

Genotype \times Environment Interaction and Stability Analysis for Selected Agronomic Traits in Cassava (*Manihot esculenta*)

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Abstract— Cassava (*Manihot esculenta* Crantz) is an important root and tuber crop worldwide. The crop is highly influenced by variations in production environments. A significant Genotype \times Environment Interaction (GEI) presents challenges in the selection of superior genotypes. This study determined the magnitude of GEI and stability performances of 26 cassava genotypes for key agronomic traits across three multi-environments. The trial was laid out in a randomized complete block design during 2016/2017 cropping season. Genotype TR0288 had the highest starch content at Pendembu and Kambia, while TR1436 performed best at Njala. Genotype TR0768 had the highest fresh storage root yield at Pendembu, TR0455 at Kambia and TR0591 and TR0657 at Njala environments. For dry matter content, genotypes SLICASS4, TR0310 and TR0740 performed best at Njala, Pendembu and Njala, respectively. Genotype TR0455 had the highest fresh storage root yield across the three production environments, TR1436 for starch content and TR0310 for dry matter content. TR0310 was the most stable and favorable genotype based on mean dry matter content and stability performance across the three production environments. Harvest index was positive and significantly correlated with storage root ($r = 0.54^{***}$), fresh storage root yield was highly and positively correlated with number of storage root ($r = 0.61^{***}$) and harvest index ($r = 0.49^{***}$). The information generated is relevant for selection initiatives targeted at superior high yielding, high dry matter content and starch content cassava genotypes combining resistance to cassava mosaic in Sierra Leone.

Keywords— Genotypic performance, multi-environment trial, stability analysis, trait correlation, cassava.

I. INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is an important starchy root crop utilized for human consumption, animal feed and various industrial applications [1]. The starchy storage roots of cassava are important source of dietary energy in sub-Saharan Africa (SSA) as they provide more returns per unit of input than any other staple crop [2–4]. Cassava serves as food security and income generation crop for resource poor farmers due to its tolerance to climate changes such as erratic rainfall and poor soil fertility. In Sierra Leone, cassava is the second most important staple crop after rice. The cassava root production in the country has increased from 82,500 tons in 1970 to 4.59 million tons in 2019 growing at an average annual rate of 12.08% [5]. However, on-farm cassava yields are significantly lower than the potential yields of improved varieties estimated at ≥ 25 t ha⁻¹ [6]. For instance, in 2019, 59,660 ha were cultivated to cassava by 101,021 households, producing 817,342 MT [6]. A wide yield variability ranging from 6.5 MT ha⁻¹ to 33.9 MT ha⁻¹ exists among genotypes, with an average yield (14.5 MT ha⁻¹) below 50% relative to yields obtained under good agronomic practices [6]. Cassava is cultivated in all regions of Sierra Leone due to its easy propagation, value of cultivation and utilization.

Despite its enormous significance, increased cassava productivity is limited by a number of biotic and abiotic factors [7]. For instance, cassava green mite attack can cause about 15 and 73% yield losses in resistant and susceptible genotypes of cassava, respectively Bellotti [8], whereas about 88% yield loss can be due to cassava mealy bug infestation in susceptible genotypes [9]. Low crop yields are also caused by low yielding varieties, environmental variability and poor environmental management or use of elite agronomic packages.

The performance of any character is a combined result of the genotype (G), the environment (E) and the interaction between genotype and environment (GE) [10]. The GE interaction (GEI) exists when the responses of two genotypes to different

levels of environmental stress are inconsistent. The GEI and yield-stability analyses have become increasingly important for measuring cultivar stability and suitability for cultivation across seasons and ecological zones [11]. Multi-environment trials (METs) have been found to be important in plant breeding for studying cultivar stability and predicting yield performance of cultivars across environments [12].

Several authors have noted the effects of GEI in cassava. Tumuhimbise *et al.* [13] reported a non-significant GEE effect for early fresh storage root yield (FSRY). Moreover, the effect of GEI on dry matter content (DMC) has been well noted [14,15]. In Sierra Leone, there is dearth of information of the GEI effects and stability performance of putative cassava genotypes developed for key agronomic traits (yield, disease resistance, root dry matter content, starch content and harvest index). A good understanding of GEI effects is useful to plant breeders for selection of suitable genotypes for specific environments. The determination of stability performance of genotypes across varying test sites requires use of specific tools and methods [10]. The univariate, bivariate and multivariate techniques are the common methods often utilized for stability analysis [16]. The additive main effects and multiplicative interaction (AMMI) multivariate analytical technique is the most widely used method for GEI assessment [10]. The AMMI method effectively captures a large portion of the GEI sum of squares [17]. The identification of yield-contributing traits and knowledge of GEI and associated yield stability are important considerations in breeding new cultivars with improved adaptation to the environmental constraints that prevail in target environments [18]. Thus, the objective of this study was to determine the magnitude of Genotype \times Environment Interaction and stability performance of genotypes for its effective utilization to improve key agronomic traits in cassava.

