G. Timpanaro, C. Bellia, V. T. Foti, and A. Scuderi, "Consumer Behaviour of Purchasing Biofortified Food Products," *Sustainability* 12, no. 16 (2020): 6297, <https://doi.org/10.3390/su12166297>.
- [4] E. Leyva-Guerrero, N. N. Narayanan, U. Ihemere, and R. T. Sayre, "Iron and Protein Biofortification of Cassava: Lessons Learned," *Current Opinion in Biotechnology* 23, no. 2 (2012): 257–264, <https://doi.org/10.1016/j.copbio.2011.12.009>.
- [5] P. Chavarriaga-Aguirre, A. Brand, A. Medina, et al., "The Potential of Using Biotechnology to Improve Cassava: A Review," *In Vitro Cellular and Developmental Biology-Plant* 52, no. 5 (2016): 461–478, <https://doi.org/10.1007/s11627-016-9776-3>.
- [6] Fao, "Food and Agricultural Division of the United Nations, Statistical Division," (FAO, 2013), <https://faostat3.fao.org/faostat-gateway/go/to/download/Q/QC/E>.
- [7] A. D. Uchechukwu-Agua, O. J. Caleb, and U. L. Opara, "Postharvest Handling and Storage of Fresh Cassava Root and

- Products: A Review," *Food and Bioprocess Technology* 8, no. 4 (2015): 729–748, <https://doi.org/10.1007/s11947-015-1478-z>.
- [8] W. G. Adebayo and M. Silberberger, "Poverty Reduction, Sustainable Agricultural Development, and the Cassava Value Chain in Nigeria," *The Palgrave Handbook of Agricultural and Rural Development in Africa* (2020): 525–551, https://doi.org/10.1007/978-3-030-41513-6_24.
 - [9] L. Luar, M. Pampolino, A. Ocampo, A. Valdez, D. F. Cordora, and T. Oberthür, "Cassava Response to Fertilizer Application," *Better Crops* 102, no. 2 (2018): 11–13, <https://doi.org/10.24047/bc102211>.
 - [10] M. A. El-Sharkawy, "Physiological Characteristics of Cassava Tolerance to Prolonged Drought in the Tropics: Implications for Breeding Cultivars Adapted to Seasonally Dry and Semiarid Environments," *Brazilian Journal of Plant Physiology* 19, no. 4 (2007): 257–286, <https://doi.org/10.1590/s1677-04202007000400003>.
 - [11] T. Sánchez, E. Salcedo, H. Ceballos, et al., "Screening of Starch Quality Traits in Cassava (*Manihot Esculenta* Crantz)," *Starch Staerke* 61, no. 1 (2009): 12–19, <https://doi.org/10.1002/star.200800058>.
 - [12] K. Shore, "Decades of Cassava Research Bear Fruit," *Gene Conserve* 1 (2002): 1–4.
 - [13] A. N. Bhanu, A. N. Bhanu, K. Srivastava, M. N. Singh, and H. A. Shreya, "Assessment of Genetic Diversity in Crop Plants-An Overview," *Advances in Plants & Agriculture Research* 7, no. 3 (2017): 279–286, <https://doi.org/10.15406/apar.2017.07.00255>.
 - [14] M. Elias, D. McKey, O. Panaud, M. C. Anstett, and T. Robert, "Traditional Management of Cassava Morphological and Genetic Diversity by the Makushi Amerindians (Guyana, South America): Perspectives for on-Farm Conservation of Crop Genetic Resources," *Euphytica* 120, no. 1 (2001): 143–157, <https://doi.org/10.1023/a:1017501017031>.
 - [15] J. Adjebeng-Danquah, J. Manu-Aduening, I. K. Asante, R. Y. Agyare, V. Gracen, and S. K. Offei, "Genetic Diversity and Population Structure Analysis of Ghanaian and Exotic Cassava Accessions Using Simple Sequence Repeat (SSR) Markers," *Heliyon* 6, no. 1 (2020): e03154, <https://doi.org/10.1016/j.heliyon.2019.e03154>.
 - [16] J. Adjebeng-Danquah, V. E. Gracen, S. K. Offei, I. K. Asante, and J. Manu-Aduening, "Agronomic Performance and Genotypic Diversity for Morphological Traits Among Cassava Genotypes in the Guinea Savannah Ecology of Ghana," *Journal of crop Science and Biotechnology* 19, no. 1 (2016): 99–108, <https://doi.org/10.1007/s12892-015-0095-8>.
 - [17] W. M. G. Fukuda, C. L. Guevara, R. Kawuki, and M. E. Ferguson, *Selected Morphological and Agronomic Descriptors for the Characterization of Cassava* (IITA, 2010).
