

## Genotype by Environment Interaction of Sugarcane (*Saccharum officinarum* L.) for Sugar Yield Based on GGE-Biplot and AMMI Analyses in Ethiopia

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### Abstract

The first goal of plant breeders in crop improvement is to develop genotypes with high yield and stable across environments. AMMI and GGE-biplot are the most effective statistical tools for the analyses of stability, adaptability and helps for proper selection of sugarcane genotypes. The present investigation was carried out on eight introduced sugarcane genotypes excluding two standard checks for three cropping cycles at Finchaa and Metehara forming together six environments. The trial was laid out in completely randomized block design. This work was conducted with objective of evaluating G x E interactions on sugar yield performances of sugarcane genotypes using AMMI and GGE statistical tools. The results of combined ANOVA and AMMI analysis of variance for sugar yield showed that highly significant ( $p \leq 0.001$ ) difference among genotypes and environments and their interactions. The sugar yield of the genotype was influenced by environments which explained 73.77% of the total variation indicating the importance of environmental main effects over genotypic main effects. The first-IPCA1 (59.08%) showed highly significant level whereas the second-IPCA2 (18.66%) were not significant and totally explained 77.74% of the variations. The analysis of the AMMI resulted that genotypes G10 (1.928), G2 (1.744), G9 (1.683) and G4 (1.633) had high mean sugar yield in ton/ha/month. The GGE-biplot analysis grouped the environments into two mega-environments and sub-divided the graph into five sectors. The first mega-environment was made up by three environments: E1, E2 and E4 while the second mega-environment was made up by E3, E5 and E6. G2 and G10 was located very nearest to the concentric circle; thus, considered to be ideal the genotype and therefore identified as the best genotype than the others. Consequently, these two genotypes could be selected for verification and recommended for commercialization.

**Keywords:** AMMI; GGE-Biplot; Mega-environment; Ideal genotype

### Introduction

Sugarcane is a field crop plant mainly having high G x E interaction and high heterozygosity (Tena et al., 2019). The production of sugarcane is affected by the environment, genotype and the interaction of both effect (GEI); of which the GEI effect causes significant variations in cultivar performance between different locations (Mohammadi et al. 2007). Sugarcane is a vegetatively propagated crop through the planting of segments of the cane stalk called sett which contains viable buds (Smit et al., 2004). A number of genotypes are evaluated over several cropping cycles and locations for selecting superior adaptable cultivars with high stability across environments for sustainable production of sugarcane in sugar industry. Multiple environment tests of the cultivar are an essential tool because of the presence of genotype and environment interactions [1].

In crop improvement, the ambition of plant breeder is to develop genotypes with high yield and stable in different environments and then, identify locations and genotypes that best represents the target factors (Luquez et al. 2002; Ahmadi et al. 2015). Consequently, it is essential that breeders are aware of the nature of G x E interactions as well as the extent of test site similarity within a multi-environmental test as this can bring change in rankings of varieties across environments [2].

There are many statistical tools to deal with multivariate analysis having a set of data in multi environment trials. Among these, agronomist and plant breeders uses AMMI (additive main effects and multiplicative interaction) (Yan et al., 2000) and GGE (genotype main effects in addition to genotype by environment interaction biplots) (Yan et al., 2007; Yan and Kang 2003) (Jamshidmoghaddam and Pourdard, 2011) which is the most effective for the analyses of stability, adaptability and ranking of genotypes and helps for proper selection of

genotypes with suitable mega environments. Both of these statistical tools integrate principal component analysis (PCA) and biplot for the explanation of genotype by environment interaction (G×E) [3].

The AMMI model combines the conventional ANOVA for the genotype main effects and environment main effects and the principal component analysis (PCA) with multiplicative factors in a single analysis. Then, it investigates the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the G x E interaction (Purchase et al. 2000) and thereby helps the breeder to identify genotypes with better performance for giving judgment (Gauch et al., 1997; Tena et al., 2019). The GGE represents the main effect of genotype (G) plus the genotype by environment interaction (GE). Based on principal components analysis GGE biplot model displays the two sources of variation G and GE. It is multivariate analytical method which contains a set of biplot interpretation models concerning various data about genotype and test-environment. This model provides an adequate graphical tool for cultivar evaluation (yield and stability), mega-environment analysis (such as 'which-won-where'

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pattern), with the scores of the genotypes and the environments of the PC1 scores against their respective scores for the PC2 scores (Burgueno et al., 2009; Crossa et al., 2002; Ding et al., 2009; Yan and Kang 2003) when many genotypes are tested across locations for more than one year and/or cropping cycles (Yan et al. 2007; Vaezi et al., 2017) [4,5].

