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Evaluation of Yellow Flesh Cassava Genotypes for Cyanogenic Potential, Total Carotenoid, Dry Matter and Yield in the Coastal Savannah Zone of Ghana

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Abstract Malnutrition, particularly vitamin A deficiency, remains a major public health challenge in Ghana. Cassava plays a crucial role in meeting the dietary needs of many Ghanaians. However, the dominated white-flesh cassava varieties fail to address vitamin A deficiency. This study aimed to evaluate the agronomic performance, cassava mosaic disease (CMD) resistance, and nutritional traits of ten cassava genotypes which included eight yellow-flesh mutant genotypes and two checks (a white-flesh and a yellow-flesh variety). Conducted at the Teaching and Research Farm of the University of Cape Coast, the experiment was laid in a randomized complete block design (RCBD) with four replications. Field evaluation were complemented by morphological and molecular (PCR) screening for CMD resistance as well as the yield and other yield component. The results showed significant ($p<0.05$) differences among genotypes in all measured traits. A negative correlation was observed between CMD severity and yield, while a positive correlation was found between total carotenoid (TC) content and dry matter content (DMC). The study identified four genotypes; 12B, 5B, 1011A, and 11B, with high TC content, dry matter content (DMC), root yield, low hydrogen cyanide levels (28.52–39.68 mg HCN/kg), and resistance to CMD. These genotypes, were selected for further evaluation and potential release as varieties. The findings highlight the potential of biofortified, high-yielding cassava varieties to improve nutrition, and contribute to sustainable agriculture in Ghana and beyond.

Keywords: *yellow flesh cassava, yield, dry matter, carotenoid, hydrogen cyanide, CMD*

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1. Introduction

The issue of food insecurity and malnutrition has long been a global challenge. The United Nations (UN) World Food Program estimates that over 700 million people globally lack sufficient food to maintain healthy, active lives [1]. Over two billion people suffer from micronutrient malnutrition, also known as "hidden hunger" [2]. Among the most widespread forms of micronutrient deficiency is Vitamin A Deficiency (VAD), which predominantly affects populations in developing regions that rely on staple crops to meet their nutritional needs.

In Africa, particularly in regions like Ghana where cassava is a dietary staple, the prevalence of malnutrition is exacerbated by the low concentrations of essential nutrients, such as vitamin A, in cassava roots [3]. This challenge has spurred a need for innovative, cost-effective, and sustainable solutions. One such approach has been the development of biofortified cassava varieties rich in provitamin A.

Breeding efforts began addressing these nutritional gaps with the development of cassava varieties exhibiting desirable traits, such as improved root and starch yields, reduced toxicity, enhanced pest and disease resistance, and higher micronutrient levels. Specifically, biofortified provitamin A cassava genotypes have been recognized for their improved carotenoid levels, which contribute to combating VAD [3,4]. Finding [4,5,6] showed higher levels of acceptance of product made from biofortified cassava over product from the known white-flesh cassava.

Despite these advancements, yellow flesh cassava varieties often exhibited low dry matter content (DMC), which lead to difficulties such as drying challenges, poor taste, and reduced cooking quality [7]. Reports from major stakeholder engagement including farmers and consumers in the Central Region of Ghana, revealed preferences and acceptance of yellow-flesh or biofortified cassava. However, concerns were raised about the need to breed

yellow flesh cassava varieties with improved nutritional traits and mealiness [8].

The University of Cape Coast (UCC), in Collaboration with the Ghana Atomic Energy Commission – Biotechnology and Nuclear Agriculture Research Institute (GAEC-BNARI) and the International Institute of Tropical Agriculture (IITA), in a joint project seek to develop yellow flesh cassava mutants. This initiative aims to incorporate farmers' preferred traits while systematically distributing these varieties to enhance the nutritional status of populations dependent on cassava as a major staple food. The objective of this study, therefore, was to evaluate ten cassava genotypes for their nutritional (carotenoid, cyanogenic potential, DMC), yield, disease resistance and genetic diversity.

2. Materials and Methods

2.1. Collection of Cassava Planting Materials

Ten cassava genotypes were used in this experiment. These genotypes include eight yellow-flesh mutants; 9A (151036), 6A (150579), 8A (151082), 12B (150306), 1011A (150029), 14B (151110), 5B (151006), 11B (150538), an international yellow-flesh check, 1A (70593) from IITA and a white flesh-check 6F (106F) (commonly known as "*fufuohene*"), a newly released variety by UCC [9].

