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Yield Stability and Genotype X Environment Interaction of Early Set Soybean Genotypes in Ethiopia

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ABSTRACT

The goal was to evaluate the genotype by environment interaction for grain yield productivity and identify genotypes stability in Ethiopia. Eighteen genotypes were assessed across 10 environments using a randomized complete block design under 3 replications. Adaptability and phenotypic stability of the genotypes were assessed using Additive main effects and multiplicative interaction (AMMI) and Genotype main effect and genotype x environment interaction (GGE). AMMI analyses elucidated highly significant ($P < 0.001$) genotype and environmental effects, as well as genotype by environment interaction regarding grain yield. In the exploration of variance, 78.8 % of the grain yield dissimilarity was demonstrated by the environment, 2.94 % of variations by genotypes, and 19.02 % by genotype by environment interaction. GGE-bi plot models illustrated that the ten environments used for this investigation belonged to three mega-environments. According to AMMI and the GGE results, G12, G10, G2, and G7 were low productive and stable genotypes, G14(TGx 1935-10E), and G16 (PC-4) high productive and unstable genotypes whereas G1, G8, G17(TGx 1988-5E) and G15 (TGx 1989-40F) were high yielder and stable genotypes. Therefore, in regard to most productivity in grain yield and relative stability, we recommended G17 (TGx 1988-5E), and G15 (TGx 1989-40F) for the test environments.

Keywords: AMMI, GxE, Genotype, Stability, Yield

Introduction

Soybean is a legume. It is an important origin of protein, oil, carbohydrates, minerals, vitamins, folic acid, fiber, isoflavones, and other nutrients for humans and animals. The increasing value of the crop has led to a huge expansion of production around the world (Sharmin *et al.,* 2021). Being the world's highly significant legume, soybean has a prominent place among recent agricultural commodities. It contributes to about 25 % of international edible oil production; two-thirds of the world's protein concentrate for livestock feeding and is a valuable ingredient in formulated feeds for poultry and fish. Furthermore, it is an important raw material for food and other industries (Maranna *et al.,* 2021).

In Ethiopia, soybeans are well suited to cultivation in lowland and low mountain areas. It is mainly grown in the northwest, southwest and west of the country (Fentahun, 2019). The soybean occupies about 75938.88 hectares of land of 188263 smallholder farmers, with an annual national production of 185522.23 tons and a productivity of 2.44 tons ha^{-1} (CSA, 2022). The same report shows that 123,205 private smallholders cultivated about 64,908.58 hectares of land and produced about 161,650.89 tons of soybeans in northwest Ethiopia, accounting for 65.4 %, 85.47 % and 87.13 % of the nationwide household, area, and production, respectively. The harvest share in Ethiopia is only 0.62 % of the area and 0.57 % of the production.

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Crop variety trial data analysis is made up three components primary: genotype evaluation, test location evaluation, and mega-environment analysis (Yan and Kang, 2003; Yan *et al.,* 2007; Yan, 2014). The first two aspects have received increasingly more emphasis because of increased awareness that a clear understanding of the target environment and the test locations is a requirement for effective and meaningful genotype evaluation (Yan, 2015). In a target environment, the effects of genotype x environment (GxE) interactions are thought to be a barrier to crop improvement and the temporal and spatial instability of crop yields. Temporal instability hurts farmers' income and, in the case of stable crops, contributes to food insecurity at the national and household levels (Begna, 2020). When the experiment is carried out at multiple locations for multiple seasons, the environmental component could be divided into years and locations, resulting in higher orders of genotype-environment interactions. Crop performance is influenced by the environment, the genotype, and the interaction of the two between genotype by environments (Mohebodini *et al.,* 2015).

More recently, the term GGE biplot was proposed and multiple biplot visualization techniques developed to tackle specific questions relative to genotype by environment data (Yan *et al*. 2000). The term GGE emphasizes the knowledge that G and GE are the two origins for variation that apply to genotype assessment and must be considered simultaneously for relevant genotype and test environment evaluation. Hence, the primary objective of this experiment was to identified high yielder and stable soybean genotype; determine the magnitude of the genotype by environment interaction, and the nature of the genotype by environment interaction.