The users always need the varieties that with high yield performance and other essential agronomic traits in commercial crop production. In most cases, in Ethiopia, the sugarcane varieties under use in a commercial farm as well as under the research are introduced from foreign countries. Besides, the locations in which these cultivars tested are also vary in soil fertility, temperature range and irrigation types. Thus, statistical evaluation of this genotype is fundamental to identify the response of genotypes in relation to the environments of the experimental conditions. Therefore, it is important to understand the causes of GEI for the determination of high-yielding genotypes and identifies sites that best represent the target environment. The objective of this study was to evaluate G x E interactions of sugarcane genotypes for sugar yield across six environments using AMMI and GGE biplot models and identify genotypes with high yield and stable performance [6].

## Materials and Methods

### Experimental site

The experiment was conducted at two most popular sugar estates of Ethiopia; Finchaa and Metehara. Finchaa was located at latitudes 90 30'N to 10000'N and longitudes 370 15' to 370 30'E and an elevation between 14550-1600 m.a.s.l. An average annual precipitation of the area reaches about 1309 mm and the average maximum and minimum temperature was 31.50C and 14.60C respectively. Metehara sugar estate was located at latitude 80 53' N and longitudes 390 52' E and at an elevation of 950 meters at sea level. It receives an average of 554mm annual rainfall with minimum and maximum temperature of 17.40c and 32.60c respectively [7].

### Plant Materials

Eight introduced sugarcane genotypes and two commercial standard checks were evaluated at Finchaa and Metehara sugar estate. These genotypes were labeled as G1, G10, G2, G3, G4, G5, G6, G7, G8 (first standard check) and G9 (second standard check) [8].

### Experimental design

The trial was laid out in randomized completely block design with three replications. The completion of the experimental period involving three crop cycles (i.e. plant cane, first and second ratoon crops) takes about four years as a single season lasts over fourteen months. The data for sugar yield and related components were collected during the crop cycles at a regular schedule at both sites. The two locations consisting of a total of six environments (sites-x-crops combinations) designated by E1-to-E6 (Table 1). Except the treatments and environments, all agronomic management practices were applied uniformly throughout the growing season as per the practice of the respective sugarcane estates [9].

### Statistical analysis

The collected data from the six environments (the combination of two locations and three crop cycles) were subjected to statistical analysis by General Linear Models (GLM) Procedure using SAS (SAS, 2002) and combined ANOVA was done to determine the significance level of genotype, environment and GxE interaction effects at each location

**Table 1:** The combinations of crop cycle with site code, environment code and year of the experiment implemented.

Codes for crop cycles, site, environment and year of implementation			
crop cycles Vs Site	Combination of Crop cycles Vs Site Code	Environment Code	Year of the crop cycles implemented
Finchaa (site one)	S1 (code of site one)		
Metehara (site two)	S2 (code of site two)		
Plant cane at Finchaa	S1Pc	E1	2014/15
First ratoon crop at Finchaa	S1R1	E2	2016/17
Second ratoon crop at Finchaa	S1R2	E3	2017/18
Plant cane at Metehara	S2Pc	E4	2014/15
First ratoon crop at Metehara	S2R1	E5	2016/17
Second ratoon crop at Metehara	S2R2	E6	2017/18

and across location (Team, 2020). The genotypes and the environments were considered as a fixed and random variables respectively [10].

AMMI model is effective in partitioning the total sum of squares into genotype main effect, environment main effect and the G x E interactions (GEI), however it does not provide full information for the GEI structure. This component is dealt with more advanced techniques such as principal component analysis (PCA) of the interaction residuals after the main effects are removed (Zobel et al., 1988; Gauch, 1992) [11].

