Genotype-By-Environment Interaction Effect on Storage Root Yield and Yield Components of Cassava (*Manihotesculenta* crantz) Genotypes in Different Agroecologies of Southwest Ethiopia

Tewodros Mulualem*, Neim Seman, and Getachew Etana
Jimma Agricultural Research Center, PO. Box 192, Jimma, Ethiopia
**Corresponding author Email: tewodrosmulualem@gmail.com*

Abstracts

The storage root yield of cassava is highly affected by genotype by environment (GEI) interactions. The objectives of this study were to assess the nature and magnitude of GxE interactions of cassava genotypes based on environment evaluation trials and to identify mega-environments for future breeding strategies. The study was conducted across six environments in southwest Ethiopia. Ten cassava genotypes and one local check were evaluated by using a randomized complete block design with three replications. Data from totalstorage root yield, root dry weight and root diameter were collected and analyzed using the additive main effect and multiplicative interaction and genotype main effect plus genotype by environment interaction bi-plot analyses. The combined analysis of variance showed significant variation for genotypes, locations, and crop year and their interactions for root dry weight and root diameter. Genotypes 8 (AAGT 191) and 6 (AAGT 108) had broad adaptability for total storage root yield, whereas, genotypes 7 (AAGT 189), 11 (local), 10 (AAGT 200) and 4 (45/72NW) were superior for root dry weight. For high total storage root yield and root dry weight, environments 2 and 4 were epitome and highly close to the ideal environment. Overall, environment 4 was the most suitable environment for discriminating among genotypes and for being a representative test environment. Three mega-environments (MGE) were identified from this study for cassava breeding; where environments 2, 5 and 6 combined into MGE-1, environments 3 and 4 fell into a separate MGE-2 and MGE-3, respectively.

Keywords: Adaptability, Bi-plot, Cassava, Genotype, Mega- Environment , Root yield, Stability.

Introduction

Cassava (*Manihotesculenta* Crantz) is an important staple crop in tropical and sub-tropical areas of the world (Joseph *et al*., 2020a; Bright *et al*., 2020). It is the sixth most important food crop globally, in terms of annual production (Aina *et al.*, 2009; Joseph *et al*., 2020b). The crop is mainly grown

for staple food of an estimated 800 million people worldwide (Tewodros *et al*., 2020; Bright *et al.,* 2020) and has the ability to give better and appreciable yields than most staple crops in areas where drought and poor soils prevails (El-Sharkawy, 1993). Cassava plays several important roles in Africa serving as a rural staple food, famine-reserve and cash crop for households and as a raw material for industrial manufacturing (Felix and Dunstan, 1995; Séri *et al*., 2013; Edwige *et al.,* 2021).

Although reliable statistical information on the distribution and production of cassava in Ethiopia is lacking, the crop has been cultivated in diverse environmental conditions in South, South West, and Western parts to overcome hunger and make a significant contribution in the diets of the people (Tewodros and Zelalem, 2015; Bright *et al.,* 2020). Furthermore, the crop is gaining fast popularity as an important industrial raw material in Ethiopia, leading to its widespread cultivation in different areas of the country (Séri *et al*., 2013; Mehari *et al*., 2015). To satisfy the growing demand of producers and consumers, cassava production needs to be extended to different parts of the country (João *et al.,* 2013). Cassava genotypes evaluated for yield in multi-location trials, wide differences are frequently observed in yield performances of the genotypes over the growing environments. This wide agro-ecological variability is the major challenge for cassava due to high genotype x environment interaction (GEI) effect (Adetoro *et al.,* 2021). In this regard, there is few efforts so far done on evaluation of cassava genotypes for yield and yield related traits in diverse environments of Ethiopia (Tesfaye *et al.,* 2017). Further, Tewodros *et al.,* (2020) reported appraisal of better type cassava genotypes for yield and quality traits in different agroecologies of southwest Ethiopia. Identification of yield contributing traits and knowledge of GEI along with root yield stability have tremendous impact for breeding of new varieties with good adaptation in the target environments (Aina *et al.,* 2009; Edwige *et al.,* 2021). The study of GEI also support cassava breeders to develop strategies for testing and selecting genotypes most adapted to the target environments under which the genotypes will be grown (Adjebeng *et al.,* 2017).

There are two dominant statistical models in G×E study, which are the additive main effect and multiplicative interaction (AMMI) and genotype plus genotype × environment (GGE) bi-plot methods (Yan *et al.,* 2000). The models can provide valuable insights in assessing the extent of G×E interactions in multi-environmental trials of cassava in Ethiopia. The current study was, therefore, designed to assess the nature and magnitude of GxE interactions and advance insights into mega-environments for cassava in southwest Ethiopia.

Materials and Methods

Description of study areas

The field experiment was conducted at three locations, namely: Jimma, Metu and Tepi Agricultural Research Centers which are considered as the representative cassava growing areas of south-west Ethiopia. The experiment was conducted for two cropping seasons (2015-2018) in all the three locations. This made a total of six environments considering one location and one cropping season as one environment. Jimma Agricultural Research Center is located at 1753 m.a.s.l., 7^o 40.00' N latitude and 36^o 47'.00' E longitude. The area receives mean annual rainfall of 1432 mm with mean maximum and minimum temperatures of 29.2 ^{0}C and 8.90 ^{0}C, respectively. The soil of experimental plot is sandy loam. Metu Agricultural Research Sub-center is situated at a distance of about 625 km to the southwest of Addis Ababa. The site is located at 8°18′ .00' N latitude, 35°35′ .00' E longitude and at an altitude of 1550 meters above sea level. The area receives mean annual rain fall ranging from 1200 to 1520 mm. The average temperature of the area is 20^{0}C. The soil of Metu sub-center is sandy loam. Tepi Agricultural Research Center is located at a distance of about 220 km to the west of Jimma. The site is located at 7^o 40.00' N latitude, 36^o 47'.00' E longitude and an altitude of 1200 meters above sea level.

