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# Multi-locations evaluation of sorghum (*Sorghum bicolor* L.) genotypes for grain yield and yield related traits at western Oromia, Ethiopia

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A field experiment was conducted on twelve sorghum genotypes against one local and two standard checks at Haro Sabu Agricultural Research Center (HSARC) sub sites for three consecutive years (2016-2018) using randomized completely block design (RCBD) to evaluate and select high yielding sorghum genotypes and to assess the impact of genotype by environment interaction on grain yield and yield components across diverse growing environments of western Oromia. Eight agronomic traits and three economically important disease reaction were collected depending on the crop descriptor. Pooled over locations analysis of variance detected significance difference among tested genotypes for all collected traits. Genotype by environment interactions (G×E) significantly affected all recorded traits excluding days to heading and thousand seed weight. Genotype and genotype by environment interaction (GGE) bi-plot analysis revealed that G3, G11 and G12 as ideal genotypes in terms of yielding ability and stability and were promoted as candidates for possible release and use as genetic resource in future breeding programs.

**Key words:** Sorghum bicolor L., Genotype by environment interactions (G×E), Genotype and genotype by environment interaction (GGE) bi-plot, stability.

## INTRODUCTION

Among grain crops cereals are the major food crops in Ethiopia, both in terms of the land coverage and volume of production (CSA, 2016). Sorghum is the most widely grown food crop in Ethiopia. It thrives in a range of agro-climatic zones including high and low altitudes. High altitude sorghums grow satisfactorily at altitudes as high

as 2,300 m where mean temperatures range from a minimum of 14 to 26°C. Sorghum (*Sorghum bicolor* L.) is an important drought tolerant rain fed cereal largely cultivated for food, feed and fodder by subsistence farmers in Ethiopia (Ayana et al., 2000). The national average production of sorghum is 2.5 tonha<sup>-1</sup> (CSA,

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**Table 1.** Passport description of the test genotypes.

S/N	Landrace code	Code	Region	Zone	Woreda	Village	Altitude	Soil type
1	SLRC-010	G1	Oromia	K/Wollega	D/sadi	Laku	1514	Sandy
2	SLRC-06	G8	Oromia	W/Wollega	Guliso	D/guda	1708	Sandy clay
3	SLRC-027	G7	Oromia	W/Wollega	Begi	Shelxa	1433	Clay loam
4	SLRC-028	G5	Oromia	W/Wollega	Begi	Meganteya	1584	Sandy loam
5	SLRC-037	G4	Oromia	K/Wollega	Gidami	Alchayajilo	1698	Sandy loam
6	SLRC-043	G3	Oromia	K/Wollega	Seyo	Minko	1690	Sandy loam
7	SLRC-046	G12	Oromia	K/Wollega	H/Galan	Mesareta	1482	Sandy loam
8	SLRC-048	G6	Oromia	K/Wollega	Y/Walel	Odamoti	1369	Clay loam
9	SLRC-058	G11	Oromia	K/Wollega	Y/Walel	Horamelka	1429	Clay loam
10	Local check	G9	Oromia	K/Wollega				
11	Gemadi	G2	Oromia	K/Wollega				
12	Lalo	G10	Oromia	K/Wollega				

2016). Of the total national sorghum production (432,3299.8 ton), Oromia region shares production (1,884,630.1 ton) of sorghum which is almost about half of the total annual production of the country (CSA, 2016). In sub Saharan Africa and south Asia sorghum is consumed as staple food and is also used in the production of a variety of by-products like alcohol, edible oil, and sugar (Wang et al., 2008). It is used as food, feed, beverage, and its stalk was used for construction of fences in Western Ethiopia and surrounding vicinities. It has a dense and deep root, has ability to reduce transpiration through leaf rolling and stomatal closure among others which in turn makes the crop to survive dry spelling periods. Hence sorghum has become a strategic crop in the face of climate unpredictability across different sorghum growing environments. In spite of all these advantages, sorghum has been a neglected crop, both at national as well as global level and the sorghum crop production is still very low (Stemler et al, 1977).

