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GENOTYPE X ENVIRONMENT INTERACTION BY AMMI AND GGE-BIPLOT STABILITY ANALYSIS IN GRAIN YIELD FOR SOYBEAN [(*Glycine Max* L.) Merrill] IN ETHIOPIA

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In multi-location trials (MET), test environments need to be identified. properly in order to discriminate between varieties and to be representative of the targeted agro-ecologies. Hence, this experiment was conducted with the objectives was to evaluate the GEI using AMMI and GGE-biplot analysis for grain yield of soybean genotypes and identify stable genotypes in the different soybean agroecologies of Ethiopia. Twenty-four soybean genotypes were planted at six soybeans agroecologies of Ethiopia with RCBD in three replications in 2015/2016 cropping season. In addition, the first two IPCAs are significant and accounted for 70.34 form a total of interaction sum squares. Stability measures viz., Additive Main Effects and Multiplicative Interactions (AMMI), AMMI stability value (ASV), and Genotype plus GEI (GGE) bi-plot analysis were used to identify the high yielding and stable genotypes across the testing environments. AMMI1 biplot showed Pawe is ideal environment; Bako is favorable environment; Asosa average environment; and the rest environments viz., Dimtu, Jimma, and Metu as unfavorable environments. Whereas AMMI-2 biplot analysis genotypes Prichard, Spry, Delsoy 4710 and Croton 3.9 were identified as stable genotypes. Bako and Metu were identified as the most discriminating environments. Mega environments and the best yielding soybean genotypes on each mega environment were revealed by GGE bi-plots analysis model. The genotypes SCS-1 and AGS-7-1 were stable across soybean growing environments and it recommended for mega environment production.

Key Words: AMMI, ASV, GGE bi-plot, GEI, IPCA*,* Stability Analysis, Soybean yield

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INTRODUCTION

Soybean (*Glycine max* L. Merrill), popularly and often called “miracle bean” as it is extraordinarily rich in protein (~40%) and oil (~20%). It is the world's foremost provider of high-quality protein and edible oil for both human food and animal feed; in addition, it can improve soil fertility through its capability to fix atmospheric nitrogen (Morsy *et al*., 1990). It contains well balanced 40% protein (Lysin rich) and 20 % oil enriched with essential fatty acids.

According to Tesfaye *et al.* (2018), with its diverse agro-ecological and climatic conditions, Ethiopia is endowed with a very large area of land, where soybean can be suitably produced, especially in rotation with maize. The land suitability analysis shows that soybean is the second among legumes in terms of land area that is moderately and highly suitable for its production in the country, with an estimated 42,067,700 (37.2%) ha of land

(According to EIAR (2017), soybean can be grown in altitudes ranging from 1250 to 2200 meters above sea level (m.a.s.l.); however, it performs well between 1300 and 1700 m.a.s.l. It can also be grown in an area receiving 450 to 1500 mm annual rainfall; however, to grow very well, and for optimum yields, soybean requires a minimum of 500 mm annual rainfall. Temperature ranging from 23- 25°C is reported to be optimum for soybean production; however, it performs well at warm temperature and medium relative humidity.

For strong breeding program of any crop such as soybean testing over diverse environment is very important to ensure that the selected genotypes have acceptable performance in variable environments within the target region (Ashraf *et al*., 2010). Effective interpretation and utilization of data in making selection decisions, however, remain a major challenge to researchers. According to Ashraf *et al*. (2010) there are two major tasks for researcher to determine whether the target region is homogeneous or should be divided into different mega environments; the second is to select superior cultivars for a given mega-environment on the basis of end product i.e. yields. Varietal adaptability to environmental fluctuations is important for the stabilization of crop production over both the regions and years. An information on GEI leads to successful evaluation of stable genotype, which could be used for general cultivation. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations; hence, the selection for superior genotypes based on yield per se at a single location in a year may be very effective. The study of GEI is crucial for indicating genotypes to each locality (Hamawaki *et al*., 2015). The recommendation of new soybean cultivars needs desirable characteristics such as pod per plant, plant height at maturity, high protein and oil, among others, together with high grain yield, production stability, and wide adaptation to diverse environments, whose variations can be found in regions where they are indicated (Polizel *et al.,* 2013).

Many investigators described the importance of GEI in stability analysis of soybean (Beaver and Johnson, 1981; Radi *et al*., 1993; Ablett *et al*., 1994; Al-Assily *et al*., 1996 and 2002). The Additive Main Effects and Multiplicative Interaction (AMMI) and GGE biplot models can be powerful tools for effective analysis and interpretation of multi environment data structure in breeding programs (Yan *et al.* 2000; Ebdon and Gauch 2002; Samonteet al. 2005). In Ethiopia the application of AMMI and site regression model GGE models for explaining and analyzing the performance of genotypes and the tested environments have been very frequent among plant breeder in recent years. Various studies have been conducted in Ethiopia to analyze the effects of GEI on soybean genotypes (Gurmu *et al*., 2009), Asfaw *et al*., 2009), but only a few studies use the GGE- bi-plot model.

The magnitude of GEI and investigate the stability of the aimed genotypes using different stability statistics. Therefore, the goal of the present study was

- To evaluate the GEI using AMMI and GGE-biplot analysis for grain yield of soybean genotypes and
- To identify stable soybean genotypes in the different agroecologies for breeding and variety testing purpose.
- To examine the usefulness of a stability model comparing with the two widely used models.

MATERIALS AND METHODS

The experiments were conducted at six different locations across Ethiopia *viz*., Dimtu, Jimma, Bako, Metu, Asosa and Pawe. These areas represent the highest potential and the main areas for soybean production in the country, with different edaphic and environmental conditions. The more detailed description biophysical description of the variation explored in the test environments is provided in Table 1.

