Phenotypic diversity assessment in a panel of 149 cassava (*Manihot esculenta* Crantz) varieties: a pre-breeding study in Togo

ABSTRACT

Aims: Evaluating the genetic diversity within a plant species is crucial for identifying genes that control important biological functions, facilitating the rationale for developing new varieties. The genetic diversity in 149 cassava varieties was explored to assess its nature, pattern, and differentiation.

Study design: Augmented Block Design (CRD) with 144 cultivars as tested genotypes and five improved and released varieties as check genotypes.

Place and Duration of Study: The experiment was conducted at the Togolese Agricultural Research Institute (ITRA) Breeding Station of Davié in the forest-savanna transition zone characterized by a bimodal rainfall pattern, between May 2017 and June 2019.

Methodology: The 149 varieties were planted in an augmented block design, with five improved and released varieties as check genotypes. Data on sixteen (16) phenotypic traits, based on cassava trait ontology were collected.

Results: A high diversity coefficient of 0.78 was observed among cultivars using phenotypic traits. Multivariate analysis revealed all assessed traits as discriminative for cassava cultivars. Principal Component Analysis identified traits such as fresh root yield, plant vigour, number of roots per plant, CMD severity, aboveground biomass, leaf lobe dimensions, Cassava Bacterial Blight severity, plant height, height to first branching, petiole length, harvest index as major contributors to the variability of the germplasm. Cluster and canonical analyses delineated seven significant groups, characterized by traits like CMD and CBB resistance, vigorous growth, high canopy and fresh root yield, elevated harvest index, and high root dry matter content.

Conclusion: The findings provide a foundation for informed selection of parental lines in developing new high-yielding and CMD-resistant cassava varieties.

Keywords: Phenotypic diversity, Phenotypic trait, Multivariate analysis, Cassava varieties, Togo.

1. INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a crucial carbohydrate source in the tropical and subtropical regions of Africa, Latin America, and Asia. The crop plays a significant role in food security for millions of families, especially in developing areas where it is grown on a subsistence basis (Amelework & Bairu, 2022 ;Soro et al., 2024). Cassava constitutes a major source of raw material for the extraction of starch, finding wide applications across various industries including food, cosmetic, chemical, and pharmaceutical sectors (Ogbonna et al., 2021). The global cassava production in 2022 reached 360.16 million tons, cultivated across 32.04 million hectares, and achieved an average yield of 10.31 tons per hectare (FAO, 2022).

In Togo, cassava plantations covered 305,160 hectares in 2022, yielding 1.22 million tons of cassava roots. The average yield was 4.02 tons per hectare, which falls below the global productivity levels (FAO, 2022). Different varieties are currently grown and used across the country in Togo (Kombaté et al., 2017). Cassava is a diploid species with 36 chromosomes (2n=36) and exhibits monoecious characteristics. Its fertilization predominantly occurs through allogamous processes, rendering it highly heterozygous (Giles et al., 2018) resulting in high genetic diversity, despite its vegetative propagation (Giles et al., 2018). Cassava exhibits remarkable adaptability to various edaphoclimatic conditions, including low-fertility soils and drought (Oliveira-Silva et al., 2014). Given these traits, the cultivation of cassava is attractive to resource-constrained farmers. Small-scale farming is vital for preserving genetic resources used in breeding programs (Houngue et al., 2018).

In traditional cassava farming, it is typical for multiple cassava varieties to grow together in the same field or adjacent fields. This coexistence, enabled by cross-pollination between the different varieties, leads to an increase in the genetic diversity of cassava plants within fields (Agre et al., 2017). Furthermore, the regular sharing of planting materials among farmers leads to a high diversity of genotypes in the fields (Oliveira et al., 2014). As a result, accessions from different localities might share the exact name, while a single accession could be known by multiple names. Often, this leads to the occurrence of duplicate accessions gathered from various locations (Filipe Schmidt Schuh et al., 2021 ; Oliveira et al., 2014 ; Hurtado et al., 2001). Eliminating duplicates from collected germplasm is essential for effective breeding

initiatives. Moreover, a comprehensive breeding program relies on a deep understanding of the variability existing at the genetic level within the current population. Consequently, evaluating the genetic diversity among genotypes is critical to supplying breeding programs with distinct genetic resources. Characterizing and understanding the genetic variability in a population, as demonstrated by morphological and agronomic characteristics, is fundamental for directing conservation efforts (Ferguson et al., 2019) management, and to aid improvement programs to identify genotypes that are superior and well adapted to new production systems (Zago et al., 2021).

Studies on cassava population structure and genetic diversity have been conducted using morphological descriptors (Oliveira et al., 2015 ; Karim et al., 2020) and low (Elias et al., 2000 ; Elibariki et al., 2013) and high-throughput molecular markers (Rabbi et al., 2014; Adjebeng-danquah et al., 2020; Soro et al., 2023). Morphological descriptors, however, are susceptible to the interaction between environment and genotype. In contrast, molecular markers are easily detectable, stable, and are not under the influence of environmental factors (Asare et al., 2011; Rabbi et al., 2014).

Agromorphological characterization, compared to molecular characterization, is straightforward, cost-effective, and easy to use. Although plant morphology and agronomic performance are influenced by environmental factors and the measurements can be subjective, agromorphological evaluations are considered the primary indicators of agronomic value and are essential for the taxonomic classification of plants (Rabbi et al., 2015b; Soyode and Oyetundi, 2009).

This study aimed to assess the diversity and the structure of a collection of cassava cultivars by examining disease and agronomic traits. This evaluation will provide important insights into the overall variation and diversity in traits of interest, which is essential for creating crossing panels with diverse characteristics. Selecting and hybridizing parental lines from the identified heterotic groups will help maximize diversity and exploit population heterosis in a cassava breeding program.

2. MATERIALS AND METHODS

2.1. Plant Material

The germplasm evaluated was composed of a set of one hundred (100) local cultivars; thirty-five (35) improved varieties introduced from the IITA Cassava Breeding Unit, seven (7) varieties obtained from the gene bank of the High School of Agronomy (ESA) and two accessions obtained from Embrapa Mandioca Fruticultura (Cruz das Almas, BA, Brazil). Five improved varieties (high yielding and CMD resistant) namely Gbazekoute, TMS 96_0409, TMS 96_0166, Sika Bankye, and Ampong bankye, released by the National Cassava breeding Unit were used as checks (Table 1).

Table 1: List of the plant material used for the characterization

N°	Code	Variety name	Type	Origin	N°	Code	Variety name	Type	Origin
1	GHCA_C1	Sika Bankye	Improved	Ghana	**27**	IITA_22	TMS 92_0326	Improved	Togo
2	GHCA_C2	Ampong Bankye	Improved	Ghana	**28**	IITA_23	TMS 96_1708	Improved	Togo
3	IITA_C3	TMS 95_0166	Improved	IITA	**29**	IITA_24	TMS 98_2132	Improved	Togo
4	IITA_C4	TMS 96_0409	Improved	IITA	**30**	IITA_25	TMS 99_0554	Improved	Togo
5	TGCA_C5	Gbazekoute	Landrace	Togo	**31**	TGCA_1	Agbede	Landrace	Togo
6	IITA_1	TMS 01_0006	Improved	Togo	**32**	TGCA_2	Agou	Landrace	Togo
7	IITA_2	TMS 00_0354	Improved	Togo	**33**	TGCA_3	Aguidagba	Landrace	Togo
8	IITA_3	TMS 00_0364	Improved	Togo	**34**	TGCA_4	Akaleyo	Landrace	Togo
9	IITA_4	TMS 01_0034	Improved	Togo	**35**	TGCA_5	Akebou	Landrace	Togo
10	IITA_5	TMS 01_0046	Improved	Togo	**36**	TGCA_6	Akoss	Landrace	Togo
11	IITA_6	TMS 01_0093	Improved	Togo	**37**	TGCA_7	Ankra atihe	Landrace	Togo
12	IITA_7	TMS 01_0098	Improved	Togo	**38**	TGCA_8	Akpadjin Feto	Landrace	Togo
13	IITA_8	TMS 01_0131	Improved	Togo	**39**	TGCA_9	Alagno	Landrace	Togo
14	IITA_9	TMS 01_0379	Improved	Togo	**40**	TGCA_10	Ankra 3	Landrace	Togo
15	IITA_10	TMS 01_1085	Improved	Togo	**41**	TGCA_11	Ankra Atiyibo	Landrace	Togo
16	IITA_11	TMS 01_1086	Improved	Togo	**42**	TGCA_12	Assiatoe	Landrace	Togo
17	IITA_12	TMS 01_1097	Improved	Togo	**43**	TGCA_13	Atidjin1	Landrace	Togo
18	IITA_13	TMS 01_1206	Improved	Togo	**44**	TGCA_14	Atidjin 2	Landrace	Togo
19	IITA_14	TMS 01_1224	Improved	Togo	**45**	TGCA_15	Atidjin Poli	Landrace	Togo
20	IITA_15	TMS 01_1368	Improved	Togo	**46**	TGCA_16	Atidokpo	Landrace	Togo
21	IITA_16	TMS 01_1368(2)	Improved	Togo	**47**	TGCA_17	Atihe1	Landrace	Togo
22	IITA_17	TMS 01_1371	Improved	Togo	**48**	TGCA_18	Atiyibo 1	Landrace	Togo
23	IITA_18	TMS 01_1610	Improved	Togo	**49**	TGCA_19	Atiyobo2	Landrace	Togo
24	IITA_19	TMS 01_1662	Improved	Togo	**50**	TGCA_20	Awou	Landrace	Togo
25	IITA_20	TMS 01_1797	Improved	Togo	**51**	TGCA_21	Awouye	Landrace	Togo

