Hindawi
International Journal of Agronomy
Volume 2023, Article ID 6759698, 13 pages
https://doi.org/10.1155/2023/6759698

Research Article

AMMI and GGE Biplot Analyses for Mega Environment Identification and Selection of Some High-Yielding Cassava Genotypes for Multiple Environments

Berhanu Bilate Daemo,[1,2] **Derbew Belew Yohannes**,[2] **Tewodros Mulualem Beyene**,[3] **and Wosene Gebreselassie Abtew**[2]

[1]*Department of Plant Science, Wolaita Sodo University, Dawuro Tarcha Campus, P.O. Box 138, Tarcha, Ethiopia*
[2]*Department of Horticulture and Plant Sciences, Jimma University College of Agriculture and Veterinary Medicine, P.O. Box 307, Jimma, Ethiopia*
[3]*Jimma Agricultural Research Centre, P.O. Box 192, Jimma, Ethiopia*

Correspondence should be addressed to Berhanu Bilate Daemo; berhanubil@gmail.com

Received 2 July 2022; Revised 16 January 2023; Accepted 10 March 2023; Published 4 April 2023

Academic Editor: Magdi Abdelhamid

Cassava (*Manihot esculenta* Crantz) is a staple food and generates income for smallholder farmers in southern Ethiopia. The performance of cassava genotypes varies in different growing environments; thus, the evaluation of genotypes tested in various environments plays an essential role in developing strategies to delineate environments, explore unstable genotypes in target environments, and identify stable genotypes for multiple environments. In this regard, there needs to be more information on the identification of mega-environments and stable genotypes with high yields for wide adaptation. Thus, this study aimed to identify mega-environment and high-yielding cassava genotypes for multiple environments using AMMI and GGE biplots. A total of 25 genotypes were evaluated in six environments using a RCBD during the 2020–2021 cropping season. The AMMI analysis of variances revealed that environments, genotypes, and genotype-environment interaction had a significant ($P \leq 0.001$) influence on cassava fresh storage root yield (t·ha^{-1}), showing genetic variability among genotypes by changing environments. The genotype-by-environment interaction showed a 61.36% contribution to the total treatment SS variation, while the environment and genotype effects explained 28.16% and 10.48% of the total treatment SS, respectively. IPCA1 and IPCA2 accounted for 33.42% and 23.5% of the GE interactions SS, respectively. The GGE biplot showed that the six environments used in this study were delineated into three mega-environments, namely, the first (Tarcha and Disa), the second (Wara and Areka), and the third (Jimma and Bonbe). Those mega-environments could be helpful for genotype evaluation and effective breeding. The GGE biplot indicated that the vertex genotypes were G16, G17, and G25. They are regarded as specifically adapted genotypes since they are more responsive to environmental change. The GGE biplot also revealed that Tarcha was ideal, having the most discriminating and representative environment, while G10 was the ideal and the overall winning genotype for the current study. Moreover, the genotypes G10 and G14 were identified as being the most stable, with a higher fresh storage root yield than the grand mean. Thus, G10 and G14 were selected as superior genotypes that could be promoted to advanced yield trials to develop stable cultivars with better storage root yield of cassava.

1. Introduction

Cassava (*Manihot esculenta* Crantz) is grown across the tropics and subtropics for its thick and starchy storage roots [1–3]. Cassava is a woody herbaceous plant that thrives in low fertility and acidic soils and requires little labor demand than other major food crops [4]. It is estimated to be the major source of daily energy for over 800 million people worldwide, with over 500 million of these people living in Sub-Saharan Africa [2, 5]. In 2019, global cassava production

reached 304 million metric tons with an average fresh storage root yield of 11.13 t·ha^{-1} [2]. The new genotype should be superior to the released genotype, and the productivity should be higher than the national productivity [6]. In Ethiopia, cassava is an essential food crop that provides food security and income as well as a significant percentage of the daily diet for humans [7, 8]. Cassava is consumed as a boiled root and processed into flour, which is mixed with cereals such as teff, barley, and wheat for bread or injera preparation [8, 9].

A significant genotype by environment interaction for quantitative traits such as yield can reduce the usefulness of subsequent analyses, restrict the significance of inferences that would otherwise be valid, and severely restrict the possibility of choosing superior genotypes [10–12]. According to Rodrigues et al. [13] and Rodrigues [14], genotype environment interaction is defined by the change in the genetic ranking of genotypes with respect to the environment; for example, a genotype that performs well in well-watered conditions may perform poorly in dry conditions. The ultimate objective of plant breeders in a crop improvement program is to develop genotypes that can be adapted to a wide variety of diverse environments [15]. Yield stability analysis can be performed to find genotypes whose performance holds stable across a range of environments [15, 16]. Hence, comparing performance across environments can assist in identifying the cassava genotypes that perform best in the target environments and those that are most adaptable to multiple environments.

Plant-breeding programs typically conduct rigorous genotype performance evaluations across environments [17]; the occurrence of genotype by environment interaction (GEI) is unavoidable in such multienvironment trials [18]. The effects of genotype and environment interactions are statistically nonadditive, demonstrating that differences in yield among genotypes depend on the environment [19]. As a result, selection strategies based on a genotype's mean yield in a particular environment are ineffective [20]. This has resulted in a greater focus on phenotypic stability in breeding programs [21] as well as a better understanding and application of various stability approaches. According to Ssemakula and Dixon [22], significant GEI variation reduces the relationship between genotype and phenotypic values and lowers yield estimation accuracy. It is also one of the key reasons why formal breeding has not been able to help smallholder farmers in marginalized areas that have limited resources [18].

Plant breeders already have a number of statistical approaches for analyzing genotype-yield adaptability and stability, which can help them with the difficult task of discovering superior genotypes in the context of significant G × E interaction [23]. According to Agyeman et al. [24], AMMI and GGE biplot analyses are two widely used methods for overcoming the problems in multienvironment trial data analysis. The AMMI and GGE biplot models are characterized as powerful tools for analyzing and commenting on multienvironment data structures in breeding operations [25, 26]. These two statistical analyses (AMMI and GGE) are of more interest to agricultural researchers since they apply to any two-way data matrix, such as the number of genotypes tested in a number of locations, and such data can come from many trials [27]. Analysis of variance (ANOVA) and principal component analysis (PCA) are used in these analyses [28]. The difference between GGE biplot analysis and AMMI biplot analysis is that the GGE biplot analysis is based on environment-centered PCA, whereas the AMMI biplot analysis is based on double-centered PCA [29]. As a result, the AMMI and GGE biplot models facilitated visual comparison and identification of superior genotypes for widely adaptable environments and each target set of environments [17].

Despite the fact that cassava is usually adapted to a wide range of environmental conditions, most cultivars are reported to have narrow adaptability and large genotype by environment interaction (GEI) effects [30, 31]. This highlighted the importance of extending research efforts to look at the differences in storage root yield among cassava genotypes across environments. In Ethiopia, the so far evaluation of performance of cassava genotypes in contrasting environments is limited. Therefore, the objectives of this study were to (1) estimate the magnitude of genotype by environment interaction, (2) identify stable genotypes with high storage root yield, and (3) identify mega-environments to guide future testing strategies.

2. Materials and Methods

2.1. Description of Study Area. The field experiment was conducted at six environments in the 2020-2021 main growing season. These locations were different in soil type, altitude, and mean annual rainfall (Table 1). Hence, each location was considered as an individual environment.

2.2. Experimental Materials. Twenty five cassava genotypes were used in the study. From the total genotypes, 4, 16, and 5 were landraces, promising and released, respectively (Table 2).

2.3. Experimental Design and Management. The experiment was laid out in 5 × 5 simple lattice designs. Mature cassava cuttings, measuring 25–30 cm long, were planted in a single row plot of 7 m long with an interrow spacing of 1 m and intrarow spacing of 1 m (7 m^2) on the top of the ridge at an angle of 45° to the ground surface. All cultural practices were conducted as recommended by Markos et al. [33] and farmers' practices in the area. The middle five plants within a row were marked and sampled for the root yield data collection. The fresh storage root yield per plot was weighed and then converted to tons per hectare (t·ha^{-1}).

2.4. Data Analysis. Statistical analyses were conducted using GenStat [34] and GEA-R described by Angela and Vargas [35]. Prior to doing the combined analysis of variance across environments, each environment's data were subjected to the analysis of variance (ANOVA) and normality test. Bartlett's tests of homogeneity of variances were used to

Table 1: Description of the test environments.

Location	Altitude (masl)	Annual rainfall (mm)*	Soil type	Temperature (0°C)		pH
				Minimum	Maximum	
Jimma	1753	1432	Eutric Nitosol	12.00	26.20	5.30
Tarcha	1250	1392	Nitosol	17.00	30.00	5.80
Disa	1244	1151	Alisols	18.00	31.30	5.60
Areka	1800	1530	Nitosol	14.00	25.00	5.20
Wara	1499	1400	Nitosols&alisols	16.50	28.50	5.47
Bobe	1701	1450	Nitosol	15.00	26.00	4.25

Source: climate data were taken from National Meterology Agency (NMA) [32].