2. Materials and Methods

2.1. Experimental Materials, Sites and Design

The materials were introduced from IITA Nigeria in 2015/16 cropping season for observation nursery trial and the remaining are our crossing recombinant inbreed lines which were crossed in 2013 (Table 1). The national variety trial was performed from 2019 to 2022 in a wider range of environments, which represents target early set production areas (Table 2). The trial was carried out in a randomized complete block design with three replications on a plot size of 2.4 x 4 m^2 (40 cm row and 5 cm between plant spacing). All the management practices were performed based on the recommendations.

Table 1: List of experimental materials.

Code	Genotype	Sources	Year	Code	Genotype	Sources	Year
G1	Line-1	PARC advanced line	2013	G10	Line-10	PARC advanced line	2013
G2	Line-2	PARC advanced line	2013	G11	Line-11	PARC advanced line	2013
G3	Line-3	PARC advanced line	2013	G12	Line-12	PARC advanced line	2013
G4	Line-4	PARC advanced line	2013	G13	Line-13	PARC advanced line	2013
G5	Line-5	PARC advanced line	2013	G14	TGx 1935-10E	IITA, Nigeria	2015
G6	Line-6	PARC advanced line	2013	G15	TGx 1989-40F	IITA, Nigeria	2015
G7	Line-7	PARC advanced line	2013	G16	PC-4	China	2015
G8	Line-8	PARC advanced line	2013	G17	TGx 1988-5E	IITA, Nigeria	2015
G9	Line-9	PARC advanced line	2013	G18	TGx 1990-55FP	ADL. TGx 1990-55F	2015

Where: ADL= Lines advanced from TGx 1990-55F, PARC= Pawe Agricultural Research Center

Table 2: Description of experimental sites.

S.No.	Location	Altitude (m. a. s. l)	Latitude	Longitude	Rainfall(mm)
1	Pawe	1120	11º 06'N	36º 24'E	1179.27
2	Assosa	1650	10º 2.92' N	34º 33.8'E	-
3	Humera	609	14º 15'N	36º 37'E	620
4	Kobo	1468	12°09′N	39°38′E	410-820
5	Metema	767	12º 46'N	36º 24'E	700-900

2.2. Statistical Analysis

The data recorded on grain yield were statistically analyzed by META-R (2016) version 6.0 for analysis of variance (Alvarado *et al.,* 2016), GEAR, and Breeding View software was used GGE biplot

analysis. For finding out mean differences among the replications, Fisher's least significant difference (LSD) test at the 5 % level of significance was applied. The basic model to analysis of AMMI is:

$$Yij = \mu + gi + ej + \sum_{n=0}^{N} \tau n\, \gamma\, in\, \delta jn + \varepsilon ij$$

Where: Yij is the yield of the i-th genotype (i=1..., I) in the j-th environment (j=1..., J); μ is the grand mean; gi and ej are the genotype and environment deviations from the grand mean, respectively, τn is the eigenvalue of the PC analysis axis n; γin and δjn are the genotype and environment principal components scores for axis n; N is the number of principal components retained in the model and εij is the error term.

3. Results and Discussion

Table 4 presents the combined analysis of variance across environments using the AMMI model, while Table 3 presents the means of the individual as well as combined environment analysis for grain yield. The findings demonstrated that there was a highly significant difference ($P < 0.01$) between environments, and genotype by environment interaction, and that the sum of squares for the environments was higher than the sum of squares for genotype and environment x genotype. Therefore, this leads to further analysis and an investigation into the stability of the genotype-environment interaction.

Regarding grain yield, environmental effects accounted for 78.04 percent of the total variation, while genotype and GE interaction effects were responsible for 2.94 % and 19.02 % of the variation, respectively, which is conceded with the earlier findings that in typical multi-environment trials, G and GE each account for roughly 10 % of the total yield variation, while E accounts for 80 % of the variation (Gauch and Zobel, 1996; Yan *et al.,* 2000). The fact that the mean squares of the environment were so large and highly significant, which implies that the environments were diverse, with a large amount of variance in the environmental means accounting for most of the variation in grain yield. This shows how dissimilar the test environments were from one another. 70.69 percent of the total interaction variations were explained by the first two PCs based on the interaction sum of squares (Table 4).