Table 1. Continued

N°	Variety code	Variety name	Type	Origin	N°	Variety code	Variety name	Type	Origin
53	TGCA_23	Badjogou	Landrace	Togo	**79**	TGCA_48	Kanbom Bantchi	Landrace	Togo
54	TGCA_24	Bazoka	Landrace	Togo	**80**	TGCA_49	Kanigbeli 1	Landrace	Togo
55	TGCA_25	Bob	Landrace	Togo	**81**	TGCA_50	Kanigbeli 2	Landrace	Togo
56	TGCA_26	Bob Assou	Landrace	Togo	**82**	TGCA_51	Kataoli	Landrace	Togo
57	TGCA_27	Bob Yegue	Landrace	Togo	**83**	TGCA_52	Katawole	Landrace	Togo
58	BRS_1	BRS Caipira	Landrace	Brazil	**84**	TGCA_53	Kidirondi	Landrace	Togo
59	TGCA_28	Degaule	Landrace	Togo	**85**	TGCA_54	Kisseimou Koutowou	Landrace	Togo
60	TGCA_29	Djakoagni	Landrace	Togo	**86**	TGCA_55	Kola	Landrace	Togo
61	TGCA_30	Djeble	Landrace	Togo	**87**	TGCA_56	Kolaoung	Landrace	Togo
62	TGCA_31	Djolaoba	Landrace	Togo	**88**	TGCA_57	Kolmon kamkam	Landrace	Togo
63	TGCA_32	Djoliba	Landrace	Togo	**89**	TGCA_58	Kossikouma	Landrace	Togo
64	TGCA_33	Donmoyibo	Landrace	Togo	**90**	TGCA_59	Koutowou 2	Landrace	Togo
65	TGCA_34	Fetonegbodji	Landrace	Togo	**91**	TGCA_60	Kperoung Felgou	Landrace	Togo
66	TGCA_35	Flawavi	Landrace	Togo	**92**	TGCA_61	Kperoung Mamougue	Landrace	Togo
67	TGCA_36	Gabonvi-ESA	Landrace	Togo	**93**	TGCA_62	Kpla	Landrace	Togo
68	TGCA_37	Gbadovi	Landrace	Togo	**94**	TGCA_63	Loki	Landrace	Togo
69	TGCA_38	Gbaze- ESA	Landrace	Togo	**95**	TGCA_64	M'beou	Landrace	Togo
70	TGCA_39	Vivigbaze	Landrace	Togo	**96**	TGCA_65	MM96/5280	Improved	Togo
71	TGCA_40	Ghana spana	Landrace	Togo	**97**	TGCA_66	MM96/JW2	Improved	Togo
72	TGCA_41	Gnidou	Landrace	Togo	**98**	TGCA_67	Nigeria Fleur	Landrace	Togo
73	TGCA_42	Hogninvo 1	Landrace	Togo	**99**	TGCA_68	Nigeria Kikpaou	Landrace	Togo
74	TGCA_43	Hogninvo 2	Landrace	Togo	**100**	TGCA_69	Nigeria Kissaimon	Landrace	Togo
75	TGCA_44	Inconnu	Landrace	Togo	**101**	TGCA_70	N'tossou	Landrace	Togo
76	TGCA_45	IRAT- Davie	Landrace	Togo	**102**	TGCA_71	Ankra atihe	Landrace	Togo
77	TGCA_46	Jhonson	Landrace	Togo	**103**	TGCA_72	Okpoli	Landrace	Togo
78	TGCA_47	Kalba	Landrace	Togo	**104**	TGCA_73	Pela	Landrace	Togo

Table 1. Continued

N°	Variety code	Variety name	Type	Origin	N°	Variety code	Variety name	Type	Origin
105	TGCA_74	Peloumkoute	Landrace	Togo	**131**	IITA_31	D00_126	Improved	IITA
106	TGCA_75	Penivi	Landrace	Togo	**132**	IITA_32	D00_54	Improved	IITA
107	TGCA_76	Sabe	Landrace	Togo	**133**	IITA_33	D00_166	Improved	IITA
108	TGCA_77	Sankara	Landrace	Togo	**134**	TGCA_94	Toma 9	Landrace	Togo
109	TGCA_78	Sassakawa	Landrace	Togo	**135**	TGCA_95	CVTM4	Landrace	Togo
110	TGCA_79	Sorad	Landrace	Togo	**136**	TGCA_96	Toma 162	Landrace	Togo
111	TGCA_80	Sawa	Landrace	Togo	**137**	TGCA_97	Unknown 02	Landrace	Togo
112	TGCA_81	Spana Assou	Landrace	Togo	**138**	IITA_34	TMS 96_1317	Improved	Togo
113	TGCA_82	Spana Yegue	Landrace	Togo	**139**	IITA_35	TMS 96_0304	Improved	Togo
114	BRS_2	BRS Tapioqueira	Landrace	Brazil	**140**	IITA_36	TMS 96_0102	Improved	Togo
115	TGCA_83	Tassiodo	Landrace	Togo	**141**	IITA _37	TMS 96_0869	Improved	Togo
116	TGCA_84	Tchigouevi	Landrace	Togo	**142**	IITA _38	TMS 96_1642	Improved	Togo
117	TGCA_85	Tetetidadjin	Landrace	Togo	**143**	IITA _39	TMS 96_0590	Improved	Togo
118	TGCA_86	TME 419	Improved	Togo	**144**	IITA _40	TMS 96_539	Improved	Togo
119	TGCA_87	TM1	Improved	Togo	**145**	TGCA_98	TMS 96_1565	Improved	Togo
120	TGCA_88	TME1	Improved	Togo	**146**	IITA _42	TMS 96_0603	Improved	Togo
121	TGCA_89	TME 696	Improved	Togo	**147**	IITA_43	TMS 30572	Improved	IITA
122	TGCA_90	Touwevi	Landrace	Togo	**148**	TGCA_99	KPEM_10_03	Improved	Togo
123	TGCA_91	Tuaka Atsu	Landrace	Togo	**149**	IITA_44	TMS 4(2) 1425	Improved	IITA
124	TGCA_92	Tuaka komi Mami	Landrace	Togo	**129**	IITA_29	D00_208	Improved	IITA
125	TGCA_93	Yabaka	Landrace	Togo	**130**	IITA_30	D00_14	Improved	IITA
126	IITA_26	D00_8300	Improved	IITA					
127	IITA_27	M94_0583	Improved	IITA					
128	IITA_28	D00_137	Improved	IITA					

2.2. Experimental Site

The experiment was run in a CMD hot spot environment at the Togolese Agricultural Research Institute (ITRA) Research station of Davié (latitude: 6° 23' 5" North; longitude: 1° 12' 18" East; altitude: 76 meters) located in the forest-savanna characterized by a bimodal rainfall pattern. A total rainfall of 1231.5 mm was recorded for 80 rainy days from June to November. July with 207.8 mm for 14 rainy days was the wet month, whereas in November only 8.7 mm was recorded for 4 days. The annual average temperature was 28.5°C. The vegetation is characterized by herbaceous vegetation (Banito et al., 2010). The soil of the experimental site is called "Terres de Barre" (sandy-clay soil) with 70% sand, 3.8% silt, 8.1% clay, acid pH (H_2O 1:1) 5.5, 1.05% organic matter, 0.41% total nitrogen (N), 10 ppm available phosphorus (P), and cation exchange capacity (CEC) of 2.89 milli-equivalents (meq)/100g of soil in the top 15 cm samples (Sogbedji et al., 2015).

