Stability Analysis of Fresh Root Yield of Sweetpotato in Southern Ethiopia using GGE Bi-Plot

International Journal of Pure Agricultural Advances
Vol. 1, No. 1, 1-9, 2017

Fekadu Gurmu[1]

[1]*South Agricultural Research Institute, Crop Research Directorate, Hawassa, Ethiopia*

ABSTRACT

The yield performance of sweetpotato is highly influenced by the effect of genotype by environment interaction (G x E) and stability analysis is required before variety release. The objectives of the study were to estimate the magnitude of G x E interactions, to select high yielding and stable elite sweetpotato clones, and to identify the most discriminating and representative test environments in Ethiopia. The study was conducted across six diverse environments in southern Ethiopia in 2014. The locations were Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla. Twenty five clones (24 elite clones and one check variety) were used for the study and were arranged in a 5 x 5 simple lattice design for field experimentation. Genotype plus Genotype by Environment Interaction (GGE Bi-plot) method was used to study the stability of the clones for fresh root yield. Significant environment, genotype and G x E interaction variances ($p < 0.01$) were observed for fresh root yield. The magnitude of environment and G x E interaction effect was higher than that of the genotype effect. Three clones, G1 (Ukrewe x Ejumula-10), G6 (Resisto x Ejumula-7) and G20 (Ejumula x PIPI-10) were identified as stable and relatively high yielding genotypes. The mean root yields of the three clones were 25.1, 26.9 and 25.5 t ha^{-1}, respectively for G1, G6 and G20. Accordingly, the above three elite clones were selected for ultimate evaluation and recommendations. Among the test locations, the highest and stable mean fresh root yield of 37.1 t ha^{-1} was recorded at Arbaminch. Therefore, Arbaminch was identified as the best environment for sweetpotato production in southern Ethiopia. The study revealed the possibility of breeding sweetpotato varieties for high yielding and stable clones that have wide adaptation in southern and similar agro-ecologies in Ethiopia.

Keywords: *Elite clones, Fresh root yield, GGE, Multi-environment, Sweetpotato, Stability analysis.*

DOI: 10.20448/813.11.1.9
Citation | Fekadu Gurmu (2017). Stability Analysis of Fresh Root Yield of Sweetpotato in Southern Ethiopia using GGE Bi-Plot. International Journal of Pure Agricultural Advances, 1(1): 1-9.

Funding: The Alliance for a Green Revolution in Africa, International Foundation for Science and Syngenta Foundation are duly acknowledged for financially supporting the study.
Competing Interests: The author declares that there are no conflicts of interests regarding the publication of this paper.
History: Received: 27 February 2017/ Revised: 17 March 2017/ Accepted: 28 March 2017/ Published: 4 April 2017
Publisher: Online Science Publishing

1. INTRODUCTION

Sweetpotato is one of the world's most important food crops ranking seventh after wheat, rice, maize, potato, barley and cassava [1-3]. It is widely grown in sub-Saharan African (SSA) countries due to its high yield potential and adaptability to a wide range of environmental conditions [4, 5]. In these countries, sweetpotato and ranks fifth after rice, wheat, maize and cassava. Sweetpotato is usually used as staple food, animal feed and a raw material for different industrial products. The root yields of sweetpotato are sensitive to the effects of genotype x environment (G x E) interaction as revealed by [6-9]. Grüneberg, et al. [10] conducted a study on genotype x environment interactions for a diverse set of sweetpotato clones evaluated across varying eco-geographic conditions in Peru and reported a significant G x E interaction of a cross-over type. This implies the presence of differential ranking of sweetpotato genotypes across locations and years. Tsegaye, et al. [11] conducted genotype x environment interactions and yield stability of orange fleshed sweetpotato varieties in Ethiopia and reported that most OFSP clones evaluated in Ethiopia were sensitive to environmental variations. Nevertheless, there is limited information on the magnitude of G x E interactions and the stability of promising sweetpotato clones in Ethiopia. Therefore, there is a need for understanding the nature of G x E interactions, quantifying its magnitude and for identifying stable and widely adapted sweetpotato clones before variety release. Identification of the most discriminating and representative test environments is also essential for further variety evaluation and production of sweetpotato in Ethiopia. Genotype plus genotype by environment interaction (GGE bi-plot) developed by [12-14] is one of the commonly used statistical methods for analyzing multi-environment data. Yan [14]; Yan and Rajcan [15] and Yan, et al. [16] noted that among genotype (G), environment (E), and G x E, only G and G x E are important and must be simultaneously considered. The authors suggested that a GGE biplot best identifies G x E interaction patterns of data and clearly shows which variety performs best in which environments, and thus facilitates mega-environment identification. Twenty five clones (24 elite clones and one check variety) were selected from a diallel cross conducted in 2013 in Ethiopia. Among these, best performing and stable clones should be ranked and selected across representative test environments in Ethiopia for release or further breeding works. Therefore, the objectives of the study were to estimate the magnitude of G x E interactions, to select high yielding and stable elite sweetpotato clones, and to identify the most discriminating and representative test environments in Ethiopia.

