



Evaluation of yield performance of early maturing soybean (*Glycine max* L. Merrill) genotypes in Ethiopia by using GGE Biplot model

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ABSTRACT

Genotype main effect and genotype by environment interaction biplot analysis is the best fit model for which-won-where pattern analysis, genotype, and test environment evaluation. Hence, the aim of this study was to identify stable and high-yielding soybean genotypes for production in diverse environments by using the genotype main effect and genotype by environment biplot stability model. Eighteen soybean genotypes were evaluated across six environments during the 2019 cropping season by using a randomized complete block design with four replications. Among evaluated environments and genotypes, Tiro-afeta gave the highest yield (3.71 t ha⁻¹); while Humera gave the lowest yield (1.37 t ha⁻¹), and genotype JM-HAR/PR142-15-SB gave the highest mean grain yield of 2.9 t ha⁻¹ across the six locations. Based on the information generated from the GGE biplot, Tiro Afeta and Areka were identified as ideal environments, whereas genotypes PR-143-(14), JM-HAR/G99-15-SD-2 and JM-HAR/PR142-15-SB were ideal genotype. The 'which won where' biplot of the GGE analysis revealed that the six environments grouped into three different mega-environments with different winning genotypes. Among the testing environments, Areka, Sirinka and Humera grouped into one mega environment; while Tiro afeta grouped into the second mega environment and Jimma and Hawasa were classified into the third mega environment with the winning genotypes JM-HAR/PR142-15-SB, PR-143-(14) and KS4895 for each mega environment, respectively. Based on the GGE biplot stability model used in the study, JM-HAR/G99-15-SD-2, JM-HAR/PR142-15SB, and PR-143-(14) were high yielder and stable genotypes. Hence, these genotypes were recommended for variety verification and release after additional evaluation for more seasons.

Keywords: Environment, Genotype, GGE Biplot, Interaction, Mega Environment

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Introduction

Soybean (*Glycine max* L. Merrill) is considered to be a miracle crop as it is extraordinary rich in proteins (~40) and is also second only to ground nut in terms of oil content (~20). Soybean is a multipurpose crop, which can be used for a variety of purposes including preparation of different kinds of soybean foods, including soy milk, tofu, and mixing soybean grain with other grains for bread and injera making, animal feed, raw material for the processing industry, and it counter effects depletion of plant nutrients in the soil resulting from continuous mono cropping of cereals, especially maize and sorghum, thereby, contributing to sustainable soil fertility management (Hailegiorgis, 2010).

According to Tesfaye *et al.* (2017) and Zerihun (2011) soybean is grown over a wider agro-ecological conditions, especially in the low to mid-altitude areas (1300 to 1700 m.a.s.l) that have moderate annual rainfall (500-1500 mm) with an average yearly temperature of between 20-25°C, and soil pH of 5.5. The global production of soybeans was 361 million tons in 2018–2019 (Hales and Coleman-Jensen, 2022). The United States, Brazil, Argentina, China and India are the world's largest soybean producers and account for more than 89% of the global soybean production (Alabdalsaid, 2021). In 2018/19, the average worldwide productivity of soybean was 2.88 t ha⁻¹ (Fão *et al.*, 2019). Foyer



et al. (2018) reported that Africa holds tremendous potential for increasing sustainable soybean production, even in the face of a changing global climate. The top four soybean-producing countries in Africa are South Africa, Nigeria, Uganda and Malawi (Fão *et al.*, 2019). Currently, the area covered under soybean production in Ethiopia is 54543 ha with a total annual production of 125,623 ton, and productivity of 2.3 t ha⁻¹ (Fão *et al.*, 2019). This shows the productivity of soybean in Africa and Ethiopia is low relative to the average productivity of USA (3.4 t ha⁻¹) and the world average productivity of 2.88 t ha⁻¹ (Fão *et al.*, 2019). This low yield is attributed to a combination of several production constraints, among which, low soil fertility, lack of high yielding varieties adapted to different soybean-producing agroecology's of the country, periodic moisture stress, diseases, insect pests, and poor crop management practices (Georgis, 1990). Among the production constraints, lack of high yielding varieties adapted to different soybean-producing agroecologies of our country is the most important limiting factors of soybean production.