Table 2: Description of cassava genotypes used for the study.

Genotype name	Genotype code	Status
AAGT108	G1	Released
Hawassa-04	G2	Released
Qulle	G3	Released
156	G4	Promising
MM 96/9361	G5	Promising
F-100	G6	Promising
M-94/0125	G7	Promising
1062630	G8	Promising
Bajk-1	G9	Landrace
1061630	G10	Promising
196/624	G11	Promising
191/0427	G12	Released
AAGT 192	G13	Promising
200	G14	Promising
AWC-5	G15	Landrace
1980510	G16	Promising
Umvure	G17	Landrace
Kello	G18	Released
45/72 white	G19	Promising
5532-4	G20	Promising
Gamo dhaske	G21	Landrace
46330/12	G22	Promising
1070539	G23	Promising
1038	G24	Promising
869	G25	Promising

determine the homogeneity of the error variances of the individual location experiments, and then the combined analysis of variance across sites was performed after confirming the homogeneity of the variances. The AMMI model was used to generate a combined ANOVA with genotypes as fixed factors and environments as random variables.

2.4.1. AMMI Analysis. A fresh storage root yield analysis was performed for the additive main effect and multiplicative interaction (AMMI) model. In the validity test, the simple lattice design MS component of the block within replication is less than the residual error in all locations; therefore, the analysis of variance was a combined analysis based on the randomized complete block design (RCBD). As described by Gauch [36], the AMMI analysis was used to adjust the main or additive genotype and environmental effects by analysis of variance and the multiplicative effects of the GE interaction by the principal component analysis. Gauch [36] suggested the following model for the AMMI analysis of variance (ANOVA).

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_\kappa \alpha_{i\kappa} \gamma_{j\kappa} + e_{ij}, \quad (1)$$

where Y_{ij} = is the yield of the i^{th} genotype in the j^{th} environment; μ = is the grand mean; G_i and E_j are the genotype and environment deviations from the grand mean, respectively; λ_k = is the eigenvalue of the PCA analysis axis k; α_{ik} and γ_{jk} = are the genotype and environment principal component scores for axis k; n is the number of principal components retained in the model, and e_{ij} is the error term.

2.4.2. AMMI Stability Value (ASV) Analysis. Purchase et al. [37] suggested an ASV measure to quantify and classify genotypes according to their yield stability because the AMMI analysis does not provide a quantitative measure of stability. The ASV is a measure of a genotype's stability. The lower the value, the stronger the stability, according to weighted IPCA1 and IPCA2 scores [37]. The ASV was determined using the following formula:

$$\text{AMMI Stability value (ASV)} = \sqrt{\left[\frac{\text{IPCA1 sum of squares}}{\text{IPCA2 sum of squares}} (\text{IPCA1 score})\right]^2 + (\text{IPCA2 sc})^2}, \quad (2)$$

where (IPCA1 sum square/IPCA2 sum square) is the weight given to the IPCA1 value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares.

2.4.3. Genotype Selection Index (GSI) Analysis. Using the formula GSI = RASV + RY, the genotype selection index was computed [38]. Here, RASV stands for AMMI stability value

ranking and RY stands for genotype mean yield ranking across environments. According to the author, GSI combines mean yield and stability into a single criterion, with a low score indicating stable genotypes with a high mean yield. As a result, the GSI with the lowest value is thought to be the most stable, with the highest storage root yield. The higher the IPCA score, either positive or negative, the better suited a genotype is to specific environments.

2.4.4. GGE Biplot Analysis. The model for a GGE biplot [25], based on singular value decomposition of the first two principal components, is

$$Y_{ij} - \mu - \hat{a}j = \ddot{e}1\,\hat{i}i1\,\varsigma j1 + \ddot{e}2\,\hat{i}i2\,\varsigma j2 + \varepsilon i\,j, \quad (3)$$

where Y_{ij} = is the measured mean of genotype i in the environment j, μ = is the grand mean, âj = is the main effect of environment j, μ − âj = is the mean yield across all genotypes in the environment j, ë1 and ë2 = are the singular values for the first and second principal components, respectively, îi1 and îi2 = are eigenvectors of genotype i for the first and second principal components, respectively, çj1 + çj2 = are eigenvectors of environment j for the first and second principal components, respectively, and $\varepsilon i\,j$ = is the residual associated with genotype i in the environment j.

3. Results and Discussion

3.1. AMMI ANOVA. The AMMI model's analysis of variance for twenty-five cassava genotypes evaluated in six environments were found that environments (E), genotypes (G), and genotype environment interaction (GEI) had a significant ($P \leq 0.001$) influence on the cassava fresh storage root yield (t·ha^{-1}) (Table 3). Additionally, the analysis of variance of the AMMI model indicated that the first two AMMI (IPCA1 to IPCA2) were very highly significant ($P \leq 0.001$). This demonstrated that there was a significant variation in yield performance among the cassava genotypes across the tested environments due to the presence of strong genotype by environment (G × E) interaction. As a result, stable genotypes or entries for a specific environment may be possible. This finding is in line with several studies that have identified significant interactions between cassava genotypes and the environment [16, 30, 39–43].

The total sum of squares factors explained (%) showed that cassava storage root yield was influenced by genotype by the environment (G × E) interaction effect (61.36%), environment effect (28.16%), and genotype effect (10.48%) (Table 3). The GEI sum of squares factor was roughly 6 times larger than the genotype sum of squares factor, indicating that genotypic response varied significantly across environments. Therefore, there is a high possibility of cultivar development for a specific environment since the GE interaction, the sum of squares, contributed more to the total variation. In agreement with these results, Hmwe et al. [43] reported that the genotype by the environment interaction effect accounted for the largest total sum of square, followed by genotype and environment. However, this was contrary to findings from Noerwijati and Prajitno [40], who reported that the environment is the most contributing, followed by the genotype by the environment interaction effect and the genotype effect, while Adjebeng-Danquah et al. [16] reported that the environment contributed a greater proportion of the treatment sum of squares, followed by the genotype effect and genotype by the environment interaction. Both studies reported that the cassava storage root yield was strongly influenced by environmental factors. This indicates that there is a large difference in storage root yield in different environments. However, the large environmental influence is irrelevant to genotype evaluation, while genotype (G) and genotype-by-environment interaction (GEI) are relevant to genotype evaluation [40].

Table 3: AMMI analysis of variance for fresh storage root yield (t·ha^{-1}) of 25 cassava genotypes evaluated in six environments.

Source of variation	DF	SS	MS	(%) SS explained
Total	299	87450	292.5	
Treatments	149	70823	475.3	
Genotypes (G)	24	7520	313.3***	10.48
Environments (E)	5	19796	3959.2***	28.16
Block within E	6	2758	459.7	
Interactions (G°×°E)	120	43507	362.6***	61.36
IPCA 1	28	14555	519.8***	33.42
IPCA 2	26	10365	398.6***	23.5
Residuals	66	18588	281.6	
Error	144	13870	96.3	

Key: *** = highly significant at 1%.

For crossvalidation of the yield variation explained by the GEI, the AMMI with IPCA1 and IPCA2 is the best predictive model [20]. In this study, IPCA1 (33.42%) and IPCA2 (23.5%) each explained a significant portion of the G × E interaction. The IPCA1 and IPCA2 sums of squares combined to contribute 57.17% of the overall GEI, with the first two terms having a sum of squares greater than genotypes. The model explained the entire genotype by environment interaction component well enough [44]. This indicates that the AMMI model with the IPCA1 and IPCA2 was acceptable for crossvalidation of the root yield variation loaded by GEI in the current data set, as it eliminates the majority of the actual variation.

The environment mean storage root yield averaged across the genotypes ranged from 32.88 t·ha^{-1} at Jimma to 60.39 t·ha^{-1} at Tarcha, while genotype mean storage root yield, averaged across the environments, ranged from 38.50 t ha^{-1} (AAGT108 = #G1) to 55.84 t·ha^{-1} (156 = #G4) (Table 4). Some genotypes in the GEI were of a crossover type, as evidenced by genotype yield rankings that differed across environments (Table 4). There was inconsistency in the top-ranking storage root yield across environments. Thus, genotypes G11, G7, G12, G25, G17, and G4 were the top-ranking genotypes at Tarcha, Jimma, Wara, Disa, Areka, and Bonbe, respectively (Table 4).

3.2. AMMI Biplot. The AMMI 1 biplot space (Figure 1) is divided into four sections, ranging from low-yielding environments in Sections 1 (upper left) and 4 (low left) to high-

Table 4: Mean fresh storage root yield (t·ha^{-1}) of 25 genotypes across environments.