2. MATERIALS AND METHODS

2.1. Study Areas and Materials used for the Study

The study was conducted at six environments in southern Ethiopia. The test sites were Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla (Table 1). These test sites represent a low to mid altitude with diverse agro-ecologies in Ethiopia where sweetpotato is widely produced. Twenty five genotypes (24 elite sweetpotato clones and one released variety) were evaluated across the six environments. The list of the clones is presented in Table 2.

2.2. Experiential Design and Field Layout

A 5 x 5 simple lattice design with two replications was used to layout the test materials. Experimental plots consisted of a four row plot of three meter long for each genotype. The spacing between each rows was 0.60 meter and between plants was 0.30 meter which resulted in a total of 10 plants per row and 40 plants per plot. The two central rows were used for data recording and harvesting. All required agronomic practices were followed as recommended for sweetpotato production in the study sites.

2.3. Data Collection

Fresh root yield (t ha^{-1}) was measured from two central rows and expressed as harvested fresh root weight in kg per plot and later converted to tonnes per hectare. Data on other agronomic parameters were also recorded but not included in the stability analysis.

2.4. Statistical Analyses

2.4.1. Analysis of Variance

A combined analysis of data across environments were analysed using GenStat 14th edition [17] and SAS version 9.3 [18] statistical packages.

The following statistical model was used for combined analysis of variance over environments:

$$Y_{ijkl} = \mu + G_i + E_j + GE_{ij} + R_{k(j)} + B_{l(k)} + \varepsilon_{ijkl}$$

Where: Y_{ijkl} is observed value of genotype *i* in block *l* and replication *k* of environment *j*, μ is grand mean, G_i is effect of genotype *i*, E_j is environment or location effect, GE_{ij} is the interaction effect of genotype *i* with environment *j*, $R_{k(j)}$ is the effect of replication *k* in environment *j*, $B_{l(k)}$ is the effect of block *l* in replication *k*, ϵ_{ijkl} is error (residual) effect of genotype *i* in block *l* and replication *k* of environment *j*.

2.4.2. G x E and Stability Analysis

G x E and stability analyses were conducted using GGE bi-plot [14, 16, 19]. The model for a GGE bi-plot based on singular value decomposition (SVD) of *t* principal components is:

$$\bar{Y}_{ij} - \mu_i - \beta_j = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where: $\bar{Y}_{ij}$ is the performance of genotype *i* in environment *j*, μ is the grand mean, β_j is the main effect of environment *j*, *k* is the number of principal components (PC); λ_k is singular value of the k^{th} PC; and α_{ik} and γ_{jk} are the scores of i^{th} genotype and j^{th} environment, respectively for PC_k; ε_{ij} is the residual associated with genotype *i* in environment *j*.

3. RESULTS

3.1. Combined Analysis of Variance

A combined analysis of variance was conducted for fresh root yield and there was a highly significant ($p < 0.001$) difference among the six test environments and the genotypes. Genotypes x environment interaction variances were significant ($p < 0.01$) for the trait studied (Table 3). Environment captured the highest portion of the total sum of squares (49.4%) followed by G x E (17.4%). Genotypic effect took relatively less (11.6%) share of the total sum of squares.

