

AMMI and GGE-biplot Analysis of Yield Performance and Stability of Soybean [*Glycine max* (L.) Merrill] Genotypes in Southern and Northwestern Ethiopia

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Abstract

The aim of this research was to examine the genotype–environment relationship for soybean genotype yield by employing AMMI and GGE biplot analysis and to identify stable genotypes in southwestern and Northwestern Ethiopia. Twenty-three introduced soybean genotypes, including two controls, were tested during 2020 and 2021 seasons, at four separate test sites. A simple lattice design was used to set up the experiment. Using additive main effects and multiplicative interactions (AMMIs) and genotype main effects and a genotype \times environment interaction (GGE), the adaptability and stability of the soybean genotypes were examined. Significant ($p < 0.01$) genotype, environmental, and genotype \times environment interaction effects were found through AMMI analysis. According to the analysis of variance, 56.9% of the soybean yield was explained by the environment, 6.3% by genotype differences, and 36.7% by the GE interaction. The overall yield variability of the soybean genotypes exhibited considerable variation in the first four PCAs. Genotypes 10 (Tgx-2010-3F), 16 (Tgx-2007-11F), and 17 (Tgx-2007-8F) could recommend to the tested environments because they were adaptive to the PW20, PW21, and AR20 environments according to the AMMI and GGE results. However, genotype 22 (Tgx-1989-19F) and genotype 5 (Tgx-1987-10F) were found to be relatively stable and adaptable.

Keywords: AMMI, GGE, Genotype, Stability, Soybean

Introduction

In the early 19th century, the soybean crop (*Glycine max* (L.) Merrill) was introduced by missionaries and is said to have originated in northern China. It is said to have arrived in Ethiopia in the 1950s. The average protein and oil contents of soybean are 42% and 20.5%, respectively (Tesfaye, *et al.*, 2018). Soybean is utilized for a number of applications, including soy food production, animal feed, alleviation of malnutrition, soil fertility improvement, and raw material for the processing sector (Hailegiorgis *et al.*, 2010).

In order to assess the performance stability of genotypes, varieties, or cultivars across each site, estimation of genotype interactions with various environments by GEI analysis is important (Lin *et al.*, 2010). The main objective of any plant

breeding program for variety development is to focus on the plant's growing environment. Towards the end of the variety development phase, breeding programs frequently carry out thorough genotype performance studies across locations and years (Asfaw *et al.*, 2009). In such type of multi-environment trials, genotype x environment interactions (GEI) are unavoidable (Ceccarelli *et al.*, 1995; Ceccarelli *et al.*, 2006).

Identifying high-yielding cultivars and locations that most closely replicate the target environment requires comparisons of numerous genotypes across various environments and/or years (Yan WeiKai and Hunt, 2002). Moreover, a highly productive prospective new cultivar should function consistently and be able to adapt to a range of situations. A genotype or cultivar is said to be stable if it is ranking constant across environments (Flores *et al.*, 1998). The environmental component (E), while frequently the largest component in studies of variance, is irrelevant to cultivar selection, and only G and GE must be taken into consideration concurrently for selection choices (Yan and Kang, 2002). By revealing how genotypes behave compared to one another in diverse contexts, stability analysis is helpful in describing genotypes (Pacheco *et al.*, 2015).

Increment of both the level of consumption per year and the population trigger high domestic soybean demand, thus, unable to be met fully soybean domestic demands. Hence, a key objective of soybean breeding in Ethiopia is increasing yields per unit area. (Derese *et al.* 2019). The goals of this study were to identify stable and suitable genotypes for Southern and Northwestern and similar agro-ecological areas in Ethiopia and evaluate the interaction effect of GEI on the grain yield of imported soybean genotypes using AMMI and GGE biplot analysis.

Materials and Method

Experimental materials

With two standard checks, the yield performance of about 23 soybean genotypes introduced from the International Institute of Tropical Agriculture (IITA) in Nigeria were evaluated as part of a National Variety Trial (NVT) at Pawe, Asosa, Jimma, and Areka/Sawla from 2020 to 2021.