Among figurative problems, a biotic and biotic factor, the effect of genotype by environment interaction and stability of released varieties across the growing environments are the major one (Tesso et al., 2004; Girma et al., 2010). It is recalled that genotype and genotype by environment interaction (GGE) bi-plot is the most recent approach for analysis of G×E and ever more being used in G×E studies in plant breeding research (Yang et al., 2007). The GGE bi-plot model was used extensively in quantitative genetics and plant breeding (Yang et al., 2007). Additionally, the additive main effects and multiplicative interactions (AMMI) model are also defined as powerful tools for effective analysis and interpretation of multi environment data structure in breeding programs. In most cases plant breeders faces instability of yield when genotypes were grown in different environments due to G×E. Therefore, multi -environment trials (MET) are required to identify specific and the

general adaptability pattern of genotypes. The aim of the present study was, therefore, to examine the stability and yielding performance of sorghum genotypes s and to identify stable and high yielding cultivar for wider cultivation.

## MATERIALS AND METHODS

Twelve sorghum genotypes were tested against one local and two standard checks (Table 1) were evaluated for three (2016-2018) cropping seasons at Haro Sabu agricultural research center on station, Hawa-Galan Farmers Training Center (FTC), Kombo FTC, and Guliso FTC of Western Oromia, Ethiopia (Table 2). The trial was planted in randomized completed block design (RCBD) with three replications. Each plot consists of six rows (with four harvestable rows) having 3 m plot length with inter-row and intra-row spacing of 0.75 and 0.15 m, respectively and 2 m spacing was used between each block. A seed rate of 25 kg $ha^{-1}$  and recommended fertilizer was applied. All other agronomic practices were performed as per the recommendation for the crop.

### Data collection method

Five plants were selected randomly before heading from each row (four harvestable rows) and tagged with thread and all the necessary plant based data were collected from these sampled plants.

Plant-based: Plant height, head height and head weight.

Plot based: Days to heading, days to physiological maturity, lodging percentage, thousand seed weight, grain yield and three economically important insect pest and disease reaction like stalk borer (*Chilo Partellus*), anthracnose (*Colletotrichum sublineolum*) and leaf blight (*Exserhilum turcicum*) were scored.

### Statistical analysis

AMMI method as described in Zobel et al. (1988) was used to analyze adaptability and phenotypic stability using the following

**Table 2.** Description of the test locations for geographical position and soil type.

Locations	Code	Geographical position		Altitude (m.a.s.l) (m)	Average rain fall(mm)	Soil type
		Latitude	Longitude			
Haro Sabu	HS	8° 19'N	35° 30'E	1550	1100	Sandy clay
Kombo	KB	8° 92 'N	35° 09'E	1440	1200	Sandy loam
Guliso	GL	NI	NI	1600	1400	Sandy clay
Hawa Galan	HG	8° 38' N	35° 50'E	1905	1600	Sandy loam

NI=not identified.

statistical model:

$$y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{kj} + r_{ij} + \varepsilon_{ij}$$

Where,  $Y_{ij}$  is the yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment;  $\mu$  is the grand mean;  $g_i$  and  $e_j$  are the genotype and environment deviations from the grand mean, respectively;  $\lambda_k$  is the eigen value of the PCA analysis axis  $k$ ;  $\alpha_{ik}$  and  $\gamma_{kj}$  are the genotype and environment principal component scores for axis  $k$ ;  $n$  is the number of principal components retained in the model and  $\varepsilon_{ij}$  is the error term.