3.2. Mean Performance of the Genotypes

Mean of fresh root yield for the genotypes is presented in Table 4. Arbaminch was the best environment for fresh root yield with a mean yield of 37.05 t ha^{-1}, followed by Halaba with 23.94 t ha^{-1}. Kokate was the poorest environment, providing a mean yield of 8.62 t ha^{-1}, followed by Areka with 11.78 t ha^{-1}. The genotypes showed stunted growth at Kokate, which is a relatively cool environment, but grew better at Arbaminch, which is a warmer environment. At Halaba about half of the genotypes studied provided a mean fresh root yield greater than 25 t ha^{-1}. At Arbaminch, some of the genotypes had mean yields that exceeded 50 t ha^{-1}. Almost all genotypes performed poorly at Kokate and Areka. Genotype G6 was the highest yielder across environments with a mean of 26.92 t ha^{-1}, followed by G20 and G1, which yielded 25.46 and 25.09 t ha^{-1}, respectively. The lowest mean fresh root yields of 7.55 and 9.64 t ha^{-1} were recorded for G25 (variety Tula) and G21, respectively. However, recommendations based solely on mean performance may be misleading if stability across environments is not analyzed. A genotype could give top yields across a few environments and less in other environments having average yields across the environments. On the other hand, there could be genotypes that consistently perform across environments regardless of environmental factors which might affect their performance. Therefore, stability analysis helps to identify such types of genotypes for recommendation for wide adaptation.

3.3. G x E and Stability Analysis

Figure 1 displays the GGE-biplot analysis of fresh root yield. The genotypes G6, G20, G1, G17 and G8 had relatively higher PC1 values and had high average fresh root yield. On the other hand, the genotypes G25, G21, G11, G4, G10, G14, G15 and G9 had lower fresh root yields that were below average. The genotypes G6, G20, G1, G22 and G3 had PC2 scores near zero. Among these genotypes, G1, G6 and G20 had relatively higher fresh root yields of 25.1, 26.9 and 25.5 t ha^{-1}, respectively.

Arbaminch and Halaba had relatively large PC1 scores and hence they better discriminated among genotypes for fresh root yield. Kokate had PC2 scores near zero but was the worst performing environment for fresh root yield (Figure 1). When the genotypes at the apex of each sector were considered, genotypes G16 and G23 were best performers at Halaba and Areka while G2, G8, G17 and G18 were the best performers at Arbaminch.

The stability of the genotypes across test environments for fresh root yield is displayed in Figure 2. Accordingly, genotypes G6, G20, G1 and G22 had shorter absolute projections and therefore they were stable across the test environments. However, G22 had lower yield than the other three genotypes (G1, G6 and G20). Most of the genotypes had above average mean fresh root yield since they were displayed at the right of the AEC *y*-axis. G21 and G25 were the worst performing genotypes for fresh root yield.

4. DISCUSSION

The presence of highly significant differences between the test environments for fresh root yield revealed that the genotypes performed differently across the six environments. The significance of environmental effects in evaluating sweetpotato clones for fresh root yield was also manifested by the significant G x E interaction effects. The current result was supported by previous similar findings [6-9, 20-23].

Yan, et al. [12] and Yan [19] indicated that large positive PC1 scores for genotypes indicate that those genotypes had relatively higher mean values. Genotypes with mean values below average and above average are separated by the line that passes through the bi-plot origin. Those genotypes to the right of this line are high yielders, while those to the left are low yielders for that specific trait [19, 24, 25].

Yan, et al. [12] and Yan [19] also indicated that the stability of a given genotypes is measured by their projection onto the average environment coordinate (AEC) on the y-axis. When the absolute length of the projection of a genotype is higher, that genotype is considered less stable. On the other hand, when the absolute length is shorter, the genotype is considered more stable. In other words, genotypes with PC2 scores near zero are the most stable [12];[13]. Genotypes G1, G6 and G20 had PC2 scores near zero and were relatively highly stable with higher fresh root yields.

Regarding the environments, environments with large PC1 scores are better in discriminating between the genotypes and those with PC2 scores near zero are more representative of an average environment [12, 19]. Two test environments, namely Halaba and Arbaminch efficiently discriminated between the test genotypes for fresh root yield and can be considered as good test sites. These environments are relatively warm. Conversely, Kokate, which is relatively cool, was not a good test environment. Most of the genotypes showed stunted growth at this environment. Therefore, warmer environments with moderate temperature not exceeding 30°C are ideal for improved yields of sweetpotato, as confirmed by a number of authors [26-28].

Genotypes at the apex of each sector are the best performing in the environments included in that sector if the GGE is sufficiently approximated by PC1 and PC2 [12, 19]. Accordingly, genotypes G16 and G23 were best performers at Halaba and Areka. Most of the genotypes performed well at Arbaminch although Arbaminch is displayed further from most of them. Hawassa, Dilla and Kokate did not well discriminate among the genotypes and were not good testing sites for sweetpotato.