Table 1. Soybean genotypes used in the experiment

Code	Designation	Source	Code	Designation	Source
1	Tgx-1990-55F	IITA	14	Tgx-1485-ID	IITA
2	Tgx-2011-3F	IITA	15	Tgx2008-2F	IITA
3	Tgx-1990-57F	IITA	16	Tgx-2007-11F	IITA
4	Tgx-1995-5F	IITA	17	TgX-2007-8F	IITA
5	Tgx-1987-10F	IITA	18	Tgx-2006-3F	IITA
6	Tgx-1935-10F	IITA	19	Tgx-2010-12F	IITA
7	TgX-1987-68F	IITA	20	Tgx-2010-11F	IITA
8	Tgx-2004-3F	IITA	21	Tgx-2008-4F	IITA
9	Tgx-1448-2F	IITA	22	Tgx-1989-19F	IITA
10	Tgx-2010-3F	IITA	23	Tgx-1990-78F	IITA
11	Tgx-2010-7F	IITA	24	Gishama (loc. check)	Released by PARC
12	Tgx-2010-15F	IITA	25	Pawe-3 (st. check)	Released by PARC
13	Tgx-2004-13F	IITA			

Where, Trt=treatment, loc. check=local check, st. check=standard check, IITA= Institute of International Tropical Agriculture, Nigeria and PARC= Pawe Agriculture Research Center.

Experimental organization and set up

The experiment was set up in five environments that are; Pawe, Jimma, Asossa, and Areka Agricultural Research Centers, during the crop seasons of 2020 and 2021. The treatment design was a randomized complete block design with three replications at each site in every year. The trial was conducted on a plots size of 4m*2.4m with four rows per plot throughout all trial sites and 60 cm and 5 cm spacing between rows and plants, respectively. The central two rows were harvested for grain yield measurement. Then, the grain yield was adjusted to 12.5% seed moisture before conversion to kilograms per hectare analysis (Malek *et al.*, 2014).

Analysis of the data

The GEA-R software was used for statistical analyses in accordance with previous methods (Pacheco *et al.*, 2015). The grain yield data were validated for normality test using the Levene test of homogeneity of error variance for each environment before undertaking the combined analysis of variance across environments.

To establish a combined ANOVA that treated genotypes as fixed factors and surroundings as random variables, the non-significant variance was first confirmed, and then the GGE biplot and AMMI methods were used.

The AMMI model often provides an agronomically meaningful interpretation of the data with the basic model:

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

where μ is the grand mean; g_i and e_j are the genotype and environmental deviations from the grand mean, respectively; Y_{ij} is the yield of the i th genotype ($i=1\dots,I$) in the j -th environment ($j=1\dots,J$); τ_n is the eigenvalue of the PC analysis axis n ; γ_{in} and δ_{jn} are the genotype and environmental principal component scores for axis n ; N is the number of principal components retained in the model; and " ε_{ij} is the error term" (Pacheco *et al.*, 2015).

Description of the study environments

Table 2. Descriptions of the study areas

No.	Location	Elev.(m.a.sl)	Long/latitude	Annual Rf(mm)	Soil type	Temp.
1	Asossa	-	10°02'N34°34'E	1130	Nitsoil	15.9-29 °c
2	Pawe	1000-1200	11°18'4N 36°24'E	1586	Clay	16.5-32.6 °c
3	Jimma	1754	7°40'N36°47'E	1572	Nitosol	11.6-26.3 °c
4	Sawla	1395	6°18'N36°53'E	-	-	18-25 °c

Where, "Elev." =elevation, "Rf" =rainfall, "Temp" =temperature

Source: Climate data were taken from the (National Meteorology Agency (NMA), 2021).

Results and Discussion

Yield performances of the soybean genotypes in the tested environments

Table 3 displays the yield and rankings of the soybean genotypes. The average grain yields (kg ha^{-1}) of the tested soybean genotypes ranged from 1272.6 to 2383.8 in PW20; 852.1-2380.1 in PW21; 341.7-1772.5 in JM20; 753.4-2701.4 in JM21; 853.4-3148 in AS20; 514.04-4216.4 in AS21; 2251.1-3955.2 in AR20; and 1075.5-1886.5 in AR21. Compared to those of the Gishama variety (check 1), the average grain yields of Tgx-2004-3F, Tgx-2008-2F, Tgx-2010-3F, and Tgx-1987-10F were 14.86%, 13.88%, 8.08%, and 7.38%, respectively, greater. The average grain yield (kg ha^{-1}) in eight environments varied from 1179.31 for JM20 to 3096.72 for AR20. The genotypes exhibited different grain yield rankings across environments, the G*E interaction crossover (qualitative type) has strong implications for breeding for a particular adaptation (Singh *et al.*, 1999) (Table 3).