Plant materials, experimental design and management

A total of 11 cassava genotypes collected from major growing areas of southwest Ethiopia were used for this study. The list of genotypes and areas of collection were presented in Table 1. The experiment was laid out in randomized complete block design with three replications in each environment. Each cassava genotype was assigned to one plot in each replication. The gross plot size for each treatment was 6m x 4m, using inter-row spacing of 1m and intra-rows spacing of 1m. Cuttings of the same size and age were used as planting material. Planting was done mid April during the main growing season of 2015-2018 following the the start of rain and sufficient soil moisture . One month after planting, seedlings were earthed up followed by frequent weeding. All other recommended agronomic practices were applied. Local materials were collected from respected tested locations of Jimma, Metu and Tepi areas.

Data collection

Data were collected from eight plants from each plot and the average values were used for data analysis. The characters that used for data collection were: total root yield (TRY) (t/ha), root dry weight (RDW) (t/ha), and root diameter (RDi) (cm).

Table 1. List of 11 cassava genotypes and their areas of collection

No	Genotypes	Zone	District	Latitude	Longitude	Altitude
1	44/72NR	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
2	44/72NW	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
3	45/72NR	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
4	45/72NW	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
5	AAGT 028	Jimma	Dedo	07°31'28N	036°53'63E	1683
6	AAGT 108	Bench maji	Sheko	07°02'91N	035°29'76E	1668
7	AAGT 189	Sheka	Yeki	07°11'22N	035°26'25E	1192
8	AAGT 191	Sheka	Yeki	07°11'22N	035°26'25E	1192
9	AAGT 192	Sheka	Yeki	07°11'30N	035°26'22E	1171
10	AAGT 200	Bench maji	Sheko	07°04'13N	035°37'74E	1320
11	*Local					

*Local materials were collected from respective testing locations around Jimma, Bench-maji and Sheka zones of southwest Ethiopia

Data analysis

The collected data were subjected to analysis of variance (ANOVA) for each location and combined over environments following the standard procedure using SAS software suggested by Fekadu *et al.* (2017) and Genstat software as prescribed by Malhotra *et al*., (2007). The mean trait value across six environments was used in this analysis. Comparison of treatment means was done using the Fisher's protected least significant difference (LSD) test at 1% and 5% probability. A second ANOVA was conducted to determine the main and interaction effects of genotype, environment, and crop-year.

The total root yield (TRY), RDW and RDI were subjected to the combined analysis of variance and AMMI analysis, which is a combination of analysis of variance and multiplicative effect analysis. The analysis of variance was used to partition variances into three components: genotype deviations from the grand mean, environment deviations from the grand mean, and G×E deviations from the grand mean. Subsequently, the multiplicative effect analysis was used to partition G×E deviations into different interaction principal component axes (IPCA), which were tested for statistical significance through ANOVA. To determine the G × E interaction for yield parameters, AMMI and GGE bi-plot analyses were performed. The following AMMI model was used (Gauch, 2013). Genotypic stability for each genotype will be computed using GenStat software, as prescribed by Malhotra *et al*.. (2007). The additive main effects and multiplicative interactions (AMMI) statistical model reported by Gauch and Zobel, (1996) was used to analyze yield data to obtain (AMMI)

analysis of variance and (AMMI) mean estimates as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda_n y_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

Where, Y_{ger} = yield of genotype g in environment e for replicate r, μ = grand mean, α_g = genotype mean deviation (genotype means minus grand mean), β_e = environment mean deviation, n = number of principal component analysis (PCA) axes retained in the model, λ_n singular value for PCA axis n,y_{gn} = genotype eigenvector values for PCA axis nδ_{en} = environment eigenvector values for PCA axis n, ρ_{ge} = residuals, E_{ger} = error term.

The AMMI stability value (ASV) proposed by Purchase *et al.,* (2000) used to quantify and rank genotypes based on yield stability. The ASV has been defined as the distance from the coordinate point to the origin in a two dimensional scatter plot of first interaction principal component axis (IPCA1) scores against the second interaction principal component axis (IPCA2) (Adjebeng *et al.,* 2017; Atung and Jeffrey, 2018). Since IPCA1 accounts for most of the GE variation, the IPCA1 scores are weighted by the ratio of IPCA1 SS (from AMMI ANOVA) to IPCA2 SS in the ASV were calculated by using the formula (Purchase *et al.,* 2000) .

$$\mathbf{ASV} = \sqrt{\left[\frac{\mathbf{SSIPCA1}}{\mathbf{SSIPCA2}}(\mathbf{IPCA1\ score})\right]^2 + (\mathbf{IPCA2\ score})^2}$$

Where, Where: $IPCA1_{Sum\ of\ squares}$/ IPCA2 Sum of squares is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares (from the AMMI analysis of variance table) by the IPCA2 sum of squares. The larger the IPCA score is, either negative or positive, the more adapted a genotype is to a certain environment. Smaller ASV scores indicate a more stable genotype across environments

Yan *et al.,* (2007) reported that genotype and genotype-by-environment effects must be considered simultaneously to make a meaningful decision in selection. Significant genotype by environment interaction was also analyzed by a GGE bi-plot which was also useful in ranking genotypes based on their average performance and stability for farmer preferred traits in cassava. The GGE bi-plot model was also used to determine the influence of GEI on total root yield, root dry weight and root diameter across test environments.The model for the GGE bi-plot based on singular value decomposition (SVD) of first two principal components were calculated by using the model (Yan *et al.,* 2007):

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where: Y_{ij}= measured mean of genotype i in environment j, μ= grand

mean, β_j = main effects of environment j, $\mu + \beta_j$ = the mean yield across all genotypes in environment j, λ_1 and λ_2= are the singular values (SV) for the first and second principle components (PCA 1 and PCA 2) respectively.ξ_{i1}andξ_{i2} = are eigenvectors of genotype i for PCA 1 and PCA 2, respectively, η_{j1} andη_{j2} = eigenvectors for environment j for PCA 1 and PCA 2, respectively.ε_{ij}= residual associated with genotype i in environment j.