2.3. Experimental Design, Field Layout and Maintenance

An augmented block design with 144 cultivars as tested varieties and 5 checks varieties (CRI Sika bankye, CRI Ampong bankye, TMS 96_0409, TMS 01_0166, and Gbazekoute), distributed in 12 blocks was used. The experimental unit is made up of four rows, each 4 meters long, containing 16 plants of a single cultivar. The two outermost rows and the end plants in the central rows were designated as borders. Soil preparation involved using a tractor rotary disk plow, followed by furrowing. Each block was delineated after plowing the experimental site, with a distance of 1.5 m separating adjacent blocks and plots. Cassava stakes, each 15-20 cm long and sourced from healthy, mature plants, were manually planted at a depth of around 10 cm. The planting followed a spacing of 1 meter between furrows and 1 meter between plants. Cultivar Main 27, highly susceptible to CMD, was planted 1.5 months in advance as spreader rows around the whole experiment and in between two adjacent blocks to ensure and enhance transmission of the disease by whiteflies (*Bemisia tabaci*) (Soyode et al., 2008; Oyetunji et al., 2009; Avijala et al., 2015). The experiment was conducted under rainfed conditions without the application of pesticides and fertilizers. Weed control was maintained through regular hand weeding to ensure a weed-free environment. The trial was harvested 12 months after planting (MAP).

2.4. Phenotypic Data Collection

Fourteen traits were recorded from the inner eight (8) plants within each plot according to the cassava crop ontology (Guevara et al., 2010). The variables, the period of collection, and the assessment method are summarized in Table 2. Data on the CMD were collected at 1, 3, and 6 MAP using a symptom severity scale of 1-5 (Adriko et al.,2011; Peter et al., 2016). CBB data were also collected at 3, 6, and 9 MAP (Banito et al., 2010). The incidence of disease was measured by recording the proportion of diseased plants in each plot. At harvest, the inner 8 plants in each plot were uprooted. Agronomic data, including fresh root yield, storage roots number per plant, above-ground biomass, storage root weight, and harvest index, were collected (Guevara et al., 2010). The specific gravity method was used to estimate the root dry matter content (Ceballos et al., 2016).

Table 2. Traits evaluated in the characterization of 149 cassava varieties

N°	Trait	Code	Assessment date	Method of assessment
1	Plant vigour	Vigour	1, 3 and 6 MAP	Guevara et al. (2010)
2	Width of leaf lobe (cm)	Wid_LeaLo	6 MAP	
3	Length of leaf lobe (cm)	Len_LeaLo	6 MAP	
4	Petiole length (cm)	Pet_Len	6 MAP	
5	Ratio length/width lobe (cm)	RaLen_WidLea	6 MAP	
6	Height to first branching (cm)	HtFi_Bra	12 MAP	
7	Plant height (cm)	PltHt	12 MAP	
8	Numbers of roots per plant	RtPlt	12 MAP	
9	Above ground biomasse (kg)	AbG_Biom	12 MAP	
10	Fresh Root Yield ($t.ha^{-1}$)	FRY	12 MAP	
11	Mean Root weight (kg)	MRW	12 MAP	
12	Harvest index	HI	12 MAP	Guevara et al. (2010)
13	Dry matter content (%)	DMC	12 MAP	
14	Fresh Root yield per plant (kg)	FRY_Plt	12 MAP	

MAP = months after planting

2.5. Data Analysis

Data collected were transformed to achieve equalization of variances and normalization of observations using the Approximate Covariance Estimation for Clustering procedure (*proc aceclus*) in SAS version 9.4. The square root transformation was used for counts data while the angular one was used for percentages data. The mixed model procedure (*proc mixed*) was employed to analyze the unbalanced dataset, enabling the calculation of means for genotypes adjusted to a common environmental effect (Federer et al., 1975; Oliveira et al., 2014; Silva et al., 2016). Analyse of variance (ANOVA) was computed based on the plot mean value following a single trial with test varieties (g) and t check varieties (c) statistical model to test the significance of entries (cultivars and checks taken together), the equality of check varieties, and varieties with check effects (Federer et al., 1975; Sraphet et al., 2011). Correlation analysis among traits was carried out using Pearson correlation analysis. The relative contribution of each trait to the diversity of the germplasm was determined through Principal Components Analysis (PCA), which was made based on the correlation matrix. Cluster analysis which constitutes a simple and less demanding model for grouping cultivars hierarchically into homogenous groups was made using Ward's method (Rabbi et al., 2015b). Based on the cubic clustering criterion (CCC), Pseudo F, and the Pseudo t^2 methods, the optimal number of clusters was determined. The indication of the optimal number of clusters is an innovative aspect of the Wards method compared with the Unweighted Pair-Group Mean Average method (Pereira et al., 2012). Canonical analysis was run in SAS 9.4 to identify traits that were relevant in grouping the clusters.

3. RESULTS

3.1. Variability and Correlation of Disease and Agronomic Traits

Significant variability was observed among treatments (tested varieties and checks taken together, among tested varieties, and checks vs tested varieties) for all the traits evaluated ($p = 0.05$). However, the coefficient of variation was moderate for traits such as leaf lobe length, dry matter content, and, plant height. The remaining 13 traits exhibited a high (greater than 20%) coefficient of variation (Table 3).

Pearson correlation analysis of disease and agronomic traits revealed significant correlations among some traits (Figure 1). CMD severity correlated negatively with plant vigour ($r = -0.78$, $p = 0.01$), number of roots per plant ($r = -0.52$, $p = 0.01$), fresh root yield ($r = -0.68$, $p = 0.01$), fresh root yield per plant ($r = -0.46$, $p = 0.01$), mean root weight ($r = -0.37$, $p = 0.05$), above ground biomass ($r = -0.64$, $p = 0.01$), harvest index ($r = -0.53$, $p = 0.01$); and positively with CMD incidence ($r = 0.90$, $p = 0.01$) and CBB severity ($r = 0.46$, $p = 0.05$) (Figure 1). Fresh root yield correlated positively with plant vigour ($r = 0.56$, $p = 0.01$), number of roots per plant ($r = 0.69$, $p = 0.01$), fresh root yield per plant ($r = 0.86$, $p = 0.01$), mean root weight ($r = 0.69$, $p = 0.01$) and the harvest index ($r = 0.35$, $p = 0.05$); and negatively with canopy yield ($r = -0.52$, $p = 0.01$) (Figure 1). Mean root weight was positively correlated with plant vigour ($r = 0.34$, $p = 0.05$), fresh root yield ($r = 0.69$, $p = 0.01$), and fresh root yield per plant ($r = 0.80$, $p = 0.01$). Significant negative correlation was also found between mean root weight and canopy yield ($r = -0.52$, $p = 0.01$). Harvest index correlated negatively with plant height ($r = -0.36$, $p = 0.05$), canopy yield ($r = -0.44$, $p = 0.01$), the width of leaf lobe ($r = -0.33$, $p = 0.05$), CMD severity ($r = -0.53$, $p = 0.05$); and positively with the number of roots per plant ($r = 0.30$, $p = 0.05$), fresh root yield ($r = 0.35$, $p = 0.05$), and the dry matter content ($r = 0.46$, $p = 0.05$) in roots (Figure 1). Plant height was correlated positively with vigour ($r = 0.36$, $p = 0.05$), above ground biomass yield ($r = 0.49$, $p = 0.01$), height at first branching ($r = 0.41$, $p = 0.01$), petiole length ($r = 0.38$, $p = 0.05$); but negatively correlated with harvest index ($r = -0.36$, $p = 0.05$). Roots dry matter content was correlated positively with harvest index ($r = 0.46$), CMD severity ($r = 0.46$), and CMD incidence ($r = 0.41$) at $p = 0.05$. However, the correlation of roots dry matter content with fresh root yield was not significant (Figure 1).

The first six PCAs with eigenvalues greater than one and explaining about 75.43% of the total variability were retained based on the Kaiser criterion (Table 4.). The first principal component (PC1) had an eigenvalue of 4.88, explaining 27.14% of the variability within the germplasm. Seven traits made significant contributions to PC1, including fresh root yield, number of roots per plant, plant vigor, root weight, fresh root yield per plant, CMD severity, and incidence. PC2 had an eigenvalue of 3.03, accounting for 16.83% of the variability, with the length of the leaf lobe, plant height, petiole length, harvest index, and the aboveground biomass, as the primary contributing traits. PC3 with an eigenvalue of 1.94 was mainly defined by CBB severity. PC4 with an eigenvalue of 1.39 was defined by the width of the leaf lobe. PC5 with an eigenvalue of 1.22 was correlated with height to first branching while the roots dry matter content was defined as the most important trait for PC6.