Table 3. Mean grain yield (kg/ha⁻¹) of 25 soybean genotypes tested across eight environments

Genotype	Environments								Over all mean	Rank
	Pawe 2020	Pawe 2021	Jima 2020	Jima 2021	Asosa 2020	Asosa 2021	Sawla 2020	Sawla 2021		
Tgx-2004-3F	1593.08	1178.27	1401.74	1519.3	2139.08	4216.39	2780.71	1886.5	2089.38	1
Tgx-2008-2F	2383.75	2033.84	612.67	802.5	2056.4	3752.88	3545.2	1385	2071.53	2
Tgx-2010-3F	1843.98	1649.8	1505.74	1267.3	2464.3	1643.93	3824.15	1528.5	1965.96	3
Tgx-1987-10F	1782.17	1808.55	1594.73	2104.05	2150.97	1669.77	2980.58	1535	1953.23	4
Tgx-1990-78F	2087	2380.07	1073.06	1177.35	2374.23	1517.97	3548.61	1075.5	1904.22	5
Tgx-2010-15F	2302.05	1382.26	1395.8	1303.85	3148.47	1306.94	3088.04	1301.5	1903.61	6
Tgx-2010-11F	1950.35	1558.5	1625.79	2322.25	2138.41	1001.03	2656.56	1718.5	1871.42	7
Gishama	1964.2	1236.94	1074.57	1511.05	1733.9	1725.72	3670.53	1635.5	1819.05	8
Pawe-3	1680.99	1619.69	1772.47	2701.35	1588.8	1675.71	2251.06	1260.5	1818.82	9
Tgx-1990-57F	1798.33	1393.88	1312.2	1480.65	2165.24	1491.09	3386.28	1487.5	1814.39	10
Tgx-2004-13F	1799.31	1702.28	1532.59	2025.15	1462.71	1222.16	3290.92	1392.5	1803.45	11
Tgx-2008-4F	2340.72	1992.58	1341.96	1637.15	2464.31	775.81	2683.55	1110	1793.26	12
Tgx-2011-3F	1761.76	1110.51	1570.06	2415.65	2010.65	938.56	2804.9	1684.5	1787.07	13
Tgx-1995-5F	1947.91	2356.41	1673.09	1688.55	904.33	1362.97	3026.13	1290	1781.17	14
Tgx-2007-11F	2226.13	1879.44	831.05	753.35	2189.18	732.78	3955.18	1555.5	1765.33	15
Tgx-1990-55F	1753.96	1927.84	1306.85	1418.6	1919.18	514.04	3344.98	1679.5	1733.12	16
Tgx-1989-19F	2287.18	1691.91	987.48	1535.95	2214.89	1599.55	2363.85	1172.5	1731.66	17
TgX-2007-8F	2211.07	1715.34	707.66	969.9	1245.89	1406.54	3818.47	1355	1678.73	18
Tgx-2010-7F	2070.29	1330.24	1322.33	1466.4	1946.1	773.66	3223.88	1160	1661.61	19
TgX-1987-68F	2196.35	1031.83	1434.3	1419.3	853.36	1267.99	3048.86	1871.5	1640.43	20
Tgx-1448-2F	1702	1098.83	816.69	963.4	1903.03	2211.86	2972.04	1193.5	1607.67	21
Tgx-1485-ID	1732.52	1576.21	341.71	1033.35	1465.12	1581.17	3139.81	1765.5	1579.42	22
Tgx-1935-10F	1804.65	1040.63	505.31	857.9	1614.15	1827.65	2626.36	1453.5	1466.27	23
Tgx-2010-12F	1847.2	852.08	1020.61	1002.05	1338.78	1075.52	2838.67	1522.5	1437.18	24
Tgx-2006-3F	1272.66	1066.04	722.24	854.8	1419.82	1139.75	2548.56	1365.5	1298.67	25
Grand Mean	48339.6	38614	29482.7	36231.2	46911.3	38431.4	77417.8	36386	43976.7	