Genotypes		Environments						
Code	Name	Tarcha	Jimma	Wara	Disa	Areka	Bonbe	Over all mean
G1	AAGT108	33.60	23.50	50.75	37.50	37.34	48.30	38.50
G2	Hawassa-04	45.90	25.00	46.67	20.00	57.20	45.23	40.00
G3	Qulle	33.95	22.30	40.34	25.00	38.25	46.63	34.41
G4	156	72.50	23.90	47.25	66.25	54.17	**71.00**	**55.84**
G5	MM 96/9361	73.55	60.17	54.95	47.50	28.84	55.40	53.40
G6	F-100	73.40	56.84	44.45	35.00	55.00	50.15	52.47
G7	M-94/0125	58.95	**63.76**	57.75	37.50	45.80	49.65	52.24
G8	1062630	73.45	26.00	50.75	37.50	67.00	58.28	52.16
G9	Bajk-1	78.70	17.67	58.34	60.00	51.55	45.50	51.96
G10	1061630	67.50	30.17	52.50	62.50	31.70	60.15	50.75
G11	196/624	**79.70**	30.84	55.84	30.00	61.25	46.67	50.71
G12	191/0427	54.45	22.00	**75.58**	58.75	52.50	39.80	50.51
G13	AAGT 192	27.00	34.30	53.34	55.00	68.34	54.85	48.80
G14	200	69.65	26.17	46.67	41.25	43.75	61.25	48.12
G15	AWC-5	65.90	40.67	28.70	55.00	36.34	39.96	44.43
G16	1980510	54.65	62.17	26.25	35.00	38.34	69.30	47.62
G17	Umvure	61.60	19.17	40.25	40.00	**77.50**	49.00	47.92
G18	Kello	62.50	26.17	46.00	50.00	54.34	40.25	46.54
G19	45/72 white	78.35	25.00	52.50	35.00	40.04	44.90	46.10
G20	5532-4	65.55	36.83	52.97	46.25	32.50	36.40	45.08
G21	Gamo dhaske	57.70	32.50	51.10	47.50	44.00	34.13	44.49
G22	46330/12	31.25	56.67	50.75	33.75	40.00	53.65	44.34
G23	1070539	55.36	25.67	64.75	31.25	45.00	36.40	43.07
G24	1038	65.70	18.33	26.25	30.00	51.25	65.34	42.81
G25	869	68.90	16.30	33.25	**75.00**	41.67	23.34	43.08
Mean		60.39	32.88	48.32	43.70	47.00	49.02	47.01
LSD (5%)		17.52	18.67	22.39	24.52	14.65	22.22	
CV (%)		13.69	26.78	21.75	26.00	14.47	21.22	
F value		**	**	*	*	**	**	

Key: *, ** = significant difference at 0.05 and 0.01 level, respectively, LSD = least significant difference, and CV = coefficient of variation. Bold indicates the highest mean yield among genotypes within environment and over all environments.

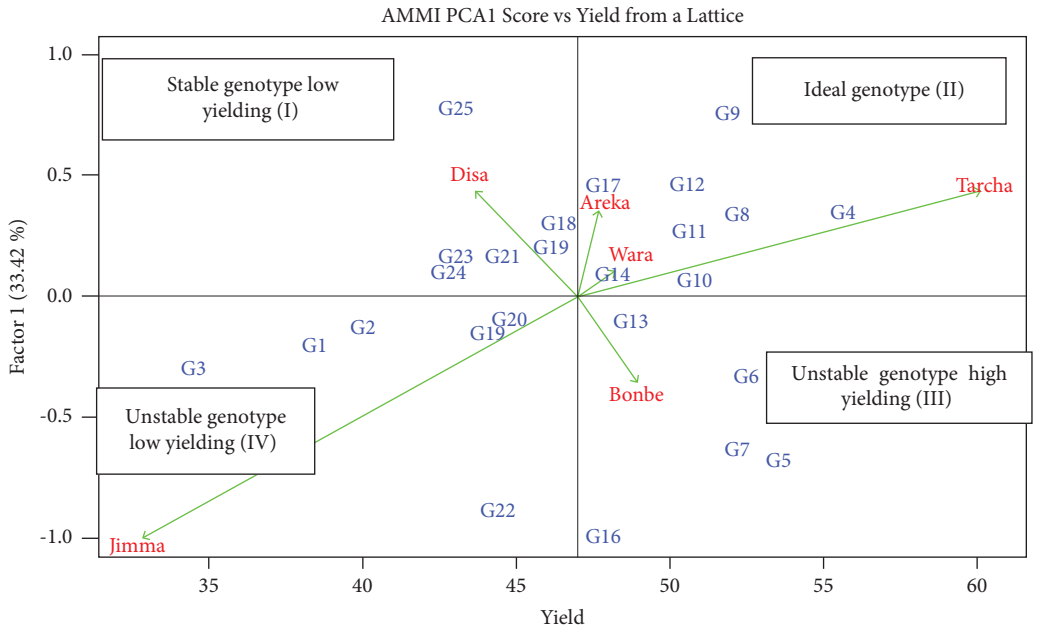

Figure 1: AMMI 1 biplot showing the main and interaction (IPCA1) effects of both genotypes and environments on mean fresh storage root yield.

yielding environments in Sections 2 (upper right) and 3 (low right). Figure 1's biplot clearly demonstrates that the points for the environment are more scattered than the points for genotypes, showing that variability due to environments is greater than variability due to genotype differences, which is in line with ANOVA (Table 3). The points for the usually adapted genotypes on the biplot would be on the right hand side of the grand mean levels (suggesting high mean performance) and near to the IPCA = 0 line (this suggests negligible or no GE interaction). In this regard, thirteen cassava genotypes, for example, G4 and four environments such as Tarcha, were positioned on the right side of the perpendicular vertical line in the AMMI biplot (Figure 1). According to the current study, these genotypes and environments were considered as high-yielding genotypes and environments. These results are supported by previous studies by Tumuhimbise et al. [31], Morais et al. [42], Hmwe et al. [43], and Esuma et al. [45] who reported that yield stability among genotypes was evaluated using mean performance and the IPCA score by graphically constructing the AMMI-1 biplot into four quadrants. They also discovered that genotypes and environments ranging from low to high yield were distributed in four quadrants.

The *X*-coordinate denotes the main effects (genotype and environment means), whereas the *Y*-coordinate denotes the interaction effects (IPCA1) in the AMMI 1 biplot (Figure 1). The differences between genotypes in terms of direction and magnitude along the *X*-axis (yield) and *Y*-axis (IPCA 1 scores) are significant in the AMMI 1 biplot. A biplot assay is interpreted, and if main effects have an IPCA score near to zero, it implies negligible interaction effects (stable), but a greater score (absolute value) shows instability and is specifically adapted to certain environments [46]. When a genotype and its environment have the same sign on the IPCA axis, their interaction is positive; when they have different signs, it is negative [47]. According to the AMMI model, genotypes with root mean yield greater than the grand mean and an IPCA score of virtually zero are generally adaptable to all environments. However, genotypes with a high mean performance and a high IPCA score are thought to be more adaptable to their environments [44].

According to Figure 1, G18, G19, and G25 (adaptive group 1 or characterized by low-yielding environments with stable genotypes) showed specific adaptability for Disa environment having a fresh storage root mean yield below the grand mean. The first adaptive group's genotypes and environments have the same sign on the IPCA axis, indicating that their interaction is positive. G4, G8, G9, G11, G12, and G17 (adaptive group 2 or characterized by high yielding/ideal environment with an unstable genotype) were found to have specific adaptability for environments such as Tarcha, Wara, and Areka, with a higher fresh storage root mean yield than the grand mean and high positive interaction. Genotypes G5, G6, G7, and G16 were in adaptive group 3 (characterized by a high-yielding environment). They revealed a specific adaptation for the Bonbe environment with a higher fresh storage root yield than the grand mean yield and positive interaction. The genotypes, G1, G2, G3, G15, and G22 (adaptive group 4, or defining a low-yielding environment with an unstable genotype), were identified as having sole adaptability for the environment of Jimma. At IPCA = 0, the genotypes G10, G13, G14, G20, G21, G23, and G24 (adaptive group 5 or stable genotypes) showed high stability and general adaptability; G20, G21, G23, and G24 had fresh storage root yields close to the grand mean yield, while G10, G13, and G14 had higher storage root mean yields than the grand mean and negligible interaction. In general, genotype G10 was screened with general adaptability for all environments (close to IPCA = 0 or insignificant interaction) with a high fresh storage root yield of more than the grand mean yield and was the overall winner with less variable yield across the environments, suggesting its eligibility as one of the leading genotypes for the current study. Agyeman et al. [24], Morais et al. [42], and Hmwe et al. [43] supported this study by discovering that genotypes with high yield were least interactive with the environment (low IPCA score), indicating that they were broadly adapted genotypes with high yield in all environments, whereas unstable genotypes with high yield were adapted to specific environments. Similarly, several studies for different crops reported that genotype-adaptive grouping in four quadrants was estimated on the basis of mean yield and the magnitude of IPCA1 scores [48–51]. Also, they observed the stable, unstable, and overall winning genotypes.

