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Stability of finger millet (*Eleusine coracana* L.) yield using additive main effects and multiplicative interaction analysis

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A B S T R A C T

In Ethiopia's mid and lowlands, where rainfall is erratic, finger millet *(Eleusine coracana* L.) is an important cereal crop. Finger millet yield is low partly due to variety instability and low yield potential. Field experiments were conducted in Boricha, Dore Bafano and Halaba districts of Southern region, Ethiopia, in 2018 and 2019, during the main cropping season from early May to October, to identify finger millet genotypes with high yield and wide adaptation. Eleven finger millet genotypes (ten improved and one local check) were grown in a randomized complete block design with four replications. AMMI analysis generated four principal components (PCs) with PC1 and PC2 being statistically significant ($p<0.01$). PC1, PC2, PC3, and PC4 contributed 49.85, 32.78, 9.27, and 7.22% of the variation in the GE interaction, respectively. E1 (Boricha2018), E2 (Boricha2019), E3 (Dore Bafano2018), E4 (Dore Bafano2019), E5 (Halaba2018), and E6 (Halaba2019) had a mean yield of 2.77, 3.47, 4.39, 4.26, 3.73, and 3.03 tons ha^{-1}, respectively. Mean yield ranged from 3.03 (genotype Bareda) to 4.42 tons ha^{-1} (Kako-01). AMMI stability value ranged from 0.23 (genotype Bako-09) to 1.55 (Boneya), and yield stability index ranged from 3 (genotype Bako-09) to 19 (Bareda). AMMI1 and AMMI2 biplots explained 87.28% and 82.63% of the treatment sum of squares, respectively. In the present study, because of its high yield (4.27 tons ha^{-1}) and stability across test environments, genotype Bako-09 would be recommended for widespread cultivation.

Keywords: AMMI analysis, Yield, Stability, Finger millet, *Eleusine coracana*

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Introduction

In the mid-and lowlands of Ethiopia, where rainfall is erratic, finger millet (*Eleusine coracana* L.) is an important cereal crop. The grain of finger millet is used to make porridge, *kita (*a thin flatbread), and traditional beverages like *areke* and *tela*, and the straw is used as livestock feed. The grain contains 7.4% protein, 74.0% carbohydrate, 3.2% fiber, and 2.6% ash. It is rich in calcium, phosphorus, iron, and tryptophan, cysteine, and methionine amino acids (NRC, 1996). Finger millet is the sixth most valuable cereal crop in area coverage and production, after tef (*Eragrostis tef*), maize, sorghum, wheat, and barley. It covers 456,172 hectares (4.46% of the cereal-growing area) and produces 1,017,059 tons (4.01% of cereal grain production) of grain per year (CSA, 2017). The average yield of finger millet is low (2.23 tons ha-1), partly due to variety instability and low yield potential.

Yield is a complex polygenic trait usually influenced by genotype, environment, and genotype by environment (GE) interaction. Because the same gene can have different effects in different environments (Yan *et al.*, 2017), a genotype's performance can vary from one environment to the other. Among the various statistical methods used in stability analysis, additive main effects and multiplicative interaction (AMMI) have been widely used to identify genotypes with wide and specific adaptations across various environments (Zobel *et al.*, 1988). Unlike traditional analysis of variance, which divides sources of variation into effects due to genotypes, environments, and GE interaction. AMMI model combines analysis of variance for additive main effects of genotypes and environments with principal component analysis for multiplicative component, or non-additive, GE interaction. Furthermore, AMMI biplots make it simple to visualize multi-environment data and identify genotypes with wide and specific adaptations (Zobel *et al.*, 1988; Gauch and Zobel, 1997). This study used AMMI analysis to identify finger millet genotypes with high yield and wide adaption.