AMMI analysis

Table 4 displays the results of the combined analysis of variance and AMMI analysis. Differences in the environment, genotype, and their relationships are quite significant. The combined AMMI ANOVA revealed that the environment, which accounted for 56.9% of the overall (G + E +GEI) variance, and the G*E interaction, which captured 36.8% of the total sum square, had a considerable effect on soybean grain yield. The experiment was conducted in diverse edaphic environments, which resulted in changes in soybean grain production, as indicated by the experiment's highest variance and substantial environmental effects. Furthermore, the AMMI model's analysis of variance revealed that the first three PCAs (PCA1 to PCA3) were highly significant ($P < 0.01$).

In accordance with the AMMI results, the environmental variance was significant and outweighed by both genotypic and GEI variations. This finding suggested that the environment played a major role in the overall variance explained by the traits. Variation due to genotype was less than the variation due to environment because of the higher genotype*environment interaction, implying that differences among genotypes are the same across environments (Ochigbo *et al.*, 2016). The existence of the genotype-by-environment (G*E) interaction caused notable variation in grain yield performance across the soybean genotypes throughout the tested environments. As a result, stable genotypes for a particular environment could be generated. This result is consistent with many studies that have shown a significant interaction between soybean genotypes and their environment (Arega *et al.*, 2018; Bilate Daemo *et al.*, 2023).

Table 4. AMMI analysis of variance over eight environments for grain yield of soybean genotypes

Source	DF	Variation Explained (%)	Cumulative	Mean squares	F statistics
Environment	7	56.9	56.9	17521846	112.6**
Genotype	24	6.28	63.25	562977.2	3.62**
GEN* ENV	168	36.75	100	470895.3	3.03**
PC1	30	43.84	43.84	1127653	9.10**
PC2	28	25.28	69.13	696669.6	5.62**
PC3	26	14.45	83.57	428739.2	3.46**
PC4	24	7.55	91.13	242849	1.96*
Residuals	200	0	0	155558.9	

Where, GEN*ENV = Genotype by Environment and DF = Degrees of freedom

Pattern of which-won-where

The genotype (Figure 1) on the polygon's vertex displayed the maximum grain yield, and it was also found that this genotype performed the best in other environments (Yan, 2002). Genotype 20 (Tgx-2010-11F) and 2 (Tgx-2011-3F) at JIM20 and JIM21 environments; Genotype 16 (Tgx-2007-11F) at AR20, PW20,

and PW21 environments; and genotype 8 (Tgx-2004-3F) at ASO20 and AR21 environments were the best genotypes in terms of grain yield, similar to the results reported for genotypes far from the biplot origin by (Yan and Kang, 2002; Baxevanos, *et al.*, 2008; Bilate Daemo *et al.*, 2023) whereas genotypes on the vertex are environment specific (Bilate Daemo *et al.*, 2023).