2.2. Experimental Site

The field experiment was conducted on sandy loam soil at the Teaching and Research Farm of the School of Agriculture, University of Cape Coast, Cape Coast, in the coastal savannah ecological zone. The study took place during 2018/2019 major farming season. The soil has been classified by [10] as Atabadze series, in agreement to Ultisol in the United States Department of Agriculture (USDA Soil Taxanomy) and Haplic Acrisol (FAO/UNESCO soil classification). It belongs to the Edina-Benya-Udu compound association, developed over Sekondian deposits. The rainfall in Cape Coast is bimodal with an annual range of 800 to 1000 mm and an average mean monthly temperature of about 26.5 ^{o}C.

2.3. Experimental Design and Field Layout

The ten cassava genotypes were grown under rain fed conditions in a randomized complete block design (RCBD) with four replications. A land size of about 680 m^2 (44 m x 24 m) was ploughed, harrowed and divided into blocks and plots. A spacing of 2.0 m was maintained between blocks and 1.0 m between plots, with each measuring 6.0 m x 4.0 m. Twenty-four (24) cm long cuttings were planted in each plot at a spacing of 1 m within rows and 1m between rows. A total of 960 plants were cultivated.

2.4. Cultural Practices

Cuttings that did not sprout were replaced two weeks after planting. Weeding was done manually with a hoe on the 1, 4, 8 and 11 months after planting. No fertilizer or insecticide were applied during the experiment.

2.5. Characterization of the Cassava Genotypes Using Agro-morphological Descriptors

The morphological characterization of cassava genotypes was based on the unique features of cassava parts which were taken at specific times during the life cycle of the plant. The standard descriptors by International Institute of Tropical Agriculture were used [11]. The characteristics that featured predominantly during this study included the colour of apical leaves, leaf retention, leaf pubescence, petiole colour, shape of central leaflet, flowering, growth habit of stem, prominence of foliar scar, colour of stem exterior and cortex colour, colour of end branches of adult plant, height at first branching, root constriction, root shape, external colour of storage root, colour of root pulp, texture of root epidermis, ease of peeling, colour of root cortex, root taste, cortex thickness, root weight per plant, weight of shoot, fresh root yield, dry matter content (%) and harvest index following the protocol of [12].

2.6. Determination of Whitefly Population and Cassava Mosaic Disease

The African cassava mosaic virus (ACMV) is transmitted by whiteflies (*Bemisia tabaci*). To evaluate the relationship between whitefly population and the intensity of cassava mosaic disease (CMD), direct counts of adult whiteflies were conducted on the top five fully extended leaves of cassava plants, following [13]. Whiteflies were counted early morning (6:00–8:00 am), when they were less active, at 3, 6, and 9 months after planting.

The resistance status of genotypes to CMD were also assessed 3, 6, and 9 MAP. This was done using the procedure outlined by [14,15] which employed a standard disease rating score of 1 to 5. A score of "1" indicating no symptoms, whereas a score of "5" indicated significant symptoms such as chlorosis, leaf distortion and plant stunting. Based on this system, plants with the mean score of "1" were classified as extremely resistant and those with mean score of "5" were classified as highly susceptible, as described also by [16].

2.7. Molecular Screening of Cassava Genotypes Against Cassava Mosaic Begomovirus Infection

To confirm resistance to Cassava Mosaic Begomoviruses (CMBs), a polymerase chain reaction (PCR) assay was performed following the protocol described by [17,18]. Leaf samples were collected from field-grown cassava genotypes and transported under ice to the laboratory of the Biotechnology Centre of the College of Agriculture and Consumer Sciences, University of Ghana, Legon for analyses. Genomic DNA was extracted using the Quick-DNA™ Plant/Seed Miniprep Kit (Zymo Research), and quality was assessed

via 0.9% agarose gel electrophoresis, as previously described by [19].

PCR amplification was carried out using species-specific primers (Table 1) targeting African Cassava Mosaic Virus (ACMV) and East African Cassava Mosaic Virus (EACMV) in a 25 µL reaction mixture containing 2X PCR Master Mix, DNA template, and primers. The cycling conditions involved 35 cycles of denaturation (94°C, 1 min), annealing (55°C, 1 min), and extension (72°C, 1 min), with a final extension at 72°C for 10 minutes [17]. Amplified products were separated by 1.2% agarose gel electrophoresis and visualized under UV light, following the method of [20].

