GENOTYPE BY ENVIRONMENT INTERACTION AND STABILITY ANALYSIS OF SWEET POTATO (*Ipomoea batatas* L.) GENOTYPES IN WEST HARARGHE ZONE, EASTERN ETHIOPIA

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ABSTRACT

Sweet potato is an important food crop in Eastern Ethiopia, including the West Hararghe Zone. However, the area is still far behind in attaining the required optimum productivity of Sweet potato, this is due to biotic and abiotic factors, inappropriate Agronomic practices and lack of improved variety, to tackle these problems; variety improvement research is the major one. Therefore, the objectives of the study were to estimate the magnitudes of genotype, environment, and genotype by environment interaction effects on Sweet potato genotypes and to identify the high yielder and stable genotypes for wide adaptability in West Hararghe Zone, Eastern Ethiopia. The experiment was carried out at two locations (Mechara on station and Habro district) in three consecutive years (2018–2020) on 20 Sweet potato genotypes using a randomized complete block design (RCBD) with three replications. Additive main effects and multiplicative interactions analysis (AMMI) indicated that the yield performances of genotypes were under the major environmental effects of genotype by environmental interactions. The first two principal component axes (PCA 1 and 2) were significant (p≤0.01) and cumulatively contributed to 73% of the total genotype by environment interaction. In GGE bi-plot analysis using genotypic and environmental scores of the first PCA 1 and lower PCA 2 scores gave high yields (stable genotypes), and genotypes with lower PCA 1 and larger PCA 2 scores had low yields (unstable genotypes), as in the sites tested. Besides, genotypes G3 and G5 were stable across tested locations and gave higher total root yields (43.94t ha^{-1} and 49.34 t ha^{-1}), respectively). However, G5 was recommended for possible release for wide adaptability in West Hararghe Zone and similar agro-ecology in the country.

INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam) is a root crop belonging to the *Convolvulaceae* family. It belongs to the family *Convolvulaceae*, genus Ipomoea, and the genus has over 600 species, of which *batatas* is the only one with economic value (Vaeasey*et al*. 2008). In many developing countries, sweet potato is reported to be the fifth most important food crop after rice, wheat, maize, and cassava (Aina*et al*., 2012). Over 110 million metric tons of sweet potatoes are produced in 2018, with China producing 53.01 million metric tons representing 65.6% of the world sweet potato production (FAOSTAT, 2018). Africa was responsible for 20.7 million tons which represents about 25.4% of the world's production.

In Ethiopia, agriculture is the main source of livelihood for about 80% of the population which contributes to 42% of Ethiopia's gross domestic product (FAOSTAT, 2009). Sweet potato has been cultivated for the last several years and over 95% of the crop is produced in the Southwest, Eastern and Southern parts. It is one of the five most important crops, in terms of production, economic value, and contribution to calories and proteins. But the productivity of sweet potato is limited to both abiotic and biotic constraints, leading to poor yields and quality at farm levels. The crop has the potential of giving over 50 to 60 ton ha-1 in Ethiopian conditions; however, the yield obtained from farmer's fields is lower than 6 to 8 tons ha-1. Thus the yields are ten times lower than the potential sought. One of the main reasons is a shortage of improved varieties of planting materials in addition to other factors (FAOSTAT, 2009). Therefore, one important way of mitigating poor root yield in farmers' fields is to develop and release new sweet potato varieties with stable and high root yield potential into the farming system.

Understanding the differential response of crop genotypes to change environmental conditions is of key importance in plant breeding. One major step toward the development of improved crop genotypes is the assessment of the nature of interactions that exist between genotypes and the production environment for a particular trait (Sabri *et al*., 2020). When genotypes are evaluated across a range of different locations and/or years, their yield performances could differ significantly. The existence of large G × E interaction usually causes serious confounding effects in comparing and recommending good genotypes for wide adaptation (Moussa *et al*., 2011). Previous G × E studies on several traits have demonstrated that sweet potato is sensitive to environmental changes. The changes in environmental conditions have been reported to affect sweet potato storage root yield and yield components (Ngailo *et al*. 2019). This analyzes G × E interaction crucial for genotype selection, cultivar release, and identification of suitable production environments for optimum yield. Therefore, having a basic understanding of G × E interactions, stability parameters, and genetic correlations for root yield and yield components is considered necessary for sweet potato breeders in making an informed choice concerning which locations and input systems should be used in their breeding efforts (Gruneberg *et al*., 2005).Statistical tools such as the additive main effect and interaction, and genotype and genotype-by-environment interaction (GGEI) biplot analysis have been reported as appropriate for use in GEI analyses (Yan and Tinker, 2006). These statistical tools have then been extensively used in several sweet potato improvement programs by authors such as (Caliskan *et al*. 2007). The AMMI model analysis for GEI and stability analysis of sweet potato genotypes across environments is different (Laurie and Booyse, 2015).Therefore, the objective of the study was to estimate the magnitudes of genotype, environment, and genotype by environment interaction effects and to identify the high yielder and stable genotypes for wide adaptability in West Hararghe Zone, Eastern Ethiopia.