Table 3. Mean square, range, and coefficient of variation of disease and agronomic traits evaluated on 149 cassava genotypes from Togo

Traits	Mean Square				Range			CV (%)
	Entries (df = 148)	Among Accessions (df = 143)	Access vs Checks (df = 1)	Error (df=44)	Min	Mean	Max	
CMD_Sev	2.07**	1.93**	34.07**	0.02	1.00	2.37	5.00	56.90
CBB_Sev	1.17**	1.09**	6.73*	0.15	1.00	2.64	4.75	36.30
Vigour	0.83**	0.78*	13.53	0.02	1.00	3.91	5.00	21.80
Len_LeaLo	6.61**	6.16**	80.71**	0.45	10.50	15.25	22.33	15.70
Wid_LeaLo	5.40**	4.93**	2.44**	1.67	1.93	4.60	14.67	29.20
RaLen_WidLea	0.60**	0.56**	1.33**	1.04	2.23	3.62	22.05	47.00
Pet_Len	38.24**	35.59**	461.07**	3.00	2.17	21.36	32.25	26.20
PltHt	2124.50*	2124.50*	7701.76*	644.53	1.49	2.36	3.47	18.20
HtFi_Bran	2353.36**	2203.34**	18699.89*	174.65	0.00	0.88	2.20	50.80
AbG_biom	400.35**	398.68**	1437.53**	99.13	5.00	29.61	87.00	56.60
FRY	406.87**	391.18**	2396.79**	112.57	3.36	37.75	75.00	43.60
RtPlt	8.084**	7.66**	121.68**	2.29	1.60	7.08	13.40	30.00
DMC	16.48**	15.67**	245.75**	4.39	20.36	28.67	39.95	12.90
HI	0.0132**	0.0127**	0.02	0.004	0.21	0.57	0.80	19.10
MRW	43.71*	42.83*	8.69	26.38	0.20	0.54	1.33	35.70
FRY_Plt	5495.82*	683.13*	63776.46**	4635.54	0.34	4.93	9.63	51.40

****, *** = significant at 5% and 1% probability levels, respectively; df = Degree of freedom;CV = coefficient of variation CMD_Sev = Cassava Mosaic Disease severity score, CBB_Sev = Cassava Bacterial Blight severity score, Len_LeaLo = Length of leaf lobe (cm), Wid_LeaLo = Width of leaf lobe (cm), RaLen_WidLea = Ratio of lobe length to lobe width of central leaf lobe, Pet_Len = Petiole length (cm), PltHt = Plant height (m), HtFi_Bran = Height to first branching (cm), AbG_biom = Aboveground biomasse (t.ha^{-1}), FRY = Fresh root yield (t.ha^{-1}), RtPlt = Number of roots per plant, DMC = Dry matter content percentage, HI = Harvest index, MRW = Mean root weigth (kg), FRY_Plt = Fresh root yield per plant (kg).

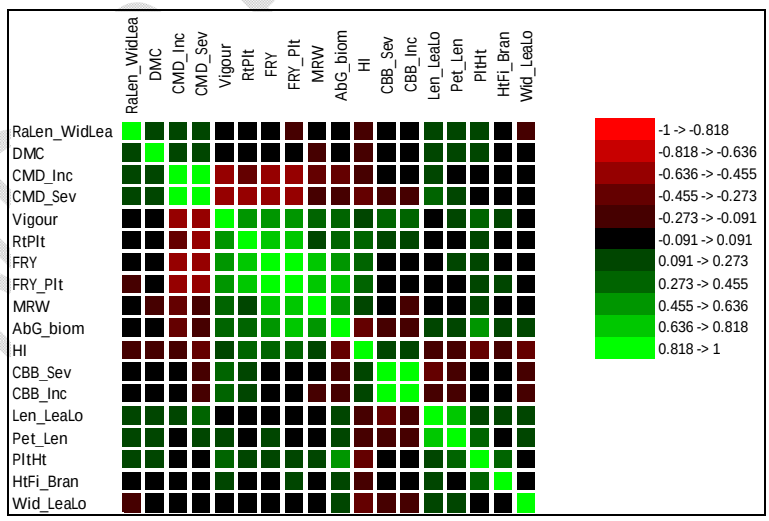

Figure 1: Correlation matrix displaying phenotypic correlations between disease and agronomic traits evaluated on 149 cassava cultivars Traits shown in the matrix are: CMD_Inc = Cassava Mosaic Disease incidence, CMD_Sev= Cassava Mosaic Disease severity score, CBB_Inc= Cassava Bacterial Blight Incidence, CBB_Sev= Cassava Bacterial Blight Severity score, Len_LeaLo= Length of leaf lobe, Wid_LeaLo= Width of leaf lobe, RaLen_WidLea= Ratio of lobe length to lobe width of central leaf lobe, Pet_Len = Petiole length, HtFi_Bran= Height to first branching, PltHt= Plant height, AbG_biom= Above ground biomasse, FRY= Fresh root yield, RtPlt= Number of roots per plant, DMC= Dry matter content percentage, HI= Harvest index, MRW= Mean root weigth, FRY_Plt= Fresh root yield per plant. Colour of the boxes represents the correlation value. The scale is indicated in the bar at the right of the matrix. Black boxes indicate non-significant correlations (p=0.05).

Table 4. PCA of 16 disease and agronomic traits and their contributions to the total variability among 149 cassava cultivars in Togo

	PC1	PC2	PC3	PC4	PC5	PC6
Eigenvalue	4.885	3.03	1.947	1.395	1.224	1.097
Variance explained (%)	**27.14**	**16.831**	**10.814**	**7.749**	**6.09**	**6.096**
Cumulative (%)	27.14	43.971	54.785	62.534	69.336	75.432
CMD_Sev	**-0.733**	0.311	0.089	0.197	-0.429	0.231
CMD_Inc	**-0.724**	0.195	0.19	0.177	-0.436	0.214
CBB_Sev	0.156	-0.516	**0.722**	-0.114	-0.227	-0.092
CBB_Inc	0.095	-0.471	**0.789**	-0.08	-0.187	-0.073
Vigour	**0.744**	0.021	0.389	-0.019	0.234	-0.036
Len_LeaLo (cm)	-0.147	**0.731**	0.128	0.377	0.117	-0.347
Wid_LeaLo (cm)	0.044	0.494	-0.029	**-0.529**	-0.134	-0.286
Pet_Len (cm)	0.021	**0.696**	0.229	0.324	0.112	-0.41
PltHt (cm)	0.241	**0.514**	0.471	-0.039	0.051	0.148
AbG_biom ($t.ha^{-1}$)	0.57	**0.581**	0.022	-0.450	-0.141	0.166
FRY ($t.ha^{-1}$)	**0.913**	0.138	-0.106	0.183	-0.237	0.153
RtPlt	**0.738**	-0.016	0.15	0.138	0.121	-0.076
MRW (Kg)	**0.693**	0.168	-0.24	0.172	-0.377	0.183
FRY_Plt (Kg)	**0.914**	0.127	-0.099	0.18	-0.236	0.151
DMC (%)	-0.148	0.236	0.334	0.276	0.1	**0.35**
HI	0.31	**-0.615**	-0.192	0.56	-0.043	-0.2

Traits that contributed most to the phenotypic variation of a particular component are in bold and underlined. CMD_Inc = Cassava Mosaic Disease incidence, CMD_Sev = Cassava Mosaic Disease severity score, CBB_Inc = Cassava Bacterial Blight incidence, CBB_Sev = Cassava Bacterial Blight severity score Len_LeaLo = Length of leaf lobe, Wid_LeaLo = Width of leaf lobe, Pet_Len = Petiole length, PltHt = Plant height, AbG_biom = Above ground biomass, FRY = Fresh root yield, FRY_Plt = Fresh root yield per plant, MRW = Mean root weight, RtPlt = Number of roots per plant, HI = Harvest index, DMC = Dry matter content percentage.

3.2. Structure of the phenotypic diversity based on disease and agronomic traits

The structure of the phenotypic diversity was visualized by plotting the PC scores with respect to PC1 vs PC2 axes (Figure 2) and PC1 vs PC3 (Figure 3). Quadrant 2 grouped the tallest cultivars with high canopy and fresh root yield, low harvest index, and tolerance to CMD. Conversely, quadrant 3 is mainly made of shortest varieties exhibiting high yield, low canopy yield, and good harvest index with a superior level of resistance to CMD. Quadrant 1 is composed of low-yielding varieties with high plant height, and highly susceptible to CMD. Varieties depicted in quadrant 4 exhibited low fresh root yield, canopy yield and plant height, good harvest index; and were susceptible to CMD (Figure 2).

With regards to Figure 3, four phenotypic groups were discerned. Group 1 (G1) cultivars are highly susceptible to CMD and low yielding. Conversely, Group 2 (G2) is made of CMD resistant cultivars with a slightly higher yield and exhibited high CBB incidence and severity. Group 3 (G3) is mainly composed of high-yielding, CMD, and CBB resistant varieties. Group 4 (G4) is composed of highly susceptible CMD varieties with a slightly lower yield and exhibited low CBB incidence and severity.