The experiments in all locations were designed in a randomized completely design (RCBD) with three replications per environment under rain feed conditions. Sowing was done manually in rows when necessary. The experimental plot consisted of four ridges, 3m long and 60cm apart. The other agricultural practices were applied as recommended for each respective location. The soil preparation was done by one plowing and two harrowing right before grooving and fertilizing the soil. At maturity, the two middle ridges of each plot were harvested to determine the seed yield in kilograms per plot ($3.6m^2$). The experiments were harvested manually when plants reached the R8 stage, according to Fehr and Caviness (1977) scale, in both central lines of each plot, eliminating 0.5 m of each line edge. Subsequently, it has proceeded the soybean threshing and drying of grains (to 13% moisture). After drying, for determining the grain yield, the grains from each useful plot had their mass weighed and extrapolated to $kgha^{-1}$. The grain yield data were subjected to AMMI and GGE biplots analysis. All statistical analyses were conducted by PBTools, version 1.4. 2014. Biometrics and Breeding Informatics, PBGB Division, International Rice Research Institute, Los Baños, Laguna.

AMMI and GGE bi-plot analysis

The results of AMMI and GGE analysis are presented by analysis of variance and biplot graph.

2.1.1. The AMMI model is

$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{x} \lambda_k \sigma_{ik} \gamma_{jk} + \varepsilon_{ijr}$,

$Y_{ijr=}$Obserbation of the r^{th} replicate of the i^{th} genotype in the environment,

μ= the overall mean,

g_i= main effect of the genotype,

e_j= main effect of the j^{th} environment,
x=matrix rank$\{ge\}_{ij}$,
λ_k=the singular value for principal component *k*,
σ_{ik} = the eigen vector score for genotype i and component k,
γ_{jk}= the eigen vector score for environment *j* and componenet *k*,

AMMI Stability Value (ASV)

Since AMMI does not provide a quantitative measurement, it is necessary to quantify and rank genotypes and based on their yield (Purchase, 1997). AMMI Stability Value (ASV), length of genotype and environment markers of the origin in a two-dimensional plot of IPCA1 sores against IPCA2 scores was calculated according to Purchase *et al*. (1997) as:

$$\text{ASV} = \sqrt{[\frac{\text{IPCA1 Sum Squares}}{\text{IPCA2 Sum Squares}}(\text{IPCA1 Score})]^2 + [\text{IPCA2 Score}]^2}$$

Where: IPCA1 = interaction principal component axis 1; IPCA2 = interaction principal component, axis 2. According to Purchase (1997) genotypes with lower values of the ASV are considered to be more stable.

2.1.2. The GGE model is

$$Y_{ij} = \mu + e_{j\,+} \sum_{k=1}^{x} \lambda_k \sigma_{ik} \gamma_{jk} + \varepsilon_{ijr},$$

$Y_{ijr=}$Obserbation of the r^{th} replicate of the i^{th} genotype in the environment, μ= the overall mean,
λ_k=the singular value for principal component *k*,
$e_{j=}$ the mean effect of the j^{th} environment,
x=matrix rank$\{gge\}_{ij}$ when $\{gge\}_{ij}$=$g_i + ge_{ij}$
$\sigma_{ik=}$the eigen vector score for genotype *i* and componenet *k,* $\gamma_{jk=}$ the eigenvector score for environment *j* and component *k,* and ε_{ijr}=the error for the genotype *i* and environment *j* and replicate *r*.

RESULTS AND DISCUSSION

GGE biplot analysis

Performance of genotypes in a specific environment

Environment's vector is <90°; it is lower than average, if the angle is >90°; and it is near average, if the angle is about 90°. In this case, Choska was below average in nearly all environments except E3 and E4 whereas Choska was above average in all environments except in E5 (Figure.1).

The Which-won-where pattern

According to Yan *et al.*, 2002 the polygon view of GGE biplot indicates the best genotypes in each environment and group of environments. In this situation, the polygon is formed by connecting the signs of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. In this case, the polygon connects all the farthest genotypes and perpendicular lines divide the polygon into sectors. Sectors help to visualize the mega-environments. This means that winning genotypes for each sector are placed at the vertex. The pattern on the environment in the above biplot suggests that the existence of three different mega-environments (Figure 2). But this pattern may not be repeatable across years (Yan *et al*. 2000). To confirm the repeatability of the mega-environment result, there need to be multiyear data (Yan *et al*. 2005).

For studying the possible existence of different mega-environments in a region, visualization of "which -won-where" Pattern of the Meta environment trial is important as described by Yan *et al*, 2000,2001). The vertex genotypes in this investigation were Hang dou No-1 (G17), AFGAT (G10), SCS-1 (G20), 5002T (G1), Choska (G15) and Princhard (G22). This means that the vertex genotypes for each sector are the one that gave the highest yield for the environments that fall within that sector. Besides, it is evident from the GGE biplot in figure 2 that environmental groupings, which suggests the possible existence of different mega environments. Thus, based on the biplot analysis of six environments of the data. The highest yielding in the environment in five and two are AFGAT (G10). And in environment six and one AGS-7-1 (G24). The other vertex genotypes are Choska (G15), Prichard (G22) and Hang douNo-1 (G17) are poor performing in all the six environments.

Ideal test environments for selecting generally adapted genotypes

Within a single mega-environment, the ideal test environment should be most discriminating (informative) and also most representative of the target environment. Figure 3 defines an "ideal test environment", which is the center of the concentric circles. It is a point on the Average Environment Coordinate in the positive direction ("most representative") with a distance to the biplot origin equal to the longest vector of all environments ("most informative"). E2 (Bako) is closest to this point and is, therefore, best, whereas E5 and E4 were poorest for selecting cultivars adapted to the whole region. Note that additional years are required to confirm that a specific test location is "ideal".