MATERIALS AND METHODS

Description of the study areas

The field experiment was carried out during the 2018–2020 cropping season at Mechara research on station and Busoytu Farmer Training Center (FTC), Habro district. Mechara on station is located in the Eastern part of the country, lying between 8.6149N latitude and 40.3220E longitude. The altitude of the area is about 1760 m.a.s.l. it has an annual mean maximum and minimum temperature of 28°C and 15.1°C. Habro district is one of the West Hararghe Zone in Eastern Ethiopia, it's located at 8051'N and 400 39' E at an altitude of 1728 meters above sea level. Gelemso town is the administrative seat of the district. Planting Materials: Sixteen sweet potato accessions, along with three released varieties, and one local check were used for the trial.

44

Res. Agric. Livest. Fish.   **Vol. 10, No. 1, April 2023: 43-52.**

Field layout and experimental design

The experiment was conducted using a random complete block design (RCBD) with three replications and a plot size of 12m^2 with 1m and 0.3 m inter-row and intra-row spacing, respectively. Data was collected from the 20 plants that were grown in two central rows. The young portion of 30 cm length of the vine cuttings planted where 2/3 of their length was covered by soil. The accessions were planted at the end of July as soon as the rain starts and the soil get sufficient moisture. All plots where receive the recommended cultural practices uniformly. Replanting was done to replace the dead vine after one week of planting. Harvesting was done after 90% of the sweet potato leaves changed to a yellowish colour. From each plot, ten plants were considered for both storage root yield and yield related traits. At harvest, the middle two rows were used for data collection. After removing vines, the ridges were opened with a hoe, and storage roots were dug. The harvested storage roots were then counted and weighed, and the average storage root weight (kg) and total storage root yield per ha were calculated from these data.

Data Collection

All Agronomic traits (mean root number, root diameter, root length, root weight, marketable, unmarketable, total root yield, and sweet potato weevil (Cylas spp. infestation) were collected. where genotype was treated as a fixed factor and replication was treated as a random variable (Steel and Torrie, 1980). The number of marketable (saleable) roots represents the number of roots that were more than or equal to 100g or with diameters at the widest point of >25mm (Levette, 1993) these were counted and the number was recorded per plot.

Statistical Data Analysis

All growth and mean root yield were subjected to analysis of variance (ANOVA) using the Generalized Linear Model procedure of SAS 9.2 (SAS INC., 2004), and the AMMI and GEI models were analyzed by Genstat's 18th edition. An analysis of variance (ANOVA) was carried out for each environment (location-year combinations) to check whether significance variation was observed among the test genotypes. This was conducted before a combined analysis of variance and other multivariate analyses of G × E interaction across the test environments. Furthermore, homogeneity of variance tests (Bartlett's test) was conducted to determine if data from individual environments could be pooled to conduct a combined ANOVA across environments to analyze G × E interactions. The environments were considered random and genotypes as fixed effects.

The combined ANOVA method sufficiently identified G × E interaction as a significant source of variation, but it is not able to explore the nature of G × E interaction, which could not show the true performance of genotypes in certain environments (Cross, 1990). Stability analysis was done using the methods of Additive main effects and multiplicative interaction AMMI ((Zobel et al., 1988). The AMMI model was done based on the formula suggested by (Cross, 1990).

$Yij = \mu + Gi + Ej + (\Sigma KnUniSnj) + Qij + eij$

Where (i = 1, 2,... 35; j = 1, 6); Yij = The performance of the i genotype in the j environment; μ = The grand mean; G = Additive effect of the i genotype (genotype mean minus the grand mean); K = Eigen value of the PCA axis n; E = Additive effect of the jth environment (environment mean deviation); U and S = the scorers of genotype i and environment j for the PCA axis n; Q = Residual for the first n multiplicative components; e = error.

RESULTS AND DISCUSSION

Combined Analysis of Variance

The analysis of variance showed highly significant differences among the tested genotypes, locations, and interaction (P≤ 0.01) for root yield (Table 1) However; significance variation (P< 0.05) was recorded on genotypes evaluated across years. This indicated the presence of variability among tested genotypes across tested environments. At the same time, GEI showed that the presence of variability among tested genotypes across environments and their interaction showed the possibility to do stability analysis, i.e to understand the nature of GEI and performance of the genotypes over locations. The analysis of variance revealed that the main effect of genotypes, location and years were significant differences (p≤0.05) on root yield.