II. MATERIALS AND METHODS

2.1 Experimental sites

The trials were conducted during 2016/2017 cropping season at three locations representing different agro-ecological zones in Sierra Leone. The mean monthly minimum and maximum temperatures, annual rainfall and soil attributes of the various sites are presented in Table 1.

TABLE 1
AGRO-ECOLOGICAL CHARACTERISTICS OF THE TRIAL SITES

Attribute	Location		
	Njala	Kambia	Pendembu
Coordinates			
Longitude	8°9'32.14"N	9°7'30.16"N	7°57'06"N
Latitude	12°25'54.05"W	12°55'5.38"W	-10°55'26"E
Elevation (m)	73	57	157
Agro-ecological zone	Transitional rainforest	Savannah	Rainforest
Weather and climate attributes			
Rainfall (mm)	2616.6	2456.0	2745.4
Temperature (min-max) (°C)	21.5–31.2	20.9–32.4	21.0–31.9
Relative humidity (min-max) (%)	62.6–83.1	64.0–87.0	70.7–83.7
Soil attributes			
pH(H ₂ O) (1:1)	5.00	4.40	5.08
OC (%)	0.54	0.21	0.31
N (%)	0.14	0.14	0.15
Bray P (ppm)	5.43	4.31	6.84
K (Cmol/kg)	0.08	0.08	0.06

2.2 Plant material and experimental design

A total of 26 genotypes comprising 23 advanced clones from IITA, one local check (COCOA) and two released checks (SLICASS 4 and SLICASS 6). The trial was laid out in a randomised complete block design with three replications. Healthy stems of each genotype were cut into 25 cm length each and planted horizontally on ridges at a spacing of 1 \times 1 m. Each plot measured 3 \times 10 m comprising three rows of 10 plants each.

2.3 Data collection

A total of six agronomic traits were collected including cassava mosaic disease (CMD); storage root number per plant (SRN); fresh storage root yield (FSRY); harvest index (HI); starch content (SC); and dry matter content (DMC). The CMD was collected at six months after planting (MAP) using the scale of 1 to 5 (1 = no visible symptom of disease; 2 = mild; 3 = low; 4 = intermediate; 5 = high) as described by Fukuda *et al.* [19].

Starch content was determined according to the method described by Sofa-Kantanka and Osei-Minta [20]. The amount of dried starch obtained from 2 kg of fresh cassava storage roots was weighed and expressed as a percentage of the weight of fresh storage roots. The starch content was calculated as follows:

$$\text{Starch content} = \frac{X}{Y} \times 100 \quad (1)$$

Where X = dry weight starch extracted and Y=fresh weight of cassava storage roots.

2.4 Data analysis

The data were subjected to combined analyses of variance using the GLM procedure of Statistical Analysis System (SAS 9.4) to determine the magnitude of the main effects and interactions. For genotypic assessment of the selected agronomic traits across environment trials, prediction assessment was conducted using the AMMI method [21]. The AMMI model was as follows:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^n \lambda_k \gamma_{ik} \delta_{jk} + \varepsilon_{ij} \quad (2)$$

where, Y_{ij} = the yield of i^{th} genotype in j^{th} environment over all replications, μ is the grand mean, α_i is the i^{th} genotype mean deviation,

β_j = the j^{th} environment mean deviation, λ_k is the singular value for IPC axis k, γ_{ik} is the i^{th} genotype eigenvector value for IPC axis k, δ_{jk} is the j^{th} environment eigenvector value for IPC axis k, and ε_{ij} is the error term.

The eigenvalue (EV) stability parameter of AMMI was calculated based on the equation by Zobel *et al.* [22]:

$$EV = \mu + \alpha_i + \beta_j + \sum_{n=1}^N \frac{\lambda_{in}^2}{n} \quad (3)$$

In this formula, γ_{in} = the genotype eigenvector for axis n, and N = the number of IPCs retained in the AMMI procedure using different F-test.

The sum of IPCs scores (SIPC) parameter was determined according to Sneller *et al.* [23]:

$$\text{SIPC} = \sum_{n=1}^N \lambda_n^{0.5} y_{in} \quad (4)$$

Where, λ_n is the eigenvalue of the IPC analysis axis n. In this equation, N = 1 for SIPC1; and for SIPCf, N is the number of IPCs retained in the AMMI model.

The GGE Biplot was done to visually assess the GEI pattern of data using GGE-biplot software [24]. The GGE Biplot is based on two concepts including the Biplot concept [25] and the GGE concept [26]. Correlation of the various plant parameters was done using Pearson correlation coefficients [27].

III. RESULTS

3.1 AMMI analysis of the measured traits

The combined analyses of variance (ANOVA) across the three environments revealed that, highly significant differences ($P < 0.001$) were observed among genotypes (G) for NSR, DM, and CMD, while non-significant differences were observed among genotypes for HI, SY and FSRY. Significant differences were observed among locations for all traits except for dry matter content. Also, genotype \times location (G \times L) interactions were significant for number of storage root, starch content, fresh storage root yield, dry matter content and cassava mosaic disease (Table 2). In the combined AMMI ANOVA, the genotype mean squares were highly significant ($P < 0.001$) for all the traits evaluated (Tables 2 and 3).