Table 1. Brief description of the experimental environments

No.	Locations	Altitude (m.a.s.l*)	Geographic Coordinates (Latitude/ Longitude)	Annual Rain Fall(mm)	Temperature (0^c) Min. to Max.
1.	Asosa (E1)	1580	10°02'N 34°34'E	1130	15.9-29
2.	Bako (E2)	1590	9° 06 N,37° 09' E	1245	9-34.4
3.	Jimma (E4)	1753	7°40'9"N,36°47'6"E	1561	18.9-26.8
4.	Pawe (E6)	1120	11019'N,036024'E	1587	16.3-32.6
5.	Metu (E5)	1550	8°18′N ,35°35′E	1810	12.5-28.6
6.	Dimtu (E3)	1640	7°55′0″N,37°20′0″E	1601	12.5-26.5

Table 2. A list of soybean cultivars for six environments and their abbreviations that are used for the trials

Genotype Code	Strain Sub-Designation	Cultivar Name	Seed Source*	Genotype Code	Strain Sub-Designation	Cultivar Name	Seed Source*
G1	Mod PI 634193	5002T	AON	G13	Mod PI 559932	Ks3496	AON
G2	Mod PI 570668	Ciaric	AON	G14	-	Clarck-63k	Released
G3	Mod PI 633970	Ozark	AON	G15	Mod PI 533050	Choska	AON
G4	Mod PI 603953	Motte	AON	G16	Mod PI 594669	Liu yue mang	AON
G5	Mod PI 595081	Ks4895	AON	G17	Mod PI 594675	Huang dou No-1	AON
G6	Mod PI	UA4805	AON	G18	Mod PI 594675	Hs93-4118	AON
G7	Mod PI 560207	Delsoy 4710	AON	G19	Mod PI 614153	Croton 3.9	AON
G8	Mod PI 553051	Spry	AON	G20	-	SCS-1	Released
G9	Mod 561702	Harbar	AON	G21	Mod PI 639740	LDOO-3309	AON
G10	TGX-1892-10F	AFGAT	Released	G22	Mod PI 612157	Prichard	AON
G11	Mod PI 594675	Graham	AON	G23	Mod PI 633610	Desha	AON
G12	Mod PI 559932	Manokin	AON	G24	Hawassa-04	AGS-7-1	Released

Sources: EIAR/JARC *AON=Advanced Observation Nursery

Ranking of genotypes based on relative to the ideal genotypes

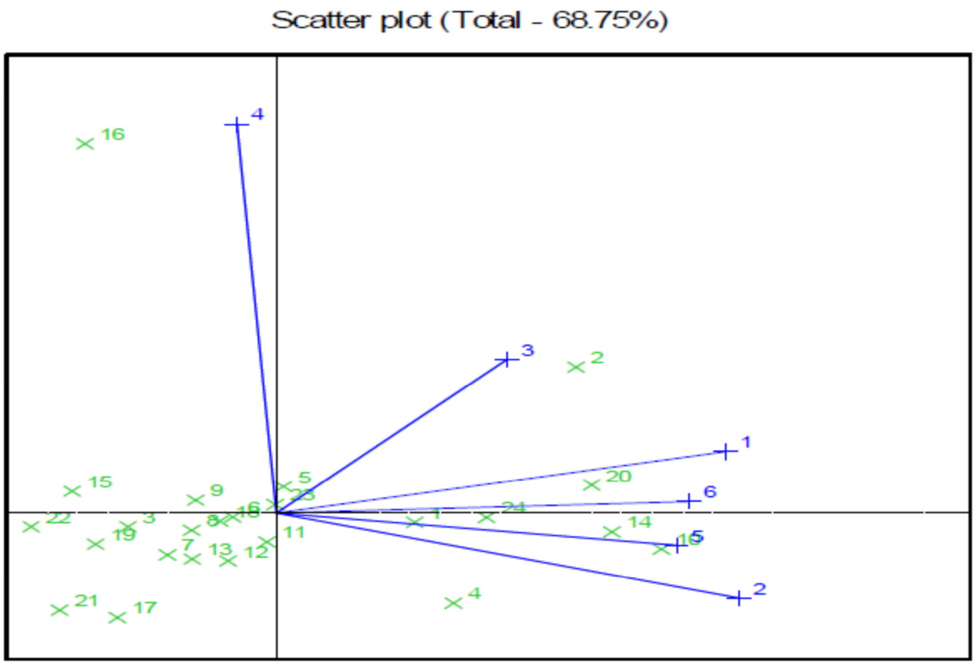
The ideal genotypes (the center of concentric circles) to be a point on AEA in the positive direction and has a vector length equals to the longest vector of the genotypes on the positive side of the AEA ("highest mean performance"). As a result, genotypes located closer to the "ideal genotypes" are more desirable than the others. Hence, the GGE biplots (Figure 4) shows that G10 is an ideal genotype, with other genotypes like G20 and G14 are desirable genotypes as they are closer to the ideal genotype on the bi-plot.

Relationships among test environments

As displayed in Figure 5 the lines that connect the environments to the biplot origin are called environment vectors, and the length of environmental vectors is proportional to their standard deviation, which measures the discriminating ability of the environments. At the same time the angle between the vectors of two environments is related to the correlation coefficient between them. According to Kroonenberg (1995) and Yan (2002) the cosine angle between the vectors of two environments approximates the correlation coefficient between them. Based on the angles of environment vectors, the six sites are grouped into three groups. Accordingly, group one includes Jimma and Dimtu; group two Asosa and Pawe, and group three Bako and Metu.