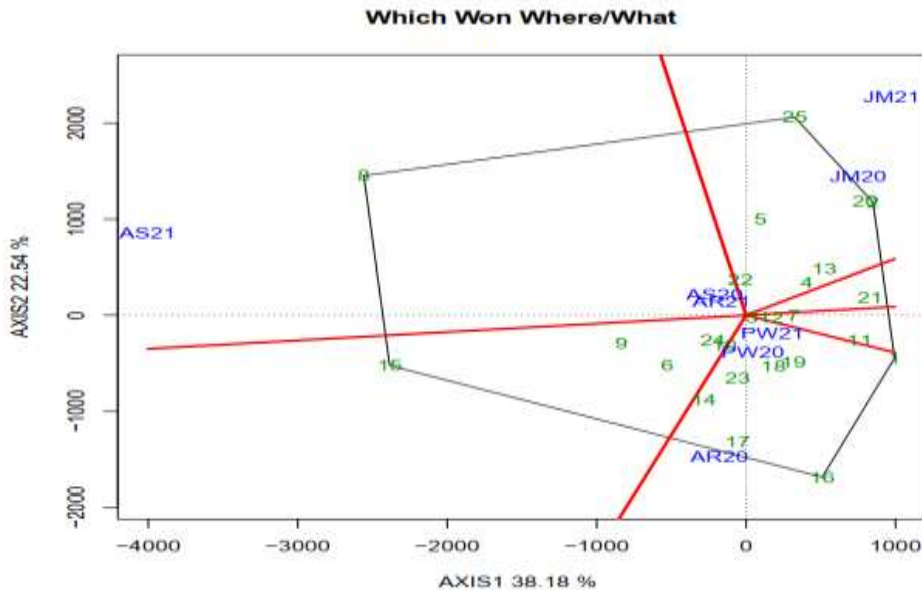


Figure 1: Genotype main effects (AXIS1) and the Genotype x Environment Interaction (GGEI) (AXIS2) biplots

Mean vs. Stability

Genotype 8 (Tgx-2004-3F) presented the greatest mean grain yield, followed by genotype 15 (Tgx-2008-2F) and genotype 25 (Pawe-3), while genotype 16 (Tgx-2007-11F) had the lowest yield.

The GGE biplot's average-environment coordination (AEC) is represented in Figure 3 and interpreted as the AEC abscissa, which has a single arrow indicating a higher mean yield across conditions, and the AEC ordinate is perpendicular to the AEC abscissa and passes through the plot origin, indicating more variability (poor stability) in either direction (Yan and Tinker, 2006). Thus, genotype 16 (Tgx-2007-11F) was highly unstable, but genotype 22 (Tgx-1989-19F) was relatively stable and adaptive.

According to the graph, the AS21 and JM21 environments were the most discriminating regarding genotypes with the longest vectors from the origin, followed by the JM20 and AR20 environments, which were moderately discriminating, and the AR21 and AS20 environments demonstrated the least discriminating regarding genotype differences (Figure 3). Less or non-

discriminating test conditions offer little insight into genotypes and therefore were not employed (Tadese, 2019).

Similarly, the biplot vector display shows relationships at acute, obtuse, and right angles, with positive, negative, and zero correlations between or among environments (Yan and Tinker, 2006).

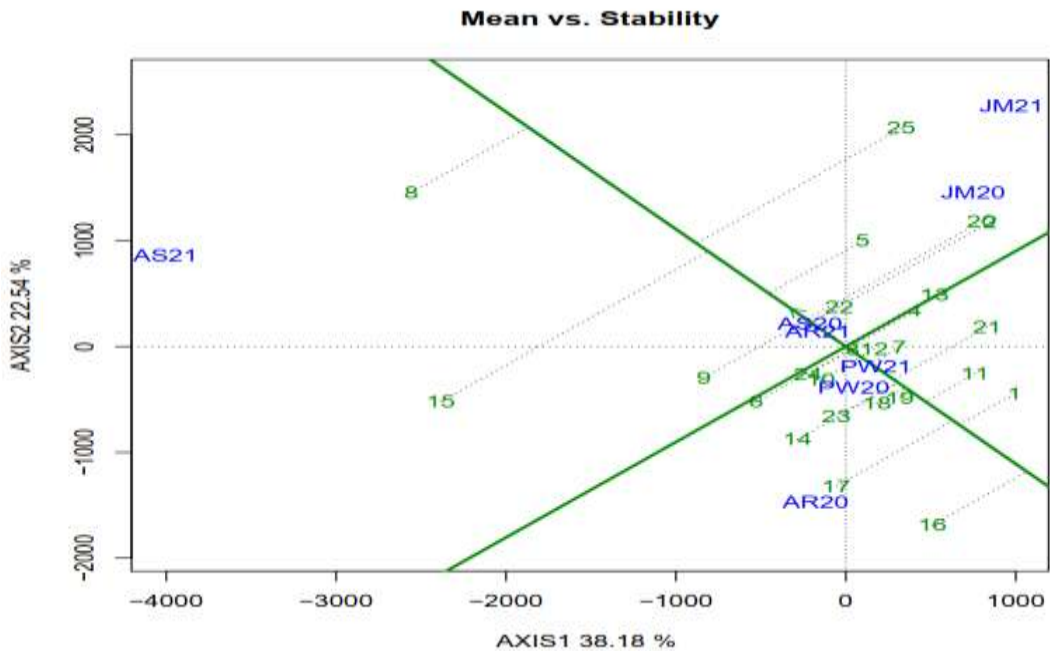


Figure 3: Outlooks of the GGE biplot using average environment coordination (AEC) based on environment-focused scaling for genotype mean performance and stability. Environments are represented by words in blue, and genotype codes are represented by green numbers.