TABLE 2
MEAN SQUARES VALUES OF COMBINED ANALYSIS FOR THE 26 CASSAVA GENOTYPES EVALUATED FOR DISEASE, ROOT YIELD AND RELATED ATTRIBUTES IN THREE LOCATIONS

Source	DF	NSR	HI	SC	FSRY	DMC	CMD
REP	2	2376.594**	0.005 ^{ns}	12.851 ^{ns}	117.304 ^{ns}	18.979 ^{ns}	0.205 ^{ns}
GEN	25	1352.410**	0.0286 ^{ns}	36.155 ^{ns}	110.077 ^{ns}	25.618**	3.507**
LOCATION	2	58213.453**	1.716**	1338.760**	3294.339**	16.056 ^{ns}	40.936**
GEN*LOCATION	50	1823.573**	0.023 ^{ns}	18.079 ^{ns}	146.047**	14.700**	1.989**
ERROR	154	394.780	0.021	20.795	71.898	7.0522	0.850
CV		42.620	32.865	45.321	48.861	7.578	43.065

P < 0.01; NSR=Number of storage root; HI= harvesting index; SC= starch content, FSRY = fresh storage root yield; DMC= dry matter content and CMD= cassava mosaic disease

TABLE 3
MEAN SQUARES OF AMMI ANALYSIS OF VARIANCE FOR THE 26 CASSAVA GENOTYPES EVALUATED FOR DISEASE, ROOT YIELD AND RELATED ATTRIBUTES ACROSS THREE LOCATIONS

Source	DF	NSR	HI	SC	FSRY	DMC	CMD
Treatments	77	1317***	0.07***	58.3***	216.1***	18.28***	3.49***
Genotypes	25	3135***	0.03 ^{ns}	36.2*	110.1***	25.62***	3.51***
Environments	2	58213***	1.69***	1338.8***	3294.4***	16.06 ^{ns}	40.94***
Block	6	1988***	0.002***	26.1 ^{ns}	54.6***	20.18 ^{ns}	0.27 ^{ns}
Interaction	50	1824***	0.02 ^{ns}	18.1 ^{ns}	146***	14.70***	1.99***
IPCA1	26	2822***	0.024 ^{ns}	21.9**	150.8***	21.63***	2.78***
IPCA2	24	742 ^{ns}	0.021 ^{ns}	13.9 ^{ns}	140.9***	7.20 ^{ns}	1.14
Error	150	357	0.021	20.5	72.8	6.66	0.86
Total	233						

P < 0.05 and P < 0.001; NSR=Number of storage root; HI= harvesting index; SC= starch content, FSRY = fresh storage root yield; DMC = dry matter content and CMD= Cassava mosaic disease

The location mean squares were highly significant ($P < 0.001$) for storage root number; harvest index; fresh storage root yield; cassava mosaic disease and significant ($P < 0.05$) for starch content. Genotype \times environment mean squares were highly significant ($P < 0.001$) for number of storage root; fresh storage root yield; dry matter content and cassava mosaic disease. The IPCA1 mean squares were highly significant ($P < 0.001$) for number of storage root; fresh storage root yield; dry matter content, starch content and cassava mosaic disease. Harvest index had non-significant IPCA1 mean squares while the IPCA2 mean squares were non-significant for all traits except for fresh storage root yield that was highly significant.

3.2 The GEI patterns of traits and genotypes based on GGE biplot analysis

The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted for 45.13% and 34.06% of GGE sum of squares, respectively, for root yield, explaining a total of 79.19% variation (Figure 1). Genotype TR0455 had the highest average fresh storage root yield and TR0657 had the lowest fresh storage root yield across three environments. Stability of each genotype is explored by its projection onto the AEC vertical axis. Thus, genotypes TR0768, TR0458 and TR0488 were the least stable. TR0024 was the most stable genotype followed by SLICASS 4, SLICASS 6 and TR0541. However, considering mean yield performance, genotype TR0455 is regarded as the most stable.