Results and Discussion

Analysis of variance

The combined analysis of variance (ANOVA) was performed to determine the effects of year (Y), location (L) and genotype (G) as presented in Table 2. Variance due to locations (L) were highly significant ($p \leq 0.01$) for all the traits studied. Similarly, genotype (G) was highly significant ($p \leq 0.01$) for RDW, conversely, RDi was significant only at $p \leq 0.05$. Likewise, year (Y) was highly significant ($p < 0.01$) for all the traits, except for TRY that was significant only at $p \leq 0.05$. The Y x L interactions were highly significant ($p < 0.01$) for all the traits considered in this study. Equally, the G x Y were highly significant ($p \leq 0.01$) for RDW, and RDi that was significant only at $p \leq 0.05$. The triple interaction effect, G x Y x L, was highly significant ($p \leq 0.01$) for RDW and RDi and non-significant for TRY (Table 2). The non-significant interaction between genotype, location, and year (environment) (G x Y x L) for TRY of cassava support no need for multi-locational testing to identify good performers for specific locations. The significance of the year effects however indicates to the unpredictability of the cassava growing seasons in southwest Ethiopia and suggests the need to evaluate for more than two year for reliable inferences to be made on performance (Semakula and Dixon, 2007) within the overall focus of the development of stable genotypes in terms of yield and yield related traits of cassava. The significant morphological traits for the nvironments (as derived from location, year, and their interaction) showed significant variation that can be stimulated from the genotypes. The additional significant genotypic effect points to indicated genotypic differences for the traits and the possibility of selection for adaptation to specific environments. These observations are consistent with those of Tesfaye *et al*., (2017) had observed similar results when seven cassava genotypes were evaluated across four locations in Ethiopia. This consistency further prompts the need for further recombination of genes to select higher performing genotypes (Adetoro *et al.,* 2021).

Table 2. Combined analysis of variance and significant tests for cassava yield and related traits of 11 genotypes tested during 2015-2018

Sources of variation	DF	TRY	RDW	RDi
Location (L)	2	8774.4**	17537.9**	11628.9**
Genotype (G)	10	367.04	743.47**	53.9*
Year (Y)	1	904.06*	68689.5**	9854.5**
Y*L	2	3787.53**	43095.45**	10692.61**
G*L	20	328.91	490.58**	45.83*
G*Y	10	297.98	540.07**	47.30*
G*Y*L	20	244.28	3220.63**	710.23**
Error	130	272.06	233.30	30.13

*, **significant at 0.05 and 0.01% of probability level; TRY= Total root yield; RDW= Root dry weight, RDi= Root diameter, Y = Year, L = Location, G = Genotype, Rep= Replication

The results further indicated the importance of testing genotypes in more locations as is currently practiced in order to preserve the high levels of genotype stability and wide adaptability. The environmental effect influencing TRY was reported in different cassava studies Aina *et al.* (2007); Agyeman *et al.,* 2015; Tesfaye *et al*., (2017) reported in multi-location yield experiments, location accounted for about 92%, 85% and 69% of the total variation, whilst genotype and G×E interaction combined contribute to 4.62 and 8.27% of the total variation. In this regards, dissimilar reports obtained from Adetoro *et al.*, (2021) who reported high significant difference on genotype, location and year on TRY of cassava genotypes collected from Nigeria. This difference might be due to the fluctuation of environments in all tested areas.

Additive main effects and multiplicative interaction analysis (AMMI)

The enormous G×E interaction was examined further by using AMMI and GGE bi-plot analysis (Yan and Tinker, 2006). The AMMI analysis of variance showed highly significant effects ($p \leq 0.01$) of genotypes, environments, and GEI on cassava yield and related traits (Table 3). Genotype, environment, and GEI contributed 8.31%, 58.96% and 32.72%, respectively, to the total variation observed in TRY. Interaction principal component axes (IPCA 1 and IPCA 2), on the other hand, were non-significant ($p > 0.05$) for IPCA 2 except for IPCA 1, which was significant only at the 5% level of probability, and explaining 44.55% and 31.84% of the total GEI. The percent of variation of genotype, environment and GEI on TRY obtained from this study is comparable with the report of Atung and Jeffrey, (2018).

Table 3.AMMI analysis of variance for cassava yield and related traits of 11 genotypes tested across six environments in Southwest Ethiopia during 2015-2018

		Total root yield (TRY)				**Root dry weight (RDW)**				**Root diameter (RDi)**			
Source of variation	DF	SS	MS	Variation explained (%)	GxE Explained (%)	SS	MS	Variation explained (%)	GxE Explained (%)	SS	MS	Variation explained (%)	GxE Explained (%)
Treatments	65	44142	679.1**	67.28		224072	3447**			57295	881**	96.05**	
Genotypes	10	3670	367.0	8.31		7435	743**	3.31		539	54**	0.94*	
Environment	5	26028	5205.6**	58.96		189956	37991**	84.77		54498	10900**	95.11**	
Block	12	2698	224.8	6.11		8028	669**	3.58		682	57*	1.19**	
Interactions	50	14444	288.9	32.72		26681	534**	11.90		2259	45*	3.94**	
IPCA-1	14	6435	459.6 *		44.55	24684	1763**		92.51	2198	157**		97.30
IPCA-2	12	4600	383.4^{ns}		31.84	1106	92^{ns}		4.14	34	3^{ns}		0.05
Residuals	24	3409	142.0^{ns}		23.60	891	37^{ns}		3.34	26	1^{ns}		0.04
Error	120	32962	274.7	74.67		23085	192			3398	28	5.93	