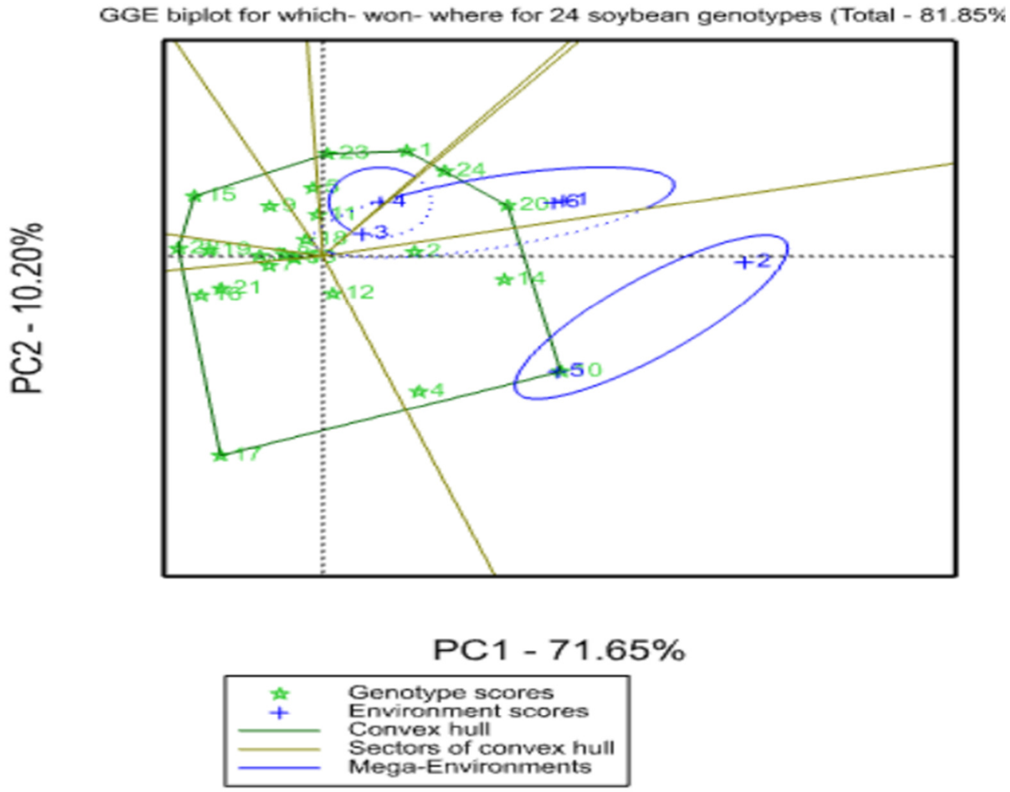
Comparison among all genotypes

The is the distance between two genotypes approximates



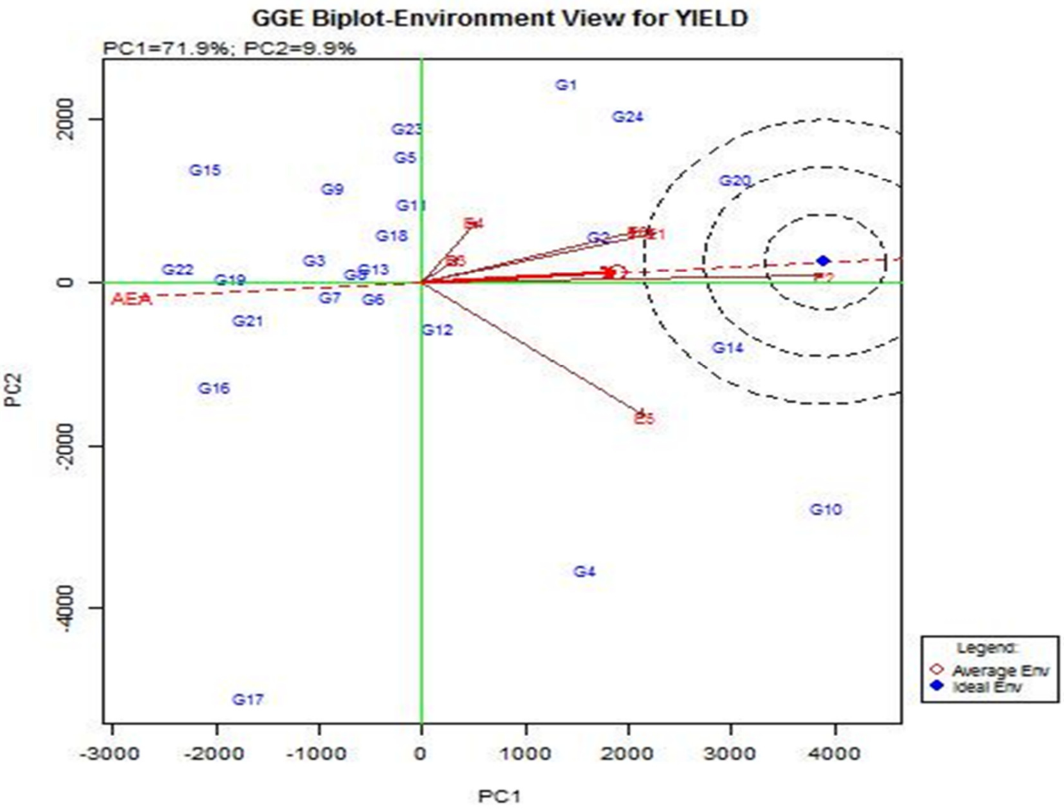
Performance of each genotype in each environment

Figure 1. The GGE biplot showing the performance of each genotype in each environment.