Table 1. Primer name and sequence (5' to 3')

Virus Strain	Name of Primer	Primer Sequence (5'- 3')	Ref
EACMV	OjaRep-F	CRTCAATGACGTTGTACCA	[17]
	EACMVRep-R	GGTTTGCAGAGAACTACATC	
ACMV	OjaRep-F	CRTCAATGACGTTGTACCA	[17]
	ACMVRep-R	CAGCGGMAGTAAGTCMGA	

2.8. Determination of Total Carotenoid and Hydrogen Cyanide (HCN) Potential

For a strong reproducibility and reliability of carotenoid analysis, the carotenoid content of cassava genotypes was determined using iCheck™ Carotene device. (BioAnalyt, Germany) [21] and [22]. Following the manufacturer's protocol, the measuring unit and reagent vials, which are commercially available, were utilised (www.bioanalyt.com). The cyanogenic potential of the genotypes was determined following a standard titration protocol outlined by [23].

2.9. Statistical Analysis

Data was analysed using Origin 2024 (10.1). Statistical means from the analysis of variance (ANOVA) among genotypes were separated using Tukey's comparison test at the 5% significance level.

3. Results

3.1. Whitefly Population on the Ten Genotypes

The mean number of adult whiteflies on cassava genotypes at 3, 6, and 9 months after planting (MAP) is recorded in Table 2. The whitefly count for the 3rd month had the high mean values of 19.7, 20.1, 20.1 and 20.3, and recorded for genotypes 6A, 5B, 1A and 12B respectively with least values of 5.4 and 6.5 for genotypes 8A and 14 respectively (Table 2).

The whitefly count at the 6th month was significantly different among the genotypes, with a mean range of 5.4 – 21.9. The high whitefly count of 21.9 was recorded for genotype 5B while the low whitefly count of 5.4 was recorded for genotype 8A. The whitefly count at the 9th month, had the high mean values of 21.3 and 21.7 for genotypes 1A and 6A respectively with a low mean value of 5.5 and 7.9 for genotypes 8A and 14B respectively. From, the overall mean for the whitefly count for the 3, 6 and 9 months ranged from 5.5 to 21.0. The high (21.0) mean value of whitefly count was recorded for genotype 5B, followed by genotype 1A with a mean of 20.9. The low overall mean value of 5.5 and 9.9 was recorded for genotypes 8A and 9A, respectively (Table 2).

Table 2. Mean number of adult whiteflies on the ten (10) Genotypes

Genotypes	3 months	6 months	9 months	Mean
9A	9.2bc	11.3cd	9.2d	9.9c
6A	19.7a	19.5ab	21.7a	20.3a
8A	5.4c	5.4d	5.5e	5.5d
1A	20.1a	21.1a	21.3ab	20.9a
12B	20.3a	20.9a	20.7ab	20.7a
14B	6.5bc	17.8abc	7.9de	10.7c
1011A	17.3a	19.2ab	18.2b	18.3ab
5B	20.1a	21.9a	20.9ab	21.0a
11B	9.7b	13.3bc	10.1cd	11.0c
6F	16.7a	20.0ab	12.3c	16.3b
Mean	14.5	17.1	14.8	15.4
Hsd	3.66	6.20	2.87	3.01
% cv	17.5	25.2	13.4	13.5

Means in a column with a common letter are not significantly different ($p>0.05$).

3.2. Severity for Cassava Mosaic Disease on the Ten Cassava Genotypes

The mean severity scores of Cassava Mosaic Disease (CMD) on cassava genotypes at 3, 6, and 9 MAP is recorded in Table 3. The ten genotypes recorded resistance, moderate resistance and susceptibility to CMD. There was significant difference among the ten genotypes for severity scores, however, the scores ranged from 1.0 to 3.8 for the 3 MAP. The high severity scores of 3.1, 3.5 and 3.8 were recorded for genotypes 1011A, 11B and 9A respectively, with the least severity scores of 1.0 and 1.1 recorded for genotypes 1A and 6A respectively. The severity score recorded for the 6 MAP showed significant difference between the ten genotypes. Genotypes 1011A, 12B, 11B, and 9A, recorded the high severity scores of 1.8, 2.5 and 3.8 respectively.