45

Res. Agric. Livest. Fish.   **Vol. 10, No. 1, April 2023: 43-52.**

Table 1. The combined mean of ANOVA for root yield of Sweet potato genotypes over six environments at Mechara on station and Habro district, West Hararghe Zone, in 2018-2020 cropping season

Source of variation	D.f.	S.S.	M.S.
Genotype(G)	19	20512.16	1079.59**
Rep(Env't)	4	2386.46	596.62**
Year(Yr)	2	9075.49	4537.75**
Location(Loc)	5	1781.53	356.31**
Genotype.Yr	38	6767.48	178.09*
Loc.Yr	10	904.14	90.35**
G.Loc	95	12676.61	133.44**
G.Yr.Loc	93	12676.61	136.31**
Residual	238	17876.77	75.11
Total	359	64309.02	

df = degree of freedom, ** and * = highly and Significant at p<0.01 and p< 0.05 probability levels, respectively

Table 2. The combined mean result of root marketable yield across locations and years of Sweet potato regional variety trial at Mechara on station and Habro district, in 2018-2020 cropping season

Genotypes name	Gen. code	Environments							Mean RY (t ha^{-1})
		Habro district				Mecharaonstation			
		2018	2019	2020	Mean	2018	2019	2020	
CN-1753-4	G4	12.75a-g	34.41cde	24.61b-e	23.92d-h	32.66	36.96abc	17.62b-e	26.5cde
Tis-9068-8	G18	31.71a-h	18.52e-h	25.47b-e	25.23d-g	25.45	27.77c-f	15.5b-f	24.07c-g
Tis-8441-1	G15	37.16a-d	35.98b-e	27.4bcd	33.51bcd	31.26	19.33d-g	9.66d-g	26.8cde
Hawaassa-09	G10	38.15abc	54.17ab	28.47bc	40.26abc	32.36	33.49a-d	23.75b	35.06 b
Tis-80/043-3	G14	19.3e-h	21.99d-h	19.67c-f	20.32fgh	26.56	13.21fg	19.58bcd	20.05fgh
CN-2065-7	G8	30.34a-g	9.35gh	13.53f	17.74gh	30.24	17.13d-g	10.28d-g	18.48gh
CN-2065-15	G7	20.54d-h	39.04bcd	25.2b-e	28.26def	24.35	31.77b-e	13.06c-g	25.66c-f
CN-1754-12	G5	41.9a	65.78a	40.07a	49.25a	39.05	48.99a	39.42a	45.87a
CN-1753-19	G3	36.62a-d	54.64ab	31ab	40.75ab	36.77	46.3ab	35.91a	40.21ab
Barkume	G1	26.77a-h	33.91c-f	24.93b-e	28.54def	26.7	26.78c-f	21.63bc	26.79cde
Hawassa-83	G11	34.71a-f	35.18cde	25.17b-e	31.69b-e	27.46	24.89c-g	21.4bc	28.14c
Tis-9468-7	G20	19.04fgh	7.77h	15.36ef	14.06h	30.25	17.91d-g	5.52fg	15.98h
CN-2059-5	G6	26.7a-h	36.96b-e	27.57bcd	30.41c-f	26.33	28.28c-f	16.98b-e	27.14cd
Tis-9065-1	G16	35.9a-e	39.73bcd	11.91f	29.18def	28.42	20.13c-g	13.28c-g	24.89c-f
Tis-70357-2	G13	16.53gh	19.51e-h	17.53def	17.86gh	28.61	8.5g	7.81efg	16.42h
Local	G12	18.65fgh	15.33fgh	11.27f	15.08gh	25.8	16.52efg	4.01g	15.26h
CN-2069-8	G9	22.91b-h	43.5bc	23.93b-e	30.11c-f	33.11	32.94a-e	11.15d-g	27.92c
Tis-9068-2	G17	37.28abc	29.6c-f	21.33b-f	29.41def	28.32	26.17c-f	11.15d-g	25.64
CN-1752-9	G2	21.04c-h	26.65c-g	19.2c-f	22.3e-h	29.73	16.86d-g	13.44c-g	21.15
Mean		27.85	32.48	22.61	27.65	29.5	25.32	16.04	25.63
CV		36.2	34.9	27.5	22.3	10.6	30.5	36.22	14.66
LSD		16.65	18.74	10.27	10.18	5.18	16.95	10.07	6.20

*, ** significant at 0.05 and 0.01 probability levels, respectively
df = degree of freedom, LSD = least significant difference, CV =Coefficient of variation.