Cluster analysis revealed that the optimal number of clusters required was ten, with a maximum R-square value of 0.736; based on the cubic clustering, Pseudo-F, and the Pseudo-t^2 criteria (Table 5). Clusters 4, 8, and 10 contained only one accession each and therefore were considered as outliers. Cluster 1 was constituted of 75 varieties, cluster 2 of 14 varieties, cluster 6 had 37 varieties, cluster 7 contained 8 varieties, cluster 3 was made of 6 varieties, cluster 9 of 4 varieties, whereas cluster 5 was composed of 2 varieties (Figure 4). The maximum likelihood cultivar assignment ranged from 0.69 to 1 (Table 6), denoting a strong phenotypic structure of the germplasm. A comparison of clusters based on the phenotypic profile plots of each cluster (Figure 5) revealed that they seemed to be similar in plant vigour, leaves characteristics (petiole length, leaf lobe length, width of leaf lobe), height to first branching, plant height, number of roots per plant, harvest index, and roots dry matter content. However, the clusters differed in terms of fresh root yield, above-ground biomass, CMD, and CBB resistance (Figure 5). Cluster 9 is composed of high-yielding cultivars with a low CMD incidence, high CBB incidence, and moderate

canopy yield. Unlike cluster 9, cluster 6 and 7 cultivars exhibited a high CMD incidence, low canopy, and fresh root yield; but differ in CBB resistance. Cluster 1 is made of varieties with a high CBB incidence, moderate CMD incidence, and fresh root yield. Cluster 2 is constituted of varieties that exhibited a low CMD and CBB incidence, moderate canopy, and fresh root yield. Cluster 3 varieties had moderate fresh root and canopy yield, low CMD incidence, and were highly susceptible to CBB (Figure 5).

The cophenetic distance matrix displaying the inter-cluster genetic distance values is summarized in Table 7. The highest genetic distance was recorded between clusters 6 and 10, followed by clusters 7 and 10, clusters 4 and 7, clusters 4 and 6, clusters 7 and 9, and clusters 1 and 10; indicating wide genetic divergence among the clusters. The shortest distance was observed between Cluster 2 and Cluster 3, followed by Clusters 1 and 3, and Clusters 3 and 5.

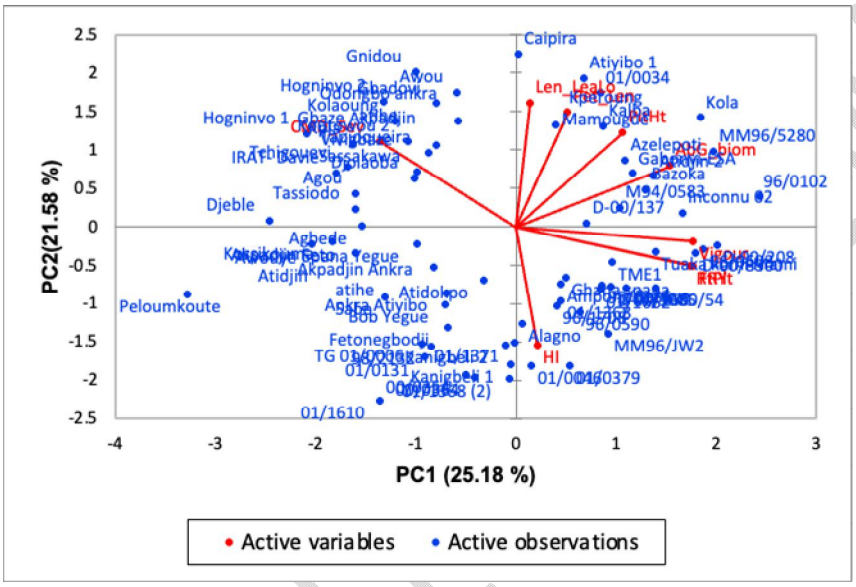

Figure 2. PCA scatter plot displaying the phenotypic diversity of 149 cassava accessions from Togo along the PC1 and PC2 axes. CMD_Sev = Cassava Mosaic Disease severity score, Len_LeaLo = Length of leaf lobe (cm), Pet_Len = Petiole length (cm), PltHt = Plant height (cm), AbG_biom = Above ground biomass (t.ha-1), FRY = Fresh root yield (t.ha-1), RtPlt = Number of roots per plant, DMC = Dry matter content percentage, HI = Harvest index.

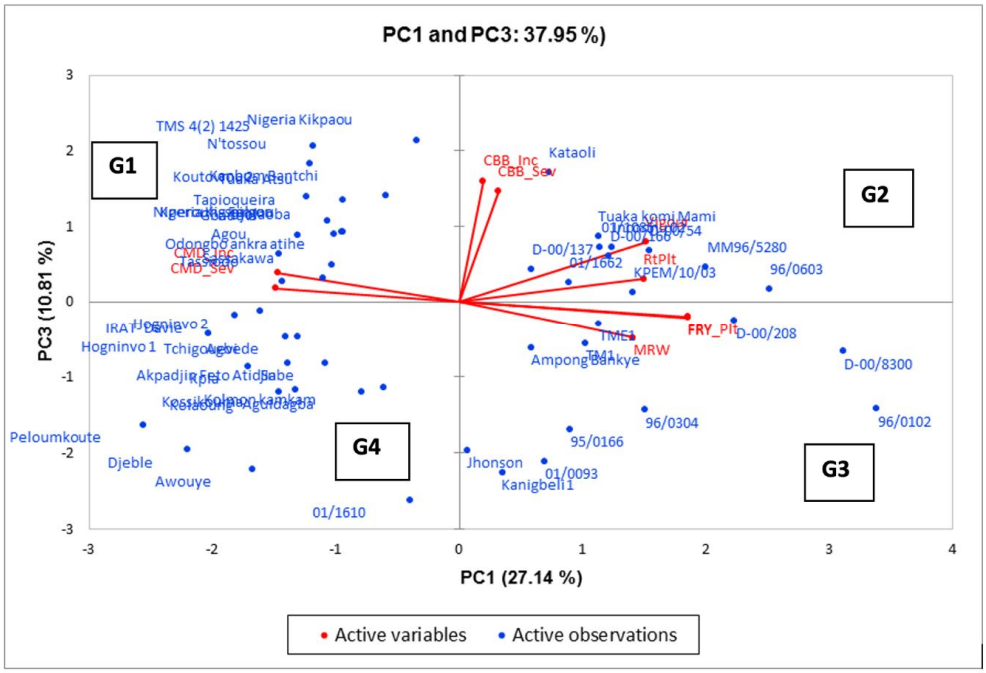

Figure 3. PCA scatter plot displaying the phenotypic diversity of 149 cassava accessions from Togo along the PC1 and PC3 axes. CMD_Inc = Cassava Mosaic Disease incidence, CMD_Sev = Cassava Mosaic Disease severity score, CBB_Inc = Cassava Bacterial Blight incidence, CBB_Sev = Cassava Bacterial Blight severity score, FRY = Fresh root yield ($t.ha^{-1}$), FRY_Plt = Fresh root yield per plant (Kg), MRW = Mean root weight (kg), RtPlt = Number of roots per plant

Table 5. Number of optimal clusters formed based on disease and agronomic traits

Numbers of clusters	Semipartial R-square	R-square	Approximate expected R-square	Cubic clustering criterion	Pseudo F statistic	Pseudo t-squared
12	0.006	0.792	0.803	-0.950	25.371	4.623
11	0.037	0.773	0.771	-2.800	24.846	16.212
10*	**0.222**	**0.736**	**0.645**	**-14.300***	**12.014***	**47.804***
9	0.026	0.729	0.743	-12.200	24.033	9.473
8	0.020	0.709	0.724	-11.950	26.851	1.682
7	0.026	0.683	0.725	-2.340	27.705	7.043
6	0.028	0.665	0.655	-10.250	29.400	7.821
5	0.061	0.593	0.676	-9.600	15.640	8.365
4	0.021	0.348	0.600	-8.400	17.100	10.123
3	0.046	0.302	0.533	-7.500	21.020	6.714
2	0.030	0.272	0.397	-4.000	36.630	5.621
1	0.271	0.000	0.000	0.000	.	36.642

***Values in bold correspond to the optimal number of clusters which occurs at the start of peak in the table.**

Table 6. Clusters formed using the Ward-MLM method based on significant disease and agronomic traits evaluated in 149 cassava varieties