The AMMI model analysis used to estimate yield of genotype, environment and G X E interaction:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij} + \epsilon_{ij}$$

Where  $Y_{ij}$  is the value of the  $i$ th genotype in the  $j$ th environment;  $\mu$  is the grand mean;  $g_i$  is the deviation of the  $i$ th genotype from the grand mean (genotype main effect);  $e_j$  is the deviation of the  $j$ th environment from the grand mean (environment main effect);  $N$  is the number of IPCA retained in the model;  $\lambda_n$  is the eigen value of the  $n$ th interaction principal component analysis (IPCA) retained in the AMMI model;  $\gamma_{in}$  is the eigen vector for the  $i$ th genotype from  $n$ th IPCA;  $\delta_{jn}$  is the eigen vector for the  $j$ th environment from the  $n$ th IPCA;  $\rho_{ij}$  is the GE interaction residual;  $\epsilon_{ij}$  is the random error term [12].

The GGE-biplot is composed of the biplot (Gabriel, 1971) and the GGE (Yan et al. 2000) concepts. It uses a biplot to show the factors (genotype and genotype x environment interaction) that are important in genotype evaluation and that are also sources of variation in GEI analysis (Yan, 2001; Yan et al., 2000). It was constructed from the first two principal components (PC1 and PC2) derived by subjecting the environment centered yield data (which contains G and GE) to singular valued composition [13].

The sums of squares of a PCA axis are termed its "eigenvalue", and its direction relative to the original axis system is termed its "eigenvector" (Sanesh, 2012). The AMMI and GGE biplot analyses were done using Genstat software (International, 2009). The GGE-biplots and AMMI are graphical images to exemplify G x E interaction and genotype ranking based on mean and stability (Zobel et al., 1988). The graph generated is based on multi environment evaluation yield trial (which-won-where pattern). Genotype evaluation (mean versus stability), and the environment are tested by their ranking (discriminative versus representative) [14].

## Result and Discussions

### AMMI analysis of variance

The results of combined ANOVA and AMMI analysis of variance for sugar yield showed that highly significant ( $p \leq 0.001$ ) difference among genotypes (G), environments (E) and genotype by environment interaction (GEI). Based on the AMMI result, the sugar yield of the genotype were influenced by environments which explained 73.77% of the total phenotypic (G + E + GEI) variation while the genotype (G) and genotype by environment interaction (GEI) accounted 8.65% and 17.58% respectively indicating the contribution of environmental main effects over genotypic main effects for the variation of sugar yield due to diverse environmental conditions of the testing locations. Similar to this result, the higher donation of environment than the genotype and their interaction was reported in sugar yield by Tena et al. (2019) and by Legesse et al. (2019) in grain yield of maize [15]. The magnitude of sum squares of GEI is greater than that of genotype effects, indicating that there are more differences in genotypic response across environments. This result was not confirm with Erol et al. (2018) that reported the highest genotypic effect than GEI in the study undertaken for the selection of the best barley genotypes to multi and special environments by AMMI.

The GE interactions effect in the AMMI model has been partitioned into two Interaction Principal Component Axes (IPCA1 and IPCA2) [16]. The first-IPCA1 showed highly significant level whereas the second-IPCA2 were not significant recording 59.08%, and 18.66%, respectively with a decrease in the subsequent axes and totally explained 77.74% of the variations observed. The rest 22.26% of the interaction effect was residual, therefore, not interpreted (Purchase et al., 2000). The significance level of the first-IPCA1 indicates that the sugarcane clones and the six environments were considerably different from one another. This end result was in agreement with Vaezi et al. (2017) and Regis et al. (2018). According to Legesse et al. (2019), such research result shows the performances of the genotypes used were varied differently in sugar yield (Table 2) [17].