3.1 Genotypes mean performance across environment

Based on results presented in Table 3, the genotype average performances were varied from 1192.65 kg ha^{-1} for Kobo to 3891.46 kg ha^{-1} for Metema-2. The environments, Pawe-2, Kobo, and Pawe-22 were low yielding environments as compare the rest, while Humera, Metema, Metema-22, Pawe-3, and Pawe were presented intermediate yielding environments in this study. Whereas high yielded environments were Metema-2, and Assosa-22. The high yielding genotypes were G16 5062.88 at Assosa-22, G14 4350.33 at Metema-2 and 4128.35 Metema, and G15 (Tgx-1989-40F) 4197 kg ha^{-1} at Metema-2. The mean grain yield of genotypes across 10 environments ranged from 1878.3 kg ha^{-1} G11 (Line-11) to 2575.1 G15 (Tgx-1989-40F). For each genotype, the mean grain yield average across all locations (seasons) was 2105.26 kg ha^{-1}. There were no significant differences in the combined mean performance of grain yield across genotypes, except for genotype G15 (Tgx-1989-40F), which has a high yield and is comparatively stable when compared to the other genotypes (Table 2; Fig 1). This genotype G15 (Tgx-1989-40F) was ranked first at Pawe, and Pawe-2, 2nd at Pawe-3, 3rd at Metema-2, 4th at Kobo and Metema, 5th at Assosa-22 and 6th at Metema-22 environments in yield performance. G15 (Tgx-1989-40F), G16 (PC-4), G14 (Tgx-1935-10E), and G17 (Tgx-1988-5E) were placed first, second, third, and fourth, respectively, in terms of overall yield performance ranking.

3.2. Mean yield performance and genotype stability

Based on the mean yield and genotype stability, an average tester coordinate (ATC or AEC) can be found at (Fig. 1). The average environment, denoted by the average PC1 and PC2 scores across all environments, is marked by the bi-plot origin and the ATC x-axis. The ATC y-axis is perpendicular to the ATC x-axis and passes through the plot origin. The projections of the genotypes' markers to the ATC x-axis approximate the genotypes average yield (Yan, 2001). As a result, genotype G11 had the lowest average yield while genotype G15 had the highest. The cultivars are ranked according to average yield using the lines parallel to the average tester coordinate (ATC y-axis). The projection of the genotypes onto the ATC y-axis serves as a proxy for genotype stability. A genotype is less stable the

Table 3: Genotype mean yield performance across 10 environments from 2019 to 2022.