Cluster	No. of varieties	Range of assignment probability	Varieties
C1	75	0.69-1	Sika Bankye Ampong Bankye, TMS 96_0409, Gbazékouté, TMS 01_0006, TMS 00_0364, TMS 01_0034, TMS 01_0046, TMS 01_0131, TMS 01_0379, TMS 01_1085, TMS 01_1086, TMS 01_1097, TMS 01_1368, TMS 01_1368 (2), TMS 01_1371, TMS 01_1662, TMS 01_1807, TMS 96_1708, TMS 98_2132, Akaleyo, Akebou, Akoss, Akpadjin Ankra atihe, Alagno, Ankra 3, Ankra Atiyibo, Atidjin1, Atidjin Poli, Atidokpo, Atihe1, Atiyobo2, Azelepoti, Bob Yegue, Degaule, Djakoagni, Donmoyibo, Fetonegbodji, Gabonvi-ESA, Gbaze- ESA, Gbaze Akpadjin Vivigbaze, Ghana spana, Kalba, Kanigbeli 2, Kataoli, Kidirondi, MM96/JW2, Nigeria Kikpaou, Okpoli, Pela, Penivi, Sorad, Spana Assou, TME1, TME 696, Tuaka komi Mami, Yabaka, M94_0583, **D-00_137**, D-00_14, D-00_126, D-00_54, D-00_166, Toma 9, CVTM4, Toma 162, Inconnu 02, TMS 96_1317, TMS 96_0869, TMS 96_1642, TMS 96_1642, TMS 96_0590, TMS 96_539, TMS 96_1565, TMS 30572, KPEM_10_03
C2	14	0.74-1	**TMS 95_0166**, TMS 01_0093, TMS 01_1610, TMS 92_0326, Atidjin 2, Atiyibo 1, Bob Assou, Flawavi, Inconnu, Kanigbeli 1, M'beou, **Tetetidadjin**, TME 419, Touwevi
C3	6	0.65-1	TMS 00_0354, TMS 01_0098, TMS 01_1224, Bob, **TM1**, TMS 96_0304
C4	1	1	**TMS 96_1206**
C5	2	0.81-1	TMS 01_1797, **TMS 99_0554**
C6	37	0.83-1	Agbede, Agou, Aguidagba, Akpadjin Feto Atidjin, Assiatoe, Awouye, Badjogou, BRS Caipira, Djolaoba, Djoliba, Gbadovi, Hogninvo 1, Hogninvo 2, IRAT- Davie, Kanbom Bantchi, Katawole, Kisseimou Koutpwou, Kolmon kamkam, Kossikouma, Kperoung Felgou, Kperoung Mamougue, Kpla, Nigeria Kissaimon, N'tossou, Odongbo ankra atihe, Peloumkoute, sabe, Sassakawa, Sawa, Spana Yegue, **BRS Tapioqueira**, Tassiodo, Tchigouevi, Tuaka Atsu, TMS 4(2) 1425
C7	8	0.95-1	**Awou**, Bazoka, Djeble, Gnidou, Jhonson, Kolaoung, Loki, Nigeria fleur
C8	1	0.85-1	**Kola**
C9	4	0.96-1	MM96_5280, D-00_208, D-00_8300, **TMS 96_0603**
C10	1	1	**TMS 96_0102**

[1]**Centroids of each cluster are in bold**

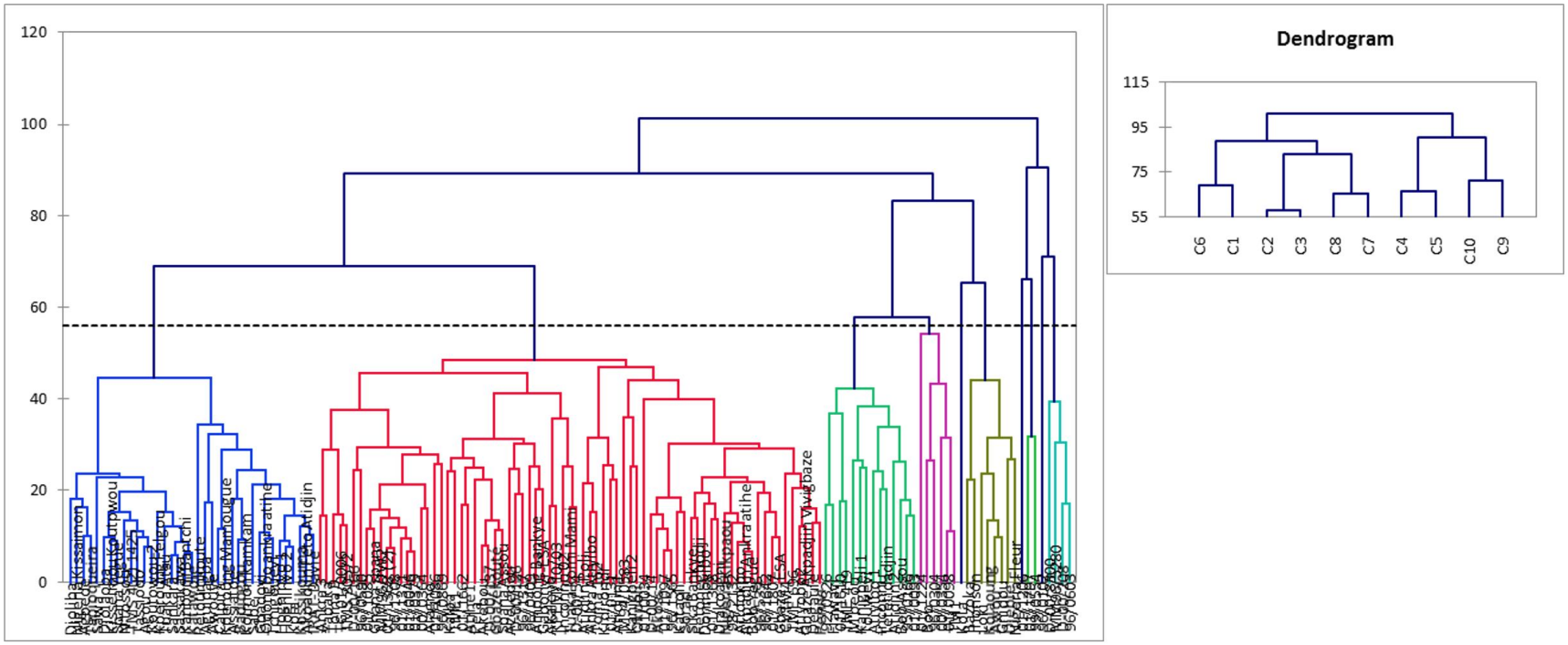

Figure 4. Dendrogram of 149 cassava varieties from Togo revealed by the Wards method based on significant disease and agronomic traits. The legend of the figure is shown at the right on top. From left to right of the dendrogram the clusters C6, C1, C2, C3, C8, C7, C4, C5, C10 and C9 are respectively represented.