5. CONCLUSIONS

The genotypes G1 (Ukrewe x Ejumula-10), G6 (Resisto x Ejumula-7) and G20 (Ejumula x PIPI-10) were identified as highly stable genotypes with higher fresh root yields. Accordingly, the above three elite clones were selected for the final evaluation and recommendations.

Arbaminch was identified as the best environment for sweetpotato screening in southern Ethiopia followed by Halaba. The candidate clones did not perform well in Kokate, which was a relatively cool environment. Warmer environments with moderate temperatures are better for consistent performance of sweetpotato genotypes. Generally, the current study revealed the possibility of breeding sweetpotato varieties for high yielding and stable clones that have wide adaptation in southern region and similar agro-ecologies in Ethiopia.

6. ACKNOWLEDGEMENTS

The Southern Agricultural Research Institute of Ethiopia is thanked for provision of facilities during execution of the field works.

REFERENCES

[1] J. A. Woolfe, *Sweetpotato: An untapped food resource*. Cambridge, United Kingdom: Cambridge University Press, 1992.

[2] B. M. Settumba, R. R. Patrick, and P. T. V. Jari, "Incidence of viruses and viruslike diseases of sweetpotato in Uganda," *Plant Disease*, vol. 87, pp. 329-335, 2003. *View at Google Scholar* | *View at Publisher*

[3] J. K. Mwololo, M. W. K. Mburu, R. W. Njeru, E. M. Ateka, N. Kiarie, J. K. Munyua, R. W. Muinga, R. Kapinga, and B. Lemaga, "Resistance of sweetpotato genotypes to sweetpotato virus disease in Coastal Kenya. In: Kasem, Z.A., editors," in *The 8th African Crop Science Society (ACSS) Conference Proceeding, El-Minia, Egypt. 27-31 October, 2007 African Crop Science Society*, 2008, pp. 2083-2086.

[4] V. Lebot, *Sweetpotato. In: Bradshaw, J.E., editors. Root and Tuber crops*. New York, USA: Springer Science+Business Media, LLC, 2010.

[5] Z. Wang, J. Li, Z. Luo, L. Huang, X. Chen, B. Fang, Y. Li, J. Chen, and X. Zhang, "Characterization and development of EST-derived SSR markers in cultivated sweetpotato (Ipomoea batatas)," *BMC Plant Biology*, vol. 11, pp. 131-139, 2011. *View at Google Scholar* | *View at Publisher*

[6] J. G. Wolfgang, K. Manrique, D. Zhang, and M. Hermann, "Genotype x environment interactions for a diverse set of sweetpotato clones evaluated across varying ecogeographic conditions in Peru," *Crop Science*, vol. 45, pp. 2160-2171, 2005. *View at Google Scholar*

[7] M. Chiona, "Towards enhancement of β-carotene content of high dry mass sweetpotato genotypes in Zambia," PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg, 2009.

[8] M. O. Osiru, O. M. Olanya, E. Adipala, R. Kapinga, and B. Lemaga, "Yield stability analysis of Ipomoea batatas L. cultivars in diverse environments," *Australian Journal of Crop Science*, vol. 3, pp. 213-220, 2009. *View at Google Scholar*

[9] S. A. M. Moussa, A. A. E. Hala, and I. A. E. Nashwa, "Stability study of sweetpotato yield and its component characters under different environments by joint regression analysis," *Journal of Horticultural Science and Ornamental Plants*, vol. 3, pp. 43-54, 2011. *View at Google Scholar*

[10] W. J. Grüneberg, K. Manrique, D. Zhang, and M. Hermann, "G x E interaction for a diverse set of sweetpotato clones evaluated across varying ecogeographic conditions in Peru," *Crop Science*, vol. 45, pp. 2160-2171, 2005. *View at Google Scholar*

[11] E. Tsegaye, M. Cherinet, A. Kifle, D. Mekonen, and T. Tadesse, *Genotype x environment interactions and yield stability of orange fleshed sweetpotato varieties grown in Ethiopia. In: Tropical roots and tubers in a changing climate: A critical opportunity for the world, 2-6 November, 2009, Lima.* Lima, Peru: International Society for Tropical Root Crops (ISTRC), 2011.