Df. degrees of freedom, ns: non-significant (P > 0.05); *, ** significant at p ≤ 0.01. SS= Sum of square, and MS= Mean square

For RDW, genotype, environment and GEI contributed 3.31%, 84.77% and 11.90% to the total variance explained, respectively. Only IPCA 1 was highly significant ($p \leq 0.01$). IPCA 1 and IPCA 2 scores explained 92.51% and 4.14% of the total GEI, respectively. Comparatively, this result was slightly lower than the report of Adetoro *et al*., (2021) on cassava genotypes from Nigeria. For RDi, the total variation contributed by genotype, environment, and GEI was 0.94%, 95.11% and 3.94%, respectively. The two IPCAs accounted for 97.35% of the total GEI explained, each contributing to 97.30% (IPCA 1) and 0.05% (IPCA 2)(Table 3). Similarly, higher total variation was reported by Akinwale *et al.,* (2011) and Aina *et al.,* (2009) on cassava genotypes from Nigeria.

Performance of genotypes across individual locations

The mean TRY, RDW and RDi of cassava genotypes across six environments was presented in Table 4. On average, genotypes 45/72NW, AAGT 108 and respective local check had the highest mean yield across environments.Genotype 45/72NR had lowest mean total root yield of all genotypes across environments. Highest RDW was observed in the environment-4, followed by environment-2 and environment-3 (Table 4). On average, genotypes 44/72NR and AAGT 028 produced the highest and the lowest root dry weight, respectively. This finding was consistent with the result of Alex *et al.,* (2021) who reported higher mean storage tuber yield of cassava (41.26 t/ha) genotype from Adjumani district of Uganda.

Similarly,the highest RDi was observed from genotypes 45/72NW, AAGT 189 and AAGT 108 with a value of 62.10, 57.17 and 55.20 cm, respectively (Table 4). Environment-6 and environment-2 were the best environments for the RDi with mean value of 63.92 and 62.91 cm, respectively (Table-4). In this regards, different scholars reported the highest and lowest root yield and related traits performances of cassava genotypes in different countres, for example Yan and Tinker (2006) and Adetoro *et al.,* (2021) from Nigeria; Tesfaye *et al*., (2017) from Ethiopia. The environments contributed significantly to the differential performance of genotypes across environments resulting in either cross over or non-cross over GxE. According to Yan *et al*., (2000) and Jandong *et al*., (2019) who reported that the cross over effects as a significant change in performance from one environment to another, while in non-crossover interaction, a ranking of genotypes remains constant across the environment.

AMMI stability value (ASV)

The AMMI stability values revealed variations in TRY and related traits stability among the 11 genotypes (Table 5). For TRY, genotype AAGT 108 was highly stable, with an ASV value of 1.18. while, 45/72NW and 44/72NW were among the least stable genotypes; other genotypes had intermediate stability.

Table 4.Mean TRY (t/ha), TDW (t/ha) and RDi(cm) performance of 11 cassava genotypes tested across six environments.

Genotypes	TRY						Over all Mean	TDW						Over all Mean	RDi						Over all Mean
	Environments							Environments							Environments						
	E-1	E-2	E-3	E-4	E-5	E-6		E-1	E-2	E-3	E-4	E-5	E-6		E-1	E-2	E-3	E-4	E-5	E-6	
44/72NR	37.1	59.4	30.8	18.6	44.9	38.1	38.1	9.09	25.6	74.3	58.4	19.4	9.41	**32.70**	49.0	54.2	44.5	36.9	48.8	42.1	45.91
44/72NW	39.7	67.9	31.7	18.2	50.5	39.5	41.3	9.94	27.3	32.8	55.5	20.2	11.2	26.17	47.3	56.4	47.9	39.7	52.5	42.8	47.79
45/72NR	32.3	47.7	23.5	23.3	33.9	48.2	34.8	4.50	24.9	52.1	58.1	13.6	12.9	27.71	28.8	61.4	44.2	41.5	41.3	75.3	48.78
45/72NW	43.7	83.3	27.0	24.8	56.8	65.4	**50.2**	13.1	37.0	26.6	19.1	20.0	31.7	**24.59**	53.9	74.2	54.8	52.8	54.1	82.5	**62.10**
AAGT 028	40.6	56.6	32.3	30.6	42.9	52.0	42.5	11.4	29.8	5.63	14.8	18.3	23.2	17.21	39.9	60.9	46.5	41.9	46.8	63.6	49.96
AAGT 108	43.7	59.3	36.8	31.8	46.6	44.4	**43.8**	14.9	27.4	22.9	25.1	23.0	16.2	21.60	57.0	65.4	48.2	44.7	49.3	66.6	**55.20**
AAGT 189	38.2	69.1	25.0	22.0	47.6	53.0	42.5	11.1	31.6	4.91	87.7	19.0	22.9	**29.55**	62.7	67.6	46.8	45.2	46.9	73.8	**57.17**
AAGT 191	42.6	54.9	37.8	30.9	44.5	35.4	41.0	12.1	23.9	20.2	57.2	18.5	17.0	24.85	49.3	62.2	46.8	42.4	47.8	62.8	51.89
AAGT 192	40.4	43.6	36.8	34.9	39.9	44.9	40.1	10.7	26.2	17.2	19.8	18.0	17.7	18.28	47.0	62.8	47.1	43.0	47.6	65.2	52.13
AAGT 200	44.3	65.5	37.7	26.8	51.2	28.7	42.4	15.2	28.7	38.6	16.1	24.6	14.1	22.91	60.3	62.5	47.7	42.7	50.6	56.8	53.46
Local	40.1	74.3	25.3	23.0	50.8	58.7	**45.3**	12.3	34.3	18.8	16.5	19.9	26.7	21.46	52.0	64.1	45.0	42.7	44.4	71.5	53.28
Mean	40.3	61.9	31.3	25.9	46.3	46.2	42.0	11.3	28.8	28.5	38.9	19.5	18.5	24.27	49.8	62.9	47.2	43.0	48.2	63.9	52.52
$LSD_{(0.05)}$	12.9	22.9	17.4	10.4	27.5	30.6	10.9	6.8	10.3	0.02	4.8	13.4	12.7	11.7	21.8	0.81	2.94	1.05	1.5	1.36	3.85
$CV_{(\%)}$	18.9	39.5	32.6	23.7	35.1	42.2	40.2	34.4	40.3	10.9	30.1	40.4	40.4	51.4	25.7	13.8	36.6	14.4	19.3	12.5	46.0