### Mean performance of genotypes

The sugar yield mean values of an introduced sugarcane genotypes ranged from 1.282 to 1.928ton/ha/month. Appropriated harvesting time of the genotypes across locations had its own yield advantage in sugarcane production; hence the unit measure ton per hectare per month is used in this result. Analysis of the AMMI indicated that genotypes G10 (1.928), G2 (1.744), G9 (1.683) and G4 (1.633) had high mean sugar yield in ton/ha/month while G6 (1.282), G7 (1.336) and G5 (1.488) were the least sugar yield. The standard check genotype

G9 (the second standard check) either at par or surpassed most of the tested new genotypes except G10 and G2. The genotype labeled by G10 observed to be the highest sugar yield mean value in ton/ha/month in four environments: E1, E2, E3 and E4 and also considered as the first cultivar among the first four AMMI selections for these sites [18].

Genotypes and/or environments with large IPCA1 scores (either positive or negative) have high interactions, whereas genotypes or environments with low IPCA1 scores show low contribution to the G×E interaction (Cossa et al., 1990; Oliveira et al., 2014). Accordingly, based on the first IPCA1 which scored 59.08% of sum squares of the interactions, G6 (0.081), G1 (-0.129) and G2 (-0.149) showed the lowest GEI interaction of the ten genotypes evaluated in six environments as listed in. Thus, these genotypes were considered as stable genotypes but except G2 the others two gave the lower sugar yield mean value in ton/ha/month. On the other hand, G3 (0.698) followed by G4 (-0.641), had the largest GE interaction and are responsive to environmental change and therefore not considerably stable [19].

Moreover, an average environmental sugar yield mean values over locations varied from 0.935(E4-plant cane at Metehara) to 2.369 (E1-plant cane at Finchaa). AMMI biplot analysis showed that the least first IPCA value of 0.040 was recorded for E3 (second ratoon at Finchaa) while the highest IPCA value (0.830) was observed for E1 (plant cane at Finchaa) indicating that low interaction of the climatic conditions at E3 and high interaction at E1. Therefore, E3 was contributed more for the stability of the genotypes. The genotypes with greater IPCA score is the more openly adapted to a specific location [20]. The genotype with IPCA score approximate to the nearest to zero is the more stable and or adapted to in overall environment (Alberts, 2004; Legesse et al. 2019). However, the sugar yield of genotypes could be changed depending on the nature of its genetic make-up; while the yield of environments could display variations based on the edapho climatic conditions (Tables 3 and 4).

### AMMI-biplot analysis

The AMMI-biplot analysis is a bi-directional method of evaluation: the main effects of genotype and environment are seen along the x-axis while the interaction effects are seen along the y-axis (Kendal et al., 2019). In another word, the genotypes and environments were evaluated based on their sugar yield mean (y-axis) and their stability value (x-axis). The genotypes are judged as stable if they are only closer to the x-axis, otherwise unstable. According to IPCA1 AMMI-biplot in Figure 1, G10, G2, G4 and G9 (the second standard check) showed good performance, because they located above or at right side to the y-axis. Moreover, G8 (the first standard check) showed relatively stable and moderately desirable average mean of sugar yield. G2 was

**Table 2:** Combined AMMI analysis of Variance on sugar yield of the 10 sugarcane lines across six environments (the combination of two sites for three cropping cycles).

Source	DF	S.S.	M.S.	v.r.	F pr	% TSS Explained	% trt	% GIE explained
Treatments	59	67.71	1.14***	7.96	<0.001	79.3		
Genotypes(G)	9	5.86	0.65***	4.51	<0.001		8.65	
Environments(E)	5	49.95	9.99***	57.04	<0.001		73.77	
Block (Env)	12	2.1	0.17	1.21	0.2825	2.46		
Interactions(GEI)	45	11.9	0.26**	1.83	0.0057		17.58	
IPCA 1	13	7.03	0.54***	3.76	<0.001			59.08
IPCA 2	11	2.22	0.20ns	1.4	0.182			18.66
Residuals	21	2.65	0.12	0.87	0.626			22.26
Error	108	15.57	0.14			18.24		
Total	179	85.38	0.47					

\*\*\*= highly Significant at 0.001; \*\*= Significant at 0.01; ns= non-significant; DF = Degrees of freedom; SS = Sum of squares; MS = Mean square; TSS= Total Sum of squares; trt= treatment

**Table 3:** The mean Performance of sugar yield (ton/ha/month) and IPCA scores of ten genotypes across six environments (the combination of two sites for three cropping cycles).