Previous studies of G x E interaction on soybean have illustrated significant interaction of genotypes with the environment for yield and yield-related traits (Mesfin *et al.*, 2019). Yan *et al.* (2000) proposed genotype plus genotype x environment interaction (GGE) biplot model for graphical representation of GE interaction pattern of multi-environment trial (MET) data. GGE bi-plot is a data visualization tool, which graphically displays a GxE interaction in a two-way table (Yan *et al.*, 2000). To understand GEI, two types of biplots, the AMMI biplot (Gauch and Zobel, 1997) and the GGE biplot (Yan *et al.*, 2000) are the most commonly used. Thus, GGE biplot is more logical and biological as compared to AMMI in explaining PC1 score, which represents genotypic effect rather than additive main effect (Yan *et al.*, 2006). GGE bi-plot is an effective tool for 1) mega-environment analysis (e.g., "which-won-where" pattern), whereby

specific genotypes can be recommended to specific mega-environments, 2) genotype evaluation (the mean performance and stability), and 3) environmental evaluation (the power to discriminate among genotypes in target environments) (Yan *et al.*, 2006). GGE biplot analysis has been carried out in understanding GEI in many crop species including soybean (Yan and Rajcan, 2002), sorghum (Rao *et al.*, 2002) and others. Fetien and Bjørnstad (2009) in barley; Farshadfar *et al.* (2011) in wheat, Fiseha *et al.* (2015) in sesame, and Mesfin *et al.* (2019) in soybean, are among the many authors who used GGE bi-plot to identify mega environments to evaluate and assess the performance and stability of the genotypes, and the test environments.

In spite of reports on utility of GEI analysis in deciding superior genotypes and/or test environments in many crops, GEI and stability analysis by GGE biplot model was not carried out on the materials considered in this study. While, as a case study we analyzed the performance of eighteen early matured soybean advanced lines across six locations using GGE biplot to demonstrate the utility of biplot graphical approach in analyzing and interpreting the complex GEI in MLT data. Hence, this research project was initiated to determine the genotype by environment interaction by using GGE-biplot analysis model and identify high yielding and stable genotypes for different agro-ecologies of the country.

Materials and Methods

Description of the study area

Eighteen (18) early maturing soybean genotypes were evaluated during the rainy season of 2019 at six locations of the major moisture stress and short growing period soybean growing areas in Ethiopia. The altitudes of the locations ranged from 608 to 2800 m.a.s.l. Detailed descriptions of the study locations are presented in Table 1.

Table 1. Description of the study area.

Location	Region	Longitude	Latitude	Altitude	Temperature	Annual Mean RF (mm)	Soil type
Tiro afeta	Oromia	37°19' E	7°54'N	2800	22°C	2000	Chromic & vertisol
Hawasa	Sidama	38°, 28'E	7°3' N	1708	20.3°C	953.4	Loam, clay or clay loam
Jimma	Oromia	36° 00'E	7°46' N	1753	16°C	1561	Nito, Combi soil
Areka	Sidama	37° 42'E	7° 4'N	1830	18°C	1450	Silt clay loam
Humera	Tigray	36°37'E	14°18'N	608	24°C	581.2	Vertisol
Sirinka	Amhara	36°38'00"E	11°45'00"N	1850	19.5 °C	945	Clay

Source: National Meteorology Agency (NMA) and Climate-data.org (2019)

Experimental materials

Eighteen early maturing (70-90 days to maturity) soybean genotypes obtained from Jimma Agricultural Research Center (JARC) were used for the study. Five of these genotypes were lines developed by JARC, from its hybridization programs, while eleven genotypes were obtained

from the University of Illinois, USA. The two varieties used as standard checks i.e., Nova and Gazale were released in 2012 and 2015, for early maturity and the seeds were obtained from Hawasa and Pawe Agricultural Research Centers, respectively.

Table 2. List of the study materials.

Trt #	Genotype Name	Seed source	Trt #	Genotype Name	Seed source
1	JM/PR142-15D	JARC	10	P1200488	USA
2	JM-HAR/G99-15-SD-2	JARC	11	JM-ALM/CRFD-15-SA	JARC
3	JM-HAR/PR142-15SB	JARC	12	P1417129B	USA
4	JM-PR142/G99-15SB	JARC	13	F6LG05	USA
5	Delsoy4710	USA	14	PR-143-(14)	USA
6	Gazale (check 2)	Pawe	15	P1203398	USA
7	Nova (check1)	Hawasa	16	Ozark	USA
8	P1417116	USA	17	KS4895	USA
9	P1506764	USA	18	Harber	USA

Experimental design and trial management

The trial was laid out in a randomized complete block design (RCBD) with four replications. Each plot consisted of four rows of 4 m length with 40 and 5 cm spacing between rows and seeds, respectively. The two middle rows were used for data collection and harvested at maturity. The experimental plot was prepared very well by ploughing three times and leveled for sowing. The plantings were done in early-June in each location. Fertilizer was applied at the rate of 122kg NPS ha⁻¹ at planting, and all other crop management practices were applied as per the recommendations for the crop. Weeds, pests and diseases are intensively controlled, using principles of integrated pest management (IPM).