The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 51.16% and 30.43% of GGE sum of squares, respectively explaining a total of 81.59% variation of the starch content (Figure 2). Genotype TR1436 had the highest average starch content, and TR0657 had the lowest mean starch content across the three environments. Genotypes TR1436, TR0048 and TR0288 were the most stable genotypes, whereas for mean fresh root yield and stability performances, genotype TR1436 is the most favorable. The PC1 and PC2 accounted for 60.39% and 27.08% explaining a total of 87.47% variation of the dry matter content (Figure 3). The average dry matter content of genotypes across the three environments was estimated by projections on to the AEC horizontal axis. Thus, genotype TR0310 had the highest average dry matter content, and TR1716 had the lowest mean dry matter content across the three environments. Stability of each genotype is explored by its projection onto the AEC vertical axis. Genotypes TR0310 and TR0488 were the

AXIS2 34.06 %

AXIS1 45.13 %

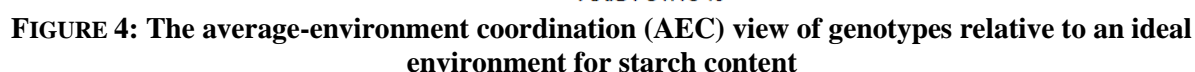
Species labels: NJALA, KAMBIA, TR0488, TR1716, TR0455, TR0768, TR0024, SLICASS4, SLICASS6, TR0545, TR0188, TR0038, TR0591, TR0657, TR0300, TR1280, TR0259, TR0904, TR0718, TR0740, TR0418, TR0244, PENDEMBU.

A PCA plot showing the separation of 15 samples into three groups: NJALA (top right), PENDEMBU (bottom right), and KAMBIA (bottom right). The x-axis is labeled 'AXIS1 51.16 %' and the y-axis is labeled 'AXIS2 30.43 %'. The samples are labeled with their IDs: TR0300, TR0768, TR0545, TR0771, TR0275, TR1436, TR0781, TR0784, TR0038, COGOA, TR0546, TR0548, TR0549, TR0550, TR0551, TR0552, TR0553, TR0554, TR0555, TR0556, TR0557, TR0558, TR0559, TR0560, TR0561, TR0562, TR0563, TR0564, TR0565, TR0566, TR0567, TR0568, TR0569, TR0570, TR0571, TR0572, TR0573, TR0574, TR0575, TR0576, TR0577, TR0578, TR0579, TR0580, TR0581, TR0582, TR0583, TR0584, TR0585, TR0586, TR0587, TR0588, TR0589, TR0590, TR0591, TR0592, TR0593, TR0594, TR0595, TR0596, TR0597, TR0598, TR0599, TR0600, TR0601, TR0602, TR0603, TR0604, TR0605, TR0606, TR0607, TR0608, TR0609, TR0610, TR0611, TR0612, TR0613, TR0614, TR0615, TR0616, TR0617, TR0618, TR0619, TR0620, TR0621, TR0622, TR0623, TR0624, TR0625, TR0626, TR0627, TR0628, TR0629, TR0630, TR0631, TR0632, TR0633, TR0634, TR0635, TR0636, TR0637, TR0638, TR0639, TR0640, TR0641, TR0642, TR0643, TR0644, TR0645, TR0646, TR0647, TR0648, TR0649, TR0650, TR0651, TR0652, TR0653, TR0654, TR0655, TR0656, 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The average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, shows the best genotypes across the three environments. Genotypes SLICASS4 and TR0024 were ideal for Pendembu, whereas SLICASS6 and TR0024 were ideal for Kambia. Genotypes TR0455, TR0768 and TR0657 were high yielding, but unstable across the three locations (Figure 4). The comparison of the relative performance of all genotypes accross the environments is shown in Figure 5. Genotype TR1436 had higher average starch content in Njala environment while genotype TR0288 had the highest starch content for Pendembu and Kambia followed by TR0329. The relative performance of genotypes for dry matter content accross the Njala, Kambia and Pendembu test sites is shown in Figure 5. Genotype TR0310 had higher average dry matter content and was the most stable genotype accross the three environments while genotypes TR0218 and TR1716 showed lower dry matter content than average performance.