Materials and Methods

Field experiments were conducted on-farm in Boricha and Dore Bafano districts and on-station in Halaba district, Southern region, Ethiopia, from early May to October, during the main cropping seasons of 2018 and 2019. Boricha is located at 6°56'04"N and 38°20'88"E, with an elevation of 1907 m above sea level, and Dore Bafano is at 7°04'68"N and 38°22'18"E, with an elevation of 1717 m above sea level, while Halaba is located at 07°18'44"N and 37° 06'50"E, with an elevation of 1763 m above sea level. The annual average rainfall in Boricha, Dore Bafano, and Halaba is 915, 997, and 912 mm, respectively. For Boricha, Dore Bafano, and Halaba, the average cropping season rainfall was 482, 602, and 480 mm in 2018 and 1112, 853, and 798 mm in 2019. Boricha, Dore Bafano, and Halaba have annual average temperatures of 20.10, 20.09, and 21.74°C, respectively, with silt loam, sandy clay loam, and loam as their respective soils.

A randomized complete block design with four replications was used to grow eleven finger millet genotypes (ten improved and one local check). Each plot consisted of four rows with 2.5 m row length. The space between rows, plots, and replications was 40, 80, and 120 cm, respectively. The seed was drilled at a rate of 10 kg ha^{-1}. Plots were given 65 kg ha^{-1} of nitrogen in the form of urea and NPS, as well as 38 kg ha^{-1} of P_2O_5 in the form of NPS at planting. Manual weeding was also used to control weeds.

The AMMI analysis was based on the following AMMI model:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \zeta_{gn} \eta_{en} + \theta_{ge}$$

Where, Y_{ge} is the yield of genotype (g); in the environment (e); μ is the grand mean; α_g is the genotype mean deviation; β_e is the environment mean deviation; λ_n is the eigenvalue of the PC axis, n; $\zeta_{gn}\eta_{en}$ are the genotype and environment PC axis scores for the PC axis, n; N is the number of PC axes retained in the model; and θ_{ge} is the residual (Zobel *et al.*, 1988). Moreover, Genstat version 18.1 (VSN International, 2015) was used for AMMI analysis.

In order to compensate for differences between PC1 and PC2 in explaining the GE sum of squares, the AMMI stability value (ASV) was calculated as:

$$\text{ASV} = \sqrt{\left[\frac{\text{PC1 sum of squares}}{\text{PC2 sum of squares}}(\text{PC1 score})\right]^2 + (\text{PC2 score})^2}$$

Where, the smaller ASV scores suggest a less interactive environment and a more stable genotype (Purchase *et al.*, 2000).

Yield stability index (YSI) was calculated as:

YSI= RASV + RY

Where, RASV is the rank of the AMMI stability value (ASV), and RY is the rank of a genotype's mean yield across environments, with 1 being the highest yield and the lowest AMMI stability value. Low YSI values are linked to high yield and genotype stability (Bose *et al.*, 2014).

Results and Discussion

According to the AMMI analysis (Table 1), the effects of genotypes, environments, and genotype by environment interaction were statistically significant ($p < 0.01$) and contributed 25.79, 48.85, and 25.36% to the treatment sum of squares, respectively. The more significant contribution of environments (48.85%) to the treatment sum of squares (G + E+ GE) would mean substantial differences across test environments, causing different genotypes to perform differently. Even though, in standard multi-environment yield trials, the environment accounts for 80% of the variation in treatments, while genotype and GE each account for 10% (Gauch and Zobel, 1997), these contributions can differ from trial to trial. For example, the contribution of the environment to the treatment sum of squares has been reported to be 2.21% (Bose *et al.*, 2014), 81% (Rashidi *et al.*, 2013), 75% (Zobel *et al.*, 1988; Hongyu *et al.*, 2014), and 78% (Ali *et al.*, 2018) in different trials.

GE interaction would imply that genotypes differed in their responses to changing environments, which could have been attributed to variations in rainfall and soil types among the test environments, which are often one of the major contributors to GE interaction in crops (Ananda *et al.*, 2009). The genotype and interaction components of the treatment sum of squares are used together for genotype and test-environment evaluations, but the main effect of the environment is irrelevant for these purposes (Gauch and Zobel, 1997; Gauch *et al.*, 2008). Thus, the variation in G plus GE explained 96.37/188.42, or 51.15% of the treatment sum of squares.