Data collected

Grain yield per plot (GYP): At maturity, the weight in a gram of seeds harvested from the middle two harvestable rows of each plot was adjusted to 13% moisture and converted to ton per hectare. Then grain yield data were subjected to GGE biplots analysis.

Statistical analysis of variance

Data of the mean values of all the experimental units were subjected to analysis of variance (ANOVA) for the randomized complete block design. The combined analysis of variance over environments was performed with the PROC GLM procedure of SAS versions 9.3 software. Comparison of treatment means was done by Fischer's least significant difference (LSD) at 5% probability levels (Gomez and Gomez, 1984).

The combined analysis of variance was carried out to estimate the effects of the environment, genotype and GEI on the studied yield and yield-related traits. Significance levels of these components were determined using the F- test.

Stability analysis

GEA-R software was used to perform stability analysis among genotypes over location based on GGE biplot analysis methods as described below.

Genotype main effect and genotype by environment interaction effect (GGE) biplot analysis

The GGE biplot was constructed, using GEA-R software. GGE biplot methodology, which is composed of two concepts, the biplot concept and the GGE concept (Yan *et al.*, 2000), was used to graphically analyze the performance of the soybean genotypes in different environments. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation that is also sources of variation in GE interaction analysis of MET data (Yan and Rajcan, 2003).

The general model used for GGE Biplot is as follow:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \epsilon_{i1} \eta_{j1} + \lambda_2 \epsilon_{i2} \eta_{j2} + \epsilon_{ij} \text{ where:}$$

Y_{ij} = the performance of the i^{th} genotype in the j^{th} environment;

μ = the grand mean; β_j = the main effect of the environment j ; λ_1 and λ_2 = singular value for IPCA1 and IPCA2, respectively; ϵ_{i1} and ϵ_{i2} = eigenvectors of genotype i IPCA1 and IPCA2, respectively; η_{j1} and η_{j2} = eigenvectors of environment j for IPCA1 and IPCA2, respectively; ϵ_{ij} = residual associated with genotype i and environment j .

Results and Discussion

Combined analysis of variance across environments for yield

Following the confirmation of homogeneity of error variances of the individual locations using Bartlett's test, the combined analysis of variance was performed to determine the effects of genotypes, environments, and GEI interactions on grain yield.

The combined analysis of variance showed that there were significant ($p < 0.01$) differences among the environments, genotypes and GEI for grain yield (Table 3). The proportions of environment, genotypes and GEI to the total sum of squares for grain yield were 55.2%, 16.0% and 27.0%, respectively (Table 3). The high percentage of the environment sum of squares indicates that environment is the major factor that influences the performance of early maturing soybean genotypes in the moisture-stressed, short-growing season environments of the study locations in Ethiopia. The G x E interaction is highly significant ($p < 0.01$), accounting for 27.3% of the sum of squares, implying the need for investigating the nature of the differential response of the genotypes to environments. [Asrat *et al.* \(2009\)](#) reported that the significance of GEI indicates that each of the genotypes interacted differently at each location.

This result is in line with the finding of [Krisnawati and Adie \(2018\)](#) who studied the effect of genotype x environment interaction on 12 soybean genotypes tested in eight environments and reported highly significant mean squares of environments, genotypes and genotype x environment interactions (GEI). The authors also reported that environments, genotypes and genotype x environment interactions accounted for 64.4%, 10.8% and 24.8% of the total sum of squares, respectively. The environmental effect was three times higher than the G and GE effects ([Cravero *et al.*, 2010](#)). However, another report revealed that GEI effects were higher than the contributions of genotypic and environmental effects to the total variation ([Bhartiya *et al.*, 2017](#)).

Table 3. Combined ANOVA for grain yield (t ha⁻¹) and the percentage sum of squares of the 18 early mature soybean advanced line tested at six locations during 2019 season.

Source of variation	DF	SS	%SS	MS
Environment	5	25547.70457	55.2%	5109.54091**
Rep. within E(R/E)	18	53.11733	0.11%	2.95096
Genotype	17	7416.31573	16.04%	436.25387**
GXEI	85	12613.19113	27.3%	148.39048**
Residuals	306	598.74742	1.3%	1.95
Total	431	46229.07619	100%	

GY Mean = 2.1945 t ha⁻¹

CV = 6.372799% s

R² = 0.987048

**indicates significance at $P < 0.001$ probability level; CV = coefficient of variation, GY = grain yield, DF = degree of Freedom, SS = sum square, MS = mean square GxE = Genotype by environment interaction.

Stability analysis for grain yield

There were numerous methods used to evaluate yield stability in crops. In this study, the stability parameters GGE biplot were used to evaluate the yield stability of 18 early maturing soybean advance lines tested across six environments.