Environmental relationships

The GGE biplot shown in Figure 3 revealed that the first and second main components together explained 69.12% of the total variance, demonstrating that this biplot could be utilized to disentangle interdependence across the environment. Additionally, a significant degree of genotype discrimination is conferred by the length of an environmental vector (Tadese, 2019).

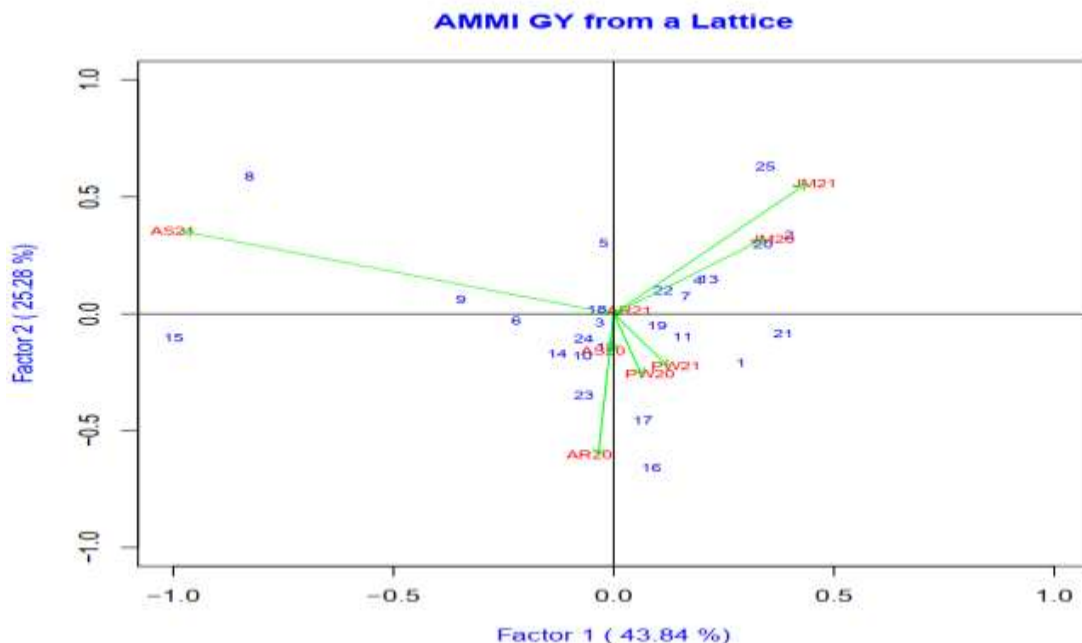


Figure 4: GGE biplot graph showing the relationships among test environments.

Conclusion

This study evaluated the yield performance and stability of soybean genotypes across representative national test locations. The tests were conducted under different climatic conditions, which resulted in different environmental means producing variation in soybean yield, as indicated by the large mean squares and significant effects on the environment. The GGE biplot and AMMI results showed that the best genotypes for grain yield were genotype 20 (Tgx-2010-11F) and genotype 2 (Tgx-2011-3F) in environments JIM20 and JIM21; genotype 16 (Tgx-2007-11F) in environments AR20, PW20, and PW21; and genotype 8 (Tgx-2004-3F) in environments ASO20 and AR21. These are the genotypes that are recommended for particular environments. However, genotype 8 (Tgx-2004-3F) had the highest mean grain yield across the environment, followed by genotypes 15 (Tgx-2008-2F) and 25 (Pawe-3). On the other hand, genotype 16 (Tgx-2007-11F) showed the lowest mean grain yield and was unstable. According to the statistical data, most of them were unable to show best grain yield performance (neither adaptable nor stable) throughout the testing locations; rather, they each displayed location-specific performances.

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