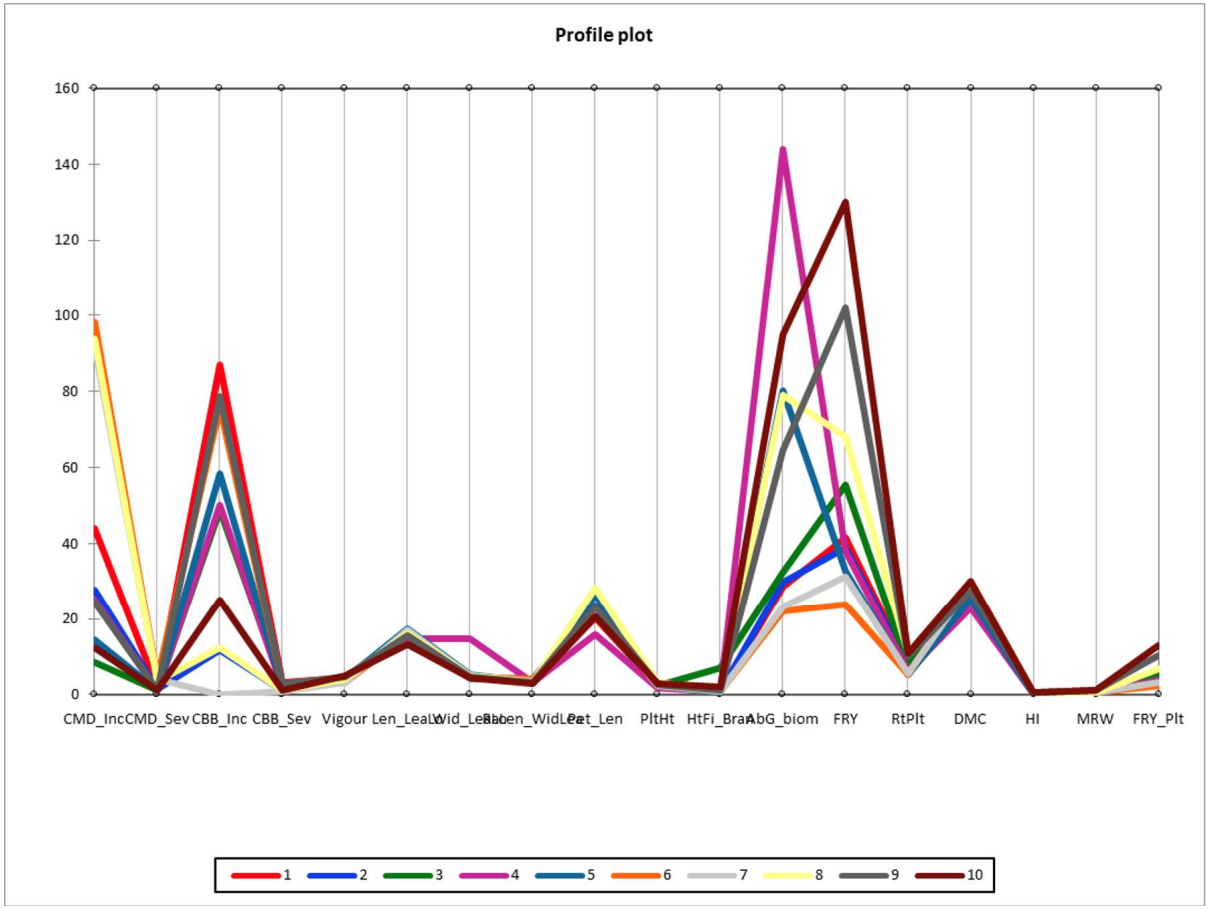

Figure 5. Profile plot describing the 10 clusters formed using the Ward-MLM method based on disease and agronomic traits evaluated in 149 cassava varieties of Togo. CMD_Inc = Cassava Mosaic Disease incidence, CMD_Sev = Cassava Mosaic Disease severity score, CBB_Inc = Cassava Bacterial Blight Incidence, CBB_Sev = Cassava Bacterial Blight Severity score, Len_LeaLo = Length of leaf lobe, Wid_LeaLo = Width of leaf lobe, RaLen_WidLea = Ratio of lobe length to lobe width of central leaf lobe, Pet_Len = Petiole length, HtFi_Bran = Height to first branching, PltHt = Plant height, AbG_biom = Above ground biomass, FRY = Fresh root yield, RtPlt = Number of roots per plant, DMC = Dry matter content percentage, HI = Harvest index, MRW = Mean root weigth, FRY_Plt = Fresh root yield per plant.

Table 7. Genetic distances between 10 optimal clusters of 149 cassava varieties from Togo

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10
C1	0									
C2	77.22	0								
C3	54.3*	45.5*	0							
C4	123.2**	121.3**	114.9**	0						
C5	66.9*	70.3*	54.8*	67.0*	0					
C6	58.8*	96.9*	99.6*	145.9**	104.0**	0				
C7	99.93*	65.7*	99.9*	147.5**	112.2**	76.5**	0			
C8	106.4**	87.8*	104.8*	107.6*	98.4*	96.4*	68.6*	0		
C9	73.5*	98.7*	66.2*	107.1**	75.0*	115.9*	132.2**	102.9**	0	
C10	130.8**	114.4**	100.6**	109.2**	104.8**	163.3**	148.1**	104.7**	69.1*	0

Cn: Cluster; (*, **) significant at 5% and 1% probability level, respectively

3.3. Differentiation of clusters based on disease and agronomic traits

Bartlett's test for eigenvalue significancy revealed that the first four canonical variables were significant and accounted for 99.61% of the divergence among the 10 phenotypic clusters delineated through cluster analysis (Table 8). The first canonical variate (CAN1) was mainly correlated with CMD severity, CMD incidence, plant vigour, and the number of roots per plant. The second canonical variate (CAN2) was positively defined by traits such as CBB severity and CBB incidence. The third canonical variate (CAN2) correlated negatively with fresh root yield, mean root weight, and fresh root yield per plant. The fourth canonical variate was correlated positively with the harvest index and negatively with the leaf lobe width and the above ground biomass (Table 8).

The Box test was also highly significant (M of Box = 38.52; F-value =1.458; p-value < 0.0001) confirming the validity of the study in terms of variety assignment to the clusters. The unidimensional test of equality of clusters means (Table 9) revealed that CMD severity, CBB severity, width of leaf lobe, dry matter content, above-ground biomass, fresh root yield, and the harvest index were key traits discriminating the clusters. The performance clusters based on discriminating traits are shown in Table 10. It was observed from the comparison of clusters revealed that clusters 7, 8, and 9 were constituted of CMD highly susceptible genotypes but differed in traits such as above-ground biomass, fresh root yield, and dry matter. In contrast, clusters 1, 4, 10, and 6 are mainly composed of CMD resistant genotypes with high fresh root yield, high canopy yield, and low dry matter, but differ in terms of harvest index. Clusters 2, 3, and 5 are made of CMD moderately susceptible varieties and differ in terms of CBB susceptibility, fresh root yield, number of roots per plant, vigour, dry matter content, and harvest index (Figure 6).

Table 8. Correlations between disease and agronomic traits evaluated on 149 cassava varieties from Togo and factors obtained from canonical analysis

	CAN1	CAN2	CAN3	CAN4	CAN5
Eigenvalue	15.406	8.279	4.013	1.532	0.509
Discrimination (%)	82.27	11.28	4.699	1.372	0.390
Cumulative (%)	82.27	93.55	98.24	99.61	100.0
Bartlett's statistic	213.23	86.431	30.254	15.811	6.373
P value	0.001	0.001	0.001	0.001	0.08
Traits	**Loading scores**				
CMD_Inc (%)	**0.847**	0.504	-0.002	-0.073	-0.111
CMD_Sev	**0.860**	0.417	-0.054	-0.135	0.243
CBB_Inc (%)	-0.498	**0.849**	0.031	0.059	-0.024
CBB_Sev	-0.502	**0.719**	-0.002	0.082	-0.047
Vigour	**-0.625**	-0.097	-0.124	-0.072	-0.257
Len_LeaLo (cm)	0.243	-0.102	0.053	-0.102	0.159
Wid_LeaLo (cm)	-0.147	-0.119	0.284	**-0.677**	0.076
RaLen_WidLea	0.083	0.104	0.065	0.029	0.032
Pet_Len (cm)	0.093	-0.115	-0.028	-0.117	0.130
PltHt (cm)	-0.071	-0.052	-0.215	-0.285	-0.025
HtFi_Bran (cm)	-0.075	-0.061	0.005	0.065	0.079
AbG_biom (t.ha^{-1})	-0.406	-0.233	-0.143	**-0.790**	-0.081
FRY (t.ha^{-1})	-0.441	-0.248	**-0.777**	-0.133	-0.143
RtPlt	**-0.393**	-0.204	-0.392	0.164	-0.250
DMC (%)	0.214	0.152	-0.127	0.240	0.103
HI	-0.064	0.019	-0.374	**0.770**	-0.057
MRW (Kg)	-0.405	-0.235	**-0.771**	-0.234	-0.040
FRY_Plt (Kg)	-0.446	-0.248	**-0.670**	-0.127	-0.136

CANn = Canonical variate; Traits that contributed most to the phenotypic variation among clusters of a particular canonical variate are in bold and underlined. CMD_Sev = Cassava Mosaic Disease severity score, Wid_LeaLo = Width of leaf lobe, Len_LeaLo = Length of leaf lobe, RaLen_WidLea = Ratio of lobe length to lobe width of central leaf lobe, Pet_Len = Petiole length, HtFi_Bran = Height to first branching, PltHt = Plant height, AbG_biom = Above ground biomass, FRY = Fresh root yield, DMC = Dry matter content percentage, RtPlt = Number of roots per plant, HI = Harvest index.