46

Res. Agric. Livest. Fish.   **Vol. 10, No. 1, April 2023: 43-52.**

Combined Mean Root Yield and Agronomic Performance of Sweet Potato Genotype

The mean root yield of the individual environments during the 2018 - 2020 main cropping seasons was highly significant at (p≤0.01) and was presented in Table 2. Habro district was the suitable environment for sweet potato production. Genotype, G5 was the highest root yielder (45.87 t ha-1) across environments, followed by G3, which yield 40.21 t ha-1. The lowest mean root yield (15.26 t ha-1) was recorded for the local check (Table 2). This high-yielding genotype (G5) produced nearly 2-3 times higher yield than local genotypes. Likewise, the result for the combined mean analysis of yield related traits across environments was showed significance differences among the genotypes in all locations (Table 2). The combined mean of tested genotypes indicated that G5 and G3 were better performers, followed by Hawasa-09 varieties, while the local check was the least performer in a trait. Besides, the highest mean of root numbers (8.29, 7.43, and 7.19) were recorded by G16, G8, and G2 genotypes, respectively. Whereas, Genotype G5 had the highest root diameter (7.21cm) followed by Hawassa-09 (6.35cm).

This may be related to the genetic potential of the individual genotypes, While G9 had the lowest mean root number(4.82) while the least mean root diameter (3.60cm) was recorded by (G20) followed by G8(4.23cm) genotypes (Table 3). In generally, genotype (G5) showed higher yield related traits are the major components of having larger storage roots produced higher total root yield in addition, the root length and number, and root diameter per varied significantly due to varietal difference(Gezahegn A. *et al*., 2020).

Table 3. The Combined analysis of overall Agronomic traits of Sweet potato genotypes regional Variety Trial at Mechara on station and Habro district, in 2018-2020 cropping season

Genotypes name	Gen. Code	RN	RL (cm)	RD (cm)	RW (kg)	RWP (kg)	My (t ha-1)	Unm (tha-1)	TY (tha-1)
CN-1753-4	G4	6.87a-e	16.74e-g	5.31cde	0.53c-f	4.12b-e	26.5cde	2.58	29.08d-g
Tis-9068-8	G18	6.36b-f	17.52b-e	4.99efg	0.49def	3.51c-e	24.07c-g	3.65	27.72d-h
Tis-8441-1	G15	7a-d	15.58gh	5.86bc	0.43efg	2.97efg	26.8cde	6.01	32.81cd
Hawaassa-09	G10	6.35b-f	18.57abc	6.35b	0.91a	5.43b	35.06 b	3.38	38.22bc
Tis-80/043-3	G14	6.00b-g	16.70e-g	5.19c-f	0.48efg	4.23b-e	20.05fgh	2.95	23ghi
CN-2065-7	G8	7.43ab	15.00h	4.23hi	0.23h	2.33fg	18.48gh	4.3	22.78hi
CN-2065-15	G7	6.41b-e	15.62hg	4.91e-h	0.40efg	3.14c-g	25.66c-f	3.82	29.48def
CN-1754-12	G5	6.57b-e	17.21c-f	7.21a	0.93a	8.41a	45.87a	3.47	49.34a
CN-1753-19	G3	6.65b-e	18.56abc	4.87fgh	0.48efg	7.34a	40.21ab	3.74	43.94ab
Barkume	G1	5.43e-g	19.91a	5.60cde	0.760b	4.83bcd	26.79cde	2.16	28.95d-h
Hawassa-83	G11	4.93fg	18.78ab	5.43cde	0.61cd	4.87bc	28.14c	2.65	30.78de
Tis-9468-7	G20	7.03a-d	17.03e-g	3.60i	0.21h	1.50g	15.98h	3.62	19.59 i
CN-2059-5	G6	5.49efg	18.31bcd	5.76bcd	0.75b	4.15b-e	27.14cd	1.54	28.68d-h
Tis-9065-1	G16	8.294a	15.92fgh	5.09def	0.53cde	3.30c-e	24.89c-f	5.2	30.09def
Tis-70357-2	G13	6.32b-f	16.17e-h	4.50fgh	0.410fg	2.01fg	16.42h	3.98	20.4i
Local	G12	4.96fg	18.79ab	4.27gh	0.53cde	1.61g	15.26h	3.33	18.59i
CN-2069-8	G9	4.82g	18.56abc	5.86bc	0.65bc	3.12deg	27.92c	2.9	30.83de
Tis-9465-10	G19	5.69d-g	17.19c-f	5.34cde	0.53c-f	2.66efg	20.65	3.2	23.85fghi
Tis-9068-2	G17	5.97c-g	17.22c-f	4.97e-h	0.54cde	3.06efg	25.64	2.48	28.13d-h
CN-1752-9	G2	7.19abc	16.65e-g	4.49fgh	0.36g	3.19c-g	21.15	3.51	24.67e-i
Means		6.29	17.3	5.19	0.54	3.79	25.63	3.42	29.06
CV%		13.9	5.1	8.65	13.53	27.92	14.66	38	13
LSD		1.44	1.45	0.74	0.12	1.75	6.2	2.57	6.24