Since it includes the majority of the treatment degrees of freedom, GE interaction contributes the most uncontrolled variation (noise) to the treatment sum of squares compared to the genotype and environment effects, even though the latter still include some noise (Gauch and Zobel, 1997; Anandan *et al.*, 2009). Such noise must be removed because it obscures true winners in test environments by reducing yield estimation accuracy (Gauch and Zobel, 1997; Hongyu *et al.*, 2014; Neisse *et al.*, 2018). Thus, the GE interaction was divided into noise sum of squares and actual structure (Gauch and Zobel,

1997). The interaction noise (*GEN*) was calculated by multiplying the degrees of freedom of GE and error mean square. Then actual structure or GE signal (*GES*) was calculated by subtracting *GEN* sum of squares from GE sum of squares. Thus, the *GEN* was 50 × 0.47 = 23.50 (49.18% = 23.50/47.78) and the *GES* was 47.78-23.50 = 24.28 (50.82%). When the interaction noise was removed, the relevant variation (G + *GES*) was 48.59+24.28 = 72.87 or 38.67% of the treatment sum of squares. On the other hand, G + PC1 accounted for 48.59 + 23.82 = 72.41, or 38.43% of the treatment SS, similar to that explained by the relevant variation (38.67%). Indeed, the relevant variation for detecting mega-environments is around 10 to 40% of the treatment variation in a yield trial (Gauch and Zobel, 1997).

Only PC1 and PC2 of the four principal components (PCs) generated by AMMI analysis were statistically significant ($p<0.01$) (Table 1), implying that PC3 and PC4 could be considered as noise (Zobel *et al.*, 1988; Crossa *et al.*, 1990; Ebdon and Gauch, 2002). PC1, PC2, PC3, and PC4 contributed 49.85, 32.78, 9.27, and 7.22%, respectively, to the variation in GE interaction. Indeed, the first two PCs usually account for most of the sum of squares of GE interaction in multi-environment yield trials (Tadesse *et al.*, 2018). Furthermore, PC1 and PC2 together explained 82.63% of the GE sum of squares, which is adequate for cross-validation of the yield variation explained by GE interaction because a model must explain at least 70% of the variation to be considered fairly reliable (Neisse *et al.*, 2018).

Table 1. Sources of variation and significance of mean squares from AMMI analysis of yield (tons ha^{-1}) for eleven finger millet genotypes grown in six environments.

Sources of variation	Degrees of freedom	Sum of squares	Mean squares	%SS of treatments	%SS of GxE
Treatments	65	188.42	2.90**		
Genotypes(G)	10	48.59	4.86**	25.79	
Environments(E)	5	92.04	18.41**	48.85	
Replication/E	18	12.62	0.70^{ns}		
GxE	50	47.78	0.96**	25.36	
PC1	14	23.82	1.70**		49.85
PC2	12	15.66	1.31**		32.78
PC3	10	4.43	0.44^{ns}		9.27
PC4	8	3.45	0.43^{ns}		7.22
Residuals	6	0.42	0.07^{ns}		0.88
Error	180	84.7	0.47		
Total	263	285.74			

** = *significant at 1% probability level; ns = not significant.*

Genotypes showed considerable variations in yield (tons ha^{-1}), PCs, ASV, and YSI (Table 2). In E1 (Boricha2018), yield ranged from 1.90 (genotype Boneya) to 3.85 tons ha^{-1} (Kako-01), and from 3.38 (genotype Bareda) to 4.98 (Boneya) in E4 (Dore Bafano2019). E1 (Boricha2018), E2 (Boricha2019), E3 (Dore Bafano2018), E4 (Dore Bafano2019), E5 (Halaba2018), and E6 (Halaba2019) had mean yield of 2.77, 3.47, 4.39, 4.26, 3.73, and 3.03 tons ha^{-1}, respectively. The mean yield across environments varied from 3.03 (Bareda) to 4.42 tons ha^{-1} (Kako-01). The following high-yielding genotypes were Gudetu (3.85 tons ha^{-1}) and Bako-09 (4.27 tons ha^{-1}).