Genotypes	Assosa-22	Humera	Kobo	Metema	Metema-2	Metema-22	Pawe-2	Pawe-22	Pawe-3	Pawe	Mean
G1	2940.68	1975.26	896.96	1928.21	3639.67	2997.46	1686.22	1683.4	1525.63	2135.86	2140.94
G2	2853.5	1985.03	640.04	2421.23	3833	2789.79	955.84	980.1	1410.55	1837.49	1970.66
G3	3558.15	2048.18	1231.86	2014.72	3687	3082.32	889.19	1638.32	1105.37	912.19	2016.73
G4	2979.92	1825.95	738.64	1782.37	4189.67	2919.63	1407.68	1091.04	1572.21	1930.01	2043.71
G5	2542.71	2057.51	1270.42	2212.51	3739	2888.9	1172.26	1804.34	1459.6	1718.59	2086.58
G6	2577.48	1209.85	1487.01	1035.61	3548.33	3007.95	1510.26	1558.38	1933.74	2260.97	2012.96
G7	2947.24	1450.31	1848.05	1862.25	3950.33	2884.13	1269.69	747.12	1674.81	2007.25	2064.12
G8	3087.35	2085.29	1370.79	2211.13	4591	1816.77	1468.66	822.3	1633.98	1671.56	2075.88
G9	2732.02	1441.19	1602.9	1303.1	3477.33	3494.32	1350.99	1771.51	1760.29	1951.54	2088.52
G10	3476.2	1388.67	902.59	1364.59	3807	2974.55	1467.39	1138.06	1434.42	1971.1	1992.46
G11	2635.22	1235.68	1178.29	1031.85	3842.33	2790.92	1444.29	1285.35	1603.45	1735.6	1878.3
G12	2778.62	1778.21	1288.92	2117.98	3953.33	2588.57	1005.64	1204.83	1609.1	1559.78	1988.5
G13	2522.24	1242.84	1328.75	940.01	3857.67	2560.08	1543.77	1452.35	1835.46	2117.29	1940.04
G14	4128.35	2520.83	1262.13	3423.86	4350.33	2563.97	955.38	797.7	1036.97	1906.95	2294.65
G15	3463.61	1771.27	1488	3120.52	4197	2956.4	2092.37	1595.98	2398.51	2667.3	2575.1
G16	5062.88	2551.22	818.3	3388.45	4093	2459.36	1056.47	1075.15	1071.19	1841.49	2341.75
G17	3138.13	1999.13	495.37	2286.66	3772	2657.78	1624.69	1837.27	2527.5	2397.37	2273.59
G18	3314.65	1840.06	1618.59	3406.86	3518.33	2348.33	1081.99	532.85	1372.66	2067.91	2110.22
Mean	3152.16	1800.36	1192.65	2102.88	3891.46	2765.62	1332.38	1278.67	1609.19	1927.24	2105.26
LSD (0.05%)	619.33	619.33	494.37	650.29	413.78	494.49	353.12	572.45	292.81	326.12	215.32
CV (%)	12.71	12.71	30.16	19.47	10.57	17.84	17.73	34.92	11.38	10.78	17.86
Genotype Variance	351722.58**	94112.56*	94197.82*	609688.20**	32787.98	46590.72	79942.85**	98412.14*	146358.39**	121792.68**	8093.21
Residual Variance	160497.74	211565.5	129412.9	167664.21	169059.7	243547.2	55826.03	199398.54	33515.2	43194.78	141368.18
Environment Variance											780568.10**
Genotype x environment (GEI)											159467.38**

Note:- the number in the sufices indicated the years when the experiment performed; Assosa-22=2022, Humera=2019, Pawe= 2019, Metema=2019, Metema-2= 2020, Metema-22=2022, Pawe-2= 2020, Pawe-3= 2021, and Pawe-22=2022

longer its projection is in absolute terms. Consequently, the genotypes G12, G10, G2, G7, and G4 were the most stable and low yielders, performing below average, while G16 and G14 were the third and fourth highest yielders and least stable. Conversely, the genotypes G1, G8, and G15 demonstrated a high level of stability and yield exhibiting performances that exceeded the average mean (Fig 1).

Table 4: AMMI analysis of variance

	DF	SS	MS	PORCENT	PORCEN AC	F	PROBF
ENV	9	389168452.5	43240939.16	78.04	78.04	258.15	0
GEN	17	14663633.33	862566.67	2.94	80.98	5.15	0
ENV*GEN	153	94824857.8	619770.31	19.02	100	3.70	0
PC1	25	54681361.42	2187254.46	57.67	57.67	13.11	0
PC2	23	12344529.51	536718.67	13.02	70.68	3.22	0
PC3	21	9654880.17	459756.20	10.18	80.87	2.76	0.0001
PC4	19	7472206.62	393274.03	7.88	88.75	2.36	0.0012
PC5	17	5947323.79	349842.58	6.27	95.02	2.10	0.0069
PC6	15	2440804.57	162720.31	2.57	97.59	0.98	0.48
PC7	13	1191828.03	91679.08	1.26	98.85	0.55	0.89
PC8	11	802814.07	72983.10	0.85	99.70	0.44	0.94
PC9	9	289109.64	32123.29	0.31	100	0.19	0.995
PC10	7	0	0	0	100	0	1
Residuals	360	60302431.23	167506.7534	0	0		