AMMI stability value of the  $i^{\text{th}}$  genotype (ASV) was calculated for each genotype according to the relative contribution of IPCA1 to IPCA2 to the interaction SS as follows (Purchase et al., 2000):

$$ASV = \sqrt{\left[ \frac{SS_{IPCA1}}{SS_{IPCA1} + SS_{IPCA2}} (IPCA1score)^2 + (IPCA2score)^2 \right]}$$

Where,  $SS_{IPCA1}/SS_{IPCA2}$  is the weight given to the IPCA1 value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. Based on the rank of mean grain yield of genotypes (RY<sub>i</sub>) across environments and rank of AMMI stability value (RASV<sub>i</sub>) a selection index called Genotype Selection Index (GSI) was calculated for each genotype, which incorporates both mean grain yield (RY<sub>i</sub>) and stability index in single criteria (GSI) as suggested by Farshadfar (2008):

$$GSI_i = RASV_i + RY_i$$

The analysis of GGE Bi-plot method was carried out for grain yield, according to the following model (Yan and Tinker, 2006).

$$\ddot{y}_{ij} = \lambda_1 \gamma_{i1} \delta_{j1} + \lambda_2 \gamma_{i2} \delta_{j2} + p_{ij}$$

where  $\lambda_1$  and  $\lambda_2$  are singular values of the first and second Principal Components (PC) associated with the matrix of the effects of genotypes added to effects of genotype  $\times$  environment interactions;  $\gamma_{i1}$  and  $\gamma_{i2}$  are eigenvectors of the first and second PC associated with the effect of the genotype  $i$ ;  $\delta_{j1}$  and  $\delta_{j2}$  are eigenvectors of the first and second PC associated with the effect of the environment  $j$ ;  $p_{ij}$  is the residual of the model associated with the genotype  $i$  in the environment  $j$ .

Bi-plots of the scores associated with two first PC were generated to better understanding the interrelationship among genotypes and/or environments, as proposed by Yan and Tinker (2006). Analysis of variance was carried using statistical analysis system (SAS) version 9.2 software (SAS Inst., 2008). AMMI analysis and GGE bi-plot analysis were performed using GenStat 15<sup>th</sup> edition statistical package (GenStat, 2012).

## RESULTS AND DISCUSSION

### Combined analysis of variance

All agronomic and yield component parameters were affected by environmental effect whereas all except grain yield were affected by cropping seasons. Days to maturity and head weight of genotypes were not affected across a cropping seasons and it agrees with the findings of Worede et al. (2020). Except days to heading and thousand seed weight all agronomic and yield components among tested genotypes were statistically affected across an environmental set. Statistically significant ( $P < 0.01$ ) difference were documented for grain yield among genotypes, environments and G $\times$ E and it's in concordance with the finding of Filho et al. (2014) and Worede et al. (2020)(Table 3).

### Yield performance of sorghum genotypes across environments

The mean performance of the tested sorghum genotypes for grain yield showed fluctuation over growing seasons and environments (Table 4). It's also noted that some genotypes consistently performed in a set of tested environments whereas some of them are irregular across locations. The highest grain yield was recorded from G11 (5.56-ton ha<sup>-1</sup>) genotype at Haro Sabu (2018) whereas the lowest was from G8 (1.27-ton ha<sup>-1</sup>) at Haro Sabu (2016). The combined over locations showed G12 as the highest yielder. In contrary, the local check included in this study was the low yielder among all tested genotypes that might be stem due to the genetic potential of the genotype (Mengistu et al., 2013). The disparity in yield rank of genotypes across the growing environments displays the prevalence of G $\times$ E interactions (Purchase et al., 2000; Yang et al., 2007).

### Agronomic performance

Delayed days to heading and days to physiological maturity were recorded from genotypes G11 (132.5) and

**Table 3.** Analysis of variance (ANOVA) for grain yield and yield related traits of sorghum genotypes evaluated in 2016-2018 main cropping seasons.