Genotypes G3, G4, G5, and G10 were the most unstable due to their high PC1 scores, while G1, G4, G7, G8, and G11 were the most unstable due to their high PC2 scores. Since PC1 contributes more to the GE interaction sum of squares than PC2, the AMMI stability value (ASV) is used to compensate for the discrepancies between PC1 and PC2 in measuring stability so that genotypes with low ASV values are the most stable (Purchase *et al.*, 2000). According to their ASV values, genotypes G2 (0.23) and G9 (0.25) were the most durable, while G3 (1.01) and G4 (1.55) were the most unstable. In addition, E2 (1.38) and E6 (0.65) were the most unstable and stable environments, respectively. However, when selecting genotypes, stability should be considered along with yield capacity since the most stable genotypes do not necessarily produce the best yield (Hongyu *et al.*, 2014). Genotype G9, for example, had a low ASV score, but its mean yield (3.21 tons ha^{-1}) was less than the average yield (3.61 tons ha^{-1}). Thus, the yield stability index (YSI), which combines yield and ASV ranks, has been suggested for selecting high yield and stability simultaneously (Bose *et al.*, 2014; Tadesse *et al.*, 2018). Accordingly, genotypes G2 and G6 were the most desirable because they combined high mean yield with a high level of stability.

Table 2. Yield (tons ha^{-1}) and AMMI analysis parameters of eleven finger millet genotypes grown in six environments.

Code	Genotype	E1	E2	E3	E4	E5	E6	Mean	PCA1	PCA2	ASV	YSI
G1	Addis-01	3.45	2.93	4.78	4.33	3.50	2.91	3.65	0.022	-0.527	0.53	8
G2	Bako-09	3.53	3.98	4.79	4.83	4.67	3.79	4.27	0.022	0.224	0.23	3
G3	Bareda	2.64	3.64	3.33	3.38	2.91	2.28	3.03	-0.659	0.144	1.01	19
G4	Boneya	1.90	2.91	4.25	4.98	4.94	3.41	3.73	0.922	0.668	1.55	15
G5	Diga-01	3.16	4.17	4.11	3.74	3.81	2.98	3.66	-0.585	0.236	0.92	16
G6	Gudetu	2.53	3.50	4.96	4.69	3.84	3.60	3.85	0.374	-0.106	0.58	7
G7	Gute	2.68	2.72	4.97	4.39	3.14	2.54	3.41	0.290	-0.724	0.85	13
G8	Kako-01	3.85	4.84	4.58	4.67	4.99	3.59	4.42	-0.484	0.505	0.89	9
G9	Urjii	2.31	3.31	3.80	3.60	3.13	3.14	3.21	-0.122	0.172	0.25	12
G10	Wama	2.09	2.83	4.34	4.38	3.40	3.33	3.39	0.507	-0.039	0.77	14
G11	Local	2.37	3.38	4.37	3.87	2.69	1.82	3.08	-0.286	-0.553	0.70	16
	Mean	2.77	3.47	4.39	4.26	3.73	3.03	3.61				
	F-ratio	**	**	*	*	**	**					
	CV (%)	20.46	21.36	15.27	16.99	19.34	22.35					
	LSD $_{(0.05)}$	0.82	1.07	0.98	1.04	1.04	0.98					
	PC1	-0.792	-0.982	0.362	0.660	0.359	0.393					
	PC2	-0.398	0.303	-0.910	-0.209	0.850	0.365					
	ASV	1.16	1.38	1.04	0.93	0.98	0.65					