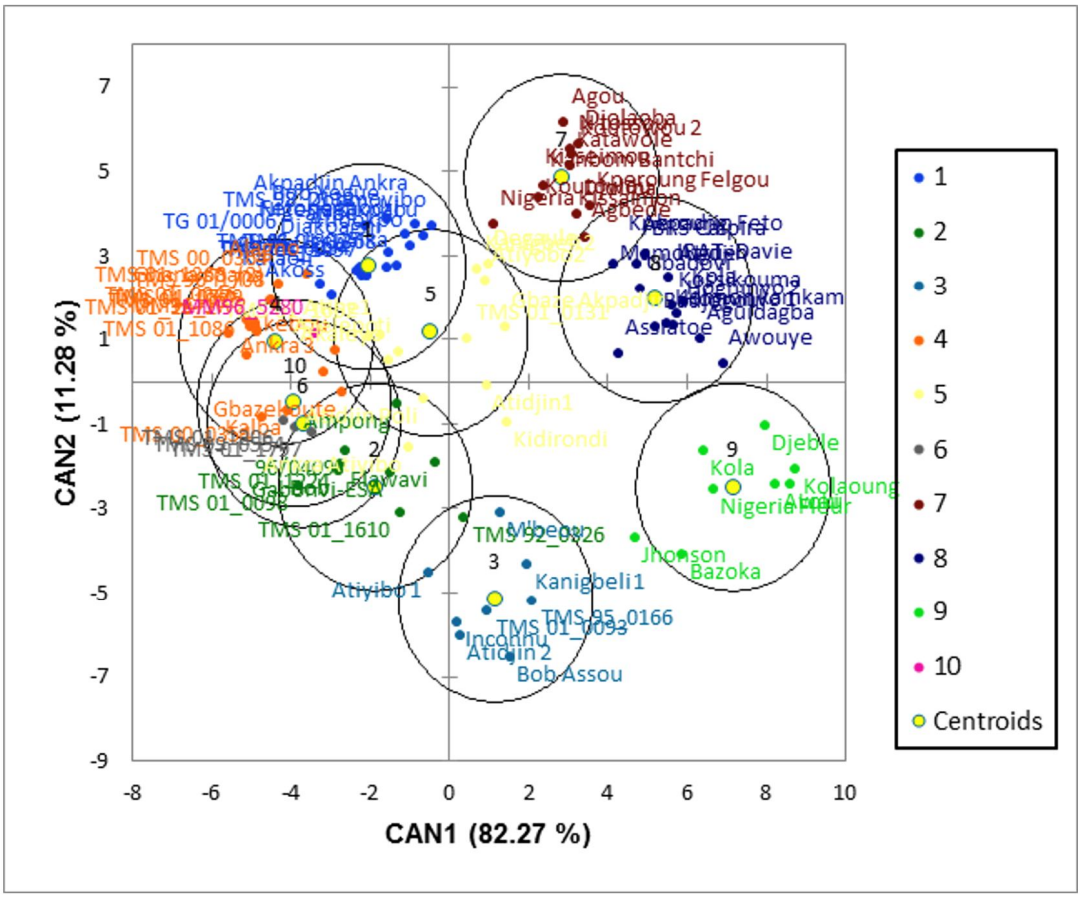

Figure 6. Canonical scatter plot displaying the relationship between 10 clusters of 149 cassava varieties from Togo along the CAN1 and CAN2 axes

Table 9. Mean performances of 10 optimal clusters identified from cluster analysis

Cluster	CMD_Sev	CBB_Sev	Vigour	Wid_LeaLo	AbG_biom	FRY	RtPlt	DMC	HI
1	1.67	3.48	4.23	4.24	22.77	32.06	7.68	28.27	0.60
2	1.21	2.03	4.18	4.37	33.29	46.05	7.68	30.35	0.59
3	1.53	1.04	3.90	4.69	31.65	42.91	7.60	27.20	0.57
4	1.23	3.12	4.30	4.27	24.67	45.80	7.97	27.55	0.65
5	2.03	2.92	4.14	4.31	34.87	47.40	7.51	28.48	0.57
6	1.24	2.57	4.47	8.71	82.86	36.73	6.36	25.27	0.32
7	4.20	3.17	3.64	4.47	22.32	23.38	5.45	30.83	0.52
8	4.39	2.03	2.69	4.75	21.93	24.29	5.35	29.10	0.52
9	3.82	1.01	3.28	4.77	29.28	36.68	6.57	29.28	0.54
10	1.26	2.68	4.86	4.75	70.60	65.60	10.12	28.05	0.61

CMD_Sev = Cassava Mosaic Disease severity score, CBB_Sev = Cassava Bacterial Blight severity score, PltHt = Plant height, AbG_biom = Above ground biomasse, FRY = Fresh root yield, RtPlt = Number of roots per plant, DMC = Dry matter content percentage, HI = Harvest index.

Table 10. Unidimensional test of equality of the means of 10 clusters

Traits	Lambda	F	DF1	DF2	p-value
CMD_Inc	0.091	152.798	9	148	< 0.0001
CMD_Sev	0.116	116.300	9	148	< 0.0001
CBB_Inc	0.120	111.946	9	148	< 0.0001
CBB_Sev			9	148	NS
Vigour	0.554	12.332	9	148	< 0.0001
Len_LeaLo			9	148	NS
Wid_LeaLo	0.620	9.394	9	148	< 0.0001
RaLen_WidLea			9	148	NS
Pet_Len			9	148	NS
PltHt			9	148	NS
HtFi_Bran			9	148	NS
AbG_biom	0.399	23.101	9	148	< 0.0001
FRY	0.260	43.601	9	148	< 0.0001
RtPlt	0.653	8.140	9	148	< 0.0001
DMC	0.826	3.230	9	148	0.001
HI	0.518	14.296	9	148	< 0.0001
MRW	0.394	23.589	9	148	< 0.0001
FRY_Plt			9	148	NS

CMD_Sev = Cassava Mosaic Disease severity score, Len_LeaLo = Length of leaf lobe (cm), Wid_LeaLo = Width of leaf lobe (cm), RaLen_WidLea = Ratio of lobe length to lobe width of central leaf lobe, Pet_Len = Petiole length (cm), HtFi_Bran = Height to first branching (cm), PltHt = Plant height (cm), AbG_biom = Above ground biomass ($t.ha^{-1}$), FRY= Fresh root yield ($t.ha^{-1}$), RtPlt = Number of roots per plant, DMC = Dry matter content percentage, HI = Harvest index. NS = non significant.

4. DISCUSSION

4.1. Phenotypic Diversity of the Cassava Germplasm

The phenotyping of plant materials based on agromorphological traits has been used to determine the phenotypic variability among genotypes and to verify the phenotypic correlation between disease and agronomic traits (Avijala et al., 2015; Agre et al., 2015; Adjebeng-Danquah & Gracen, 2017; Carine et al., 2017). In this study, high morphological variability was observed within the germplasm based on qualitative traits. The petiole colour, leaf colour, flowering ability, colour of leaf vein, levels of branching, seed set ability, colour of stem epidermis, leaf lobe margins, colour of end branches, and the stem growth habit were underscored by the MCA as the most relevant traits for cultivars identification. Asare et al. (2011), Adjebeng-Danquah & Gracen (2017), Agre et al. (2017) and Gmakouba et al. (2018) observed similar findings.

Substantial variation was observed for disease and agronomic traits under selection, which indicates the possibility of genetic gains through selection. Genetic variation for cassava agronomic traits has been documented in various studies across Africa (Agre et al., 2015; Adjebeng-Danquah & Gracen, 2017) and in Brazil (Oliveira et al., 2015).

Strong phenotypic correlations were identified among disease and agronomic traits in this study. CMD severity was negatively correlated to yield related traits, which confirms significant yield losses due to CMD across the country. This agrees with earlier studies on cassava (Ojulong et al., 2010; Sing et al., 2015; Adjebeng-Danquah & Gracen, 2017).

4.2. Structure of the Germplasm Phenotypic Diversity

The population structure analyses revealed that the accessions were not grouped based on the geographical origin distribution. Accessions collected from places such as Vogan, Wetrope, Akebou, Danyi, Aouda, Davie, and Assoukoko were clustered in cluster 1. Likewise, accessions from Bafilo, Assoukoko, Danyi, and Bouronde were also clustered together in cluster 2. The remaining clusters

also included accessions from different collection regions. The informal farmers-to-farmers seed supply system practiced in the country could explain this result. Similar results were reported by Gmakouba et al. (2018) in characterizing 54 cassava accessions sourced from different regions of Burkina Faso. Furthermore, cassava accessions collected from the same region were grouped into distinct clusters, indicating significant genetic diversity within each collection area. Similar observations were also reported by Agre et al. (2017) in Bénin. Furthermore, similar to the findings reported by Kombo et al. (2012), this study found no clear distinction or significant structuring between local and improved accessions. Morphotypes identified may be valuable in cassava germplasm management and accession identification, while the ten divergent groups identified based on disease and agronomic traits may be useful in the national cassava breeding programs. From this study, a high amount of heterotic expression is expected from crosses involving parents selected from clusters 5 and 7 followed by clusters 4 and 7. However, to make the best of these clusters, the breeder needs to specify his breeding objectives based on farmers' varietal preferences.

5. CONCLUSION

The study demonstrated that the germplasm exhibited substantial genetic diversity at the phenotypic level. The variation observed among the varieties for traits such as CMD resistance, root dry matter content, fresh root yield, above-ground biomass, and harvest index was significant. Within the germplasm, phenotypic groups with desirable traits such as CMD resistance, high root dry matter content, high canopy, fresh root yield, and a high harvest index were identified. The study provided crucial insights into the overall variation and diversity of traits that are of economic importance, aiding in the development of crossing panels with diverse characteristics. Selecting and hybridizing parent lines from the identified phenotypic groups will enhance diversity and leverage population heterosis in the National Cassava Breeding Program. However, identifying heterotic groups requires a combined analysis of genotypic and phenotypic data.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

DATA AVAILABILITY

The data of the study are available upon request from the corresponding author.

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