Sov	DF	DH	DM	PH	HH	HW	LGD	TSW	YLD
Year	2	653.0**	22.5**	627.9**	55.6*	1158.1**	3274.8**	413.7**	0.56ns
Env	3	3472.5**	4859.5**	620.5**	157.0**	191.4**	431.2**	136.6**	61.2**
Rep	2	27.6**	10.3ns	3.58ns	18.2ns	6.7*	2.3ns	61.8**	17.1*
Gen	11	484.7**	1005.8**	223.6**	180.0**	5.1**	4.06**	29.4**	203.87**
YearxEnv	2	60.4**	226.6**	493.9**	100.7**	0.04ns	15.4*	99.0**	0.89ns
YearxGen	22	125.6**	3.4ns	66.3**	20.1*	0.91ns	4.22ns	27.3**	0.97*
GenxEnv	33	4.3ns	9.6**	35.71**	20.8*	2.41**	7.46**	13.4ns	33.43**

Key: ns=non –significant, \*-significant at ( $P \leq 0.05$ ), \*\*-significant at ( $P \leq 0.01$ ), DH- Days to heading; DM- Days to maturity; PH- Plant height in cm; HH- Head height in cm; HW-Head weight in gm, LGD- Lodging percentage, TSW- Thousand seed weight in gm, YLD – Yield in ton.

**Table 4.** Mean grain yield (tonha<sup>-1</sup>) of sorghum genotypes evaluated at four environments.

Genotype	Grain yield in tonha <sup>-1</sup>								
	2016		2017			2018			
	Kombo	Haro Sabu	Haro Sabu	Guliso	Hawa Galan	Haro Sabu	Guliso	Hawa Galan	Comb. mean
G1	2.23 <sup>fg</sup>	3.39 <sup>cd</sup>	3.99 <sup>c</sup>	3.56 <sup>ef</sup>	3.96 <sup>de</sup>	3.76 <sup>d</sup>	3.83 <sup>e</sup>	4.01 <sup>bc</sup>	3.59 <sup>d</sup>
G2	2.89 <sup>d</sup>	4.36 <sup>a_c</sup>	4.29 <sup>b</sup>	3.82 <sup>d</sup>	4.12 <sup>cd</sup>	4.40 <sup>c</sup>	4.12 <sup>d</sup>	4.29 <sup>bc</sup>	4.04 <sup>c</sup>
G3	4.52 <sup>a</sup>	4.92 <sup>a</sup>	5.18 <sup>a</sup>	4.82 <sup>b</sup>	5.28 <sup>a</sup>	5.33 <sup>a</sup>	4.89 <sup>b</sup>	4.88 <sup>ab</sup>	4.98 <sup>a</sup>
G4	2.58 <sup>e</sup>	2.83 <sup>de</sup>	4.34 <sup>b</sup>	4.39 <sup>c</sup>	4.35 <sup>bc</sup>	4.77 <sup>b</sup>	4.69 <sup>bc</sup>	4.46 <sup>bc</sup>	4.05 <sup>c</sup>
G5	3.39 <sup>c</sup>	3.13 <sup>d</sup>	3.62 <sup>d</sup>	3.67 <sup>ed</sup>	3.86 <sup>de</sup>	3.83 <sup>d</sup>	3.86 <sup>e</sup>	3.81 <sup>c</sup>	3.65 <sup>d</sup>
G6	4.49 <sup>a</sup>	3.17 <sup>d</sup>	4.50 <sup>b</sup>	4.34 <sup>c</sup>	4.61 <sup>b</sup>	4.63 <sup>bc</sup>	4.53 <sup>c</sup>	4.81 <sup>ab</sup>	4.39 <sup>b</sup>
G7	3.11 <sup>cd</sup>	3.66 <sup>b_d</sup>	3.55 <sup>d</sup>	3.36 <sup>f</sup>	3.69 <sup>e</sup>	3.36 <sup>e</sup>	3.46 <sup>f</sup>	2.36 <sup>d</sup>	3.32 <sup>e</sup>
G8	2.08 <sup>g</sup>	1.28 <sup>f</sup>	2.89 <sup>e</sup>	2.62 <sup>g</sup>	2.48 <sup>g</sup>	2.78 <sup>f</sup>	2.58 <sup>g</sup>	2.86 <sup>d</sup>	2.45 <sup>f</sup>
G9	1.75 <sup>h</sup>	1.69 <sup>f</sup>	2.58 <sup>f</sup>	2.64 <sup>g</sup>	2.82 <sup>f</sup>	2.59 <sup>f</sup>	2.54 <sup>g</sup>	2.73 <sup>d</sup>	2.42 <sup>f</sup>
G10	2.38 <sup>ef</sup>	1.79 <sup>ef</sup>	2.50 <sup>f</sup>	2.39 <sup>g</sup>	2.50 <sup>g</sup>	2.64 <sup>f</sup>	2.60 <sup>g</sup>	2.78 <sup>d</sup>	2.45 <sup>f</sup>
G11	3.86 <sup>b</sup>	3.81 <sup>b_d</sup>	5.33 <sup>a</sup>	5.01 <sup>b</sup>	5.33 <sup>a</sup>	5.56 <sup>a</sup>	4.92 <sup>b</sup>	5.48 <sup>a</sup>	4.91 <sup>a</sup>
G12	3.26 <sup>c</sup>	4.46 <sup>ab</sup>	5.46 <sup>a</sup>	5.48 <sup>a</sup>	5.34 <sup>a</sup>	5.39 <sup>a</sup>	5.25 <sup>a</sup>	5.46 <sup>a</sup>	5.02 <sup>a</sup>
Mean	3.05	3.21	4.03	3.84	4.03	4.09	3.94	3.99	3.77
CV%	5.75	19.54	4.3	3.86	4.21	4.13	3.72	13.05	8.52
LSD(5%)	2.95	1.06	2.92	2.49	2.86	2.85	2.47	8.78	1.83
F test	**	**	**	**	**	**	**	**	**