 - [18] P. P. Acheampong, E. O. Danquah, K. Agyeman, K. O. Dankwa, and M. Addison, "Research and Development for Improved Cassava Varieties in Ghana: Farmers' Adoption and Effects on Livelihoods," in *Cassava-Biology, Production, and Use* (IntechOpen, 2021).
 - [19] R. N. A. Prempeh, V. A. Amankwaah, A. Oppong, and M. D. Quain, "Breeding Cassava for End-User Needs," in *Cassava-Recent Updates on Food, Feed, and Industry* (UK: IntechOpen, 2023).
 - [20] R. T. Sayre, "Biofortification of Cassava: Recent Progress and Challenges Facing the Future," *Biofortification of Staple Crops* (2022): 417–438, https://doi.org/10.1007/978-981-16-3280-8_16.
 - [21] H. E. Bouis, C. Hotz, B. McClafferty, J. V. Meenakshi, and W. H. Pfeiffer, "Biofortification: A New Tool to Reduce Micro-nutrient Malnutrition," *Food and Nutrition Bulletin* 32, no. 1 (2011): S31–S40, <https://doi.org/10.1177/15648265110321s105>.
 - [22] W. M. G. Fukuda, C. L. Guevara, R. Kawuki, and M. E. Ferguson, "Selected Morphological and Agronomic Descriptors for the Characterization of Cassava" (IITA, Ibadan, Nigeria, 2010).
 - [23] P. A. Asare, I. K. A. Galyuon, J. K. Sarfo, and J. P. Tetteh, "Morphological and Molecular Based Diversity Studies of Some Cassava (*Manihot Esculenta* Crantz) Germplasm in Ghana," *African Journal of Biotechnology* 10, no. 63 (2011): 13900–13908, <https://doi.org/10.5897/ajb11.929>.
 - [24] J. I. Lenis, F. Calle, G. Jaramillo, J. Perez, and H. Ceballos, "Leaf Retention and Cassava Productivity," *Field Crops Research* 95, no. 2-3 (2006): 126–134, <https://doi.org/10.1016/j.fcr.2005.02.007>.
 - [25] R. S. Kawuki, M. Ferguson, M. T. Labuschagne, et al., "Variation in Qualitative and Quantitative Traits of Cassava Germplasm From Selected National Breeding Programmes in Sub-Saharan Africa," *Field Crops Research* 122, no. 2 (2011): 151–156, <https://doi.org/10.1016/j.fcr.2011.03.006>.
 - [26] I. R. M. Benesi, "Characterisation of Malawian Cassava Germplasm for Diversity, Starch Extraction and Its Native and Modified Properties" (2005).
 - [27] E. Kosh-Komba, S. Akpavi, A. W. Yao, et al., "Diversité Agromorphologique De Manihot esculenta Crantz.(Euphorbiaceae) Cultivée Dans Trois Zones Agroclimatiques En République Centrafricaine (RCA)," *European Scientific Journal* 10, no. 3 (2014).
 - [28] T. Sánchez, A. L. Chavez, H. Ceballos, D. B. Rodriguez-Amaya, P. Nestel, and M. Ishitani, "Reduction or Delay of Post-Harvest Physiological Deterioration in Cassava Roots With Higher Carotenoid Content," *Journal of the Science of Food and Agriculture* 86, no. 4 (2006): 634–639, <https://doi.org/10.1002/jsfa.2371>.
 - [29] L. F. Turyagyenda, E. B. Kizito, M. E. Ferguson, et al., "Genetic Diversity Among Farmer-Preferred Cassava Landraces in Uganda," *African Crop Science Journal* 20, no. 1 (2012).
 - [30] F. Laila, C. U. Zanetta, A. Karuniawan, and B. Waluyo, "Classifying Cassava (*Manihot Esculenta* Crantz.) Clones Based on Principal Component Analysis of Specific Characters for Use as Selection Criteria," *IOP Conference Series: Earth and Environmental Science* 911, no. 1 (2021): 012007, <https://doi.org/10.1088/1755-1315/911/1/012007>.
 - [31] M. C. C. Maia, L. B. D. Araújo, C. T. D. S. Dias, et al., "Selection of Mango Rosa Genotypes in a Breeding Population Using the Multivariate-Biplot Method," *Ciência Rural* 46, no. 10 (2016): 1689–1694, <https://doi.org/10.1590/0103-8478cr20130722>.
 - [32] H. F. Ojulong, M. T. Labuschagne, L. Herselman, and M. Fregene, "Yield Traits as Selection Indices in Seedling Populations of Cassava," *Crop Breeding and Applied Biotechnology* 10, no. 3 (2010): 191–196, <https://doi.org/10.1590/s1984-70332010000300002>.
 - [33] J. C. Nwabueze, "Cluster Analysis of Improved Cassava Varieties Cultivated at Onne, Nigeria by the International Institute of Tropical Agriculture," *African Journal of Mathematics and Computer Science Research* 2, no. 9 (2009): 196–201.