[12] 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, pp. 597-605, 2000. *View at Google Scholar*

[13] W. Yan, P. L. Cornelius, J. Crossa, and L. A. Huntt, "Two types of GGE biplots for analyzing multi-environment trial data," *Crop Science*, vol. 41, pp. 656-663, 2001. *View at Google Scholar*

[14] W. Yan, "Singular-value partitioning in biplot analysis of multienvironment trial data," *Agronomy Journal*, vol. 94, pp. 990-996, 2002. *View at Google Scholar*

[15] W. Yan and I. Rajcan, "Prediction of cultivar performance based on single- versus multiple-year tests in soybean," *Crop Science*, vol. 43, pp. 549-555, 2003. *View at Google Scholar*

[16] 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, pp. 643-655, 2007. *View at Google Scholar*

[17] R. W. Payne, D. A. Murray, S. A. Harding, D. B. Baird, and D. M. Soutar, *GenStat for windows introduction*, 14th ed. Hemel Hempstead, UK: VSN International, 2011.

[18] SAS, *Version 9.1.* Cary, NC: SAS Institute Inc, 2003.

[19] W. Yan, "GGE biplot: A windows application for graphical analysis of multi-environment trial data and other types of two-way data," *Agronomy Journal*, vol. 93, pp. 1111-1118, 2001. *View at Google Scholar*

[20] E. Tsegaye, N. Dechassa, and E. V. D. Sastry, "Genetic variability for yield and other agronomic traits in sweet potato," *Journal of Agronomy*, vol. 6, pp. 94-99, 2007. *View at Google Scholar | View at Publisher*

[21] Z. Mbwaga, M. Mataa, and M. Msabaha, "Quality and yield of orange fleshed sweetpotato (Ipomoea Batatas) varieties grown in different agro-ecologies. In: Kasem, Z.A., Editors," in *The 8th African Crop Science Society (ACSS) Conference Proceeding, El-Minia, Egypt. 27-31 October, 2007. African Crop Science Society*, 2008, pp. 339-345.

[22] L. Z. Nasayao and F. A. Saladaga, "G x E interaction for yield in sweetpotato [Ipomoea Batatas (L.) Lam.]," *Philippine Journal of Crop Science*, vol. 13, pp. 99-104, 1988. *View at Google Scholar*

[23] W. Collins, L. G. Wilson, S. Arrendel, and L. F. Dickey, "Genotype x environment interactions in sweetpotato yield and quality factors," *Journal of American Society of Horticultural Science*, vol. 112, pp. 579-583, 1987. *View at Google Scholar*

[24] W. Yan and M. S. Kang, *GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists.* Boca Raton, Florida: CRC Press, 2003.

[25] F. Gurmu, E. Lire, A. Asfaw, F. Alemayehu, Y. Rezene, and D. Ambachew, " Research Article GGE-Biplot Analysis of Grain Yield of Faba Bean Genotypes in Southern Ethiopia," *Electronic Journal of Plant Breeding*, vol. 3, pp. 898-907, 2012. *View at Google Scholar*

[26] J. M. Negeve, S. K. Hahn, and J. C. Bouwkamp, "Effect of altitude and environments on sweetpotato yield in Cameroon," *Tropical Agriculture-Trinidad*, vol. 69, pp. 43-48, 1992. View at Google Scholar

[27] T. Belehu, "Agronomical and physiological factors affecting growth, development and yield of sweetpotato in Ethiopia," PhD Thesis, University of Pretoria, Pretoria, 2003.

[28] DAFF, *Sweetpotato [Ipomoea Batatas (L.) Lam] production guide.* Pretoria, South Africa: Department of Agriculture, Forestry and Fisheries, 2011.