Table 3. Mean severity scores of Cassava Mosaic Disease (CMD) by the ten (10) genotypes

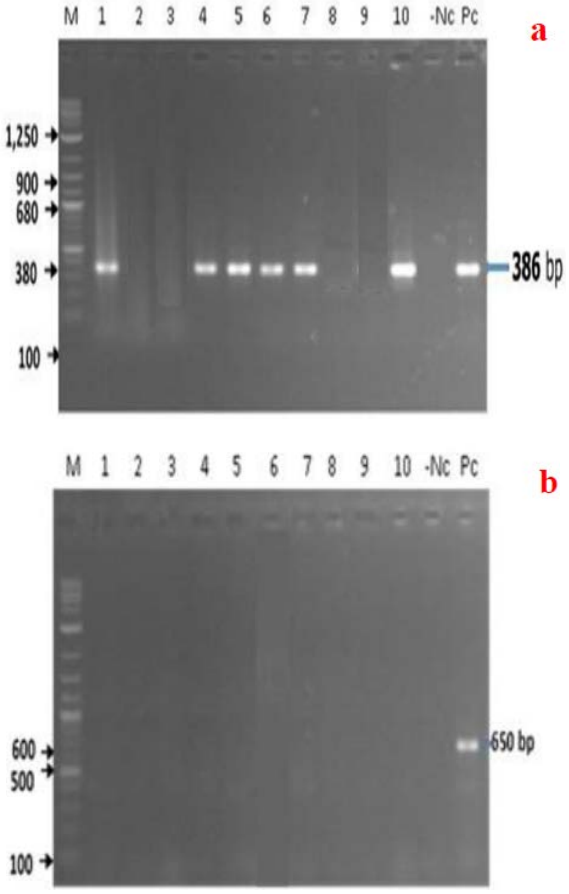
Genotypes	3 months	6 months	9 months	Mean
9A	3.8a	3.8a	3.7a	3.8a
6A	1.1c	1.0d	1.1b	1.1de
8A	1.1c	3.1ab	1.2b	1.8c
1A	1.0c	1.0d	1.0 b	1.0e
12B	1.0c	1.0d	1.8b	1.3cde
14B	2.0b	1.4cd	1.8b	1.7cd
1011A	1.4c	1.1d	1.0b	1.2cde
5B	1.0c	1.4cd	1.3b	1.3cde
11B	3.6a	2.5bc	3.1a	3.1b
6F	1.0c	1.1d	1.8b	1.3cde
Mean	2.1	1.8	1.5	1.7
Hsd	0.52	1.11	1.09	0.60
% cv	5.6	21.3	8.3	9.1

Means in a column with a common letter are not significantly different ($p>0.05$).

There was significant difference for severity scores for the 9 MAP. The high severity scores of 2.5 and 3.7 were genotypes by 9A and 11B respectively. The overall mean severity scores (Table 3) for the 3, 6 and 9 months ranged from 1.0 to 3.8 with a grand mean of 1.4. There were significant differences in the overall mean severity scores recorded at 3, 6 and 9 months after planting.

Genotypes 11B and 9A recorded a high overall mean severity score of 2.4 and 3.8 respectively, however, genotypes 6A, 1011A and 14B all recorded a low severity score of 1.1. The lowest severity scores of 1.0 was recorded for most of the genotypes; 6F, 1A, 12B and 5B.

3.3. PCR Screening of the Cassava Genotypes for ACMV and EACMV



Lanes: 1 = 11B; 2= 14B; 3= 12B; 4= 8A; 5= 1A; 6= 6A; 7= 9A; 8 = 5B; 9 = 1011A; 10 =N6F; M = Molecular size marker, Quick-Load Purple 2-Log DNA Ladder (0.1- 10.0 kb); -Ve = Negative control (nuclease-free PCR water), and; +Ve = Positive control (known ACMD and EACMV sample respectively).

Figure 1. Amplified DNA fragments of ACMV (a) and EACMV (b) from cassava leaves sampled from UCC Farm with species specific primer pairs (OJAREP- ACMVRep)

The results for the PCR screening of the genotypes for ACMV and EACMV are presented in Figure 1. The amplification of the ACMV with the species-specific primer pairs (OjaRep/ACMVRep) generated PCR products at 386 bp in all most of the cassava genotypes had ACMV DNA bands except four genotypes (2= 14B; 3= 12B; 8 = 5B; 9 = 1011A) (lanes: 1-10) Although genotype 1=11B had ACMV band but it does not always show symptom on the field and therefore should be considered as tolerant to ACMV (Figure 1a).