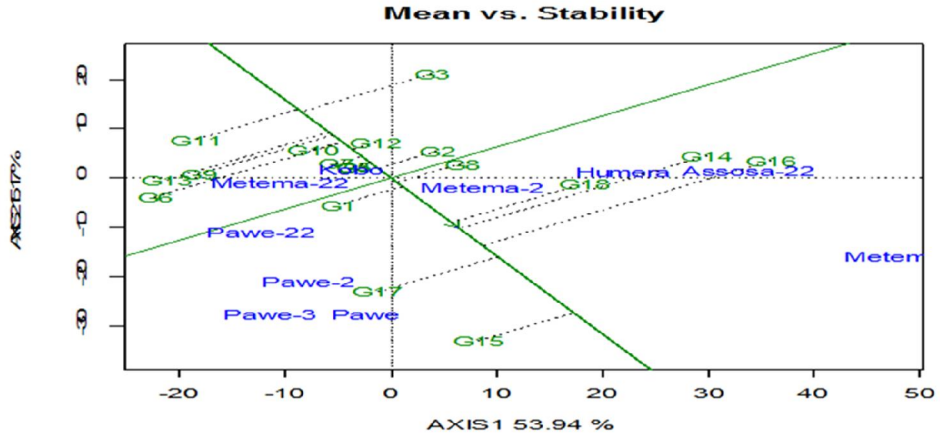

Fig. 1: GGE biplot indicating ranking of 18 soybean genotypes against mean versus stability

3.2 Best genotype selection for each environment

Fig. 2 is present the which, won where/ what view of GGE biplot for soybean grain yield in 2019–2022 at 10 environments. The genotypes with the highest or lowest performance in one or more environments were those found on the polygon's vertices (Yan and Thinker, 2006). The biplot was divided into five sectors, delimited by the lines perpendicular to each side of the polygon. The 10 environments fell into three of the five sectors. For locations within a sector, the nominal, the best performer's genotype is at the vertex. G15 and G6 were the wining genotypes on three environments, whereas G16 was the winning genotype at four environments. The best performer's genotype and the corresponding environments in Fig. 2 were summarized as: Metema-2, Humera, Metema, and Assosa-22 the wining genotype was G16; Pawe, Pawe-2, and Pawe-3 the winner genotype was G15; and Kobo, Pawe-22, and Metema-22 the winner genotype was G6.

3.3. Discrimination of genotypes and environmental representativeness

GGE bi-plot enables the evaluation of discriminative genotypes and representative abilities of an environment. A GGE bi-plot based on the 2019-2022 yield data is depicted in Fig. 3. The bi-plot explained 69.11 % of the total variation. This result is consistent with the results reported in the previous study (Amogne *et al.,* 2023). A test location that is highly representative of a target mega-environment

in all or most environments can be used as a core test location. However, the degree of representativeness of test locations used in multiple location trials should have varied (Yan, 2014).