E=Environments, TRY= Total root yield; RDW= Root dry weight, RDi= Root diameter

CV=Coefficent of variation(%), LSD= Least significant difference at 5% level of probablity

For RDW, genotypes 45/72NR was highly stable with ASV values of 1.46; whereas genotype AAGT 108 remained the least stable among others (ASV of 3.96). For RDi, genotypes AAGT 191, 44/72NR and local were the most stable, with ASV values of 0.14, 0.94 and 0.95, respectively; whereas genotypes AAGT 189 and AAGT 200 were the least stable genotypes due to higher ASV values. On the other hand, data in Table 6 showed that environments ENV-1 and ENV-5 had a low ASVs score in TRY as compared to RDW and RDi and these environments were considered highly discriminating of genotypes. Comparatively, similar ASV vslues were reported by Esther *et al.*, (2020) on taro genotypes from Ghana. The AMMI model does not make provision for a quantitative stability measure (Atung and Jeffrey, 2018; Jandong *et al.*, 2019). Such a measure is essential in order to quantify and rank genotypes into their TRY stability.

The ASV measure was proposed by Yan *et al*., (2007) to cope with this problem. The ASV is the distance from zero in a two-dimensional scatter gram of IPCA1 scores against IPCA2 scores. Since the IPCA1 score contributed more to G × E sum of squares, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total G × E sum of squares. In the ASV method, a genotype with the least ASV score is the most stable. Accordingly, genotype AAGT 108 (TRY), 45/72NR (RDW) and AAGT 191 (RDi) were the most stable. Therefore, these genotypes can be used as checks in genotype evaluations. According to Atung and Jeffrey, (2018), the larger the ASV value, either negative or positive the more specifically adapted a genotype was to certain environments. However, according to Purchase (1997), a small ASV value indicated a more stable genotype across environments (Purchase, 1997).

Additive main effect and multiplicative interaction bi-plot analysis

The AMMI 2 bi-plot analysis was conducted by plotting IPCA 1 scores against IPCA 2 scores for genotypes and environments. The AMMI 2 bi-plot analyses of TRY, RDW, and RDi of the 11 genotypes evaluated in six environments are shown in Figure 1a-c, respectively. For TRY, the percentage of variation accounted by the IPCA 1 and IPCA 2 axes was 44.55% and 31.85%, respectively (Figure 1a). Comparatively, this result was lower than the report of Adetoro *et al*., (2021) on the percent variation of the IPCA 1 (56.4%) and IPCA 2 axes (32.91%) for storage root yield of cassava genotypes from West Africa. Genotypes 8 (AAGT 191) and 6 (AAGT 108) had broad adaptability as they were located closer to the center of the bi-plot. Genotypes 4 (45/72NW), 11 (local), 2 (44/72NW), and 1 (44/72NR) are placed furthest from the point of origin, showing specific adaptation to the environments within their proximity on the bi-plot Similar findings reported by Akinwale *et al*, (2011) on 43 cassava genotypes at three different agro-ecologies of Nigeria.

Table 5.AMMI stability values (ASV) and IPCA scores TRY, RDW and TDi of 11 genotypes tested in six environments in SW Ethiopia during 2015-2018

Genotype	**TRY**				**RDW**				**RDi**			
	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV
44/72NR	34.82	2.77	-1.21	3.24	20.19	1.26	1.50	2.29	11.94	-0.06	-0.93	0.94
44/72NW	37.95	2.74	-2.41	4.23	20.75	1.65	1.30	2.61	11.88	0.32	-1.08	1.29
45/72NR	34.85	-1.59	1.9	2.77	18.15	1.05	-0.23	1.46	9.20	1.67	0.52	3.73
45/72NW	50.20	-3.07	-2.37	4.56	32.44	-1.00	-2.44	2.80	14.31	-0.54	0.56	1.32
AAGT 028	42.52	-1.01	1.56	2.02	32.84	-1.79	-1.02	2.66	10.99	1.69	-0.06	3.74
AAGT 108	43.81	0.39	1.07	1.18	34.83	-2.74	1.23	3.96	14.07	-1.23	0.14	2.73
AAGT 189	42.50	-1.9	-1.08	2.64	28.81	0.87	-0.97	1.54	15.12	-2.20	0.60	4.91
AAGT 191	41.04	1.53	1.28	2.33	37.81	-1.10	0.40	1.56	12.59	0.06	-0.03	0.14
AAGT 192	39.59	0.28	3.62	3.64	31.79	-1.49	0.05	2.05	12.26	0.48	0.04	1.06
AAGT 200	42.38	2.35	-0.84	3.10	30.45	0.09	1.76	1.76	14.40	-1.87	-0.27	4.15
Local	45.37	-2.5	-1.52	3.52	30.29	-1.17	-1.54	2.23	13.13	-0.37	0.49	0.95

IPCAg = integrated principal component analysis, TRY=total root yield per hectare, RDW = root dry weight, RDi = root diameter

Table 6. AMMI stability values (ASV) and IPCA scores TRY, RDW and RDi of six environments tested 11 genotypes in SW Ethiopia