On the other hand, some environments stood out as having a small contribution to the interaction (Wara); a moderate contribution (Disa, Areka, and Bonbe); and a large contribution (Tarcha and Jimma) (Figure 1). Tarcha, Wara, and Bonbe environments, produced a higher mean storage root yield than the grand mean (47.01 $t \cdot ha^{-1}$), indicating that these were ideal sites to acquire high means. With a high positive IPCA 1 score, the environments with the most potential (Tarcha, Wara, and Areka) demonstrated differential performance of genotypes for fresh storage root yield (Figure 1). The low-yielding environment (Jimma) had the lowest yield but a negative IPCA1 score, indicating that all genotypes performed poorly in this environment. Similar observations were reported by Kadhem and Baktash [49], Erdemci [50], and Wardofa et al. [51], who observed high-yielding and low-yielding environments with varied contribution interactions.

3.3. AMMI Stability Value (ASV). To determine the genotypes' stability, an AMMI stability value was calculated (Table 5). In a two-dimensional scatter graph of IPCA1 (interaction principal component analysis axis 1) scores against IPCA2 scores, ASV is the distance from zero. The proportional difference between the IPCAs (1 : 2) can be used to compensate for the difference in stability measurements of the two principal components, which can then be computed using the Pythagorean theorem to the effect of the AMMI stability value [37]. According to Purchase [52], the AMMI stability value (ASV) does not give a quantitative stability metric but rather quantifies and ranks genotypes based on their yield stability. In this sense, genotypes with lower ASV values are thought to be more stable, while those with higher ASV values are thought to be unstable. Genotype

Table 5: Grand mean fresh storage root yield (FSRY) t·ha^{-1}, RY, ASV, GSI, RASV, IPCA1, and IPCA2 of 25 cassava genotypes across environments.

Genotypes	FSRY	RY	ASV	GSI	RASV	IPCA1	IPCA2
G1	38.50	24	1.72	31	7	−0.8313	−1.2568
G2	40.00	23	2.86	40	17	−0.7991	−2.6335
G3	34.41	25	2.34	37	12	−1.2845	−1.4919
G4	55.84	1	2.35	14	13	1.6625	0.2291
G5	53.40	2	4.17	23	21	−1.9305	3.1704
G6	52.47	3	2.50	17	14	−1.6865	0.8082
G7	52.24	4	4.02	24	20	−2.8103	0.7640
G8	52.16	5	2.03	16	11	0.8827	−1.6108
G9	51.96	6	4.23	28	22	2.9934	0.4963
G10	50.75	7	1.25	12	5	0.6708	1.9761
G11	50.71	8	1.30	14	6	0.7334	−0.8003
G12	50.51	9	2.85	25	16	1.8497	−1.1771
G13	48.80	10	3.53	29	19	−0.8493	−3.3262
G14	48.12	11	0.58	12	1	0.3538	0.3055
G15	44.43	18	2.70	33	15	0.0983	2.6960
G16	47.62	13	5.74	37	24	−3.9447	1.5038
G17	47.92	12	3.48	40	18	1.4424	−2.8272
G18	46.54	14	1.83	23	9	1.2957	−0.2178
G19	46.10	15	1.73	23	8	1.0541	0.9025
G20	45.08	16	1.93	26	10	0.1970	1.9061
G21	44.49	17	0.88	20	3	0.5194	0.4981
G22	44.34	19	5.49	42	23	−3.8854	−0.5730
G23	43.07	21	1.07	25	4	0.2584	−1.0047
G24	42.81	22	0.78	24	2	0.1662	−0.7483
G25	43.08	20	5.78	45	25	3.7438	2.4114

Key: RY = ranking mean storage root yield, ASV = AMMI stability value, GSI = -genotype selection index, and RASV = AMMI stability value ranking.

G14 was the most stable, with an ASV value of 0.58, followed by genotypes G24 and G21 with ASV values of 0.78 and 0.88 in fresh storage root yield, respectively, and the genotypes G9, G16, G22, and G25 were the most unstable, with ASV values of 4.23, 5.74, 5.49, and 5.78, respectively (Table 5). A similar procedure was used by Adjebeng–Danquah et al. [16], Tumuhimbise et al. [31], and Esuma et al. [45], who found a more stable genotype with a lower ASV value.

3.4. Genotype Selection Index (GSI) Analysis. Stability is not the only parameter for selection because the most stable genotypes would not necessarily give the best yield performance. The term "high stability" only has significance if it is linked to average performance [53]. Hence, there is a need for approaches that incorporate both mean yield and stability into a single index [38]. The lowest GSI value is considered the most stable, with a high mean yield. Therefore, G14 and G10, with a GSI value of 12, were the most stable genotypes with a high fresh storage root yield, followed by G4, G11, and G8, with GSI values of 14, 14, and 16, respectively, indicating that they were stable (widely adaptable) and high-yielding. Based on the value of the genotype selection index, the genotypes G2, G3, G17, G22, and G25 were unstable genotypes (Table 5). This finding is in line with previous studies, which stated that stable genotypes with high yields were identified by analysis of the genotype selection index based on the ranking mean yield and ranking AMMI stability value [31, 45, 54].

3.5. GGE Biplot

3.5.1. Which Won Where View of GGE Biplot. The polygon view of the GGE biplot graphic analysis is presented (Figure 2) for the identification of winning genotypes by visualizing the interaction patterns between genotypes and environments [55]. It is helpful in identifying crossover and noncrossover genotype-by-environment interactions as well as the possible existence of different mega-environments in multilocation yield trials [19, 56]. As displayed by (Figure 2) genotypes, G3, G5, G13, G16, G17, G22, and G25 were the vertex genotypes. These genotypes perform best or worse in some or all environments because they are the furthest from the biplot's commencement [55], and they are regarded as specifically suited genotypes since they are more responsive to environmental change. They thrive in environments that are part of their specific sector in the GGE's polygon view-biplot [55]. At Tarcha and Disa, G25 was the most successful genotype, while G16 at Bonbe and Jimma and G17 at Wara and Areka. As a result, G25 won in Tarcha and Disa environments, while G16 and G17 won in Bonbe and Jimma and Wara and Areka environments, respectively. On the other hand, the vertex genotypes G3, G5, G13, and G22 were the poorest genotypes in almost the entire test environments because they were the furthest from the biplot's origin on the opposite side of the environments. Similar results were reported by Agyeman et al. [24], Akinwale et al. [30], Noerwijati and Prajitno [40], and Sholihin [57], who characterized genotypes' which-won-where patterns. They found that some genotypes performed better in a specific environment than others and that some genotypes performed worst in some environments.

The biplot was divided into seven sections by the equality lines in Figure 2. The environments were distributed across three sectoral areas, whereas the genotypes were distributed throughout all the seven. The three mega-environments were, namely, first (Tarcha and Disa), second (Wara and Areka), and third (Jimma and Bonbe). This suggests that comparable genotypes do better in a homogeneous environment. Therefore, the identified mega-environments could be useful in managing the genotype-by-environment interactions and then generalizing the results to similar agroclimatic locations. The genotypes that are located near the sector's vertex are the most yielding genotypes in that sector [56]. Two environments (Tarcha and Disa) were found in the first sector (I). This sector encompassed nine genotypes: G4, G9, G11, G12, G14, G15, G19, G20, and G25 (Figure 2). The first sector's vertex genotype was G25, indicating that this was the better genotype for these two environments and that environments within the same sector had the same winning genotype, while it was not clearly separated since G4 and G9 were also very near to the side of that vertex, the second sector (II) contained five genotypes without any environment, and G5 was the vertex genotype (Figure 2). The third sector (III) contained two environments (Jimma and Bonbe) and two genotypes, G7 and G16. The vertex and best-yielding genotype for this

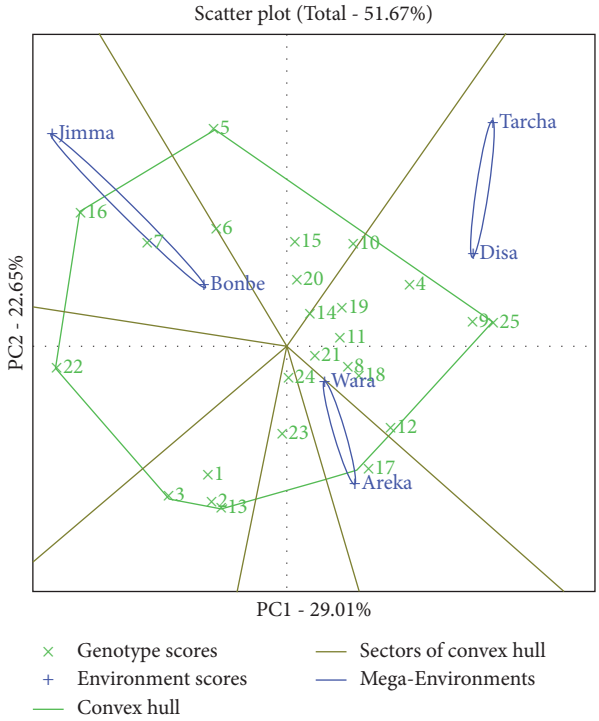

Figure 2: The GGE biplot shows which genotypes won where and their related mega-environments.