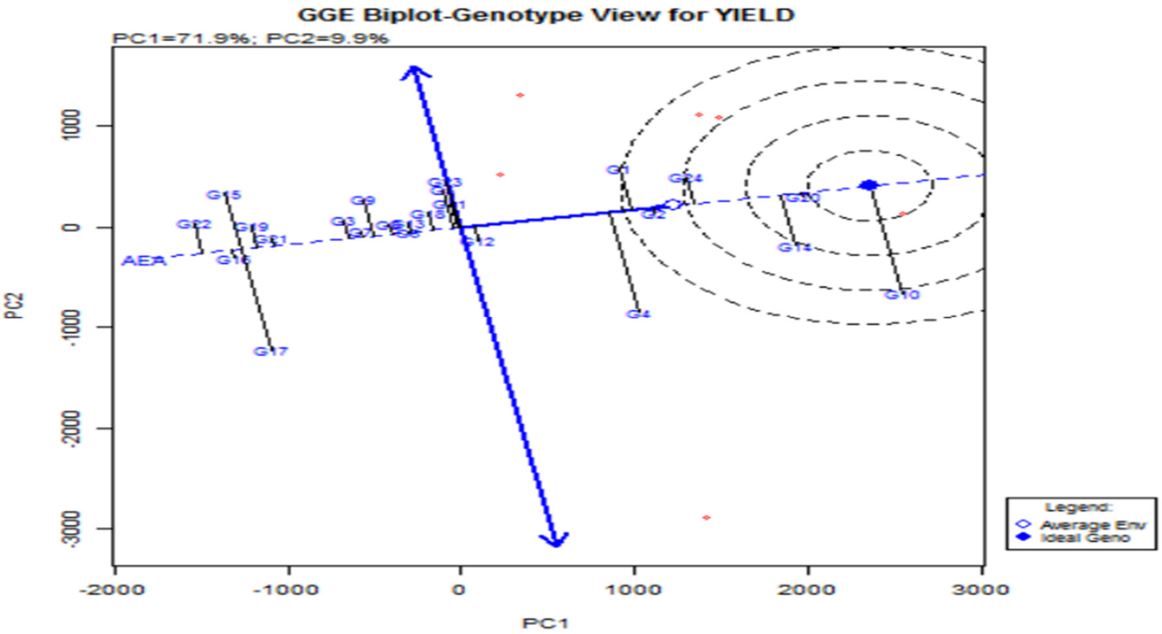
Which genotype won where?

Figure 2. “Which-won-where” or “Which is best for what’’ pattern of GGE biplot based on 24 soybean genotypes evaluated in six soybean agro-ecologies of Ethiopia.



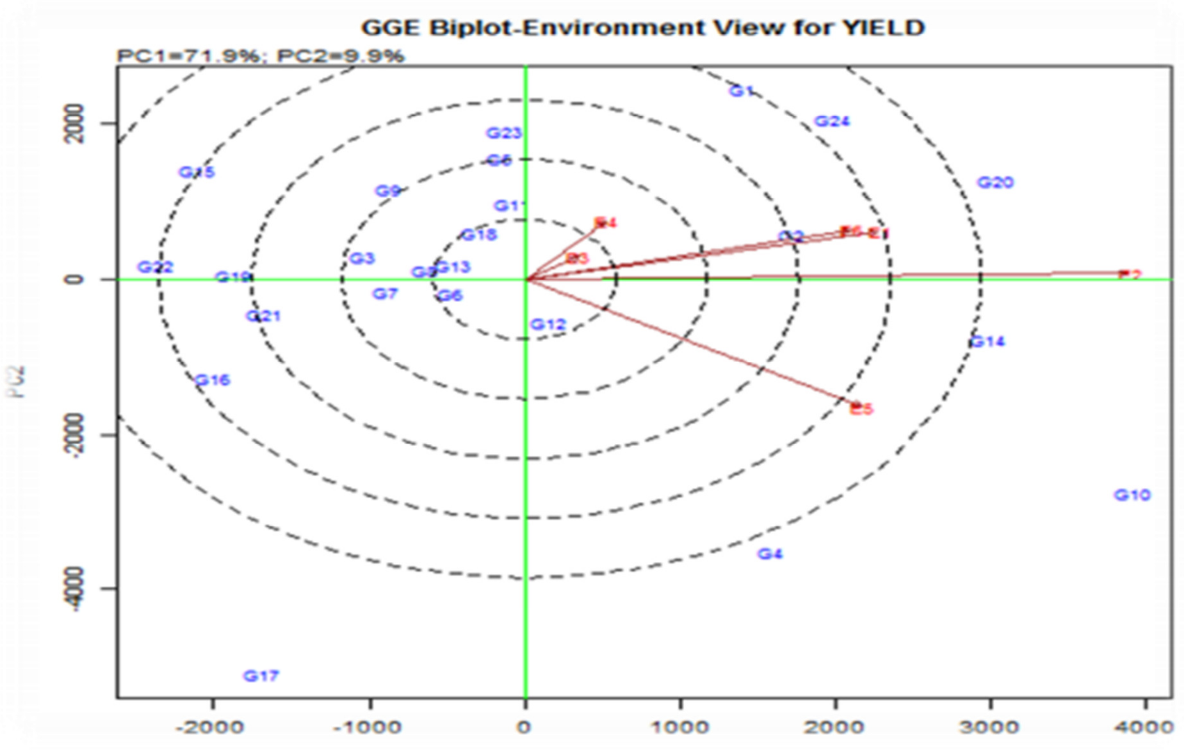
Ranking environments based on discriminating ability and representativeness

Figure 3. The discrimination and representatives view of the GGE biplot to rank test environments relative to the ideal environments.



Ranking genotypes based on both mean and stability

Figure 4. The average-environment coordination (AEC) view to rank genotypes relative to an ideal genotype.



Discrimitiveness vs. reperesentativeness of test environments

Figure 5.GGE biplots based on environment focused scaling for environments to show relationship among test environments in discriminating genotypes.