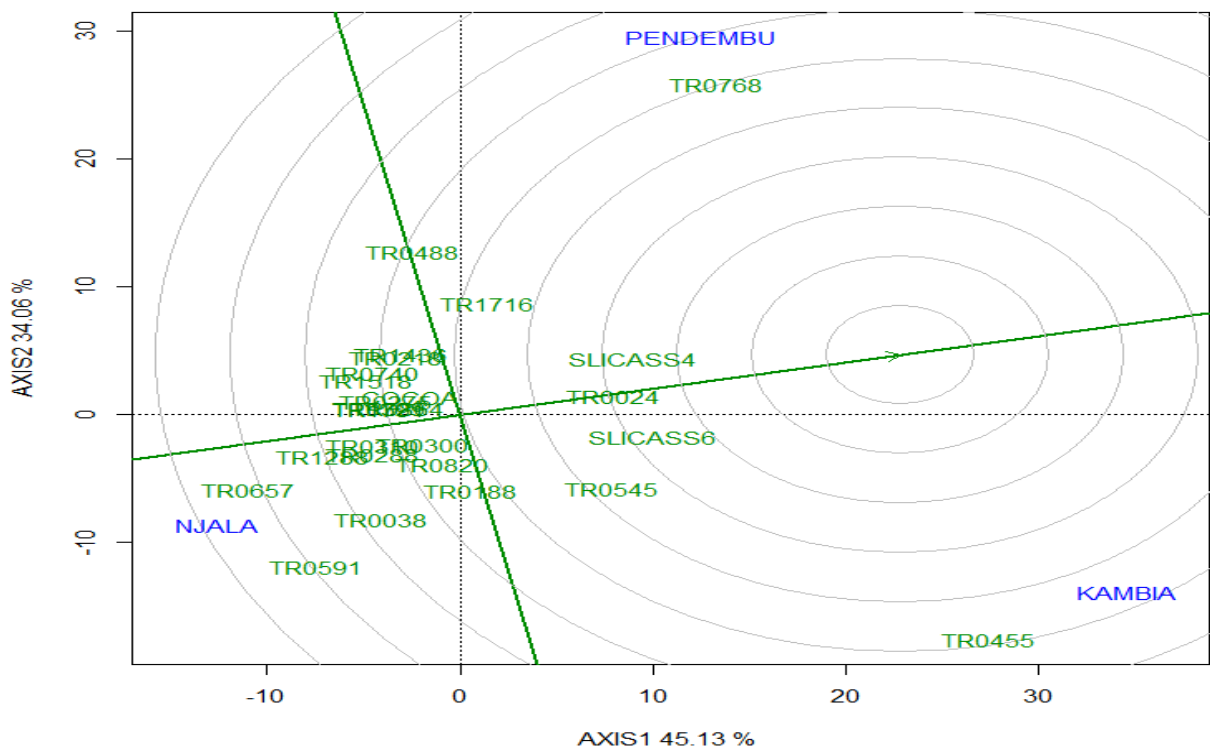


FIGURE 5: The average-environment coordination (AEC) view of genotypes relative to ideal environment for fresh storage root yield

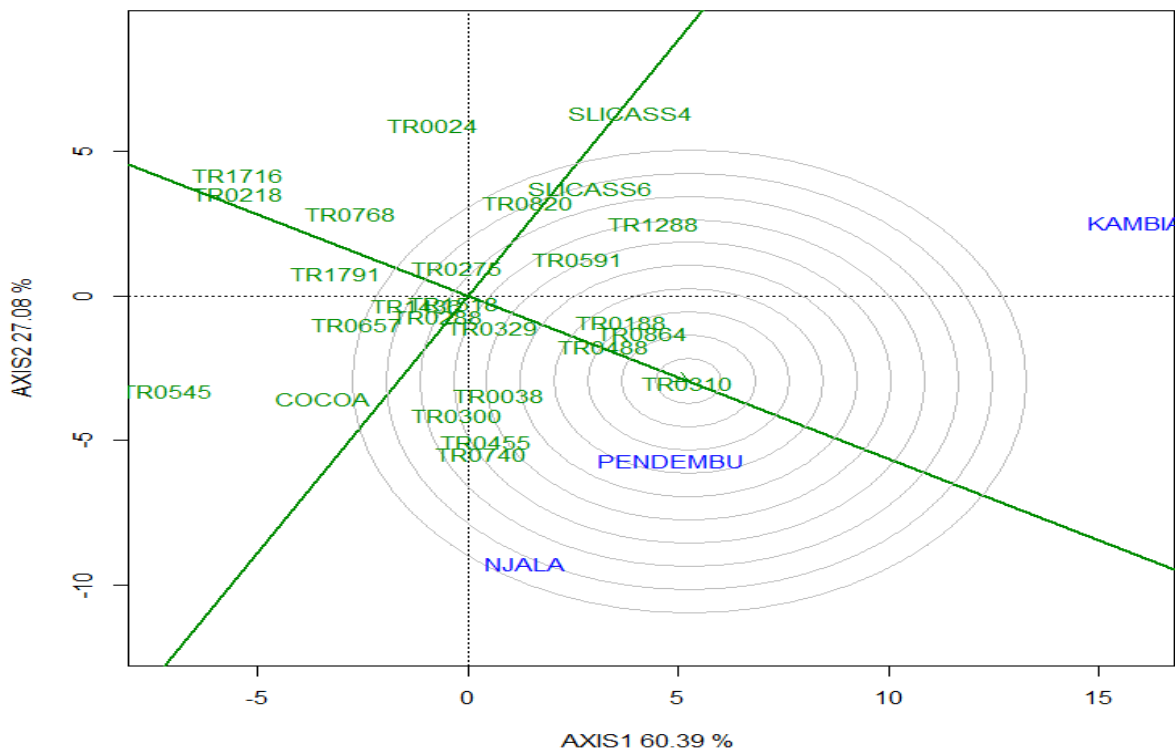


FIGURE 6: The average-environment coordination (AEC) view of genotypes relative to an ideal environment for dry matter content

The polygon view of cassava genotypes evaluated across Kambia, Pendembu and Njala environments is shown in Figure 7. The vertex genotypes TR0768, TR0488, TR455, TR0591 and TR0657 were the best performers or winning genotypes for storage root yield at the studied enironments because they are farthest away from the biplot origin. Genotype TR0768 is the winning genotypes in the Pendembu enviroment. The Kambia has TR0455 as the winning genotype. The Njala enviroment

has genotypes TR0591 and TR0657 as the winning genotypes. The genotype TR0488 performed poorly in all the three enviroments.