Genotype Main Effect and Genotype by Environment (GGE) Bi-plot Analysis for Grain Yield

The GGE biplot displays the graphic analyses of the studied early maturing soybean genotypes tested across the six environments are presented in figures below (Fig. 1).

Figure 1 indicated that genotype s that closed center of origin were stable genotype across the studied area but genotype that far from center of origin were unstable genotype with in studied area accordingly G9, G10 and G13 were unstable genotype and G2, G3, G4, and G14 were stable genotype (Fig. 1).

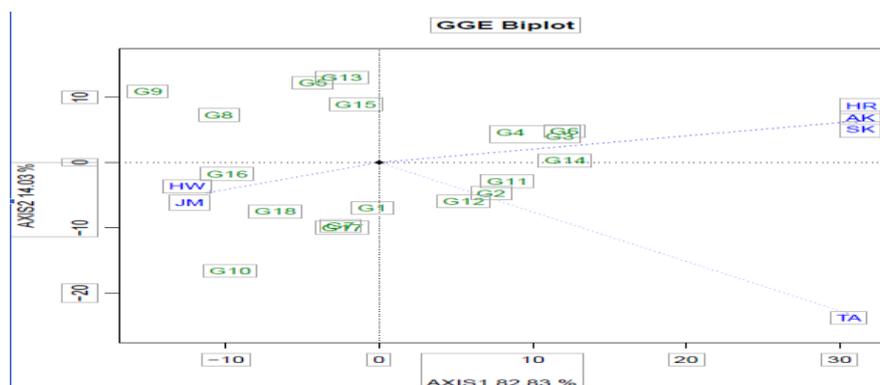


Fig. 1. GGE Biplot of 18 early matured soybean genotypes.

G1=JM-DAV/PR142-15D, G2=JM-HAR/G99-15-SD-2, G3=JM-HAR/PR142-15-SB, G4=JM-PR142/G99-15-SB, G5=Delsoy 4710, G6=Gazale, G7=Nova(check1), G8=PI417116, G9=PI506764, G10=PI200488, G11=JM-ALM/CRFD-15SA, G12=PI417129B, G13= F6 LG05-4321x LG05 4550, G14= PR-143-(14), G15= PI203398, G16= Ozark, G17= KS4895, G18= Harber TA=Tiro afeta, AK=Areka, JM=Jimma, HW=Hawasa, SK=Sirinka and HM=Humera.

Mean yield and stability performance

In the GGE biplot methodology, the estimation of yield and stability of genotypes was established using the average environment coordinate (AEC) methods (Yan and Rajcan, 2002). The best genotype can be defined as the one with the highest yield and stability across environments.

The line passing through the biplot origin the AEC which is defined by the average of PC1 and PC2 scores for all environments is called the Average Environment Coordinate (AEC) (Yan and Tinker, 2006). The axis of the AEC abscissa, or “average environment axis” is the single-arrowed line that passes through the biplot origin and at the centre of the small circle. The genotypes on the left side of the ordinate line had yields lower than average mean yield. Accordingly, the genotypes G8, G9, G5, and G13 the genotypes have mean grain yield lower than the grand mean (2.19 t ha⁻¹). But, the genotypes on the right side of the ordinate line have yield performance greater than mean yield and according to this genotypes G14, G3, G6, G4, G11, G2 and G12 had mean grain yield greater than the grand mean (2.19 t ha⁻¹) (Figure 2). A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GE

interaction of a genotype, which means it is more variable and less stable across environments or *vice versa*. Hence, considering simultaneously yield and stability, genotypes G2, G3, G4, G6, G11, G12 and G14 showed the best performances (Figure 2), suggesting their adaptation to a wide range of environments.

In a similar study, Fentaw (2011) reported that a genotype which has a shorter absolute length of projection in either of the two directions of AEC ordinate (located closer to AEC abscissa) represents a smaller tendency of GEI, which means it is the most stable genotype across the different environments or *vice versa*. Hence, genotypes G14, G11, G2, G3, and G16 with the short absolute value of projection from the AEC abscissa were the most stable genotypes. The genotype G3 had high yield and a relatively short distance from the AEC abscissa indicating this genotype is high yielding as well as stable. The fact that the genotype G16 showed a very short distance from the AEC abscissa and AEC ordinate shows that this genotype is poor yielder and stable, and this result was in line with the results reported using the ASV as this genotype was ranked first by ASV, however by mean grain yield it was ranked 16th.