G12 (131.04) whereas G5 (169.17) and G6 (169.17) were early to days to heading and days to physiological maturity suggesting a great flexibility for developing improved varieties suitable for various agro-ecologies with variable length of growing period. G1, G4, G8, G9 and G10 were high in terms of plant height indicating that these genotypes might be susceptible to root and/or stem lodging (Mengistu et al., 2019). Contrariwise, G3, G11 and G12 genotypes were medium in terms of plant height indicating that the possibility to develop resistant variety against lodging problems. Moreover, G3, G11 and G12

were recorded the highest grain yield and they had 23.33, 21.72 and 24.3% yield advantage over the best standard check G2 (Table 5). Those genotypes that had better grain yield among tested genotypes had correspondingly low scores to economically important insect pest and disease reactions. Maximum anthracnose disease reaction score was recorded from G2 and G6. Likewise, maximum leaf blight disease reaction was recorded from G2 and G10. Conversely, G3, G11 and G12 genotypes were better tolerant to stalk borer, anthracnose and leaf blight (Table 6).

**Table 5.** Combined mean grain yield and other agronomic traits of sorghum genotypes.

Genotypes	DH	DM	LDG	PH	HH	HW	TSW	YAD (%)
G1	127.67 <sup>d</sup>	172.83 <sup>d</sup>	2.5 <sup>b</sup>	420.70	32.87	99.82 <sup>c</sup>	24.76 <sup>e</sup>	-11.09
G2	122.60 <sup>f</sup>	172.92 <sup>d</sup>	2.25 <sup>cd</sup>	327.12 <sup>ef</sup>	26.28 <sup>de</sup>	101.50 <sup>c</sup>	32.79 <sup>b</sup>	0
G3	130.37 <sup>bc</sup>	174.00 <sup>d</sup>	1.04 <sup>h</sup>	349.80 <sup>d</sup>	33.07	114.75 <sup>b</sup>	32.58 <sup>b</sup>	23.33
G4	124.02 <sup>e</sup>	165.62 <sup>f</sup>	2.08 <sup>d</sup>	407.95 <sup>b</sup>	31.66	106.35 <sup>bc</sup>	26.56 <sup>c-e</sup>	0.37
G5	124.42 <sup>e</sup>	169.17 <sup>e</sup>	2.62 <sup>b</sup>	388.83 <sup>c</sup>	31.83	118.88	25.36 <sup>e</sup>	-9.47
G6	122.71 <sup>f</sup>	169.17 <sup>e</sup>	1.7 <sup>ef</sup>	353.3 <sup>d</sup>	29.60 <sup>b</sup>	99.32 <sup>c</sup>	25.69 <sup>de</sup>	8.64
G7	129.83 <sup>c</sup>	175.83 <sup>c</sup>	1.83 <sup>e</sup>	344.05 <sup>de</sup>	28.81 <sup>bc</sup>	103.96 <sup>bc</sup>	27.47 <sup>c-e</sup>	-17.77