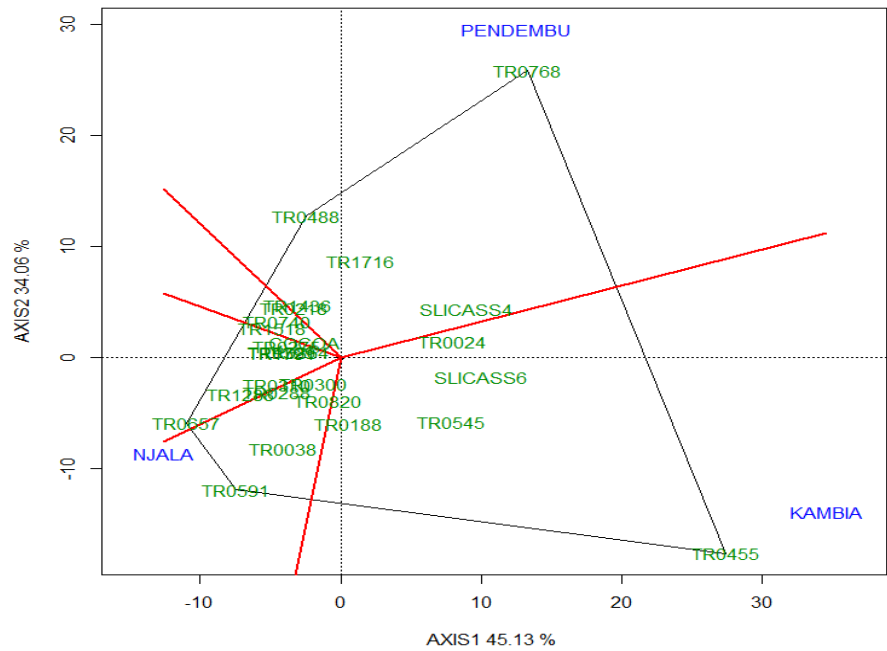


FIGURE 7: GGE biplot for best genotypes for fresh storage root yield across different environments

The polygon view of cassava genotypes across the three environments (Kambia, Pendembu and Njala) is shown in Figure 8. The vertex genotypes in this study are; TR0329, TR0288, TR1436, TR0300, TR0657 and TR1716. The first section contains Kambia and Pendembu environment with TR0288 as the winning genotype. The second section contains Njala enivironment with genotype TR1436 as the winning genotype. The other vertex genotypes TR0300, TR0657, TR1716 and TR0329 were not the top yielding genotypes in any of the three environments. The vertex genotype in each sector is the best genotype within the environments.

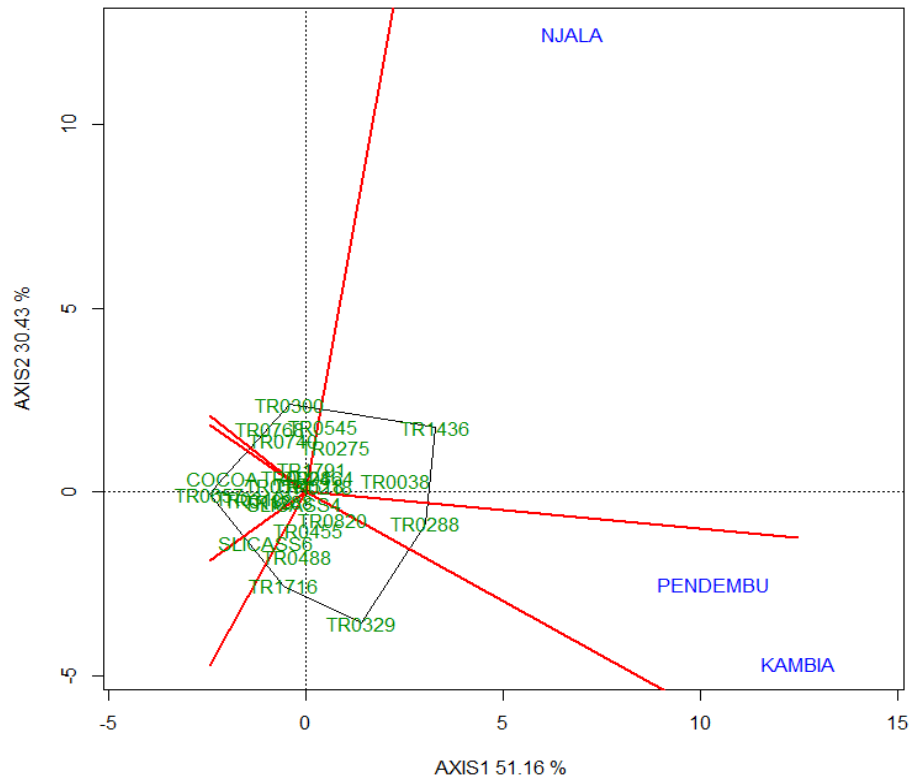


FIGURE 8: GGE biplot for the best performing genotypes for starch content evaluated across three production environments

The polygon view of cassava genotypes across the three environments (Kambia, Pendembu and Njala) for dry matter content is presented in Figure 9. The vertex genotypes in this study are SLICASS4, TR0310, TR0740, TR1716, TR0545 and TR0624. The Kambia environment has SLICASS4 as the winning genotype. The winning genotype in Pendembu environment was TR0310. The Njala environment had genotype TR0740 as the winning genotype. The other vertex genotypes TR1288, TR0455, and TR1716 were not the top genotypes in any of the three environments.