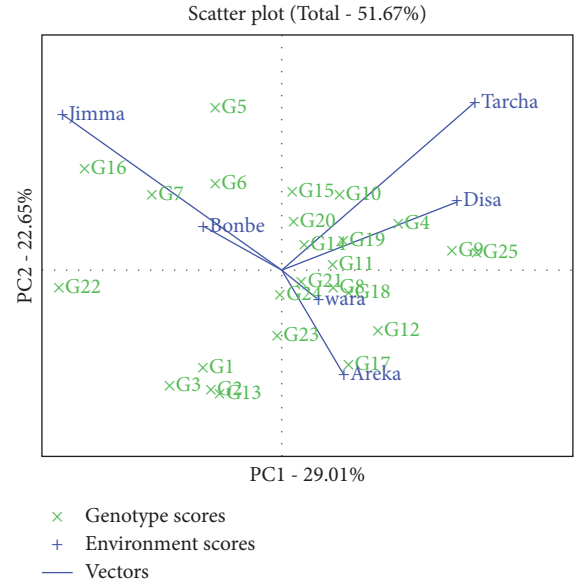

Figure 3: GGE biplot graph showing relationships among test environments.

section was G16. Without any environment, the fourth (IV), the fifth (V), and the sixth (VI) sectors contained one, four, and two genotypes, respectively (Figure 2). Under these sectors, the vertex genotypes were G3, G13, and G22. However, these were not the highest yielding genotypes in any environment; rather, they were the poorest genotypes in all or some environments. As a result, these genotypes are thought to be well suited to their environment. The last sector (VII) comprised two environments (Wara and Areka) and one (G17) vertex genotype. GEI variation was lower in the genotypes near the origin than in the vertex genotypes. Thus, the G8, G11, G14, G21, and G24 genotypes were close to the biplot origin, indicating roughly average performance, and their GEI variation was lower than that of the vertex genotypes. This finding was similar to that of Noerwijati and Prajitno [40], Esuma et al. [45], Sholihin [57], Akter et al. [58], and Bakare et al. [59], who reported that the testing environment was delineated into different mega-environments with winning genotypes and sectors containing various numbers of genotypes.

3.5.2. Relationship among Environments. The GGE biplot demonstrates in Figure 3 that the first (PC1) and second (PC2) principal components combined explained 51.67 percent of the total variation, indicating that this biplot can be used to separate interrelationships across the environments. The angle between the biplot origin and the markers of test environments is connected to the correlation coefficient [25]. Furthermore, the length of an environmental vector confers a high level of genotype discrimination [19]. In the present study, environments Tarcha and Jimma were the most discriminating (holding more information) about the genotypes having the longest vectors from the origin, followed by Disa and Areka, which were medium discriminating, and environments Bonbe and Wara, little or no discriminating about the genotype differences (Figure 3). Nondiscriminating (noninformative) test environments provide minimal information about genotypes and should not be used as test environments [53]. Furthermore, the biplot vector view is primarily used to find test environments with acute, obtuse, and right-angle relationships, respectively, with positive, negative, and zero correlation between environments [56].

Based on the angle test between environment vectors, the six environments were clustered into three groups. The first group was discovered to have a small angle between environments Jimma and Bonbe, Tarcha with Disa and Wara, and Areka with Disa and Wara, that there was a highly positive correlation between them and that they provided similar information on genotypes (Figure 3). It implies that the environment provides unnecessary information on their ability to discriminate between genotypes. Obtaining reliable information on environment similarity and clustering should allow breeders to employ fewer test environments, reducing testing costs and enhancing breeding efficiency. The second group possesses the large angle revealed between the environments of Jimma and Tarcha, Disa, Wara, Areka, and Bonbe with Tarcha, Disa, Wara, and Areka. Hence, they were negatively correlated. The presence of wide obtuse angles among the test environments is an indication of strong crossover GE, and the largest angle is slightly larger than 90°, implying that the GE is moderately large. The third group, which had the right angle, was formed between Disa and Areka. This indicates that these two environments have little or no correlation between them and the genotype performing differently. Akter et al. [58], Lule et al. [60], and Baraki et al. [61] reported similar findings in the relationship

among environments characterized based on the angle method. They found that some environments between them had large angles or low or negative correlations, whereas the associations with small angles had strong positive correlations and offered similar data on genotypes.

3.5.3. Evaluation of Genotypes Based on the Ideal Genotype. The GGE biplot model is an interesting application for the evaluation of genotypes relative to an ideal genotype. Several authors Diriba [53], Yan and Tinker [56], and Farshadfar et al. [62] described that an ideal genotype has a high mean performance as well as high stability across environments. According to Nimlamai et al. [63], the ideal genotype with high mean performance and high stability was identified by using the ideal position (the center of the concentric circle). An ideal genotype has large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability). Even though such an "ideal" genotype may not be present in reality, it might be used as a benchmark for genotype evaluation [64]. Concentric circles were formed in a GGE biplot graph based on genotype-focused scaling to better visualize the distance between genotypes and the ideal genotype [56, 65]. In early breeding cycles, genotypes that are far from the ideal genotype can be ruled out, while genotypes that are close to it can be considered in subsequent tests [55]. A genotype is more desirable if it is closer to the "ideal" genotype, which is located in the first concentric circle of the GGE biplot graphic [64, 66].

According to the GGE biplot graph (Figure 4), genotype G10 was positioned in the first concentric circle. Therefore, G10 was the ideal genotype position, followed by G15, G4, G20 G19, G14, and G11, making it more desirable than other cassava genotypes. In spite of this, G1, G2, and G3 improved cultivars were more undesirable than other cassava genotypes, and they were adapted to specific environments. G14, G21, and G24 were placed near the biplot origin, and they were less sensitive to an environmental change. This is similar to what Akinwale et al. [30], Erdemci [50], and Naheif and Alaa [67] reported as one ideal genotype and some other desirable genotypes located in the first and next concentric circles, respectively. Similarly, Noerwijati and Prajitno [40] identified ideal genotypes using different approaches; their criteria were that an ideal genotype should have large PC1 scores (high mean yield) and a small absolute PC2 score (high stability), but this approach was not able to identify desirable genotypes.

3.5.4. Evaluation of Environments Relative to Ideal Environments. According to Yan and Tinker [56], an ideal environment has the highest discriminating capability and representativeness, which are important properties of a test environment. Yan and Kang [55] defined an ideal environment as one that is highly differentiating for the tested genotypes while at the same time representative of the target environments. In this regard, Tarcha had a smaller angle with the average environment axis (AEA), while Wara, Bonbe, and Areka had a large angle with the average environment axis (Figure 5). Bonbe and Wara were close to the

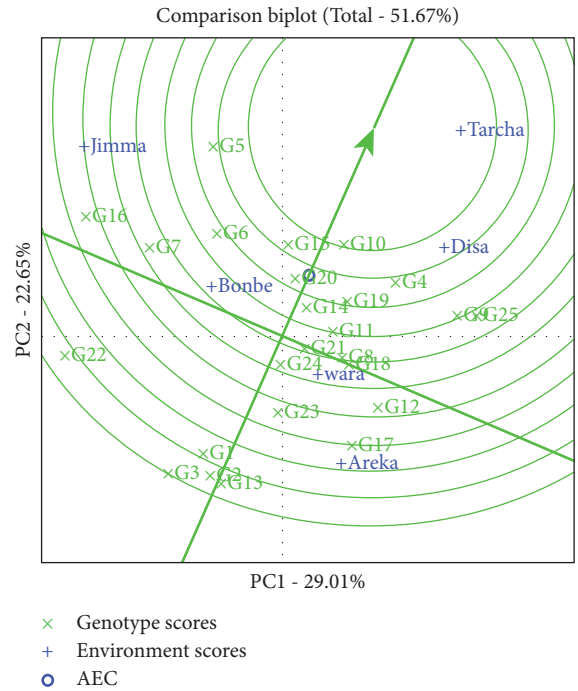

Figure 4: GGE biplot graph based on genotype-focused scaling for comparison of genotypes with an ideal genotype.

center with very short vectors (Figure 5) and provided less helpful discriminating information about the genotypes. As a result, Tarcha was the most representative environment, whereas Wara, Bonbe, and Areka were the least representative. Also, Tarcha had the highest discriminating capability of the genotypes (Figure 5). As a result, Tarcha is the most favorable environment for the selection of superior genotypes.