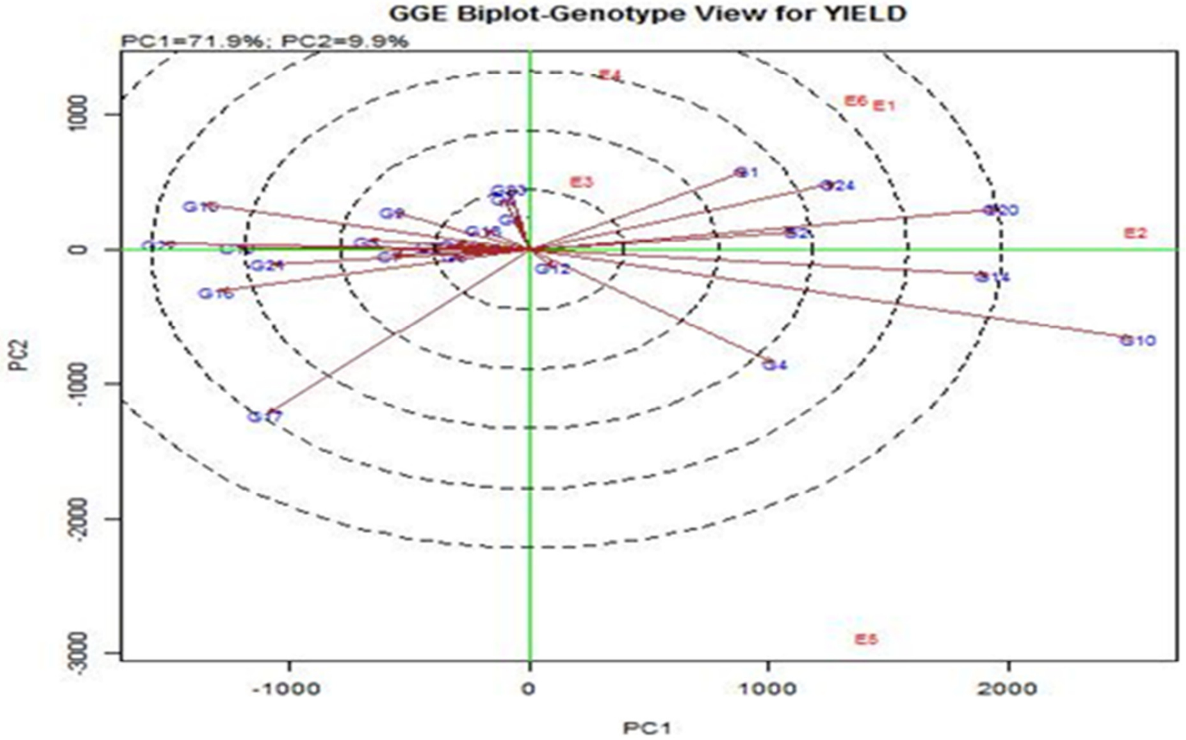
the Euclidean distance between them, which is a measure of the overall dissimilarity between them (Yan *et al*., 2006). In this case, Ciaric (G2) and SCS-1 (G20) are quite similar, whereas Hang douNo-1 (G17) and AFGAT (G10) are very different. This implies that the dissimilarity is because of the variation in mean yield and or interaction with the environments. In addition, the biplot origin represents a "virtual" genotype that assumes an average value in each of the environment. This "average" genotype has zero contributions to both G and GE (Yan *et al*.,2006) and inversely genotypes with larger vectors have large contributions to either G or GE or both. In this case Manokin (G12) and other genotypes in the smaller concentric circle are the average genotypes.

Additive Main Effects and Multiplicative Interactions (AMMI)

According to AMMI analysis for grain yield, the first two interaction principle components have taken the largest portions (70.34%) of the interaction sum squares with 50.3% and 20.04 and 27 and 25 degree of freedom respectively (Table 3). The AMMI model integrates the analysis of variance into a unified approach (Gauch, 1988; Gauch and Zobel, 1996). IPCA scores of genotypes in the analysis are an indication of the stability of a genotype over the environments (Guach and Zobel, 1997).

The combined analysis of variance (ANOVA) of twenty-four genotypes at six locations according to AMMI model 2 is shown in Table 3. The ANOVA showed that a highly significant ($P \leq 0.01$) between environments, genotypes and genotype by environment interaction (GEI) for grain yield. The IPCA 1 axis was very highly significant ($P \leq 0.001$) for grain yield, while IPCA 2 axis was significant ($P \leq .0.05$). IPCA 1 and IPCA 2 axes explained 50.30% and 20.04% of the total GEI, while the remaining 29.66% were shared between other IPCA's. This showed that AMMI model 2 was best suited because gave for this data set.

The AMMI model summarizes patterns and relationships of genotypes and environments. Figure 7(a). Shows the AMMI model 2 biplot of grain yield for six locations. The IPCA2 score plays a major role in GEI (Purchase, 1997), so they should be plotted against the IPCA1 scores to further explore the adaptations. Genotypes closer to zero or center of the figure are more stable Figure 7(a) indicates the IPCA1 and IPCA2 score for grain yield to further explore further adaptations. The further away from zero the IPCA score for the



Similarity among genotypes

Figure 6. The genotype vector views to show similarity among genotypes in their performances in their individual environments.

Table 3. Analysis of Variance of AMMI model for grain yield (Kg ha^{-1}) of 24 soybean genotypes.

				Sum Square Explained		GEI
Source of Variation	DF	SS	MS	% TT	%GEI	Cumulative (%)
Treatments	143	325088528	2273346***	77.38		
Genotypes	23	66486177	2890703***	15.83		
Environments	5	198793045	39758609***	47.32		
Reps within E	12	22104567	1842047***	5.26		
GEI	115	59809305	520081***	14.24		
IPCA1	27	30081895	1114144***		50.30	
IPCA2	25	11984468	479379*		20.04	70.33
Residuals	63	17742941	281634ns		29.67	
Error	276	72917426	264194			
Total	431	420110521	974734			

CV (%) =24.98 R^2=0.83

***P<0.001; *P<0.05; IPCA=Interaction Principle components axis term 1 to 2; DF=Degree of freedom; SS=Sum of Squares; MS=Mean Square, =Coefficient of variation; R=Coefficient determination.