Genotype	TRY				RDW				RDi			
	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV
ENV-1	40.26	1.42	0.41	1.60	11.32	1.40	1.28	1.98	9.77	-1.74	0.03	2.60
ENV-2	61.99	-0.56	-4.53	4.57	28.33	2.18	-1.03	2.57	6.29	0.90	0.09	1.35
ENV-3	31.36	2.92	1.76	3.63	11.00	1.88	1.16	2.34	4.72	0.95	-0.54	1.52
ENV-4	25.93	0.99	2.89	3.08	15.40	-2.67	0.20	2.89	4.30	0.94	-0.17	1.42
ENV-5	46.08	1.00	-2.11	2.37	19.52	1.74	1.93	2.70	4.82	0.89	-0.89	1.60
ENV-6	42.59	-5.78	1.57	6.47	18.48	1.46	-3.37	3.72	6.39	1.05	1.49	2.17

IPCAg = integrated principal component analysis, total root yield per hectare (TRY), root dry weight (RDW), root diameter (RDi)

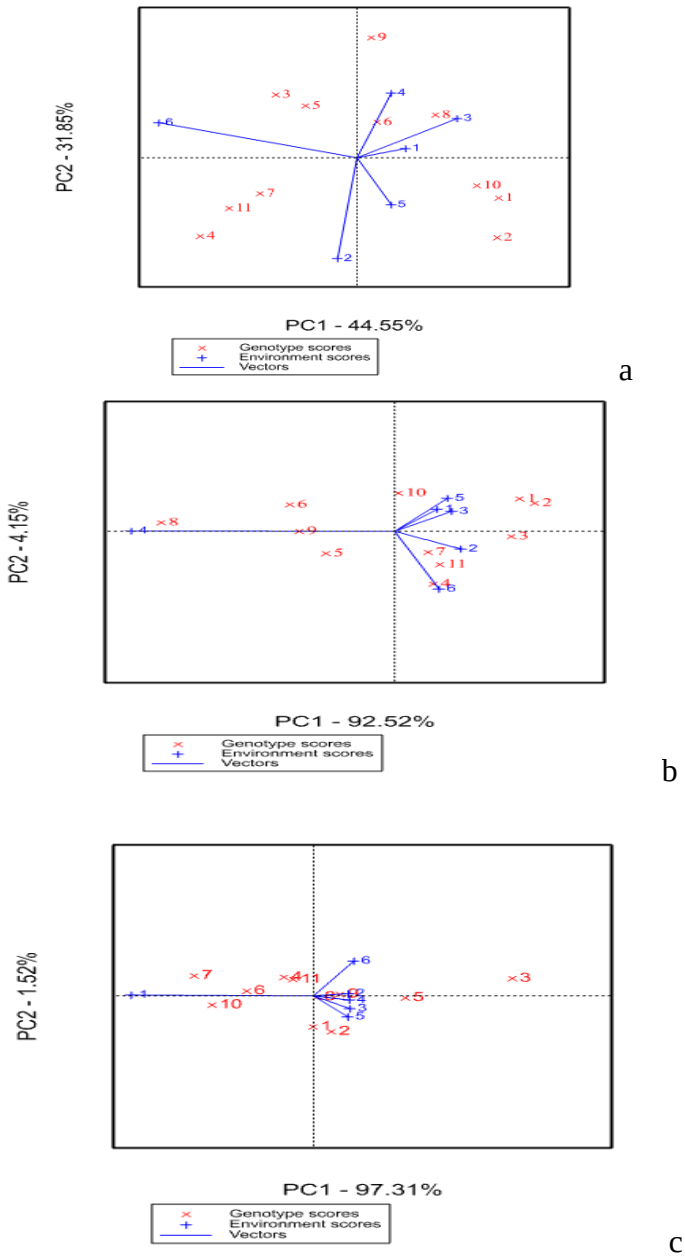


Figure 1a-c. AMMI 2 bi-plot for IPCA 1 against IPCA 2 scores for 11 cassava genotypes and six environments on (a) total root yield (TRY), (b) root dry weight (RDW) and (c) root diameter.

Moreover, genotypes 9 (AAGT 192), 8 (AAGT 191), and 6 (AAGT 108) had above-average yields and were located at the acute angle of PC1. Genotypes located on the right-hand side of the bi-plot were positively correlated with the environments on the same side. Based on this analysis, environment 6 was considered highly discriminating and had similar discriminating ability of the site since it had longer vector. Environments 1, 3 and 4, were highly positively correlated, indicating that genotypes ranked similarly with respect to TRY in these environments. This suggested that these environments might form part of the same mega-environment.

For RDW, the AMMI-2 bi-plot explained 96.67% of the total GEI (Figure.1b). The percentage of variation accounted for by IPCA-1 and IPCA-2 was 92.52% and 4.15%, respectively. According to Adetoro *et al*., (2021), the percent variation of the IPCA 1 and IPCA 2 axes was 84.1% and 12.93%, respectively. On the other hand, Fekadu *et al*., (2017), reported the variation of the IPCA 1 (61.63%) and IPCA 2 axes (13.99%) for root dry weight of orange fleshed sweet potato genotypes from South Ethiopia. Genotypes 7 (AAGT 189), 11 (local), 10(AAGT 200) and 4 (45/72NW) were close to the bi-plot origin; these genotypes had yields close to the overall mean yield. The following genotypes were positively correlated with environments closer to them: 10 (5), 7 and 11 (2), 4 (6)and 8 (4). Genotypes located on the right-hand side of the bi-plot were positively correlated with the environments found on that side. To that extent, environment 4 highly discriminating in this analysis. This environment showed high discriminating ability based on longer vector. Environment 3 and 2 had longer vectors, indicating the similar discriminating ability of the site at different right angles. Environment 1 had the shortest vector, suggesting poor genotype discriminating ability.