The amplification of the EACMV with the species-specific primer pairs (OjaRep/EACMVRep) did not generate any PCR products at 650 bp in all the tested cassava genotypes, however, the positive control amplified (Figure 1b).

3.4. Total Carotenoids Content and Cyanogenic Potential

The results for total carotenoid contents and cyanogenic potential of the genotypes are presented in Table 4. The results of total carotenoid (TC) recorded among the YFC roots ranged 1.9 ug/g to 10.38 ug/g with a significant difference ($p<0.05$) among the ten genotypes (Table 4). The carotenoid for the positive and negative checks; 1A and 6F were 1.77 and 7.97 respectively. These genotypes; 11B, 5B, 12B and 1011A recorded the high total carotenoid of 9.57, 9.83, 10.01 and 10.38 ug/g respectively that was above the positive check (Table 4). However, these genotypes; 6B, 14B, 9A and 8A also recorded total carotenoids of 5.41, 6.88, 6.07 and 6.64 ug/g respectively which were lower than the positive check value of 7.97 ug/g (Table 4). There was a significant difference ($p<0.05$) between genotype 6F that recorded lowest total carotenoids value of 1.77 ug/g and the rest of the genotypes (Table 4).

The result of the cyanogenic potential is also presented in Table 4. There was a significant difference ($p<0.05$) between the ten genotypes. The concentration of cyanide in genotype 9A, 8A, 12B, 11B and 5B were the high (36.54, 37.16, 38.24, 38.96, and 39.68 mgHCN/kg) respectively, while genotypes 6A and 14B had low cyanide concentrations of 28.52 and 30.32 mgHCN/kg respectively. The concentration of cyanide in cassava genotypes that recorded the high HCN was significantly different ($p<0.05$) from the cassava genotypes 1A, 6F and 1011A, that recorded cyanide concentration of 30.04, 31.71 and 33.92 mgHCN/kg respectively. The cassava genotypes 14B and 6A that recorded low cyanide concentration were significantly different from the rest of the genotypes.

Table 4. Mean total carotenoids and cyanogenic potential of the ten (10) genotypes

Genotypes	Total carotenoid (ug/g)	Cyanogenic potential (mgHCN/kg)
9A	6.07c	37.11c
6A	5.41c	29.15f
8A	6.64c	37.70c
1A	7.97abc	31.36e
12B	10.01a	38.54b
14B	6.88bc	34.41d
1011A	10.38a	30.87e
5B	9.83a	40.13a
11B	9.57ab	39.28b
6F	1.77d	31.15e
Mean	7.45	34.97
Hsd	1.526	0.762
% cv	9.0	1.3

Means in a column with a common letter are not significantly different (P>0.05)

3.5. Yield and Yield Components of Ten (10) Genotypes of Cassava

Results obtained showed that, there were significant differences ($p<0.05$) between the number of roots, root length, fresh root yield and dry matter (Table 5). There was a significant difference ($p<0.05$) for the number of roots/plant with a range of 3.0 to 7.0 and percentage coefficient of variation (% cv) of 2.63. Genotypes 8A and 1011A recorded the high mean of 6.75 and 7.0 respectively for the number of roots/plants, followed by genotypes 5B and 11B with the mean number of root/plant of 5.5. Genotypes 9A and 6F recorded low number of roots/plant of 3.0 and 4.1 respectively (Table 5).

There was a significant difference ($p<0.05$) among the genotypes in relation to the mean root length. There were however no significant differences between genotypes 11B and 6F which recorded the longest mean root length values of 44.92 cm and 55.53 cm respectively. This was followed by genotypes 1A with the mean root length of 41.85 cm (Table 5). There was significant difference ($p<0.05$) between genotype 9A and 5B that recorded a shorter mean root length of 19.12 cm and 23.82 cm respectively than the rest of the genotypes.

The fresh root yield ranged from 17.22 to 44.70 with a mean of 30.54 t ha-^{1} (Table 5). The yellow fresh root highest yield of 44.70 t ha-1 was recorded for genotype 12B. This was not significantly different from the yield of 44.7 t ha^{-1} recorded for the white flesh genotype 6F that was used as a checked. The fresh root yields obtained showed a significant difference ($p<0.05$) among all the genotypes. Genotypes 5B, 1101A, 11B and 6A also gave a high yield of 32.92 t ha^{-1}, 32.58 t ha^{-1}, 33.15 t ha^{-1} and 33.30 t ha-1 respectively (Table 5). Lower yields of 23.15 t ha^{-1}, 19.95 t ha^{-1} and 17.22 t ha^{-1}, were recorded for genotypes 11B, 9A and 14B, respectively which were about two times lower than the highest root yield recorded. Six genotypes had fresh root yields above the genotype means (30.54 t ha^{-1}) while four of the genotypes yielded less than the genotype means (Table 5).