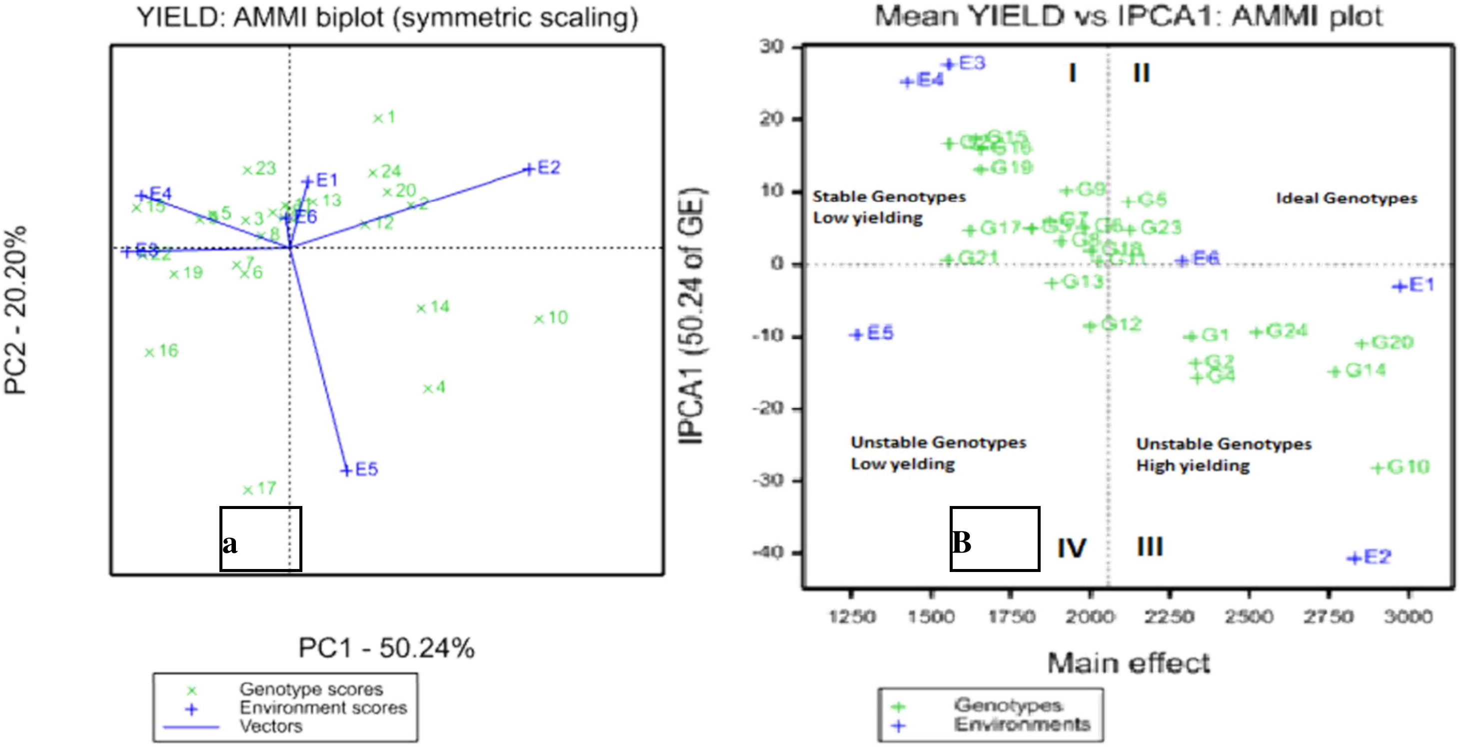


Figure 7(a). Biplots principle component analysis (PCA) vs mean yield (Kg ha^{-1}) for twenty-four soybean genotypes grown in six environments in 2015/2016 cropping season and (b)Biplots of principle components analysis (PCA) axis 2 vs axis 1 for yield.

environments is the more interaction the environment has with the genotypes, thus making difficult to choose genotypes for that environment.

In AMMI biplot 1 showing main effects means on the abscissa and principal component (IPCA) values as the ordinates, genotypes (environments) that appear almost on a perpendicular line have similar means and those that fall on the almost horizontal line have similar interaction patterns. Genotypes that group together have similar adaptation while environments which group together influences the genotypes in the same way. Genotypes (environments) with large IPCA1 scores (either positive or negative) have high interactions whereas genotypes (environments) with IPCA1 score near zero have small interactions.

Genotypes having a zero IPCA1 score are less influenced by the environments and adapted to all environments. Since IPCA1 scores of varieties Graham, LD00-3309, Hs93-4118, ks3496 and Spry were close to zero, they were most stable genotypes that across these environments (Figure 7(a)). However, the mean yield of genotype Spry was higher than genotype the remaining genotypes, hence it is more preferable since it had a mean yield above average, but the rest four genotypes have mean below average. In summary, a stable variety might not be the highest yielding. These results are in line with Asfaw *et al.* (2009).

The environments having a small score had small interaction effects indicating all genotypes performed well in these locations. Pawe (E6) was relatively close to zero than other locations, it was more stable. But its mean yield is third compared with the rest locations; it might not be the best location with respect to yield. Generally, genotypes and environments with IPCA1 scores of the same sign produce positive interaction effects, thus higher yield of the genotype at that particular location, whereas combination of the IPCA 1 scores of the opposite sign produce specific negative interactions. A genotype showing high positive interaction in an environment has the ability to exploit the agroecological and agro-management conditions of the specific environment and is therefore best suited to that

Table 4. The first and second IPCA, Grain Mean yield and various yield _stability statistics investigated in soybean genotypes over rain feed conditions.

Genot. ID	Genotypes	GM (Kgha^{-1})	Rank	IPCA1	IPCA2	ASV	Rank	YSI
G1	5002T	2319	7	-10.71	14.67	22.44	16	23
G2	Ciaric	2385	5	-14.42	6.57	23.78	17	22
G3	Ozark	1815	18	5.30	3.72	9.18	7	25
G4	Motte	2337	6	-15.66	-17.05	30.10	23	29
G5	ks4895	2121	8	8.63	3.88	14.22	11	19
G6	UA4805	1981	13	4.99	-3.08	8.49	6	19
G7	Delsoy 4710	1871	17	6.25	-1.72	10.05	8	25
G8	Spry	1909	15	3.24	1.62	5.39	3	18
G9	Harbar	1926	14	10.07	3.46	16.33	12	26
G10	AFGAT	2903	1	-28.11	-8.55	45.35	24	25
G11	Graham	2027	10	0.36	4.80	4.83	2	12
G12	Manokin	2000	12	-8.15	3.02	13.26	10	22
G13	ks3496	1880	16	-2.55	5.59	6.90	5	21
G14	Clarck-63k	2770	3	-14.54	-7.84	24.33	18	21
G15	Choska	1641	21	16.97	5.00	27.35	20	41
G16	Liu yuemang	1656	19	15.77	-12.34	27.87	21	40
G17	Hang dou No-1	1623	22	5.04	-28.54	29.63	22	44
G18	Hs93-4118	2003	11	2.17	4.44	5.61	4	15
G19	Croton 3.9	1656	20	13.20	-3.02	21.13	15	35
G20	SCS-1	2853	2	-11.07	6.55	18.72	14	16
G21	LD00-3309	1554	24	0.92	3.91	4.18	1	25
G22	Princhard	1558	23	16.52	-0.36	26.18	19	42
G23	Desha	2072	9	4.92	7.04	10.51	9	18
G24	AGS-7-1	2522	4	-9.16	8.20	16.67	13	17