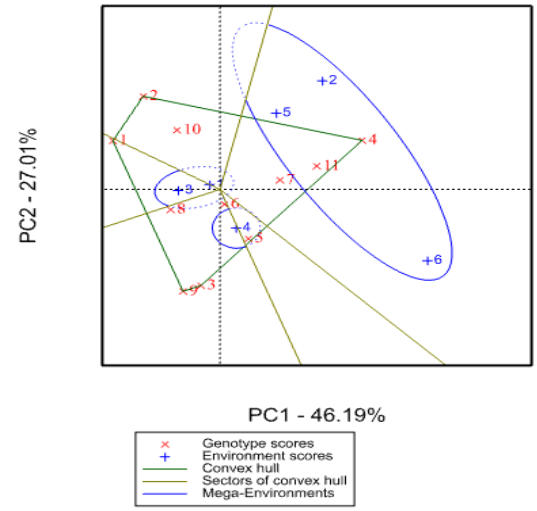
The percentage of variation of AMMI 2 bi-plot for RDi accounted for by IPCA 1 and IPCA 2 was 97.31% and 1.52%, respectively (Figure.1c). Genotypes 1 (44/72NR), 2 (44/72NW) and 5 (AAGT 028), 8 (AAGT 191), 9 (AAGT 192) were much closer to the bi-plot center, showing broader adaptability across the environments and had positively correlated with environments located on the right-hand side of the bi-plot. Genotype 1 (44/72NR) was positively correlated with environment 5 (AAGT 028), suggesting specific adaptation to this environment. In this analysis, except environment 1, all environments had shorter vectors, which imply the low discriminating ability of the site. Most environments in this study had positive correlations. This was expected, since almost similar

environmental conditions existed between environment 1 and 2, and 3, 4 and 5 and 6 (Table 2). The positive correlation obtained between test environments also suggests that indirect selection for TRY can be applied across the sites (Otoo *et al*., 1994). Combining these environments into a single test environment can give similar genotypic responses, thus reducing unnecessary costs and improving breeding efficiency (Gauch and Zobel, 1997). For TRY, which is the trait of economic interest, environment PC1 had both positive and negative scores. Similar results were reported by Aina *et al*. (2007) indicated the existence of cross over G×E interactions. Genotypes with large PC1 scores can be easily recognized in environments with larger PC1 scores (Yan *et. al.,* 2007; Agyeman *et al.,* 2015).

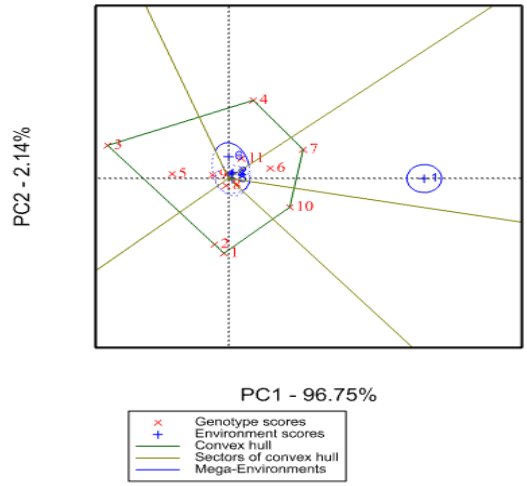
Mega-environment analysis using GGE bi-plots

The polygon views of the GGE bi-plot for TRY, RDW and RDi are shown in Figure. 2a-c, respectively. In each bi-plot, different mega environments (MGEs) were grouped into sectors. Environments within the same MGE were assumed to have a similar effect on genotype performance and were considered a homogeneous group. Similarly, genotypes within the same MGE were assumed to have a similar response to the environments located in the MGE sector. The genotype located at the vertex of the sector was considered the best-performing variety in the MGE. For TRY (Figure. 2a), principal component 1 (PC1) explained 46.19% of the total variation, while PC 2 explained 27.01%, with both axes accounting for 73.20% of the total variation. Perpendicular lines were drawn to each side of the polygon, all lines starting from the bi-plot origin.

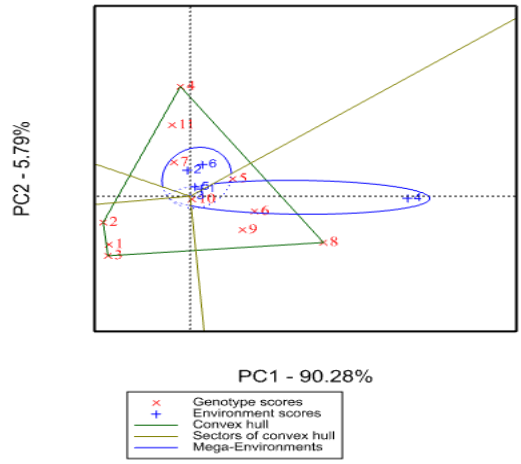
In this analysis, three mega-environments were found, environments 2, 5 and 6 combined into MGE-1, environments 3 and 4 fell into a separate MGE-2 and MGE-3, respectively. Genotypes 4 (45/72NW), 7 (AAGT 189) and 11 (local) were the highest-yielding genotype in MGE-1. Genotype 5 (AAGT 028) won in the MGE-2. Genotype 8 (AAGT 191) was positively correlated with the environment 4 site and was the winning genotype in MGE-3.



a



b



c

Figure 2a-c. The "which-won-where" polygon view for (a) TRY , (b) RDW and (c) RDiof the GGE bi-plot analysis representing the performance of 11 cassava genotypes tested across six environments