G8	120.02 <sup>g</sup>	163.08 <sup>g</sup>	2.29 <sup>c</sup>	407.08 <sup>b</sup>	27.24 <sup>cd</sup>	114.03 <sup>b</sup>	25.36 <sup>e</sup>	-39.43
G9	127.75 <sup>d</sup>	166.17 <sup>f</sup>	1.60 <sup>f</sup>	394.66 <sup>bc</sup>	33.52	110.00 <sup>c</sup>	29.80 <sup>c</sup>	-40.18
G10	116.44 <sup>h</sup>	163.08 <sup>g</sup>	2.88	403.34 <sup>bc</sup>	27.09 <sup>c-e</sup>	110.22 <sup>c</sup>	29.40 <sup>b-d</sup>	-39.33
G11	132.58	181.88 <sup>b</sup>	1.29 <sup>g</sup>	326.33 <sup>f</sup>	25.24 <sup>e</sup>	106.56 <sup>c</sup>	33.45	21.72
G12	131.04 <sup>b</sup>	183.42	1.10 <sup>h</sup>	344.03 <sup>de</sup>	29.39 <sup>b</sup>	105.36 <sup>bc</sup>	32.48 <sup>b</sup>	24.3
Mean	125.78	171.44	1.93	372.26	29.71	106.81	28.83	
CV%	1.68	1.2	15.83	8.1	11.1	20.5	22.85	
LSD (5%)	120	1.17	0.17	17.19	1.89	12.47	3.75	

Key: DH-Days to heading, DM-Days to maturity, PH- Plant height in cm, HH-Head height in cm, LDG- Lodging percentage, HW-head weight in gm, TSW- Thousand seed weight in gm, YAD- yield advantage of genotypes over G2.

**Table 6.** Combined mean of disease and insect pest reactions of sorghum genotypes evaluated in 2016-2018 main cropping seasons.

Genotypes	Stalk borer	Anthracnose	Leaf blight
G1	1.00 <sup>e</sup>	1.36 <sup>d</sup>	2.04 <sup>e</sup>
G2	1.169 <sup>a</sup>	2.5 <sup>a</sup>	2.88 <sup>a</sup>
G3	1.027 <sup>de</sup>	1.4 <sup>d</sup>	2.04 <sup>e</sup>
G4	1.022 <sup>de</sup>	2.29 <sup>b</sup>	2.04 <sup>e</sup>
G5	1.00 <sup>e</sup>	2.29 <sup>b</sup>	2.54 <sup>b</sup>
G6	1.078 <sup>bc</sup>	2.417 <sup>a</sup>	2.38 <sup>c</sup>
G7	1.00 <sup>e</sup>	1.44 <sup>d</sup>	1.88 <sup>f</sup>
G8	1.11 <sup>b</sup>	1.56 <sup>c</sup>	2.21 <sup>d</sup>
G9	1.056 <sup>cd</sup>	1.08 <sup>e</sup>	2.04 <sup>e</sup>
G10	1.167 <sup>a</sup>	2.33 <sup>b</sup>	2.88 <sup>a</sup>
G11	1.00 <sup>e</sup>	1.63 <sup>c</sup>	1.57 <sup>g</sup>
G12	1.083 <sup>bc</sup>	1.37 <sup>d</sup>	1.29 <sup>h</sup>
CV%	4.79	8.61	1.37
LSD (5%)	0.03	0.09	0.02

#### Additive main effects and multiple interaction (AMMI) model

AMMI analysis of variance (ANOVA) with the appropriate AMMI model was indicated in Table 7. The analysis of variance (ANOVA) indicated highly significant differences ( $P \leq 0.01$ ) for environments, genotypes and importantly G×E.