NB:GM=Grain Mean; IPCA1= interaction principle component one; IPCA1= interaction principle component two; YSI=Yield Stability Index.

Table 5. Ranking of four AMMI selections per environment for grain yield (Kg ha^{-1}).

Number	Environment	Mean (Kg ha^{-1})	IPCA Score	Genotype Ranking 1st	2nd	3rd	4th
3	Dimtu	1557	28.09	G20	G5	G14	G24
4	Jima	1426	25.46	G20	G5	G24	G14
6	Pawe	2291	1.07	G20	G10	G14	G24
1	Asosa	2973	-5.28	G20	G10	G14	G24
5	Metu	1268	-9.13	G10	G14	G4	G17
2	Bako	2830	-40.22	G10	G20	G14	G2

environment. In this case, Choska, Prichard, Liu yuemang , and Croton 3.9 are suited for E4 (Jimma). While SCS-1is suited for E1 (Asosa).

AMM 2 biplot presents the spatial pattern of the first two IPC axes of the interaction effect corresponding to the genotypes and helps in the visual interpretation of the GEI pattern and identify genotypes or environments that exhibit low, medium, or high level of interaction effects (Sharma *et al.*, 1998). IPCA1 and IPCA2 of grain yield accounted for 50.30% and 20.04% of interaction respectively. The stability of a genotype or an environment is determined by the end point of its vector from the origin (0,0). Genotypes near the origin are non-sensitive to environmental interactive forces, hence may be considered stable ones and those distant from origin are sensitive and have large interactions. Genotypes Prichard, Spry, Delsoy 4710, Croton 3.9, and Manokin were closer to the origin than any of other genotypes, hence they are most stable (Figure.7b). In AMMI 2 biplot, the environment scores are joined to the origin by the site lines. Environments with short spokes (length of arrow lines) do not exert strong interactive forces. Those with long spokes (length of arrow lines) exert strong interaction. Metu (E5) and Bako (E2) having longer spokes exert high interaction while Asosa (E1), Pawe (E6), Dimtu (E3) and Jimma (E4) having shorter spokes produce a relative weak interaction.

The graph space Figure.7 (b) are divided into IV quadrant from lower yielding environments in quadrant I and IV to high yielding in quadrants II and III. In Addition, quadrant II considered as ideal environment. So, from the graph in Figure.7b, Asosa (E1), Bako (E2) and Pawe (E6), which is in quadrant II, are ideal environments, while quadrant II characterizes in high yielding environment with unstable genotypes, in this quadrant Metu (E5) is found. Similarly, in quadrant I characterized, stable genotypes and low yielding and in contrast quadrant IV unstable genotypes with the low yielding environment.

AMMI stability value (ASV)

The ASV measure was proposed by Purchase *et al.* (2000) to cope up the fact that the AMMI model does not make a provision for a quantitative stability measure. In this method, as described by Purchase (1997) was calculated for each genotype. Depending on this method, genotype with least ASV score is the stable, accordingly, genotype LD00-3309 followed by Graham and Spry in third place were the most stable respectively. While genotypes AFGAT (G10), Motte, Hang dou No-1, Liu yuemang and Choska were undesirable. This result also similar to the three genotypes grain mean yield rank. This method illustrated in Table 4 Shows the ASV for 24 genotypes compared with mean grain yield.

The greater the IPCA scores (Negative or Positive), the more specifically adapted a genotype is to certain environment. The closer the IPCA scores to zero, the more stable the genotype over the tested locations. The further away from zero the IPCA score for the environments is the more interaction the environment has with the genotypes, thus making difficult to choose genotypes for that environment.

Yield Stability Index (YSI)

Yield stability index incorporates both mean yield and stability in a single criterion. The minimum values of YSI desirable genotypes with high mean yield and stability.

AMMI Selections for the highest four yielding cultivars across six environments

The AMMI model selected four best genotypes for in each environment and illustrated in Table 5.

The genotype that appeared in the top four environments in at least six environments was Clarck-63k, which is followed by; SCS-1(five env.), AFGAT (four), AGS-7-1(four), Ks4895(two). The other cultivar, Hang douNo-1, Ciaric and Motte appeared only once.

CONCLUSIONS

From the present investigation, it is concluded that multiple methods were employed to analyze stability. Those methods provided a good understanding of the adaptation level of soybean genotypes across a diverse range of environments. The AMMI and GGE biplot analysis permitted estimation of interaction effect of a genotype in each environment and it helped to identify genotypes best suited for specific environments. GGE biplot analysis showed that the polygon view of a biplot is the best way to visualize the interaction models between genotypes and environments. The polygon views of the GGE biplot pointed out that there existed three possible mega environments. The first mega environment consisted of two environments (E3 and E4), the second mega environment consisted of two environments (E1 and E1) and the third with two environments (E5 and E2). In addition, the discriminating power vs. representativeness view of the GGE biplot has been an effective tool for test environments evaluation. Environment E2 were the most discriminating for grain yield of the tested soybean genotypes, whereas E5 and E4 were poorest for selecting cultivars adapted to the whole region. The results indicated that GGE and AMMI biplot are facilitated visual comparison and informative methods to detect genotypes stability and in the preferential genotypes recommendations.

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