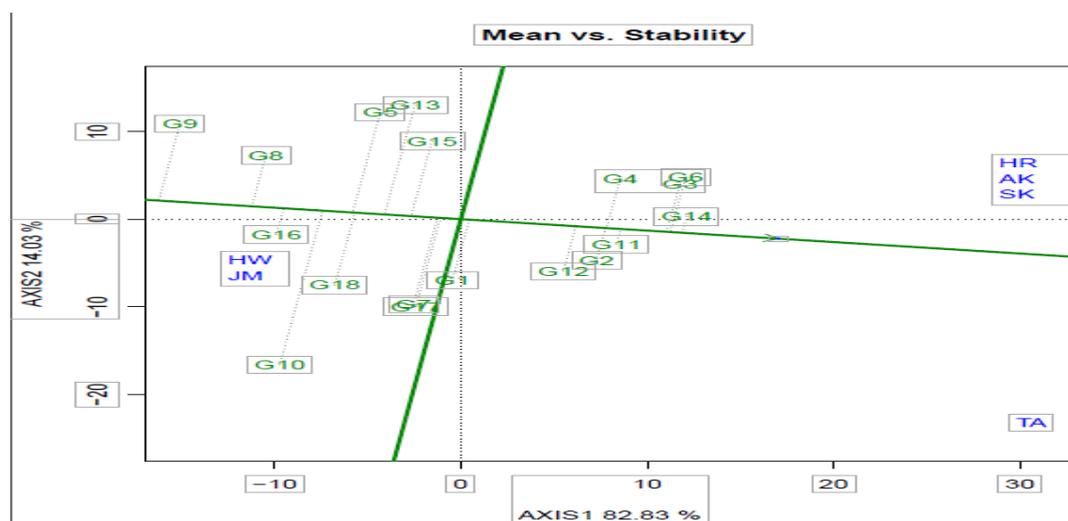


Fig. 2. Mean yield and stability performance of 18 early matured soybean genotypes.

Ranking of genotypes

The center of the concentric circles represents the position of an ideal genotype, which is defined by a projection onto the mean environment axis that equals the longest vector of the genotypes that had above-average mean yield and zero projection onto the perpendicular line (zero variability across environments). Located at the center of the concentric circle, G14 (PR-143-(14)) was identified as the “ideal” genotype in this study, followed by G11, G2, G3, G6, G4 and G12 which are closer to the ideal genotype (Fig. 3).

Hence, these genotypes are desirable for high yield and stability, as compared to other genotypes. On the other hand, genotypes G8, G9, 10 and G16 were unstable and the lowest yielding genotypes while considered to be undesirable because they are placed far from the ideal genotypes. Our results confirm those who found outstanding genotypes near to the ideal genotype in wheat for five consecutive years and those of Akter *et al.* (2015) who reported an ideal genotype of hybrid rice in the first concentric circle, Mesfin *et al.* (2019) in soybean.

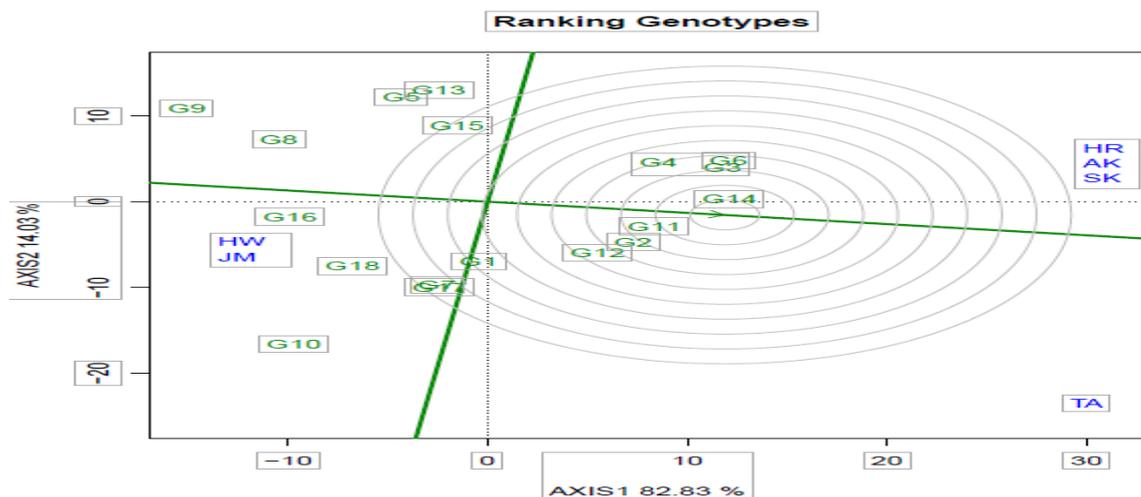


Fig. 3. Evaluation of genotypes relative to ideal genotypes.