The genotype, environment and genotype by

environment interaction explained 23.1, 69.5 and 7% of the total variation indicating the prevalence of considerable environmental variation. The interactive principal component axis (IPCA-1) and IPKA-2 axis of the G×E were highly significant ( $P \leq 0.01$ ). The first principal component managed over 68.6% of the G×E sum squares while the second principal component revealed 18.6% of the interaction, and the remaining 12.8% is due to residual (noise) and it is difficult to interpret and thus

**Table 7.** Partitioning of the explained sum of square (SS) and mean of square (MS) from AMMI analysis for grain yield of sorghum genotypes evaluated at four environments.

Source of variation	D.F	S.S	EX.SS%	M.S
Total	287	31574	100	110
Treatments	95	30462	96.5	320.7**
Genotypes	11	7061	23.1	641.9**
Environments	7	21181	69.5	3025.8**
Block	16	120	0.4	7.5 <sup>ns</sup>
Interactions	77	2220	7	28.8**
IPCA 1	17	1528	68.6	89.9**
IPCA 2	15	407	18.6	27.1**
Residuals	45	285	12.8	6.3 <sup>ns</sup>
Error	176	992		5.6

**Table 8.** AMMI stability value, AMMI rank, yield, yield rank and genotype selection index.

Genotype	ASV	ASV rank	YLDtonha <sup>-1</sup>	YLD rank	GSI
G12	28.26	10.00	5.02	1.00	11.00
G3	18.38	6.00	4.98	2.00	8.00
G11	20.20	7.00	4.91	3.00	10.00
G6	24.18	9.00	4.39	4.00	13.00
G4	30.03	11.00	4.05	5.00	16.00
G2	20.43	8.00	4.04	6.00	14.00
G5	13.11	2.00	3.66	7.00	9.00
G1	16.78	4.00	3.59	8.00	12.00
G7	40.22	12.00	3.32	9.00	21.00
G10	16.80	5.00	2.45	10.00	15.00
G8	16.66	3.00	2.45	11.00	14.00
G9	4.29	1.00	2.42	12.00	13.00

need to be discarded. Considerable percentage of G×E was explained by the first two IPCA axes. Different authors suggest the importance of apprehending most of the G×E sum squares in the first axis, to attain accurate information (Purchase et al., 2000; Kaya et al., 2002).

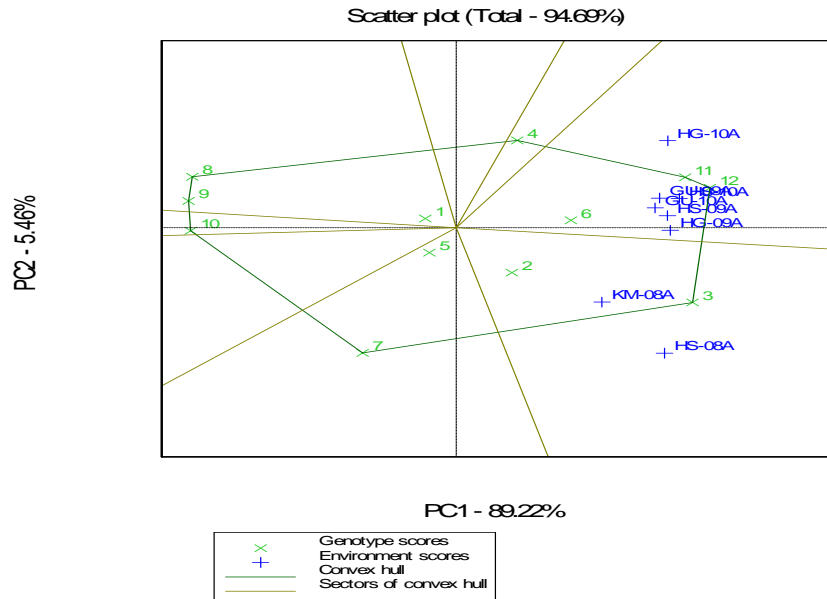
#### AMMI stability value (ASV) and genotype selection index (GSI)