Table 5. Mean yield and yield component of the ten (10) genotypes

Genotypes	Number of roots/plants	Root length (cm)	Fresh root yield (t ha^{-1})	Dry matter %
9A	3.00c	19.12f	19.95d	31.93d
6A	4.62bc	24.84e	33.30b	22.33i
8A	6.75a	26.80de	25.07c	25.33g
1A	4.25bc	41.85b	32.10b	23.52h
12B	6.50a	32.23c	44.70a	36.12b
14B	4.25bc	32.30c	17.22e	15.53j
1011A	7.00a	29.88cd	32.58b	27.13f
5B	5.50ab	23.82e	32.92b	30.13e
11B	5.50ab	44.92b	33.15b	33.52c
6F	4.12bc	55.53a	44.7a	38.12a
Mean	5.11	30.76	30.54	28.37
Hsd	1.002	2.815	2.698	1.703
% cv	19.6	8.5	6.1	1.1

Means in a column with a common letter are not significantly different ($p>0.05$).

The combined analysis of variance for dry matter content (DMC) of the yellow flesh cassava genotypes showed significant differences ($p<0.05$) among the genotypes. The mean root DMC ranged from 15.53 to 38.12 %. The highest dry mater of 38.12 % was recorded for a white flesh variety 6F and this was significantly different ($p<0.05$) from the DMC of 36.12 % recorded for a yellow flesh genotype 12B which had the second highest DMC (Table 5). DMC of 30.13, 31.93 and 33.52 % which were recorded for yellow flesh genotypes 5B, 9A and 11B respectively were also significantly different from each other. The low DMC of 15.53, 22.33 and 23.52 % were recorded for yellow flesh genotypes 14B, 6A and international check 1A respectively (Table 5).

3.6. Correlation Coefficient for Whitefly Population, Cassava Mosaic Disease (CMD), Yield, Dry Matter and Total Carotenoids (TC) Contents

The results of the combined correlation analysis, as shown by their coefficients of correlation (Figure 2) revealed that Cassava Mosaic Disease (CMD) exhibited a significant negative correlation with both the whitefly population and root yield. In contrast, a significant positive correlation was observed between dry matter content and yield. Additionally, the correlation between dry matter content and total carotenoid content was highly significant and positive. The positive correlation between dry matter content and the flesh colour of cassava mutants suggests that deeper flesh colour (indicating higher carotene levels) corresponds to higher dry matter content, and this relationship was highly significant. However, the correlation observed between yield and total carotenoid content was positive but not statistically significant (Figure 2).

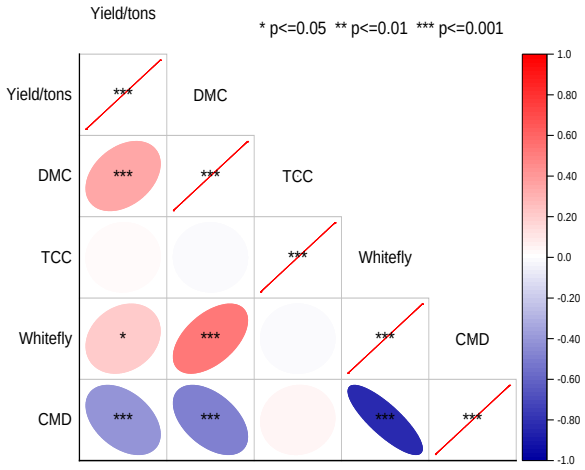


Figure 2. Correlation coefficient for whitefly population, Cassava Mosaic Disease (CMD), yield, dry matter and total carotenoid (TC) contents

3.7. Dendrogram of the Phylogenetic Relationship among the Ten Cassava Genotypes

A dendrogram (Figure 3) using 42 agro-morphological traits grouped the 10 Cassava genotypes into three main clusters based on genetic distance [24] using Power Maker version 3.25 unweighted pair grouped method with arithmetic average (UPGMA) cluster analysis [25] at a

dissimilarity of 24 % (Figure 3). The 10 cassava genotypes appeared to have emerged from common ancestry and were distinguished into 3 major clusters (A, B and C). Cluster B consisted of 70% of the cassava genotypes that were distributed into 3 sub-clusters at 17.5% dissimilarity coefficient. Cluster C was made of 6A, which was an outlier as shown in Figure 3