Ranking of environments

According to Yan and Rajcan (2002), discriminating ability and representativeness are important properties of a test location. An ideal location should be highly differentiating (discriminating) for the tested genotypes and at the same time be representative of the target locations (Yan and Tinker, 2006). The ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). Accordingly, the location Tiro Afeta had the longest vector with small IPCA, which fell

into the center of the concentric circles was considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes, followed by Sirinka, Areka and Humera that were close to the ideal environment (Figure 4). Therefore, these locations might be as the most suitable to select widely adapted genotypes. This result in line with Yan *et al.* (2000), Yan and Rajcan (2002) and Fiseha *et al.* (2015); Gadissa *et al.* (2018); Yirga (2016).

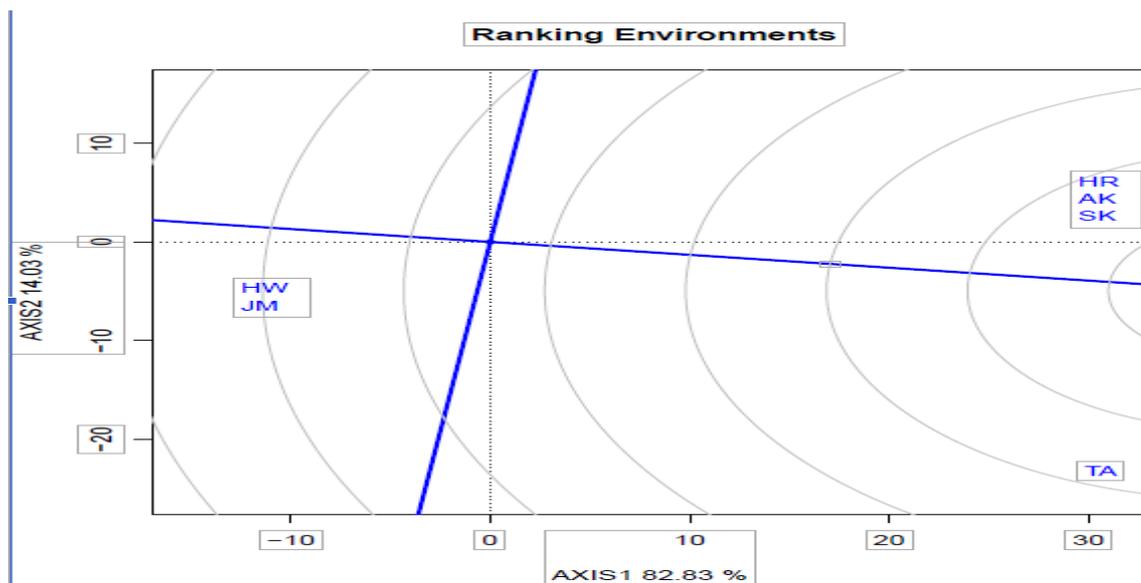


Fig. 4. Evaluation of environments relative to ideal environments.

Where, TA=Tiro Afeta, HR=Humera, AK=Areka, SK=Sirinka, HW=Hawasa, JM=Jima

Relationship among environments

The summary of the interrelationships among the environments was earlier presented in Figure 5. The lines that connect the bi-plot origin and the markers for the environments are environment

vectors, and the angle between the vectors of the two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of the two environments approximates the correlation coefficient between them (Yan and Rajcan, 2002). Based on the

angles between the test location vectors, the six locations are grouped into three major groups. Group one includes Areka, Sirinka, and Humera, group two includes Tiro afeta and group three includes Jimma and Hawasa. The smallest angle is between environments Sirnka, Areka, and Humera, and Jimma and Hawassa, implying that there is a very high positive significant correlation between these locations ($r=1^{***}$ between predicted yield by GGE2). Tiro Afeta was also closer to the locations Sirinka, Areka, and Humera indicating a close correlation between these locations with Tiroafeta ($r = 0.65^{**}$). Therefore, the first group Sirinka, Areka and Humera were closely correlated (Figure 5) suggesting that these locations provide redundant information on their capacity in discriminating between the genotypes.

The second group included Tiro afeta alone and it had the longest vectors from the origin. The third group included Jimma and Hawasa and they have a very short vector and are solitary. The angle between Tiro and Jimma, Tiro and Hawasa

was greater than 90° , showing a negative correlation between these locations with $r = -0.43761^*$ and $r = -0.43840^*$, respectively. The angle between Areka and Tiro afeta was less than 90° indicating that there was some positive correlation between them ($r=0.65^{**}$). Obtaining reliable information on the similarity of environments and their subdivision into groups can enable breeders to use fewer test environments reducing the cost of testing and increasing breeding efficiency. With the longest vectors from the origin, environments Tiro afeta and Humera were the most discriminating environments. Areka and Sirinka were moderately discriminating, while Jimma and Hawasa were the least discriminating locations. Discriminating ability and representativeness are the important properties of a test location. An ideal location should be highly differentiating for the tested genotypes and at the same time representative of the target locations. This result is in line with Yan *et al.* (2000); Yan and Rajcan (2002); Fiseha *et al.* (2015); Yirga (2016).