In the environment-focused GGE biplot, the ideal environment is positioned in the first concentric circle, and the desired environments are defined as those that are closest to the ideal environment. In this regard, Tarcha is in the first concentric circle and has been in the ideal environment (Figure 6). Tarcha's PC1 score was high, while its PC2 score was low. Hence, genotype evaluation in the Tarcha environment maximized the observed genotypic variation among genotypes for the fresh storage root yield of the tested cassava genotypes and should be regarded as the most suitable to select widely adapted genotypes. Disa's environment was close to the ideal environment (Tarcha), and this environment has been identified as a desirable environment (Figure 6). On the other hand, the Jimma and Areka environments were located far away from ideal environments, so they might be regarded as undesirable environments (fewer representatives) for selecting widely adapted cultivars but can be used for selecting specifically adapted cultivars. This variation among environments can be associated with soil fertility, rainfall, and other environmental variability across the environments. The composition of genotypes affects a location's discriminating capacity, but the presence of GEI makes finding an appropriate test location more difficult [25]. The test

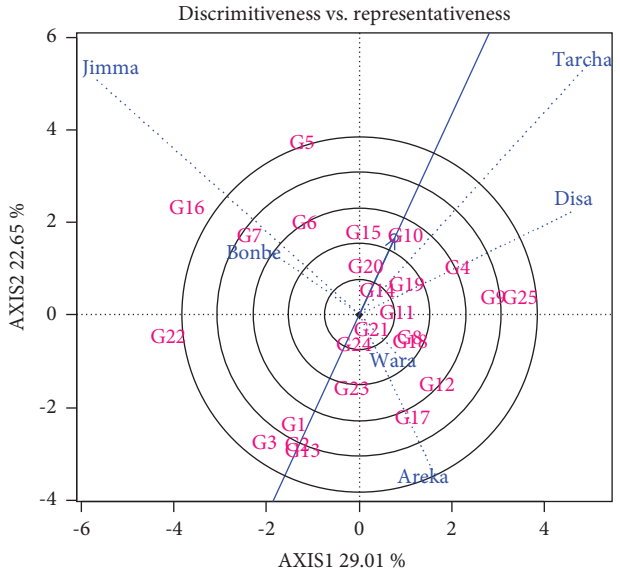

Figure 5: Discrimitiveness and representativeness of the test environments.

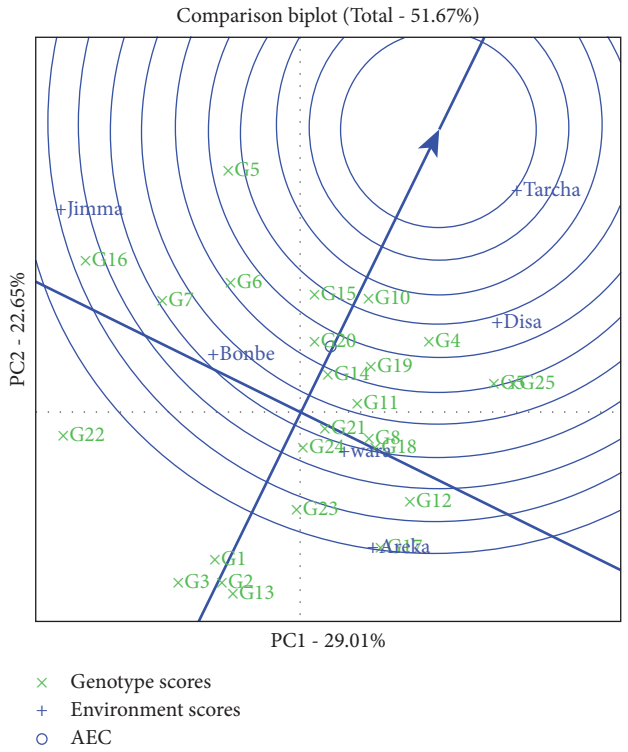

Figure 6: GGE biplot graph based on environment-focused scaling for comparison of environments with an ideal environment (Tarcha).

environments should have high PC1 scores to discriminate genotypes in terms of the genotypic main effect and low PC2 scores in an absolute value to be more representative of the overall locations [44]. As far as the testing environment is concerned, the environment obtained directly concurs with that described by [27, 50, 58, 67]. In their study, they

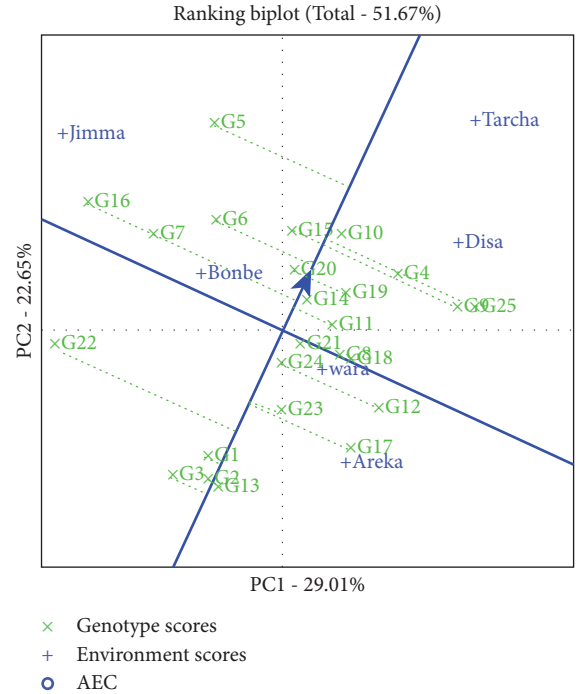

Figure 7: Average environment coordination views of the GGE-biplot graph showing the ranking of genotypes for mean root yield and stability performance over environments.

classified the testing environment as ideal, desirable, discriminating, and representative, where the ideal environment was situated in the first concentric circle, and the desirable or potential environment was closest to the ideal. In the same way, they reported that the ideal environment is the most discriminating and representative environment. Furthermore, they suggested that the most representative environments can be used for widely adapted genotype selection, while nonrepresenting environments can be useful for specifically adapted genotype selection.

3.5.5. Ranking of Genotypes Based on Mean Yield and Stability Performance. In the GGE biplot, the assessment of mean root yield and stability of genotypes (Figure 7) was conducted by using the average environment (tester) coordinate (AEC) methods [31, 68]. The average environmental (tester) coordinate (AEC) is defined by the average PC1 and PC2 scores for all the environments [55]. The AEC *X* axis (PC1) line passes through the biplot origin with an arrow indicating the positive end of the axis and indicates the mean yield performance axis of genotypes. The line, which passes through the origin and is perpendicular to the average environmental axis, measures the stability of genotypes (PC2) in either direction (Figure 7). Stable genotypes had the smallest perpendicular lines and were close to AEC (PC1) with PC2 scores of almost zero. On the other hand, any direction on the axis away from the biplot origin suggests increased GE interaction and decreased stability. The best genotypes for selection criteria are those with both

high mean yield and high stability. In this regard, in the present study (Figure 7), the single arrowed line was pointed to higher yield across environments. Therefore, genotype G5 had the highest mean yield, followed by G10 and G4. Genotype G18 had a mean yield similar to the grand mean, and G3 had the lowest mean yield. Furthermore, genotypes G14 and G10 were the most stable, while G22 and G16 were highly unstable. Mostly, genotype G22 was a highly unstable and poor-performing genotype in the environments where genotype G5 was the winner but not in the Areka environment. The present study's findings are in line with the report made by [24, 30, 69–71]. They ranked genotypes based on mean performance and stability across environments. In this way, they found some genotypes to be the most stable with a high mean yield and some unstable high yielders, while some other genotypes were unstable with a poor yield and a stable low yielder.

4. Conclusions

According to the combined analysis of variance, the degree of GEI had the greatest influence on cassava fresh storage root yield performance, followed by the environmental effect, while genotype had the least effect on the total treatment SS. The AMMI and GGE biplot models were good tools for visual multienvironment trials data analysis and allowed the estimation of the interaction effects of a genotype in each environment. The three mega-environments have been identified that could be helpful for genotype evaluation and productive breeding. The GGE biplot revealed that Tarcha was the ideal and the most representative environment, while G10 was the ideal genotype and overall winner. According to the AMMI, GGE biplot model, and GSI analysis genotypes, G10 and G14 were identified as being the most stable, with a higher fresh storage root mean yield than other genotypes and the grand mean. As a result, G10 and G14 were selected as superior genotypes that could be exploited in a cultivar development program as widely adaptable genotypes for all environments.

Data Availability

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

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors' Contributions

Berhanu Bilate carried out the field work, performed the statistical analysis, and drafted the manuscript. The rest of the authors coordinated the study, supervised fieldwork, and contributed to the writing of the manuscript. The final manuscript has been read and approved by all authors for submission.