Genotype Label	Genotype Mean	IPCAg[1]	IPCAg[2]	AMMI-estimates per environment †					
				E1	E2	E3	E4	E5	E6
G1	1.527	-0.129	-0.534	2.198	2.249	1.513	0.546	1.205	1.453
G10	1.928	0.432	-0.048	3.082	2.775	1.547	1.278	1.445	1.443
G2	1.744	-0.149	0.238	2.4	2.241	1.377	1.251	1.699	1.498
G3	1.51	0.698	0.328	2.897	2.378	0.886	1.109	0.998	0.792
G4	1.633	-0.641	0.073	1.899	1.965	1.456	1.016	1.795	1.665
G5	1.488	0.164	0.218	2.428	2.144	1.046	0.995	1.241	1.071
G6	1.282	0.081	0.12	1.15	1.927	0.907	0.725	1.052	0.933
G7	1.336	-0.277	0.063	1.905	1.837	1.076	0.728	1.289	1.185
G8	1.591	0.295	-0.568	2.613	2.512	1.488	0.605	1.017	1.3
G9	1.683	-0.444	0.108	2.114	2.094	1.442	1.965	1.745	1.606
<b>Env't Mean</b>				<b>2.369</b>	<b>2.212</b>	<b>1.274</b>	<b>0.935</b>	<b>1.348</b>	<b>1.295</b>

†= Environments (E) are a combination of sites and crop cycles.

**Table 4:** The first four AMMI selections per environment and Environment means and IPCA scores.

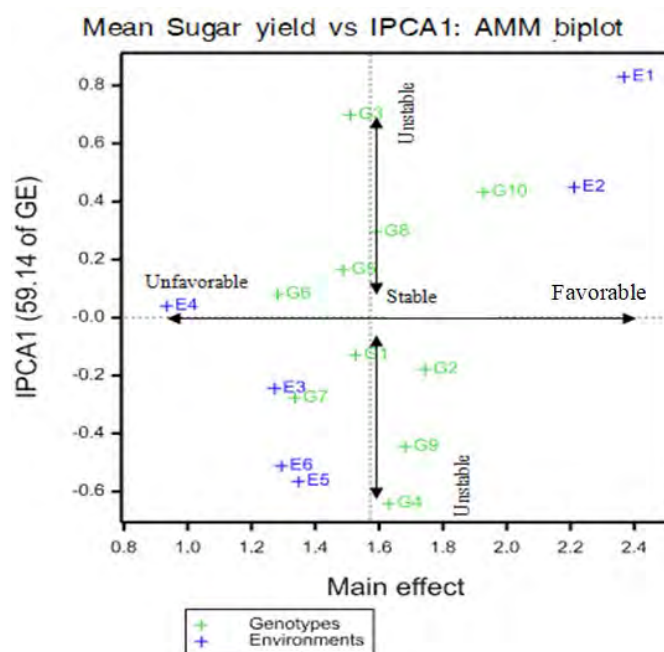
Environment	The first four AMMI selections per environment				Environmental IPCA scores	
	1	2	3	4	IPCAe[1]	IPCAe[2]
E1	G10	G3	G8	G5	0.83	0.034
E2	G10	G8	G3	G1	0.45	-0.262
E3	G10	G1	G8	G4	0.04	0.633
E4	G10	G2	G3	G9	-0.244	-0.472
E5	G4	G9	G2	G10	-0.511	-0.255
E6	G4	G9	G2	G1	-0.564	0.322

demonstrated with the highest potential of sugar yield mean value next to G10 and is also directed to the stable range and could be considered as the most preferable genotypes. G10 had the highest yield of all genotypes (main effect) but it observed as a moderately stable line [21]. On the other hand, G6 and G7 were the lowest yielder (lowest main effects), but the most stable genotypes and were categorized under poor cultivars. The genotype G4 and G3 revealed relatively high main effect value (average mean yield), but both replied to unfavorable direction because of high IPCA1 score which made them the most unstable genotypes of all the lines under test.