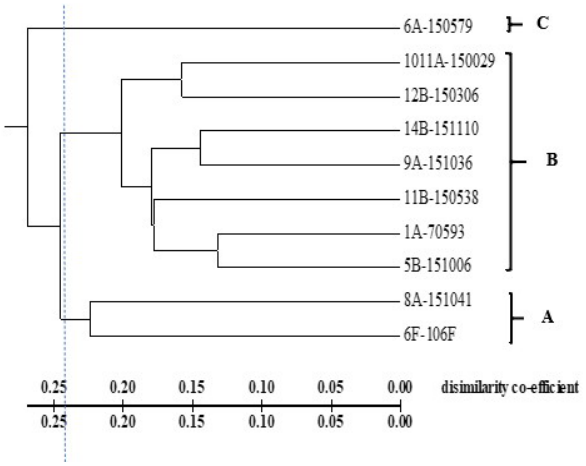


Figure 3. A dendrogram illustrating the relatedness of 10 genotypes, which was generated using 42 phenotypic (morphological) descriptors and the sequential clustering algorithm (UPGMA) based on genetic similarity [26]

4. Discussion

Morphological characterization has been used to analyse the genetic diversity of cassava germplasm due to its cost-effectiveness, simplicity, and timeliness compared to biochemical or molecular techniques [27,28] Morphological characteristic can be correlated with agronomic performance, making them useful for preliminary evaluations. In this study, the clustering of mutants with their parent genotype demonstrated their shared morphological traits, suggesting similar ancestry. Conversely, genotypes exhibiting distinct morphological characteristics from the parent (1A) clustered with the white-flesh cassava check (6F), further highlighting their phenotypic variation. Genotype 6A, which did not relate to any other genotype in the cluster analysis (Figure 3), exhibited clear morphological divergence. These findings align with earlier reports of low phenotypic variability among cassava genotypes cultivated in Ghana [29]. This limited variability is consistent with cassava's narrow genetic base, a bottleneck associated with its vegetative propagation and low cross-pollination rates during domestication.

Whitefly (*Bemisia tabaci*), a major pest of cassava, serves as a vector for cassava mosaic begomoviruses (CMVs), the causal agents of cassava mosaic disease (CMD) [30]. Previous studies [13,31] have reported yield losses exceeding 50% in CMD-affected varieties. In this study, the highest mean whitefly population was observed during the first six months of cassava growth, coinciding with its vegetative stage (Table 2). This finding contrasts with [32], who reported consistently high whitefly populations across cultivars at two months after planting (MAP), followed by a gradual decline by four MAP. Again, CMD-resistant genotypes exhibited the highest mean whitefly populations (Table 2), suggesting that whiteflies may shelter under these varieties to evade predators and harsh sunlight, later migrating to CMD-susceptible plants for feeding. This observation aligns with [31] who noted that CMD-resistant varieties are more prone to whitefly invasion, despite their resistance to CMD.

The severity of CMD varied among genotypes, with resistance, moderate resistance, and susceptibility observed (Table 3). CMD-resistant genotypes identified in this study align with previous reports [33] and have been utilized in breeding programs to enhance resistance. Resistance to CMD is known to be genetically controlled [34], further supporting the genetic basis of the observed variations in severity. Notably, some genotypes exhibited recovery from CMD symptoms by 9 MAP, suggesting potential resistance. This aligns with findings by [32,35], who reported recovery in moderately susceptible genotypes as they matured.

Yield losses in CMD-susceptible genotypes were consistent with earlier findings on the impact of CMD, where chlorosis-induced reductions in photosynthesis led to decreased tuberization and yield [36].

Genotypes that expressed CMD symptoms at 3 MAP support previous findings that, among susceptible cultivars, the first viral symptoms can appear within two weeks after infection. This observation is corroborated by [35], who noted CMD symptoms between 3 and 5 weeks after infection. Some genotypes that exhibited symptoms at 3 and 6 MAP appeared to recover from CMD, as evidenced by lower severity scores at 9 MAP. This rapid recovery is a promising indicator of resistance. Similarly, [32] found that moderately susceptible CMD varieties, though initially symptomatic, were able to recover as they matured. These findings align with the observed differences in recovery levels among genotypes throughout the season.