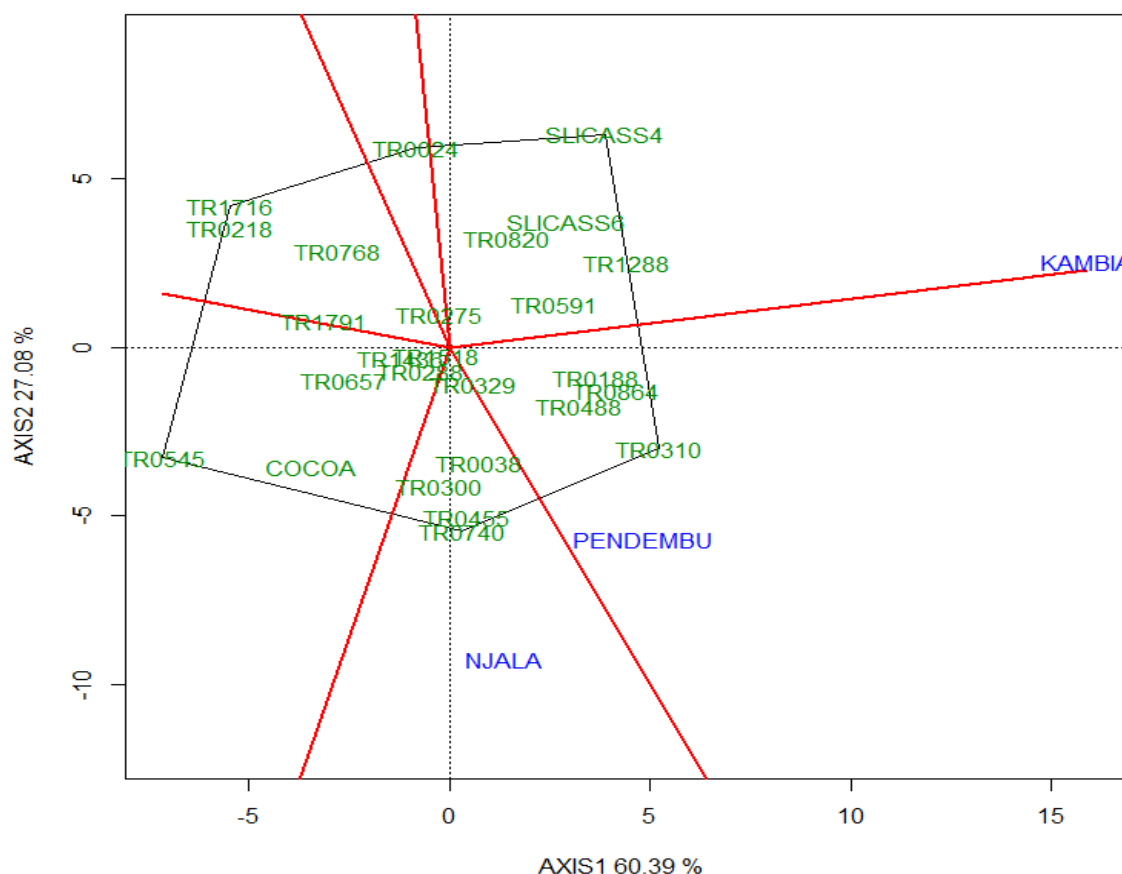


FIGURE 9: GGE biplot for best genotypes in different environments for dry matter content

3.4 Phenotypic correlations among measured agronomic traits

The phenotypic correlation among root yield and its related traits revealed that, number of storage root was positive and significantly correlated with harvest index ($r = 0.54^{***}$), and fresh storage root yield root ($r = 0.61^{***}$). The relationship between fresh storage root yield and harvest index ($r = 0.49^{***}$) was also was positive and significant (Table 4).