The AMMI-biplot indicated that E1 had the highest main effects followed by E2 and were favorable to the performance of most of the genotypes because of their high yield potential and located above or at right side to the y-axis. On the contrary, E3, E4, E5 and E6 had low yield potential environment as these located below average yield and at left side to the y-axis. The nearness of genotype G10 and G7 to environments E2 and E3 respectively indicates specific genotype adaptability to their position of environments. Generally, the environment E2 was favorably engaged for importance since it observed by having the highest main effect together with lower interaction to the stable direction to test the sugarcane genotypes more than the others (Figure 1) [22].

**The GGE-biplot analysis**

**Which-won-where pattern:** A polygon view was drawn connecting the genotypes with largest vectors in their respective directions that are further away from the biplot origin. Accordingly, the following genotypes named by G10, G4, G7, G6 and G3 are located at the corner of a polygon vertex. The polygon view of the GGE-biplot clearly displays ‘which-won-where’. It summarizes the GEI pattern of a multi-environment trial (MET) data set by answering which genotype is best performed in each environment (Yan, 2011; Hongyu et al., 2015) [23]. The magnitude of the vector (vector length and direction) is very important in representing the extent of the response of the genotypes



**Figure 1:** The AMMI-biplot graph showing interaction of PCA1 scores of the ten sugarcane genotypes in six environments.

to the tested environments. The GGE analysis is important to group more or less homogeneous and/or similar environments into mega-environments with which genotypes evaluated (Yan and Rajcan, 2002) although some information might be lost (Manjit, 2000).

A set of lines drawn from the biplot origin (0; 0) intersecting the sides of the polygon at right

angles and divided the graph into five sectors. Then, the GGE-biplot subdivide the target environment into sub-regions called

mega-environments which comprise one or more environments. Consequently, the environments were grouped into two mega-environments [24]. The first mega-environment made up by three environments: E1 (plant cane at Finchaa), E2 (first ratoon at Finchaa and E4 (plant cane at Metehara). The second mega-environment was made up by E3 (second ratoon at Finchaa), E5 (first ratoon at Metehara) and E6 (second ratoon at Metehara). This GGE-biplot polygon view indicates that the ratoon crops were grouped together in the second mega-environments except E2 showing the uniformity of this group in evaluating the tested genotypes. This suggests that the environments which located in the same sectors are strongly correlated (Solonechnyi et al., 2015). The vertex genotype observed with the highest yield in the first mega-environment was found to be only G10 while the vertex genotype G4 was obtained higher yield in the second mega-environment. Among the five vertex genotypes, G7, G6 and G3 were out of the mega environments. And were the poorest-yielding because of the fact that these genotypes were observed far away from all of test environments, reflecting as they yielded lower at each location [25].

The winning genotype on the vertex of the polygon contained in a mega-environment had the highest yield in at least one environment and was one of the best-performing genotypes in the other environments (Yan and Rajcan, 2002). In another word, these genotypes indicated highly and positively correlated with these locations. Similarly, Adu et al. (2013) and Yan et al. (2007) reported the vertex genotype in each sector had the highest yield in the environment that falls within that particular sector. The other genotypes which had smaller vectors are contained within the polygon and this means, they are less responsive in relation to the interaction with the environments within that sector (Tena et al. 2019; Mattos et al., 2013; Yan and Rajcan, 2002) (Figure 2).

### The GGE-biplot ranking

An average environment coordination (AEC) was used for ranking and identifying the top yielder and stable genotypes by GGE-biplot based on the principles suggested by Yan and Rajcan (2002). The AEC is a line crosses through the biplot's origin based on genotype focused single value portioning (SVP = 1) and helps to simplify the genotype assessment based on the mean performance and stability under a wide range of environment. When moving away from the axis

of AEC ordinate and from the biplot origin, it indicates the instability of the genotype increases and hence, the interaction effect with the environments will also increases (Tena et al., 2019) [26,27].

In this investigation, the ranking biplot AEC indicated that G2, G9 (standard check) and G4 observed with above-average means and were always considered among the best genotypes. Particularly, G2 could be noted as the stable and best leading and an ideal genotype as compared to the others due to its nearness to the arrowhead. The genotype G10 was observed as above average sugar yield mean value, but positioned at moderately stable direction. Therefore, based on the genotype G2 could be selected because of superiority and stability followed by G10 due to its above mean value and moderate stability. Conversely, G6, G7, G3 and G5 were those genotypes scored with below-average means performance [28,29]. This research result is confirmed with the report of Mebrahtom et al. (2018) and Tena et al., (2019) for GEI evaluation in sugarcane genotypes at the same location with this work and Legesse et al. (2019) in quality protein maize (Figure 3).