For RDW, the percentage of GGE explained by PC 1 and PC 2 was 90.28% and 5.79%, respectively (Figure. 2b). The bi-plot explained 96.07% of the total variation. The bi-plot consisted of two MGEs; where environments 2, 6 and 5 are combined into MGE-1;environments 1, 3, and 4 fell to form MGE-2. Perpendicular lines were drawn to separate the respective sides of the polygon. Genotypes 7 (AAGT 189), 4 (45/72NW) and 5 (AAGT 028) were the highest yielding vertex genotype in MGE-1, whereas genotype 6 and10 was the winner in MGE-2. Similarly,

for RDi, the percentage variation accounted for by PC 1 and PC 2 was 96.75% and 2.14%, respectively (Figure. 2c); the total variation explained by the bi- plot was 98.89%.In this bi-plot, only two mega-environments were found; whereenvironments 2, 3, 4 5 and 6 combined into MGE-1 and environment 1 was fell in MGE-2. Most genotypes were the highest-yielding vertex cultivar in MGE-1, whereas, genotype 7 (AAGT 189) and 10 (AAGT 200) was the highest-yielding vertex genotype in MGE-2.

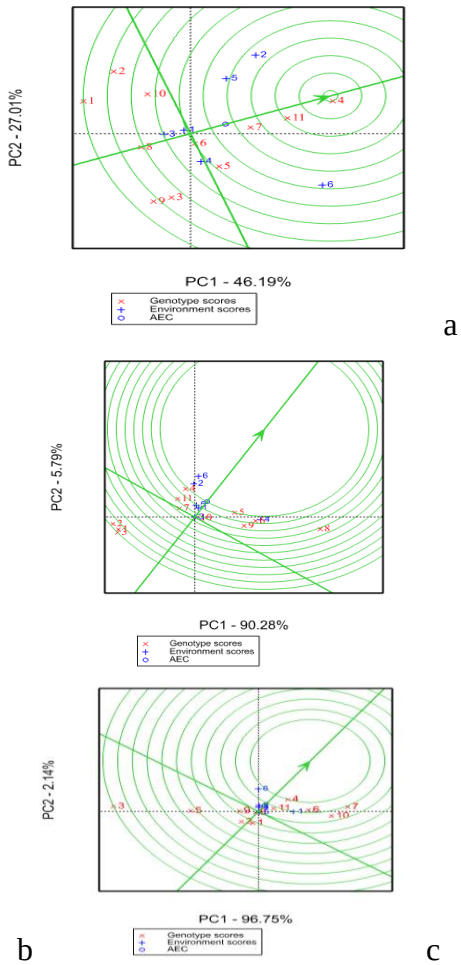
The GGE bi-plots confirm the crossover G × E interactions observed in the AMMI analysis. It is noteworthy that when crossover GEI patterns are not repeatable across years, the GE cannot be exploited (Adetoro *et al*., 2021). Instead, it can be eluded by selecting high yielding and stable genotypes across target environments (Otoo *et al.,* 1994; Sbongeleni *et al*., 2019). The bi-plots on RDW indicated that MGE-1 consisted of environments 2, 6 and 5; while MGE-2 had environments 1, 3, and 4. Since a mega-environment is defined as a group of locations that consistently share the best set of genotypes across years, data from multiple years are essential to decide whether or not the target province can be divided into different mega-environments (Yan *et al.*, 2007).

Genotype yield and stability using GGE bi-plots

For TRY, PC1 explained 46.19% of the variation and PC 2 explained 27.01% and a total of 73.20% of the variation (Figure.3a). This result slightly consistent with the data reported by Dumaetal *et al.,* (2019) who observed that the percentage variation of total cane yield accounted for by PC 1 and PC 2 was 45.19% and 34.93%, respectively. Genotype 4 (45/72NW) was the ideal genotype and, therefore, it was considered the most desirable genotype of all the evaluated genotypes, followed by genotypes 11 (local) and 7 (AAGT 189). The same interpretation is applicable to RDW (Figure. 3b); the percentage of PC 1 and PC 2 were 90.28% and 5.79%, respectively, (96.07% of the total variation). Genotype 5 (AAGT 028) had high RDW and was more stable than other genotypes, confirmed by its closest position to the ideal genotype.

For RDi (Figure. 3c), the PC1 explained 96.75% and PC 2 explained 2.14% of the variation (total = 98.89%). Also lower percent of variation on RDi were reported on different crops, Fekadu *et al.,* (2017) on sweet potato, Atung and Jeffrey, (2018) on taro Tesfaye *et al.,* (2017) on cassava genotypes from Ethiopia. Genotype 4 (45/72NW) was located closer to the ideal genotype, making the highest-yielding and most stable genotype of all genotypes tested. Yan

et al., (2007), suggested that an ideal genotype should have both high mean performance and high stability within a mega-environment. The arrow shown on the axis of the AEC abscissa compares and ranks performance of the test genotypes relative to the "ideal genotype". Yan *et al.* (2000) defined an "ideal" genotype based on both mean performance and stability, and the genotypes types can be ranked based on their distance from the ideal genotype. This study showed that genotype 4(45/72NW) is ideal for TRY and RDi evaluated. This genotype is high yielding and more stable because of proximity to the ideal genotype.



igure 3a-c. The average environment coordination (AEC) view showing mean performance and stabilityof 11 cassava genotypes tested in six environments on (a) Total root yield (TRY), (b) root dry weight (RDW) and (c) diameter (RDi).

Conclusion and Recommendation

The result of this study showed that the storage root yield of cassava was highly affected by genotype and location (environment) and the GEI contributed to the variation among the genotypes studied. This also further indicated the yields and related traits studied were varying across the six environments. Genotypes 45/72 NW, AAGT 108, and AAGT 189 were found to be widely adaptable and had yield stability across environments. Therefore, these genotypes should be recommended for release to farmers in southwest Ethiopia for production. In addition, three mega-environments were identified from the current study, further multi-environment trials (METs) need to be conducted for confirmation of the result for cassava breeding and production in the southwest Ethiopia.

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