*E1= Boricha2018, E2 = Boricha2019, E3 = Dore Bafano2018, E4 =Dore Bafano2019, E5 =Halaba2018, E6 = Halaba2019; ASV = AMMI stability value, YSI = yield stability index; *, ** = significant at 5% and 1% probability level, respectively.*

The AMMI1 biplot (Figure 1) captured genotype SS of 48.59, environment SS of 92.04, PC1 SS of 23.82, and was effective in describing 87.28% of the treatment SS, with the remainder in the residual having no predictive value (Zobel *et al.*, 1988; Crossa *et al.*, 1990). The abscissa (x-axis) in the AMMI1 biplot depicts the main effects of genotypes and environments, while the ordinate (y-axis) depicts genotype and environment interaction, or PC1 scores (Zobel *et al.*, 1988; Crossa *et al.*, 1990; Gauch *et al.*, 2008; Roostaei *et al.*, 2014; Neisse *et al.*, 2018). The horizontal line passing through the PC1 score of zero in this biplot represents the interaction score of zero, while the middle vertical line represents the average yield. Thus, genotypes G1, G5, G4, G6, G2 and G8, and environments E5, E4 and E3 had above average yield, while genotypes G7, G10, G9, G11 and G3, and environments E2, E6 and E1 had below average yield. High PC1 scores (positive or negative) of genotypes and environments suggest a high level of interaction (Zobel *et al.*, 1988; Crossa *et al.*, 1990; Anandan *et al.*, 2009; Rashidi *et al.*, 2013; Roostaei *et al.*, 2014). As a result, genotypes G9, G1, and G2 were less interactive in test environments, while environments E1 and E2 had a high level of interaction.

Genotypes or environments may have similar mean yield and/or interactions in the AMMI1 biplot (Crossa et al., 1990; Rashidi *et al.*, 2013). Thus, except for variations in interactions, genotypes G2 and G8 had similar mean yield, and genotypes G1 and G2 had similar interactions except for the mean yield difference. Similarly, environments E3, E5, and E6 had low and similar interactions, with the exception of differences in mean yield. On the other hand, genotypes and environments situated at diagonal or opposite corners have different main effects and interactions (Ebdon and Gauch, 2002). For example, the yield performances and interactions of environments E1 and E4 were quite different.

The genotypes farthest from the biplot's origin have a high level of interaction (positive or negative) and show particular adaptation to specific environments (Chimonyo *et al.*, 2014; Mafouasson *et al.*, 2018). For example, genotype G6, which had a high mean yield and a large PC1 score, was specifically adapted to environments E3 and 4, which also had a high mean yield and large PC1 score. The additive part (main effects) of the AMMI1 biplot for any genotype-environment combination is equal to the genotype mean plus the environment mean minus the grand mean, and the multiplicative part (interaction effect) is the product of genotype and environment PC1 scores (Zobel *et al.*, 1988; Crossa *et al.*, 1990; Gauch and Zobel, 1997; Ebdon and Gauch, 2002). For example, the AMMI1 model estimated yield for genotype G3 in E1 was 2.64 + 2.77-3.61 + (-0.659 x-0.792) = 1.80 +0.522 = 2.322 tons ha^{-1}. The AMMI estimated yield is closer to the observed yield of 2.64 tons ha^{-1} than the additive ANOVA estimated yield of 1.80 tons ha^{-1}. Similarly, genotype G4 interacted negatively with E1 and E2 (-0.730 vs.-0.905), but positively with E3 and E4 (0.334 vs. 0.609). When genotypes and environments have the same sign on PC1 axis, their interaction is positive; if they have opposite signs, it is negative (Zobel *et al.*, 1988; Crossa *et al.*, 1990; Anandan *et al.*, 2009; Rashidi *et al.*, 2013). Thus, genotypes G3 and G11 were adapted to Boricha (E1 and E2) but not Dore Bafano (E3 and E4).