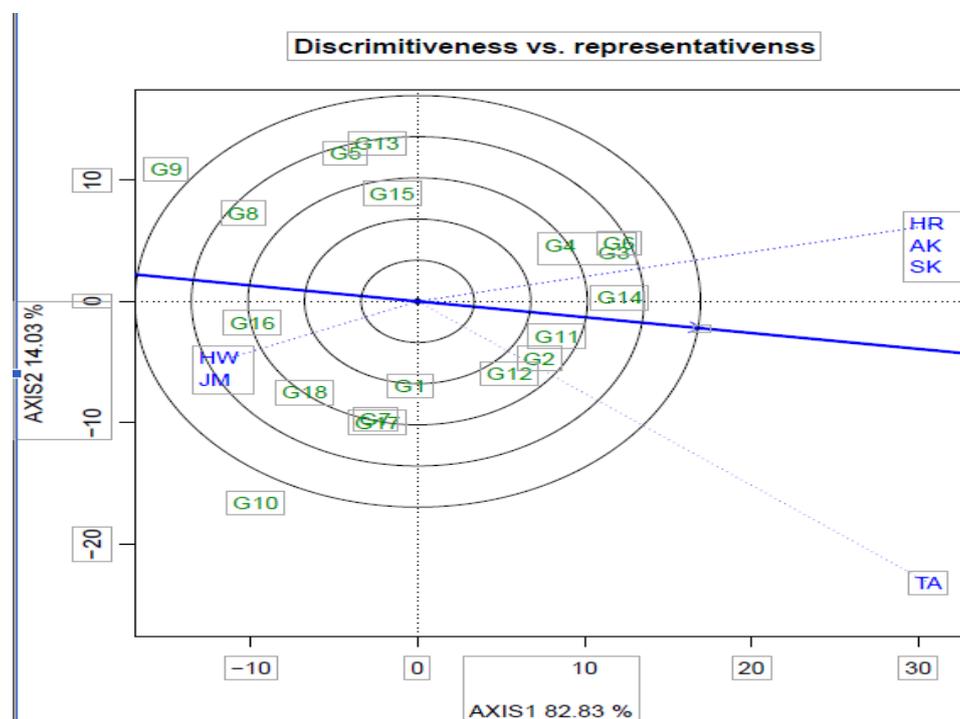


Fig. 5. The discrimination and representativeness view of the GGE biplot to rank test environments relative to an ideal test environment.

Which-Won-Where pattern of GGE biplot

One of the most attractive features of a GGE biplot is its ability to show the 'which-won-where' pattern of the GEI. Yan and Tinker (2006) reported that the use of a bi-plot is intriguing, as it graphically addresses important concepts, such as crossover GE, mega-environment differentiation and specific adaptation.

In the present study, the first two principal components of GGE biplot explained 96.83% ($PC_1=82.83\%$ and $PC_2=14.03\%$) of the total variations (Fig. 6). According to Fig. 6, genotypes G8, G9, G10, G13, and G5 were the best or worst in some or all the environments because they are furthest from the origin of the biplot (Yan and Tinker, 2006).

They are more responsive to environmental change and are considered as specifically adapted genotypes. They are best in the environments lying within their respective sector in the polygon view of the GGE-biplot (Yan and Tinker, 2006). Hence, the genotypes G6, G3, G4, were best yielding genotypes at Humera, Areka and Sirinka. Genotypes G11, G12, G2, and G14 were best yielding genotypes at Tiro. Genotypes G18, G17, G16 and G7 were the best-adapted genotypes at Hawassa and Jimma. Since Genotypes G10, G9 and G13 have the longest distance from the origin of the biplot on the opposite side of the environments the mean yield performance of these genotypes were poor. The genotypes: G1, G2, G3, G4, G6, G11 G12 and G14 are located near to the origin, and hence, according to Abay and Bjørnstad (2009) such genotypes were broadly adapted. It had also been observed that no environments fell into sectors where genotype G9 and G13 were the vertex genotypes indicating that these genotypes were not the best in any of the test environments. The present result was) in line with the work of Abay and Bjørnstad (2009) in

soybean, Karimizadeh *et al.* (2013); Yirga (2016) in sesame and lentil, Gadissa *et al.* (2018) in bread wheat identified three different growing mega-environments.

Connecting the extreme genotypes on a GGE biplot forms a polygon and the perpendicular lines to the sides of the polygon form sectors of genotypes and locations (Kaya *et al.*, 2006). The environments fall into three quadrants, while the genotypes fall into four quadrants (Figure 6).