### The GGE-biplot comparison

Genotype which is the highest sugar yield mean values in all test environments and well stable is said to be an ideal genotype (Yan and Kang, 2003). This is decided as in the center of the concentric circles or otherwise located closer to the ideal circle (Kendal et al., 2016). The center of the concentric circle is a point in the positive direction and has the longest vectors of the genotypes and helps to visualize the distance between each genotype and the ideal genotype [30]. Accordingly, depicts that G10 was located on very nearest to the concentric circle; thus, closest to the ideal genotype and therefore identified as the best genotype than the others. Genotype G2 and G9 (standard check) were categorized in the second and third desirability respectively, in terms of their higher yielding performance and stability [31]. This genotypes are ordered as G10>G2>G9 in their sugar yield performance and ordered as G2 > G10>G9 in their stability attraction. Consequently, it is very important to decide that G10 and G2 were recommended for commercial production and for broad adaptation than the others. On

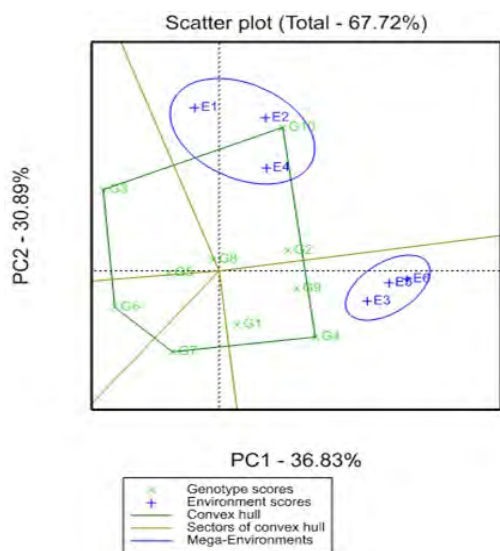


Figure 2: The 'which-won-where'-polygon view of GGE-biplot model based on sugar yield data of ten genotype analysis tested across six environments.

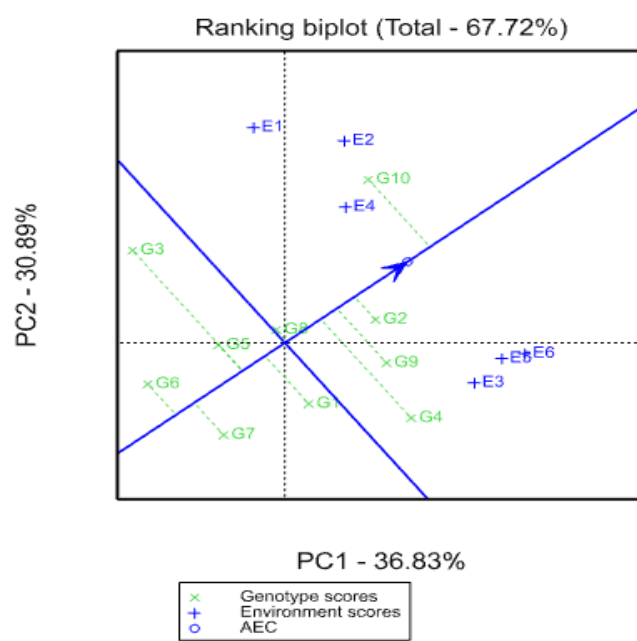
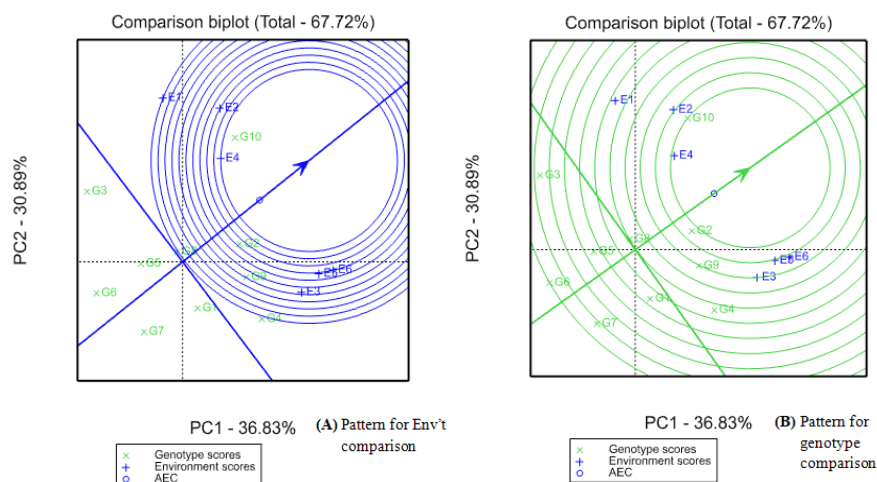