The most desirable genotypes (e.g., G2) combine above-average yield with a near-zero PC1 scores (Rashidi *et al.*, 2013). However, since high and low-performing genotypes are usually adapted to different environments, such high performance across environments (both favorable and unfavorable) is rare. On the other hand, the main effects and/or interactions of a location can differ greatly from year to year, making it less predictable (Ebdon and Gauch, 2002). Year-to-year variations in interaction lead to year-to-year changes in genotype rankings, making it difficult to recommend a specific variety to specific locations (Zobel *et al.*, 1988; Ebdon and Gauch, 2002). In the present study, the substantial year-to-year variability in yield of Boricha and Halaba sites would make it difficult to predict the performance of these sites.

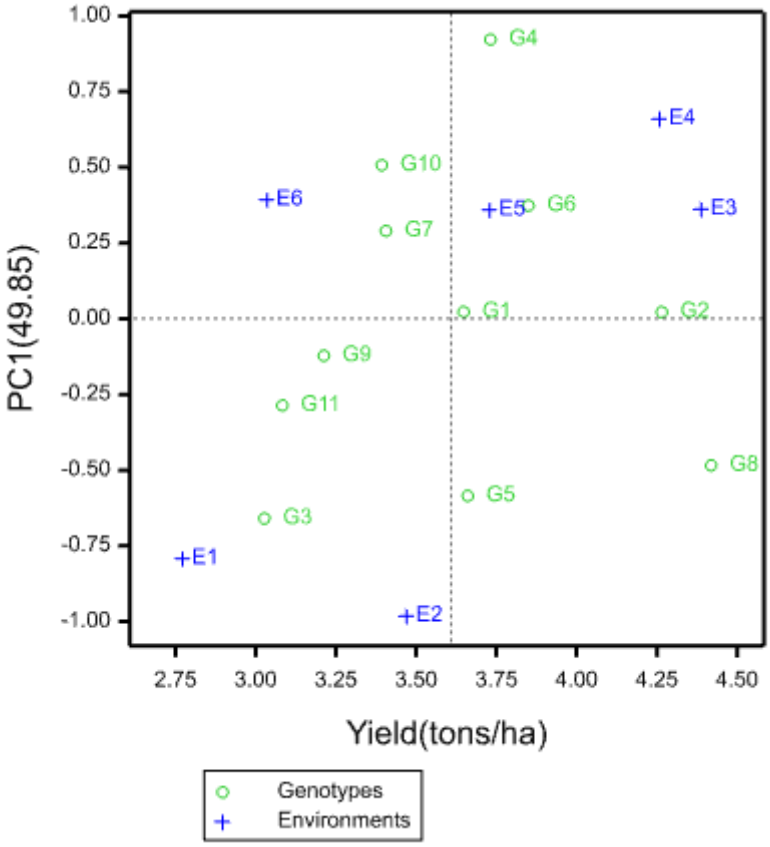

Figure 1. AMMI1 biplot for yield (main effect) and PC1 of eleven finger millet genotypes and six environments; genotype (G) and environment (E) designations are presented in Table 2.

The abscissa represents PC1 scores, and the ordinate represents PC2 scores in the AMMI2 biplot (Figure 2), which explains 82.63% of the treatment sum of squares. Since the AMMI2 biplot provides information on GE but not G (Gauch *et al.*, 2008), it can be used to distinguish genotypes with similar or different patterns of responses across environments, but it cannot be used to display the specific performance of genotypes across test environments (Gauch and Zobel, 1997; Anandan *et al.*, 2009). The vector length from the origin (0, 0) in the AMMI2 biplot indicates the amount of interaction displayed by genotypes or environments, with genotypes and environments far from the biplot origin (positive or negative) being more interactive than those near the biplot center (Gauch *et al.*, 2008; Anandan *et al.*, 2009). Since genotypes G9 and G2 are close to the biplot origin, they are less interactive than genotypes G11 and G4, which are far from the center. Because of their short vector lengths, environments E4 and E6 were less interactive and discriminative among genotypes, while E1 and E2 were more discriminative.