The GGE biplot identified three different soybean growing mega-environments. The first mega environment consisted of three locations i.e., Areka, Sirinka and Humera that contains four genotypes (G3, G4, G6 and G14) as the best performing genotypes in these locations. The second mega environment consists of only one location: Tiroafeta and four genotypes G2, G11, G12 and G14 fall under this mega environment. The third mega environments included Hawassa and Jimma, and the genotypes that fall under this mega environment are G16, G18, G10 and G7.

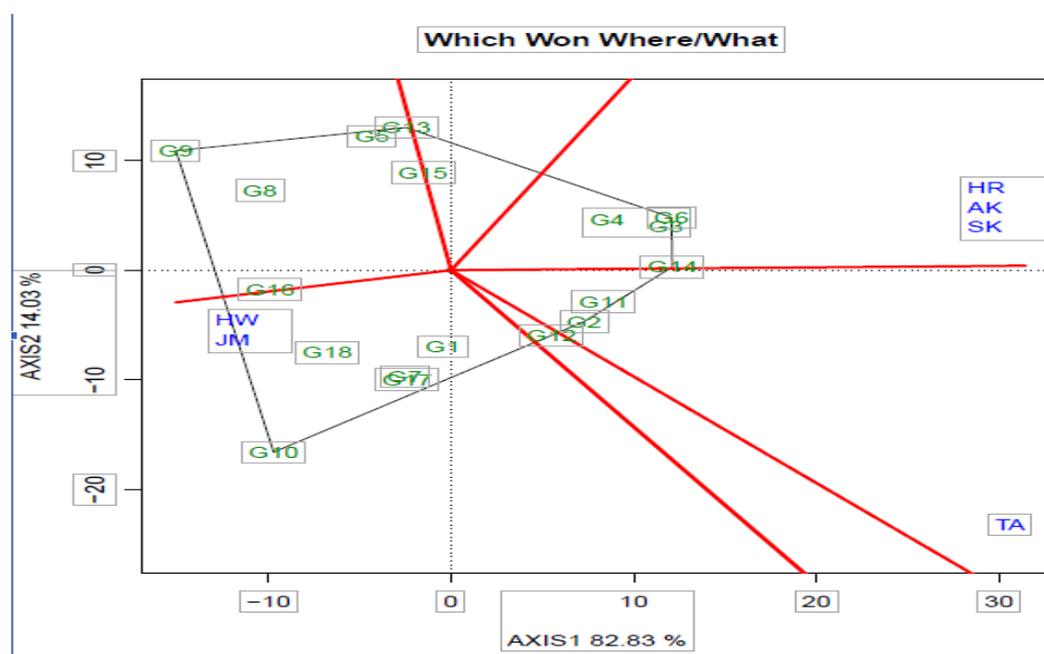


Fig. 6. Which won where? bi-plot of the GGE bi-plot analysis.

Discussion

The significant genotype by environment interaction indicates that, there is impact of environment and genotypes on soybean grain yield across the studied area. Hence, the genotypes performed differently across the different environments revealing the complication of selecting a single genotype for all environments. The same as, the significant genotypic difference indicates the presence of genetic causes of variation among the tested genotypes. In addition, the presence of highly

significant differences between the six test environments for the yield trait indicates the significance of testing soybean genotypes across environments. The current study indicated that on grain yield of early maturing soybean genotypes the impact of genotype, environment and G x E interactions were; 16.00%, 55.32% and 27.30%, respectively. In other way, this result shows high variance (55.20%) was generated by the impact of environment that means yield potential of early maturing soybean genotypes was determined by the environment.

Based on the result of GGE biplot analysis, among the tested genotypes, G2, G3 and G14 were the most stable genotypes with high yield across all location. However, Genotypes, G8, G9 and G10 were unstable genotypes and give lowest yield across all location. From the Six evaluated environments, namely Tiro-afeta, Areka, Jimma, Hawasa, Sirinka and Humera; Tiro-afeta and Areka were efficiently discriminated the tested genotypes for grain yield and can be considered as good environments for production of early maturing soybean genotypes. Some of the genotypes showed specific adaption to some environments. Accordingly, G3, G4, G6, and G14 were the best performers at Humera, Areka, and Sirinka. G16 and G18 were the best performers at Jimma and Hawasa, while, G2, G11 and G12 were best performers at Tiro-afeta. Therefore, these genotypes can be recommended for adaptation to specific environments. However, among these genotypes, only G2, G3, and G14 were stable and give highest yield across environments. According to the result of this study, from the evaluated environments Sirinka and Humera location was not a good environment for production of early maturing soybean. However, Tiro-afeta and Areka location was a good environment for production of early maturing soybean.

Generally, based on result generated from combined ANOVA and GGE biplot analysis genotypes; G2, G3 and G14 were high yielder and stable across all locations.

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