Figure 3: The GGE model environmental focused genotypes ranking for sugar yield performance and stability of genotypes across six environments.



**Figure 4:** The GGE Comparison of sugar yield of ten genotypes (A) pattern for environmental focused comparison scaling and (B) pattern for genotype focused scaling as the desirable genotypes to the ideal center.

the contrary, genotype G3, G6 and G7 were extremely far away from the concentric circle and thus not in the category of ideal genotype. This implies they are poor yielding mainly because of their distance from the concentric circle. Other reports also found that an ideal genotype having the highest yield and stable; the genotypes with poor yield and unstable (Kendal et al., 2016, Tena et al., 2019, Legesse et al., 2019) [32].

Ideal environments have two features; discriminativeness (the ability of an environment to distinguish genotype) and representativeness (the ability of an environment to represent all other evaluated environments) [33]. Environment-focused scaling of comparison the GGE biplot is measured based on AEC and concentric circles which helps to evaluate the tested environments as this measures showed the distance of the environments from the biplot origin. The ideal environment is the one that is close to the center of concentric circles. In this case, E4 (plant cane at Metehara followed by E2 (first ratoon crop at Finchaa) were found for being an ideal environment as placed close to the concentric circles (representativeness of suitable environment) having the smallest vector length from the biplot origin. This implies that sugarcane genotypes selected in that environment as well as cropping cycle would have high probability to perform well in other locations of the same region [34].

The environments that were placed far from the comparison biplot origin indicated the discriminating ability of the environments as the discrimination power of an environment is proportional to the length of the environmental vector (Vargas et al., 2013). Hence, from the six-tested environments, E1 (plant cane at Finchaa) had strong ability to discriminate the genotypes for sugar yield as it was placed far from the biplot origin (longest vector). In line with these findings reported on the discriminative and representative ability of the environments, Mebrahtom et al. (2018) and Tena et al. (2019) for sugar yield at similar locations and Enyew et al. (2021) analysis for grain yield and other agronomic traits in sorghum (Figure 4A and 4B) [35,36].

## Conclusion

The variation due to environments explained 73.77% out of total phenotypic variation indicating the importance of environmental main effects over genotypic main effects to influence sugar yield of the genotype. Analysis of the AMMI observed to be the genotypes G10 (1.928) had high mean sugar yield in ton/ha/month while G6 (1.282) recorded the least sugar yield.

The genotype labeled by G10 was considered as the first cultivar in obtaining the highest sugar yield mean value in ton/ha/month in four environments: E1, E2, E3 and E4. The GGE-biplot grouped the target environment into two mega-environments in which both of them were made up by three environments indicating most probably the ratoon crops were merged together.

Both E4 (plant cane at Metehara and E2 (first ratoon crop at Finchaa) were found for being representativeness of suitable environment while E1 (plant cane at Finchaa) had strong ability to discriminate the genotypes for sugar yield. In general, the GGE-biplot ranking analysis showed that G2 was categorized as an ideal genotype and stability followed by G10 due to its above mean value and moderate stability over location for making effective selection. Therefore, these two genotypes could be recommended for verification and release for commercial farm.

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## Competing Interests

The authors declare that there is no conflict of interest.

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