The acute angle between the vectors of genotypes or environments indicates a positive relationship, the right angle indicates a negligible relationship, and the obtuse angle indicates a negative relationship (Ndhlela *et al.*, 2014). Environments E1 and E2, E3 and E4, and E5 and E6 had similar effects on genotype performance and were most related because their vectors were at acute angles. Similarly, genotypes G3 and G5 had a similar relationship and were supposed to have a similar pattern of responses across the test environments, but this was not the case with genotypes G4 and G11. In the present study, because of its high yield (4.27 tons ha^{-1}) and stability across test environments, genotype Bako-09 would be recommended for widespread cultivation.

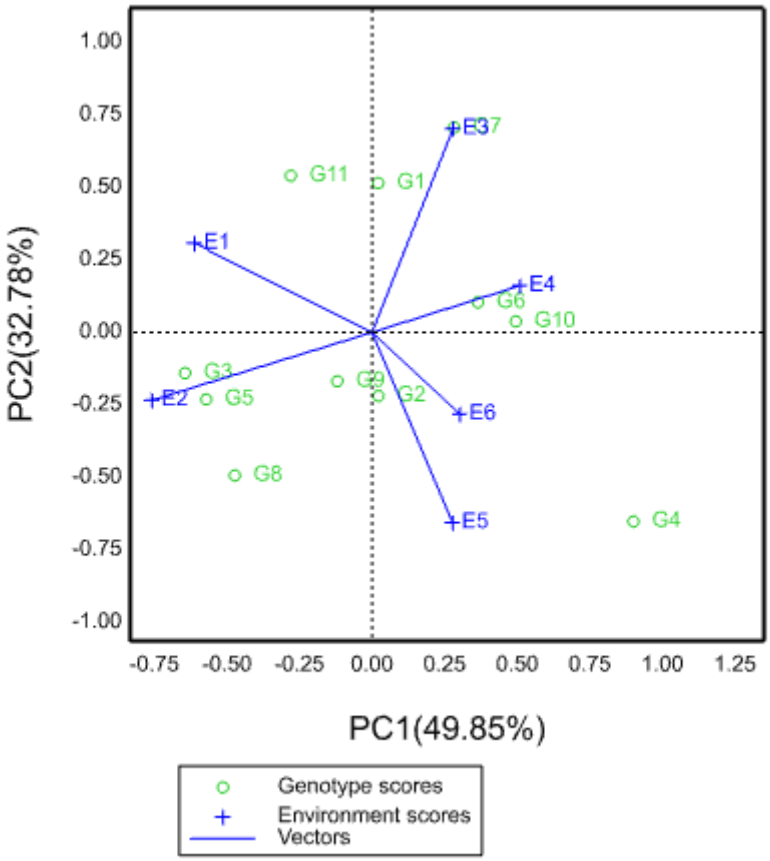

Figure 2. AMMI2 biplot for the yield of eleven finger millet genotypes grown in six environments; genotype and environment designations are presented in Table 2.

Conclusion

The substantial contribution of environments to the treatment sum of squares would suggest the differences in test environments, causing different genotypes to perform differently. The significant contribution of PC_1 and PC_2 to the variation in GE interaction relative to PC_3 and PC_4 would show that PC_3 and PC_4 would be considered as noise. Moreover, the more significant contribution of PC_1 to the GE interaction sum of squares than PC_2, suggested that AMMI stability value, which compensates for the discrepancies between PC_1 and PC_2 would be used to measure the stability of genotypes. However, the existence of stable genotypes with below average yield would suggest the use of the yield stability index, which combines both AMMI stability value and yield ranks to obtain high-yielding and stable genotypes. Finally, the present study showed that besides identifying specific and widely adapted genotypes, AMMI biplots would be used to distinguish genotypes with similar or different patterns of responses across test environments.

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