TABLE 4
PHENOTYPIC CORRELATIONS AMONG AGRONOMIC TRAITS

	NSR	HI	SC	FSRY	DMC	CMD
NSR	1					
HI	0.54 ^{***}	1				
SY	0.33	0.20	1			
FSRY	0.61 ^{***}	0.49 ^{***}	0.23	1		
DMC	-0.06	-0.05	0.03	-0.06	1	
CMD	0.09	-0.01	-0.13	0.04	-0.06	1

NSR=number of storage root; HI= harvesting index; SC= starch content, FSRY = fresh storage root yield; DMC = dry matter content and CMD= cassava mosaic disease

IV. DISCUSSION

Genotypes should be evaluated based on both mean performance and stability across environments [28]. Genotype effects were significant for number of storage root, dry matter content and cassava mosaic disease. The significant location effects

for harvesting index, starch content, fresh storage root yield and cassava mosaic disease indicate that the overall mean performances of the genotypes in each location were significantly different for these traits. This variation underlines the need to conduct multi locational trials in order to identify both generally and specifically adapted genotypes with good performance for the traits. The location effect was the major source of variation for fresh root yield in this study. Akinwale *et al.* [29] also found higher location effects for fresh root yield in cassava.

Elite cassava genotypes that out-performed at specific locations were identified using AMMI analysis. In this study, the IPCA1 in AMMI captured interaction exclusively in a sequence that decreases from the first and largest component to the last and smallest component. This also indicated the response patterns of genotypes to changes in location; so that the genotypes could be evaluated in terms of their performances across the three locations. This agrees with the view that the significant IPCA1 scores sufficed in enabling visual assessment of the genotype and location performances and their interactions for the AMMI1 [30]. The AMMI has been effective in identifying cassava genotypes for specific locations [29, 30]. The significant GEI for dry matter content and cassava mosaic disease demonstrate the combined effects of environment and genotype on the expression of these traits. The significant $G \times E$ interaction effect of dry matter content in this study was similar to the finding reported by Ssemakula and Dixon [14], who reported the influence of environment on cassava dry matter content. In the case of starch content, location effects had the greatest impact on the variation of the trait, suggesting the need to evaluate genotypes for more than a year in different environments for reliable inferences to be made on genotype performance. Fresh storage root yield, dry matter content and starch content are yield related traits and therefore, subject to influence from the environment.

Although the performances of some genotypes were location specific, some genotypes performed best in more than one location. Genotype TR1436 performed best at Njala, while genotype TR0288 performed best at Pendembu and Kambia for starch content. For fresh storage root yield, TR0768 performed best at Pendembu, TR0455 at Kambia and TR0591 and TR0657 at Njala environments. For dry matter content SLICASS4, TR0310 and TR0740 performed best at Njala, Pendembu and Njala, respectively. The high impact of genotype on fresh storage root weight indicates that evaluation and selection can be done in different environments to distinguish genotypes with high and stable performance. The superior yielding genotypes across the locations had consistently high number of roots per plant and low CMD attack. These results agree with the report that fresh storage root yield of cassava increases with increasing number of roots [31]. The low starch content observed in this study may be due to physiological changes that starch undergoes during the growth cycle, a comprehensive study would have to factor in time of harvesting, climatic changes and it may require testing in diverse and multiple environments to identify genotypes with broad and specific adaptation due to the high impact of location and interaction. However, $G \times E$ interaction on the three traits (fresh storage root yield, dry matter and cassava mosaic disease) indicates that some genotypes may not respond positively.

The results of correlation analysis showed a highly significant correlation ($P < 0.001$) between fresh root yield and number of roots and harvest index. Harvest index and number of storage roots that showed a strong positive correlation with fresh storage root yield were also found as good indicators of root yield in cassava [32]. In the present study, the functional relationship between root dry matter content and fresh storage root yield is negative indicating that genotypes with high root dry matter content may exhibit low fresh storage root yield. The negative correlations between CMD and harvest index, CMD and starch content, CMD and dry matter content, indicate that severe attacks of these diseases contribute to low performance of the genotypes for these traits in cassava. These findings are partly consistent with Karim *et al.* [33], who found that severe attack of CMD contributes to poor growth, low storage root yields and dry matter content in cassava. Selection for high dry matter content, high storage yield, and starch content are among major breeding objectives of the crop [31, 34].

V. CONCLUSION

The high degree of variation within locations compared to the variation due to genotypic differences and GEI for the measured traits could be exploited for selection of genotypes possessing desired traits for the targeted production environment. The GEI was significant for harvest index and starch content indicating that the ranking of the genotypes for the traits varied across locations resulting in the identification of genotypes with specific adaptation. Although genotypes did not significantly interact with locations for starch content, there were changes in ranking of the genotypes at each environment. The biplot identified best genotypes in each location for all the traits studied. Genotype TR0288 had the highest starch content at Pendembu and Kambia, while TR1436 performed best at Njala. Genotype TR0768 had the highest fresh storage root yield at Pendembu, TR0455 at Kambia and TR0591 and TR0657 at Njala environments. For dry matter content,

genotypes SLICASS4, TR0310 and TR0740 performed best at Njala, Pendembu and Njala, respectively. Genotype TR0455 had the highest fresh storage root yield across the different environments, TR1436 for starch content and TR0310 for dry matter content. Findings of this study present an opportunity for the genetic improvement of cassava for target environments in Sierra Leone.

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