**,*, significant at 0.05 and 0.01 probability levels, respectively

df = degree of freedom, TY=total yield, RW=root weight, RL=root length, RD=root diameter

47

Res. Agric. Livest. Fish. **Vol. 10, No. 1, April 2023: 43-52.**

Response to Major Insect Pest (Sweet potato weevil)

From analyzed of SP weevil, genotypes CN-1754-12(G5) and CN-1753-19(G3) were the least *Cylas spp* damage in environments in both locations (Table 4). The least mean SP weevil score value was recorded (1.89) from CN-1754-12 genotypes. The differential expression of tolerance by the genotypes in different environments is unexpected as tolerance to *Cylas spp.* is known to be largely influenced by strong environmental control. Sweet Potato weevil tolerance, and stability, thereby enhances the probability of identifying highly tolerant genotypes that could be deployed across many environments.

Table 4. The mean result of Sweet potato weevil (*Cylas s*pp) scores across a location for the twenty Sweet potato genotypes at Mechara on station and Habro district, in 2018-2020 cropping season

Genotypes name	Gen. code	Habro district				Mecharaonstation			
		2018	**2019**	**2020**	**Mean**	**2018**	**2019**	**2020**	**Mean (1-5score)**
CN-1753-4	G4	1.67	1.67	2.33	1.89	2.20	2.13	2.00	2.00
Tis-9068-8	G18	2.00	2.00	2.00	2.00	1.96	1.95	1.67	1.95
Tis-8441-1	G15	2.00	2.33	2.67	2.33	2.48	2.10	2.00	2.30
Hawaassa-09	G10	2.00	2.33	3.33	2.55	2.92	2.16	2.00	2.53
Tis-80/043-3	G14	1.67	2.67	3.33	2.56	2.90	2.28	1.67	2.50
CN-2065-7	G8	1.67	2.00	3.67	2.45	3.08	1.86	2.00	2.47
CN-2065-15	G7	2.00	2.33	2.00	2.11	2.00	1.81	2.00	2.04
CN-1754-12	G5	1.67	1.33	2.67	1.89	2.28	1.31	1.67	1.89
CN-1753-19	G3	2.33	2.33	2.00	2.22	1.94	1.89	1.33	2.01
Barkume	G1	2.00	2.33	3.00	2.44	2.59	1.52	1.67	2.28
Hawassa-83	G11	2.00	2.33	2.67	2.33	2.46	1.98	2.00	2.28
Tis-9468-7	G20	2.00	2.33	3.00	2.44	2.66	2.10	1.67	2.36
CN-2059-5	G6	2.00	3.33	3.33	2.89	2.99	2.63	1.67	2.74
Tis-9065-1	G16	2.00	2.67	2.67	2.45	2.41	1.71	1.67	2.26
Tis-70357-2	G13	1.67	2.33	3.33	2.44	2.85	2.33	1.33	2.39
Local	G12	2.00	2.33	2.33	2.22	2.15	1.64	1.67	2.07
CN-2069-8	G9	1.33	2.33	4.33	2.66	3.44	1.52	1.67	2.60
Tis-9465-10	G19	1.67	1.67	3.33	2.22	2.79	1.49	2.00	2.24
Tis-9068-2	G17	2.00	3.00	2.33	2.44	2.23	2.01	1.67	2.25
CN-1752-9	G2	2.00	2.33	2.33	2.22	2.13	1.42	1.67	2.04
Mean		1.88	1.21	2.83	1.97	1.89	1.89	1.75	1.92
CV		19.80	31.90	35.20	28.97	32.01	32.00	33.10	30.50
LSD		0.61	1.21	1.65	1.16	1.06	1.02	0.95	1.09

*, ** significant at 0.05 and 0.01 probability levels, respectively df = degree of freedom, LSD= Least significant difference, CV= Coefficient of variation.

Additive Main Effects and Multiple Interaction (AMMI) Model Analysis

The AMMI analysis of variance of root yield (tons ha-1) of 20 sweet potato genotypes tested in six environments was presented in (Table 5). The analysis showed that sweet potato root yield was significantly ($p \leq 0.01$) affected by genotypes (G), Environment (E) and genotype x environment interaction (GEI). The AMMI of twenty genotypes tested in six environments showed that 31.9% of the total sum of squares was attributable to genotype effects, 16.9 Environment effects, and 19.7% to GEI effects (Table 5). A large sum of squares for genotypes indicated that the genotypes were diverse with large differences among genotypes means causing most of the variation in root yield. The result is agreed with the previous findings (Mehmet, E *et al.*, 2007). The magnitude of the GEI sum of squares showed that there was a significance difference, indicating there were substantial differences in genotypic response across environments.