Acknowledgments

The universities of Jimma and Wolita Sodo are acknowledged by the authors for providing funding for the study. The authors are also pleased to acknowledge Jimma and Hawassa Agricultural Research Centers and International Institute for Tropical Agriculture for providing planting materials used for the study. Jimma and Wolita Sodo Universities financed all the research work.

References

[1] A. Nduwumuremyi, R. Melis, P. Shanahan, and A. Theodore, "Interaction of genotype and environment effects on important traits of cassava (Manihot esculenta Crantz)," *The Crop Journal*, vol. 5, no. 5, pp. 373–386, 2017.

[2] Faostat, "Food and agriculture organization of the united nations" databases agricultural production; FAO statistics databases: rome,Italy," 2019, https://www.fao.org/faostat/en/.

[3] A. S. Wassie, "Cassava production and field management in Ethiopia," *Journal of Agriculture and Horticulture*, vol. 2, no. 1, pp. 31–40, 2020.

[4] D. I. Roslim, Herman, N. Sofyanti, M. Chaniago, R. Restiani, and L. Novita, "Characteristics of 22 cassava (manihot esculenta Crantz) genotypes from riau province, Indonesia," *SABRAO J. Breed. Genet*, vol. 48, no. 1, pp. 109–126, 2016.

[5] W. Esuma, "Genetic analysis and genome-wide association mapping of carotenoid and dry matter content in cassava," Doctoral dissertation, University of the Free State, Bloemfontein, South Africa, 2016.

[6] K. N. Sholihin and M. J. Mejaya, "Genotypic variability in cassava (Manihot esculenta Crantz) mutants (M1V4) using gamma irradiation," *SABRAO J. Breed. Genet*, vol. 51, no. 2, pp. 109–126, 2019.

[7] E. Shonga, T. Addis, M. Gemu, and T. Tadesse, "Cassava scale: a new threat for a food security crop in Ethiopia," *The African Journal of Plant Science and Biotechnology*, vol. 6, no. 1, pp. 80–83, 2012.

[8] T. Tadesse, G. Degu, E. Shonga, S. Mekonen, T. Addis, and B. Yakob, "Current status, Potentials and challenges of Cassava production, processing, marketing and utilization: evidence from Southern Ethiopia," *Greener Journal of Agricultural Sciences*, vol. 3, no. 4, pp. 262–270, 2013.

[9] A. Tafesse, B. Mena, A. Belay et al., "Cassava production efficiency in southern Ethiopia: the parametric model analysis," *Frontiers in Sustainable Food Systems*, vol. 5, pp. 1–12, 2021.

[10] J. T. Anderson, C. R. Lee, and T. Mitchell-Olds, "Strong selection genome-wide enhances fitness trade-offs across environments and episodes of selection," *Evolution*, vol. 68, no. 1, pp. 16–31, 2014.

[11] P. C. Rodrigues, M. Malosetti, H. G. Gauch, and F. A. van Eeuwijk, "A weighted AMMI algorithm to study genotype-by-environment interaction and QTL-by-environment interaction," *Crop Science*, vol. 54, no. 4, pp. 1555–1570, 2014.

[12] F. A. Van Eeuwijk, D. V. Bustos-Korts, and M. Malosetti, "What should students in plant breeding know about the statistical aspects of genotype× environment interactions?" *Crop Science*, vol. 56, no. 5, pp. 2119–2140, 2016.

[13] P. C. Rodrigues, A. Monteiro, and V. M. Lourenço, "A robust AMMI model for the analysis of genotype-by-environment data," *Bioinformatics*, vol. 32, no. 1, pp. 58–66, 2016.

[14] P. C. Rodrigues, "An overview of statistical methods to detect and understand genotype-by-environment interaction and QTL-by-environment interaction," *Biometrical Letters*, vol. 55, no. 2, pp. 123–138, 2018.

[15] T. Begna, "The role of genotype by environmental interaction in plant breeding," *International Journal of Agriculture and Biosciences*, vol. 9, no. 5, pp. 209–215, 2020.

[16] J. Adjebeng-Danquah, J. Manu-Aduening, V. E. Gracen, I. K. Asante, and S. K. Offei, "AMMI stability analysis and estimation of genetic parameters for growth and yield components in cassava in the forest and Guinea savannah ecologies of Ghana," *International Journal of Agronomy*, vol. 2017, Article ID 8075846, 10 pages, 2017.

[17] A. Asfaw, F. Alemayehu, F. Gurum, and M. Atnaf, "AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia," *Scientific Research and Essays*, vol. 4, no. 11, pp. 1322–1330, 2009.

[18] S. Ceccarelli, S. Grando, and R. H. Booth, "International breeding programmes and resource-poor farmers: crop improvement in difficult environments," in *Workshop on Participatory Plant Breeding*, pp. 26–29, IPGRI, Wageningen, Netherlands, 1996.

[19] W. Yan, M. S. Kang, B. Ma, S. Woods, and P. L. Cornelius, "GGE biplot vs. AMMI analysis of genotype-by-environment data," *Crop Science*, vol. 47, no. 2, pp. 643–653, 2007.

[20] A. A. Hopkins, K. P. Vogel, K. J. Moore, K. D. Johnson, and I. T. Carlson, "Genotype effects and genotype by environment interactions for traits of elite switchgrass populations," *Crop Science*, vol. 35, no. 1, pp. 125–132, 1995.

[21] C. S. Lin, M. R. Binns, and L. P. Lefkovitch, "Stability analysis: where do we stand?" *Crop Science*, vol. 26, no. 5, pp. 894–900, 1986.

[22] G. Ssemakula and A. Dixon, "Genotype X environment interaction, stability and agronomic performance of carotenoid-rich cassava clones," *Scientific Research and Essays*, vol. 2, no. 9, pp. 390–399, 2007.

[23] K. M. Eskridge, "Selection of stable cultivars using a safety-first rule," *Crop Science*, vol. 30, no. 2, pp. 369–374, 1990.

[24] A. Agyeman, E. Parkes, and B. B. Peprah, "AMMI and GGE biplot analysis of root yield performance of cassava genotypes in the forest and coastal ecologies," *International Journal of Agricultural Policy and Research*, vol. 3, no. 3, pp. 222–232, 2015.

[25] W. Yan, L. A. Hunt, Q. Sheng, and Z. Szlavnics, "Cultivar evaluation and mega-environment investigation based on the GGE biplot," *Crop Science*, vol. 40, no. 3, pp. 597–605, 2000.

[26] S. O. P. Samonte, L. T. Wilson, A. M. McClung, and J. C. Medley, "Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analyses," *Crop Science*, vol. 45, no. 6, pp. 2414–2424, 2005.

[27] M. N. Rad, M. A. Kadir, M. Y. Rafii, H. Z. Jaafar, M. R. Naghavi, and F. Ahmadi, "Genotype environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (Triticum aestivum) under normal and drought stress conditions," *Australian Journal of Crop Science*, vol. 7, no. 7, pp. 956–961, 2013.

[28] H. G. Gauch, "Statistical analysis of yield trials by AMMI and GGE," *Crop Science*, vol. 46, no. 4, pp. 1488–1500, 2006.

[29] H. G. Gauch, H. P. Piepho, and P. Annicchiarico, "Statistical analysis of yield trials by AMMI and GGE: further considerations," *Crop Science*, vol. 48, no. 3, pp. 866–889, 2008.

[30] M. G. Akinwale, B. O. Akinyele, A. C. Odiyi, and A. G. O. Dixon, "Genotype X environment interaction and yield performance of 43 improved cassava (Manihot esculenta Crantz) genotypes at three agro-climatic zones in Nigeria," *British Biotechnology Journal*, vol. 1, no. 3, pp. 68–84, 2011.

[31] R. Tumuhimbise, R. Melis, P. Shanahan, and R. Kawuki, "Genotype× environment interaction effects on early fresh storage root yield and related traits in cassava," *The Crop Journal*, vol. 2, no. 5, pp. 329–337, 2014.

[32] National Meterology Agency (Nma), "Hawassa Meterology Agency,Hawassa branch, Ethiopia," 2021, http://www.ethiomet.gov.et/galleries/album_viewer/1/Hawassa%20Branch%20Office.

[33] D. Markos, L. Hidoto, and F. Negash, "Achievements of cassava agronomy research in southern Ethiopia in the last two decades," *Agriculture and Food Sciences Research*, vol. 3, no. 1, pp. 12–18, 2016.

[34] R. W. Payne, D. B. Baird, A. Cherry et al., "GenStat release 6.1 reference manual.Part2. Directives," 2002, https://repository.rothamsted.ac.uk/item/88z4y/genstat-release-6-1-reference-manual-part-2-directives.

[35] P. Angela and M. Vargas, "GEA-R (genotype x environment analysis with R for windows) version 2.0," *International Maize and Wheat Improvement Center*, vol. 36, 2015, https://gea-r.software.informer.com/.

[36] H. G. Gauch, "Model selection and validation for yield trials with interaction," *Biometrics*, vol. 44, no. 3, pp. 705–715, 1988.