CMD-susceptible genotypes recorded the highest severity scores and yield losses. These results extend previous findings on yield losses caused by CMD, which have been shown to vary based on cultivar and environmental factors [36]. Yield losses associated with CMD have also been documented previously [36,38]. Reduced tuberization and lower yields have been linked to CMD-induced chlorosis, which decreases photosynthetic activity [39,40,41].

Recent studies by [37] showed that PCR techniques based on DNA sequences are valuable for identifying and analysing CMD resistance. This is due to the presence of highly conserved repetitive sequences in the genomes of cassava mosaic Begomovirus, their vectors, and host plants, which are useful for strain differentiation. Although morphological screening of the ten genotypes for CMD resistance was carried out using the 1-5 disease rating by [15,42], advanced resistance screening with PCR and ACMV strain-specific primers revealed that most of the cassava genotypes were susceptible to CMD (Figure 1). This result contrasts with the morphological screening, which identified only three genotypes as susceptible to CMD (Table 3). Similarly, [27] found cassava genotypes to be asymptomatic to CMD during field screening but positive for CMD in molecular screening. These findings suggest, as noted by [43], that field resistance does not necessarily indicate true resistance to viral infection.

The absence of EACMV strains across all ten genotypes suggests either true resistance of the genotypes to EACMV or the absence of the virus at the experimental site (Figure 1). This finding aligns with [44], who also did not detect EACMV strains in cassava genotypes studied at UCC and Asuansi. However, it contrasts with [45], who detected EACMV strains in cassava genotypes at UCC. Studies by Gibson and [41] indicate that EACMV occurs widely across West Africa, including Ghana. Given its systemic nature, EACMV-free genotypes could be multiplied and distributed to farmers across Ghana.

The total carotenoid (TC) range recorded for the genotypes (Table 4) was consistent with values reported by [46], who found TC levels ranging from 8.32–16.40 µg/g in yellow cassava varieties from Colombia. The higher TC recorded in this study compared to the check variety may be attributed to the mutagen, which enhanced TC in these genotypes. Such genotypes could contribute to reducing vitamin A deficiency in Ghana by providing a richer dietary source of vitamin A. High TC values recorded in this study are also consistent with findings by [47], who reported comparable results. However, the TC values reported in the current study were higher than those reported by [3] and [48], who observed TC levels of 3.6 µg/g and 5.0 µg/g, respectively, in IITA breeding populations.

The genotypes in this study had cyanogenic glycoside (HCN) levels ranging from 28.5–39.68 mg HCN/kg fresh weight (Table 4), which falls well below the safe threshold [49] ensuring their safety for consumption. The differences in cyanide concentration can likely be attributed to genetic variation among the genotypes [50].

Dry matter content (DMC) is crucial for cassava products like gari, where processing recovery depends on the DMC of the tubers. In this study, the average DMC was 28.12% (Table 5), consistent with ranges reported by [3,42]. Four yellow-root cassava genotypes (12B, 5B, 9A, and 11B) recorded high DMC levels, while the white-root check genotype (6F) outperformed all yellow-root genotypes. Genotypes with high DMC generally showed a positive correlation with TC, which contradicts reports of an inverse relationship between DMC and TC [7,51]. The positive correlation observed here could be attributed to mutation breeding, as it introduces genetic modifications that are difficult to achieve through conventional breeding methods. This finding highlights the potential for combining high DMC and TC in breeding programs for provitamin A cassava varieties.

High fresh root yields were recorded for most of the yellow-flesh cassava genotypes (Table 5). This aligns with studies by [47], who reported high yields in yellow cassava varieties, and [52], who also identified several yellow-flesh varieties with higher fresh root yields compared to checks.

5. Conclusion

The research revealed that four (4) genotypes had total carotenoid (TC) content exceeding that of the released yellow-flesh variety used as a check, while achieving yields that were not significantly different from the white-flesh check variety. These genotypes also exhibited higher dry matter content and resistance to CMD. Additionally, the cyanogenic potential (CP) for all genotypes ranged from 28.52 to 39.68 mg HCN/kg, which is within the safe threshold of 50 mg HCN/kg recommended by the FAO. Based on these findings, genotypes 12B, 5B, 9A, 1011A, and 11B have been selected for further evaluation (multi-locational trials) across three agro-ecological zones in Ghana.

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