Table 5. The AMMI analysis of variance for root yield (t ha^{-1}) of twenty sweet potato genotypes grown at six environments at Mechara on station and Habro district in 2018-2020 cropping season

Source	D.F	S.S	M.S	% GXE Explained	Cumulative%
Total	359	64309	179.1	-	
Block	12	4024	335.4**	6.3	
Genotypes	19	20512	1079.6**	31.9	
Environments	5	10857	2171.4**	16.9	
GxE	95	12677	133.4**	19.7	
IPCA 1	23	6750	293.5**	53.2	53.3
IPCA 2	21	2492	118.7*	19.6	19.7
IPCA 3	19	1620	85.2ns	12.8	12.6
IPCA 4	17	1177	69.2ns	9.2	9.2
IPCA 5	15	638	42.6ns	5.0	99.99
Residuals	51	3434	67.3*		
Error	228	16239	71.2		

*, ** significant at 0.05 and 0.01 probability levels, respectively

df= degree of freedom, IPCA1=Interaction Principal Component Axis I & II.

Results from AMMI analysis revealed that the mean square of the first and second interaction principal component axis (IPCA1 and (IPCA2) were found to be highly significant (P≤0.01). The first principal component axis (IPCA 1) of the interaction captured 53.21% followed by PCA 2 (19.6%), together (IPCA 1 and PCA 2) they accounted for 73% of the GE interaction SS, the remaining 23% value of IPCA 3, 4 and 5).

In addition, genotypes found closer to the origin showed stable performance over the testing environment (Emanuel *et al.*, 2021). this indicates as those genotypes found close to the origin showed more general adaptability than those found at a far distance away from the origin likewise those environments found the closest distance to the origin were stable and not changed across seasons. In the present study, G3 and G5, which are found close to the origin showed general stability. In other word they had broad adaptability as they were located closer to the center of the bi-plot, whereas, environment Mechara showed less change across seasons allowing stability for the genotypes tested in these locations (Figure 1).

GGE Biplot Analysis

The value in table 5 showed sweet potato genotypes based on the yield character shown in Figures 1-3. Biplot in the AMMI analysis showed the genotype and environmental magnitude that contributed to the interaction. Figures 1-3 illustrated 85.25% of the total GGE variation, where PC1 explained 76.16% and PC2 9.09% of total variation respectively. From Figure 1, it can be seen that G5 and G3 were the closest to the ideal environment; therefore, it was most stable of all genotypes. Genotypes that have a small vector distance from the center of the biplot are considered as stable genotypes (Emanuel *et al.*, 2021). While G13 and G8 were the least unstable genotypes (Figure 1) in other word, those are placed furthest from the point of origin, showing specific adaptation to the environments within their proximity on the bi-plot. Moreover, these ideal genotypes were represented by the small circle with an arrow pointing to its defined as having the highest yield in all environments (Yan *et al.*, 2007). So, the G5 genotype was also capable of producing maximum yield at all environments, so it can be recommended as a new superior variety. Moreover, genotypes that fall in the central (concentric) circle are considered as stable genotypes (Fekadu G *et al.*, 2017). In this study, there were some genotypes with high stability and low mean root yields. But, Aim this study was to select a stable and high yielder genotype that was desirable for the area. Furthermore, the stability analysis aims at helping the breeder identify which genotypes have specific and/or general adaptability to various production environments. It also helps in the analyses of the test environment for prudent decision-making for future evaluation.

49

**Res. Agric. Livest. Fish.**   **Vol. 10, No. 1, April 2023: 43-52.**
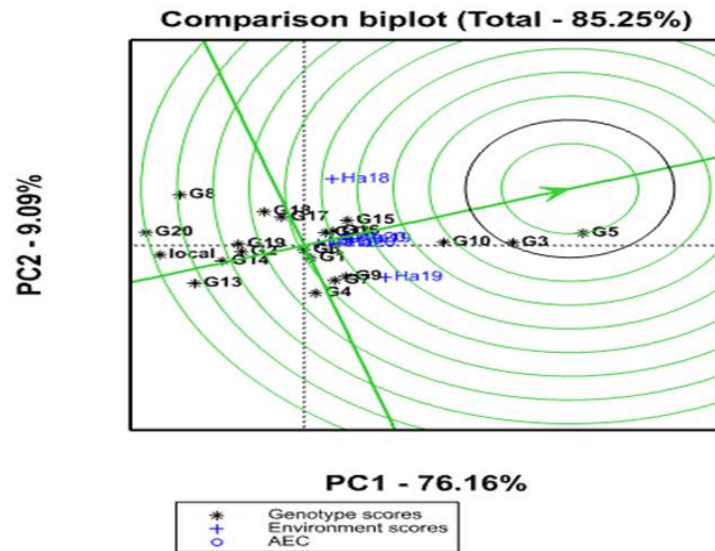
Figure 1. GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability
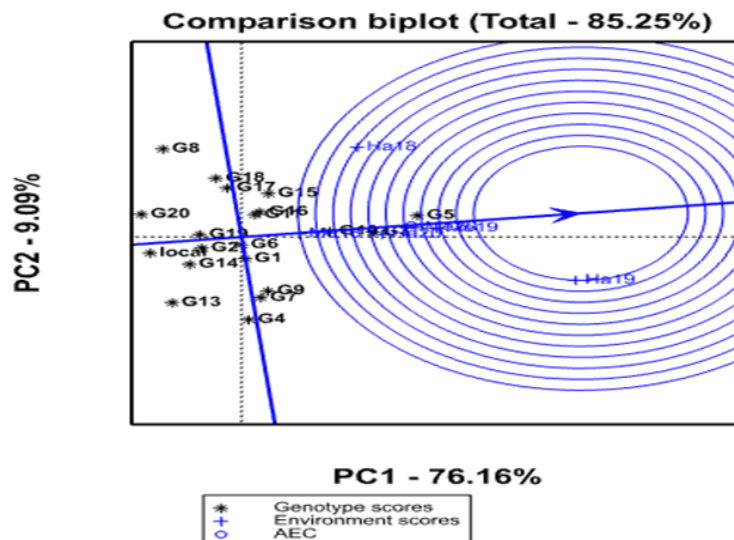
Figure 2. GGE bi-plot based on environment-focused scaling for comparison of their ideal environment for sweet potato production