[37] J. L. Purchase, H. Hatting, and C. S. van Deventer, "Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance," *South African Journal of Plant and Soil*, vol. 17, no. 3, pp. 101–107, 2000.

[38] E. Farshadfar, "Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat," *Pakistan Journal of Biological Sciences*, vol. 11, no. 14, pp. 1791–1796, 2008.

[39] E. F. N. Costa, H. W. L. Carvalho, V. S. Santos et al., "Adaptability and stability of cassava cultivars via bisegmented and multivariate regression," *Embrapa Tabuleiros Costeiros Research Bulletin*, vol. 78, pp. 1–20, 2013.

[40] K. Noerwijati and D. Prajitno, "Fresh tuber yield stability analysis of fifteen cassava genotypes across five environments in East Java (Indonesia) using GGE biplot," *Energy Procedia*, vol. 47, pp. 156–165, 2014.

[41] A. D. Santiago, L. K. Morais, and M. H. B. Cavalcante, "Recomendação de diferentes épocas de colheita de mandioca tipo indústria em Alagoas," *Comunicado Técnico da Embrapa Tabuleiros Costeiros*, vol. 164, pp. 1–6, 2015.

[42] L. K. D. Morais, A. D. Santiago, and M. H. B. Cavalcante, "Phenotypic stability in cassava estimated by the AMMI analysis with supplementary genotypes," *Crop Breeding and Applied Biotechnology*, vol. 17, no. 4, pp. 366–372, 2017.

[43] S. S. Hmwe, T. M. Htun, S. Win, M. M. Aung, and A. M. Than, "Genotype and environment interaction on yield in cassava (manihot esculenta)," *Journal of Agricultural Research*, vol. 5, no. 2, pp. 62–66, 2018.

[44] W. Yan and I. Rajcan, "Biplot analysis of test sites and trait relations of soybean in ontario," *Crop Science*, vol. 42, no. 1, pp. 11–20, 2002.

[45] W. Esuma, R. S. Kawuki, L. Herselman, and M. T. Labuschagne, "Stability and genotype by environment interaction of provitamin A carotenoid and dry matter content in cassava in Uganda," *Breeding Science*, vol. 66, no. 3, pp. 434–443, 2016.

[46] H. F. Gollob, "A statistical model which combines features of factor analytic and analysis of variance techniques," *Psychometrika*, vol. 33, no. 1, pp. 73–115, 1968.

[47] M. J. Alberts, "2A comparison of statistical methods to describe genotype x environment interaction and yield stability in multi-location maize trial," M.Sc. thesis, University of the Free State, B loemfontein, Bloemfontein, South Africa, 2004.

[48] M. Rashidi, E. Farshadfar, and M. M. Jowkar, "AMMI analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments," *The International Journal of Agriculture and Crop Sciences*, vol. 5, no. 3, p. 253, 2013.

[49] F. A. Kadhem and F. Y. Baktash, "AMMI analysis of adaptability and yield stability of promising lines of bread wheat (Triticum aestavum L.)," *The Iraqi Journal of Agricultural Sciences*, vol. 47, no. 7, pp. 1–10, 2016.

[50] I. Erdemci, "Investigation of genotype× environment interaction in chickpea genotypes using AMMI and GGE biplot analysis," *Turkish Journal of Field Crops*, vol. 23, no. 1, pp. 20–26, 2018.

[51] G. A. Wardofa, H. Mohammed, D. Asnake, and T. Alemu, "Genotype x environment interaction and yield stability of bread wheat genotypes in Central Ethiopia," *Journal of Plant Breeding and Genetics*, vol. 7, no. 2, pp. 87–94, 2019.

[52] J. L. Purchase, "Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat," Doctoral dissertation, University of the Free State, Bloemfontein, South Africa, 1997.

[53] T. Diriba, *Stability Analysis Using Gge Biplot And Linear Mixed Model Analysis By R Technical Manual*, Ethiopian Institute of Agricultural Research, Addis Ababa. Ethiopia, 2019.

[54] M. M. Chipeta, R. Melis, P. Shanahan, J. Sibiya, and I. R. Benesi, "Genotype X environment interaction and stability analysis of cassava genotypes at different harvest times," *Journal of Animal & Plant Sciences*, vol. 27, no. 3, pp. 901–919, 2017.

[55] W. Yan and M. S. Kang, *Gge Biplot Analysis: A Graphical Tool For Breeders, Geneticists, And Agronomists*, CRC press, Boca Raton, Florida, 2002.

[56] W. Yan and N. A. Tinker, "Biplot analysis of multi-environment trial data: principles and applications," *Canadian Journal of Plant Science*, vol. 86, no. 3, pp. 623–645, 2006.

[57] A. Sholihin, "GGE and AMMI biplot for interpreting interaction of genotype X environments of cassava promising genotypes," in *AIP Conference Proceedings,* vol. 2331, no. No. 1 AIP Publishing LLC,Woodbury, Long Island, New York, Article ID 50006, 2021.

[58] A. Akter, M. J. Hasan, U. Kulsum, M. H. Rahman, M. Khatun, and M. R. Islam, "GGE biplot analysis for yield stability in multi-environment trials of promising hybrid rice (Oryza sativa L.)," *Bangladesh Rice Journal*, vol. 19, no. 1, pp. 1–8, 2015.

[59] M. A. Bakare, S. I. Kayondo, C. I. Aghogho et al., "Exploring genotype by environment interaction on cassava yield and yield related traits using classical statistical methods," *PLoS One*, vol. 17, no. 7, Article ID 268189, 2022.

[60] D. Lule, M. Fetene, S. de Villiers, and K. Tesfaye, "Additive Main Effects and Multiplicative Interactions (AMMI) and genotype by environment interaction (GGE) biplot analyses aid selection of high yielding and adapted finger millet varieties," *Journal of Applied Biosciences*, vol. 76, no. 1, pp. 6291–6303, 2014.

[61] F. Baraki, Z. Gebregergis, Y. Belay, M. Berhe, and H. Zibelo, "Genotype x environment interaction and yield stability analysis of mung bean (Vigna radiata (L.) Wilczek) genotypes in Northern Ethiopia," *Cogent Food & Agriculture*, vol. 6, no. 1, Article ID 1729581, 2020.

[62] E. Farshadfar, R. Mohammadi, M. Aghaee, and Z. Vaisi, "GGE biplot analysis of genotype × environment interaction in wheat-barley disomic addition lines," *Australian Journal of Crop Science*, vol. 6, no. 6, pp. 1047–1079, 2012.

[63] T. Nimlamai, P. Banterng, S. Jogloy, and N. Vorasoot, "Starch accumulation of cassava genotypes grown in paddy fields during the off-season," *Sabrao Journal of Breeding and Genetics*, vol. 52, no. 2, pp. 109–126, 2020.

[64] B. Mitrovic, D. Stanisavljevi, T. Sanja et al., "Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analysis," *Turkish Journal of Field Crops*, vol. 17, no. 1, pp. 35–40, 2012.

[65] M. R. R. Naroui, M. A. Kadir, M. Y. Rafii, Z. E. Hawa Jaafar, M. R. Naghavi, and F. Ahmadi, "Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (Triticum aestivum L.) under normal and drought stress conditions," *American Journal of Sociology*, vol. 7, no. 7, pp. 956–961, 2013.

[66] Y. Kaya, M. Akcura, and S. Taner, "GGE-biplot analysis of multi-environment yield trials in bread wheat," *Turkish Journal of Agriculture and Forestry*, vol. 30, pp. 325–337, 2006.

[67] E. M. Naheif and A. A. Alaa, "Additive main effects and multiplicative interaction (AMMI) and GGE-biplot analysis of genotype Ã—environment interactions for grain yield in bread wheat (Triticum aestivum L.)," *African Journal of Agricultural Research*, vol. 8, no. 42, pp. 5197–5203, 2013.

[68] W. Yan and L. A. Hunt, "Interpretation of genotype× environment interaction for winter wheat yield in Ontario," *Crop Science*, vol. 41, no. 1, pp. 19–25, 2001.

[69] O. O. Aina, A. G. O. Dixon, I. Paul, and E. A. Akinrinde, "G× E interaction effects on yield and yield components of cassava (landraces and improved) genotypes in the savanna regions of Nigeria," *African Journal of Biotechnology*, vol. 8, no. 19, 2009.

[70] M. K. Mtunguja, H. S. Laswai, E. Kanju, J. Ndunguru, and Y. C. Muzanila, "Effect of genotype and genotype by environment interaction on total cyanide content, fresh root, and starch yield in farmer-preferred cassava landraces in Tanzania," *Food Sciences and Nutrition*, vol. 4, no. 6, pp. 791–801, 2016.

[71] F. Gurmu and S. Mekonen, "Root yield stability analysis of white-fleshed sweet potato genotypes in Ethiopia," *Advances in Crop Science and Technology*, vol. 7, no. 427, p. 2, 2019.