G3, G11 and G12 were the highest yielder genotypes with relatively moderate ASV (Table 8). G9 and G5 showed the lowest ASV accompanied with the lowest grain yield. However, stability alone cannot be considered in production agriculture and hence identifying genotypes with high grain yield coupled with consistent stability across growing environments has paramount importance (Farshadfar, 2008). In this regard, GSI was utilized to further identify stable genotypes with better yield performance. Accordingly, G3, G11, G12, and G5 were

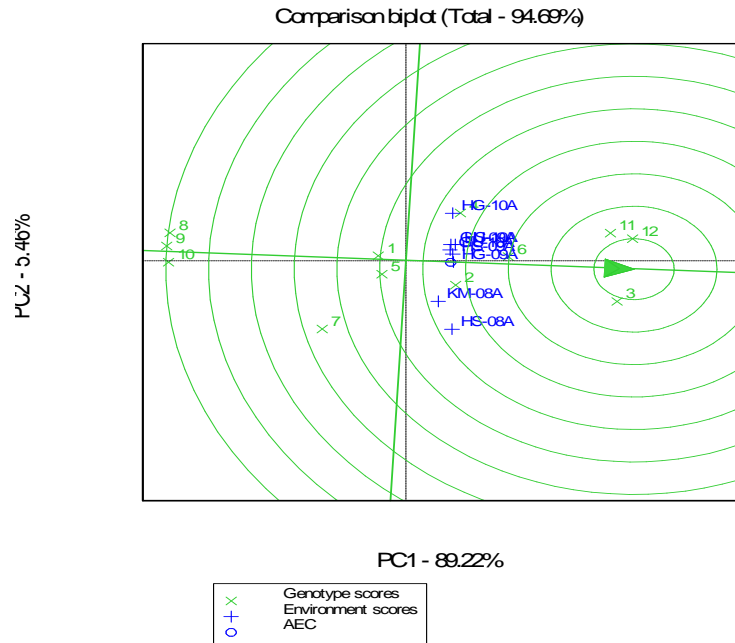
considered as most stable genotypes whereas; G7 was the least stable genotypes.

#### Genotype and genotype by environment interaction (GGE) biplot analysis

The polygon is drawn by joining the cultivars (G3, G4, G8, G10, G7 and G12) that are located farthest from the biplot origin so that all other cultivars are contained in the polygon. These vertex cultivars are the highest-yielding cultivar in all environments that share the sector with it. Vertex cultivars in which any environments fell in their sectors were the poor performing genotypes. Genotypes such as G1, G5 and G6 located at the origin would rank the same in all environments and is not responsive to the change in environments. G3, G11 and G12 genotypes were the best yielder among tested genotypes and relatively stable genotypes across various environments (Figure 1). G1, G5, G8 and G9 genotypes were inferior in



**Figure 1.** The scatter plots showing the which-won-where pattern of the GGE biplot. Hs= Haro Sabu, GU= Guliso, KM= Kombo, HG= Hawa Galan.



**Figure 2.** GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability.

yield performance and stable genotypes and G7 was the most unstable genotypes.

Genotype-focused scaling considers stability and mean grain yield concurrently and environments as well as genotypes that fall in the central (concentric) circle of

genotype-focused scaling are considered as an ideal environments and stable genotypes, respectively (Gauch and Zobel, 1997). Genotype G3, G11 and G12 fell in and around the center of concentric circle and therefore, ideal genotypes (Figure 2). Contrariwise, G8, G9 and G10

are located far from ideal genotypes and thus they are undesirable genotypes.

## CONCLUSION AND RECOMMENDATIONS

The genotypes were significantly influenced by environment, genotype and their interaction. GGE biplot and GSI index incorporating with the ASV and the yield capacity of the different genotypes in a single non-parametric index were found to be useful for discriminating genotypes with superior and stable grain yield. Depending on yield performance and reasonable stability G3, G11 and G12 genotypes were the best in the test environments and they can be used as candidates for possible release and for use as parents in future breeding programmes.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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