Set of concentric lines that serve as a ruler to measure the distance between an environment and the ideal environment. In (Figure 2) also showed that Ha19 was the closest to the ideal environment, and, therefore, is the most desirable of all seven environments. Ha19 is followed by Me19, which is followed in turn by Me18 and Ha18 were the least desirable test environments. However, Me19 and Ha 20 had the worst performing environments for fresh root yield. Environments in different sectors show that genotypes located in these locations have unequal yields and that genotypes belong to region-specific genotypes. A ranking of genotypes in (Figure 3) showed that an ideal genotype should have both high mean performance and high stability across environments. The center of the concentric circle (Figure 3) is the location of the ideal genotype. Among the test genotypes, the one closest to the point is the best. Though G3 and G5 had the highest storage root yield among the 20 genotypes, while, G3 possessed both high mean root yield and high stability and is closest to the ideal genotype for root yield with the consistency of performance across environments.

50

Res. Agric. Livest. Fish.   **Vol. 10, No. 1, April 2023: 43-52.**
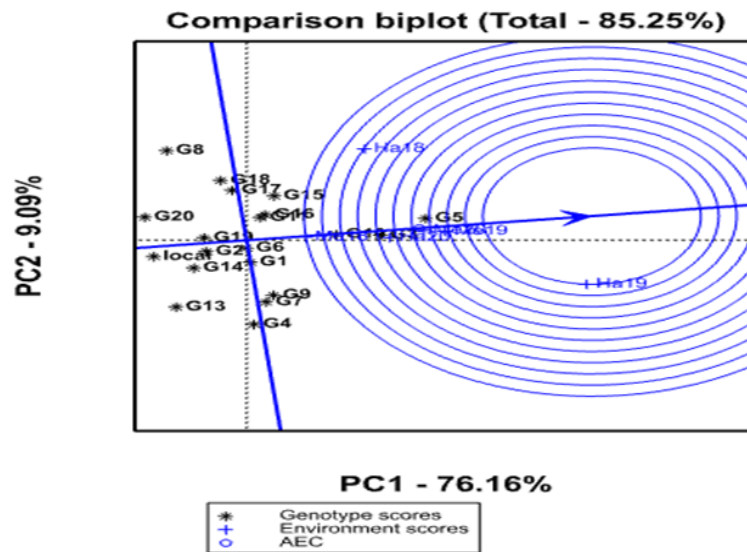
Figure 3. GGE bi-plot based on genotypes ranking of their "stable" genotypes and stability performance of eight tested genotypes

CONCLUSION AND RECOMMENDATION

In conclusion, AMMI analysis, regression coefficient, deviation from regression and GGE biplot results revealed that G3 and G5 were relatively stable genotypes with optimum root yield. However, the G5 genotype was optimum stable across tested locations and had a high root yield, From the present study it was concluded that G5 gave the highest mean total root yield than the rest of the genotypes with a yield advantage of 29% over the check (G10) and showed moderate stability over the testing sites, is identified as candidate genotypes to be verified in the coming cropping season for possible release after being evaluated by the National Variety Releasing Committee.

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CONFLICT OF INTEREST

The authors declared that there is no conflict of research interest.