Tables and Figures

Table-1. Description of the experimental areas

Location	**Code**	**Altitude (masl)***	**Coordinates**	**Annual rainfall (mm)**	**Mean annual temperature (°C)**		**RH (%)**
					Min	**Max**	
Halaba	HAL	1772	07°18’38”N, 38°05’38’E	928.8	14.6	28.6	58.3
Kokate	KOK	1854	06°49’18”N, 37°44’56”E	1352.9	12.7	25.5	63.1
Areka	ARE	1752	07°03’45”N, 37°42’28”E	1499.8	13.2	27.9	60.8
Arbaminch	AM	1400	06°03’56”N, 37°33’40”E	940.9	17.4	30.6	55.9
Hawassa	HAW	1700	07°03’54”N, 38°28’59”E	1046.3	13.3	27.6	62.1
Dilla	DIL	1519	06°22’49”N, 38°18’25”E	1354.6	12.9	28.1	65.0

***masl** = meter above sea level, RH = relative humidity.
Source: National Meteorological Agency, Hawassa Main Branch.

Table-2. Description of sweetpotato genotypes used for the study

	Genotypes	**Code**	**Flowering habit**
1	Ukrewe x Ejumula-10	G1	None
2	Ukrewe x Ejumula-13	G2	None
3	Ukrewe x PIPI-1	G3	None
4	Ukrewe x Naspot-1	G4	Moderate
5	Ukrewe x Ogansagan-5	G5	None
6	Resisto x Ejumula-7	G6	None
7	Resisto x PIPI-1	G7	None
8	Resisto x PIPI-2	G8	Profuse
9	Resisto x PIPI-4	G9	Sparse
10	Resisto x PIPI-14	G10	None
11	Resisto x Temesgen-10	G11	Sparse
12	Resisto x Temesgen-12	G12	None
13	Resisto x Temesgen-14	G13	None
14	Resisto x Temesgen-17	G14	None
15	Resisto x Temesgen-23	G15	Moderate
16	Resisto x Ogansagen-5	G16	Profuse
17	Resisto x Ogansagen-16	G17	None
18	Resisto x Ogansagen-20	G18	Moderate
19	Resisto x Ogansagen-23	G19	Profuse
20	Ejumula x PIPI-10	G20	Sparse
21	Ejumula x PIPI-18	G21	Moderate
22	Ejumula x PIPI-19	G22	Profuse
23	Ejumula x Temesgen-15	G23	None
24	Ejumula x Ogansagen-17	G24	None
25	Tula	G25	None

Source: The parental lines were introduced from CIP-Kenya.

Table-3. Analysis of variance of fresh root yield of sweetpotato genotypes evaluated across six environments

Source of variation	df	Sum of squares (SS)	Mean square (MS)	%SS
Environment (E)	5	25684.0	5136.80***	49.4
Block (B)	9	2698.2	299.80ns	5.2
Replication (R)	5	1954.5	390.90***	3.8
Genotype (G)	24	6019.2	250.80***	11.6
G x E	120	9036.0	75.30***	17.4
Error	136	6596.0	48.50	12.7
Total	299	51987.9		

df =degrees of freedom, *** significant at $p < 0.001$ probability level, Rep = replication, ns = not significant, RDMC = root dry matter content, G x E = genotype by environment interaction.

Table-4. Mean fresh root yield (t ha^{-1}) of sweetpotato genotypes evaluated across six environments

Genotypes code	Environments						
	Halaba	Kokate	Areka	Arbaminch	Hawassa	Dilla	Mean
G1	29.36	11.84	15.23	54.04	19.16	20.93	25.09
G2	19.67	11.72	12.91	48.65	18.58	20.42	21.99
G3	24.06	11.03	13.68	37.94	19.23	20.73	21.11
G4	23.41	5.21	9.52	13.59	15.47	16.42	13.94
G5	19.22	9.93	11.55	42.28	17.31	19.01	19.88
G6	32.70	13.23	17.09	55.28	20.75	22.47	26.92
G7	29.8	11.09	15.18	34.48	20.12	21.42	22.01
G8	23.13	11.47	13.42	54.44	18.17	20.07	23.45
G9	36.67	5.30	12.60	22.08	16.09	16.97	18.29
G10	1.81	7.98	6.09	30.66	14.72	16.51	12.96
G11	21.43	5.73	9.47	12.74	15.87	16.84	13.68
G12	31.27	10.22	14.88	33.56	19.48	20.72	21.69
G13	20.49	9.89	11.78	44.49	17.20	18.93	20.46
G14	14.09	3.64	5.73	27.64	11.84	13.32	12.71
G15	14.23	5.32	7.09	26.99	13.57	15.03	13.70
G16	34.68	11.47	16.54	40.16	20.48	21.81	24.19
G17	27.39	9.50	12.93	53.60	16.69	18.49	23.10
G18	23.50	7.62	10.58	51.16	14.67	16.50	20.67
G19	31.08	8.73	13.58	37.78	17.62	18.98	21.30
G20	33.00	10.58	15.08	56.23	18.07	19.82	25.46
G21	8.27	2.92	3.96	18.61	11.34	12.73	9.64
G22	25.26	9.19	12.42	43.04	17.09	18.69	20.95
G23	38.05	9.62	15.91	39.98	18.98	20.24	23.80
G24	27.99	11.44	15.06	32.95	20.43	21.72	21.60
G25	7.90	0.77	2.30	13.86	9.58	10.87	7.55
Mean	23.94	8.62	11.78	37.05	16.90	18.39	19.45

ID = identification.