REFERENCES

1. Aina A J, Falade K O, Akingbala J O, and Titus P. 2012. Physicochemical Properties of Caribbean Sweet Potato (*Ipomoea Batatas* (L) Lam) Starches. Food and Bioprocess Technology, 5: 576-583.
2. Caliskan S M, Aslan M, Uremis I, and Caliskan M E, 2007. The Effect of Row Spacing on Yield and Yield Components of a Full Season and Double-Cropped Soybean. Turkish Journal of Agriculture, 31: 147-154.
3. Cross J, 1990. Statistical Analysis of Multi-Location Trails. Advance in Agronomy, 45: 56-86.

51

Res. Agric. Livest. Fish.   Vol. 10, No. 1, April 2023: 43-52.

4. Ebem E C, Afuape S O, Chukwu S C, and Ubi B E, 2021. Genotype × Environment Interaction and Stability Analysis for Root Yield in Sweet Potato [*Ipomoea Batatas* (L.) Lam]. Frontiers in Agronomy. Https://Doi.Org/10.3389/Fagro.2021.665564.

5. Fekadu Gurmu, Shimelis Hussein and Mark Laing. 2017. Genotype-By-Environment Interaction And Stability of Sweet Potato Genotypes for Root Dry Matter, β-Carotene and Fresh Root Yield. Open Agriculture, 2: 473-485.

6. Food and Agriculture Organization of the United Nations (Faostat), 2018. Food and Agricultural Organization of the United Nations, Production Statistics. Available Online At: Http://Faostat.Fao.Org/ (Accessed Dec 12, 2021).

7. Food and Agriculture Organization of the United Nations (Faostat). 2009. Statistical Database.

8. Gezahegn Assefa, Sintayehu Girma, Dereje Deresa, 2020. Evaluation of Orange Flesh Sweet Potato Varieties (*Ipomoea Batatas*) in West Hararghe Zone of Oromia Region, Eastern Ethiopia, Biochemistry and Molecular Biology, 5(3): 37-43.

9. Gruneberg W J, Manrique K, Zhang D and Hermann M, 2005. Genotype X Environment Interactions For a Diverse Set of Sweet Potato Clones Were Evaluated Across Varying Eco-Geographic Conditions in Peru. Crop Science, 45: 2160-2171.

10. Levette M P, 1993. The Effects of Methods of Plant Cuttings of Sweet Potato (*Ipomoea Batatas* (L) Lam) on Yield. Tropical Agriculture, Trinidad, 70: 110-115.

11. Mehmet E, ÇAlışKan E, Tahsin S, Erkan B and Halis A, 2007. Genotype by Environment Interaction and Stability Analysis of Sweet Potato (*Ipomoea Balatas*) Genotypes, New Zealand Journal of Crop and Horticultural Science, 35: 87-99.

12. Moussa SAM, Hala AAE, and Nashwa I A E, 2011. Stability Study of Sweet Potato Yield and Its Component Characters under Different Environments by Joint Regression Analysis. Journal of Horticultural Science, Ornamental Plants, 3: 43-54.

13. Ngailo S, Shimelis H, Sibiya J, Mtunda K, and Mashilo J, 2019. Genotype by Environment Interaction of Newly-Developed Sweet Potato Genotypes for Storage Root Yield, Yield-Related Traits and Resistance to Sweet Potato Virus Disease. Heliyon; (5): E01448.

14. Sabri R S, Rafii M Y, Ismail MR, Yusuff O, Chukwu S C, and Hasan N, 2020. Assessment of Agro-Morphologic Performance, Genetic Parameters and Clustering Pattern of Newly Developed Blast-Resistant Rice Lines Tested In Four Environments. Agronomy 10: 1098.

15. Sas Institute Inc., 2004. Sas/Stat Software 9.2 Sas Institute Inc, Cary, N.C., Usa.

16. Steel R G D, and Torrie J A, 1980. Principles and Procedures of Statistics, 2nd Edn. New York, Ny: Mcgraw-Hill, 183-193.

17. Sunette M Laurie, Marde´ Booyse, 2015. Employing the Gge Sreg Model Plus Elston Index Values For Multiple Trait Selection In Sweet Potato. Euphytica, 204: 433-442.

18. Vaeasey E A, Borges A, Rosa M S, Queiroz-Silva J R, Bressan E A, and Peroni N, 2008. Genetic Diversity in Brazilian Sweet Potato (*Ipomoea Batatas* (L.) Lam., Solanales, Convolvulaceae) Landraces Assessed Within Microsatellite Markers. Genetics and Molecular Biology, 31: 725-733.

19. Yan W, Tinker Na, 2006. Biplot Analysis of Multi-Environment Trial Data: Principles and Application. Canadian Journal of Plant Science, 86: 623-645.

20. Zobel R W, Wright M J and Gauch H G, 1988. Statistical Analysis of a Yield Trial. Agronomy Journal, 80: 388-393.

52

Res. Agric. Livest. Fish.   **Vol. 10, No. 1, April 2023: 43-52.**