FIGURES

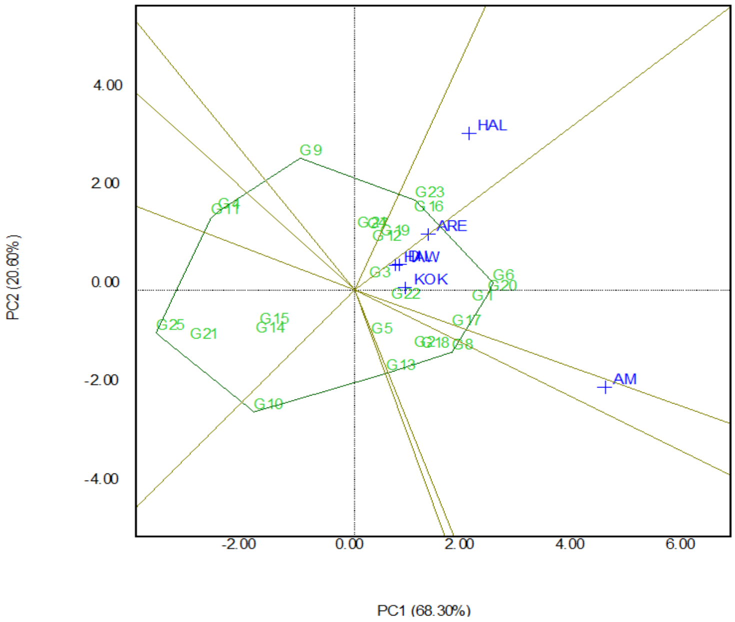

Figure-1. GGE-biplot showing environments and respective sweetpotato genotypes for fresh root yield.

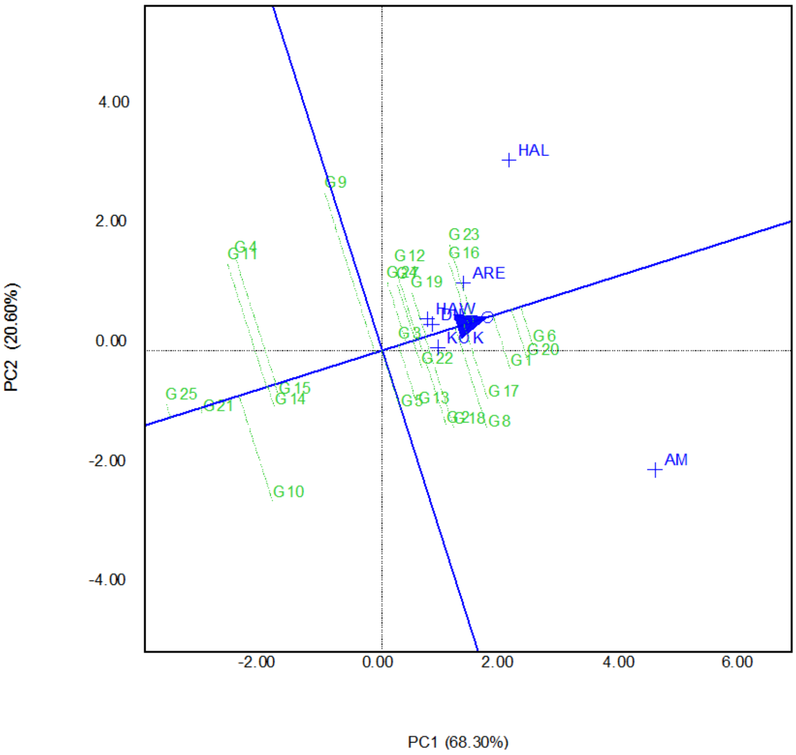

Figure-2. Genotypes mean yield performance and stability across environments for fresh root yield.