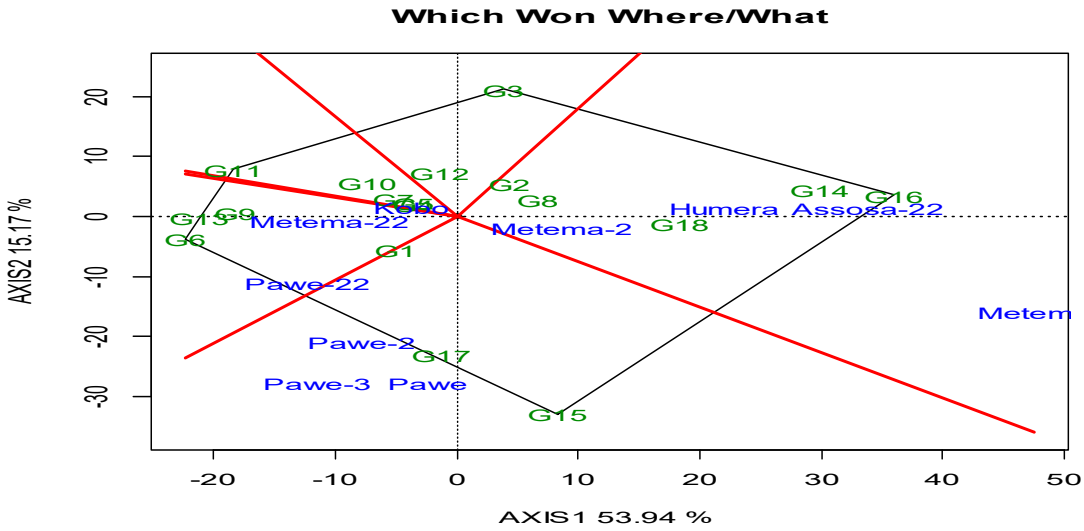

Fig. 2: Polygon views of the GGE biplot based on symmetrical scaling for which won where pattern for 18 soybean Genotypes under 10 environments

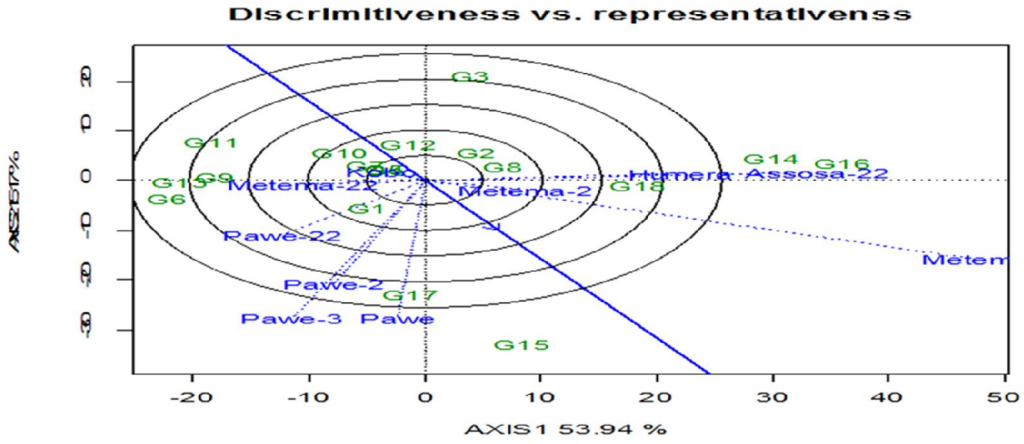

Fig. 3: GGE biplot representing discriminating ability of soybean genotypes and representativeness of test environments

Environment points with greater vector length and with acute angle are more discriminative (Yan, 2001). Environment Metema, Assosa-22, Pawe-3 and Pawe had the longest vector length and were the more discriminative environments. Kobo, Metema-2, Metema-22, and Pawe-22 were represented by shortest vector, and had least discriminative ability. It means that all genotypes performed similarly and provided little or no information about the genotype differences. Hence, they are not desirable for genotype evaluation. About discriminating, Kobo was the least discriminative location, whereas Metema was the most discriminative environment. Therefore, Metema is an ideal environment to select superior genotypes for yield performance. Test locations for use in multiplication trials, however, should have varying degrees of representativeness (Yan, 2014). Regarding representativeness, Pawe and Metema are more discriminating genotypes and representative of environments. While Assosa-22 and Pawe-3 were relatively discriminating genotypes, they were none representative environments, which means they are useful for selecting specifically adapted genotypes and serve for discarding unstable genotypes since the target environments were divided into five mega-environments (Fig. 2).

3.3 Genotype ranking

Ranking genotypes relative to the ideal genotype: An ideal genotype is defined as one that is the highest yielding across test environments and is stable in performance. In Fig. 4, the hypothetical ideal genotype is shown as a small circle on the axis of average genotype yield. To use the ideal genotype as the measurement center, concentric circles were drawn in the bi-plot to graphically determine the distance between the test genotypes and the ideal one. According to the GGE biplot, a genotype that is located at the center of the circles or is the genotype closest to the hypothetical genotype is considered a superior genotype with high grain yield and good yield stability. G15 was the closest to the ideal genotype and therefore identified as the best, and G17 and G18 were the second and third order of desirability soybean genotypes. G11 and G3 were positioned far away from the ideal genotypes; therefore, they are not an ideal genotype in this study.

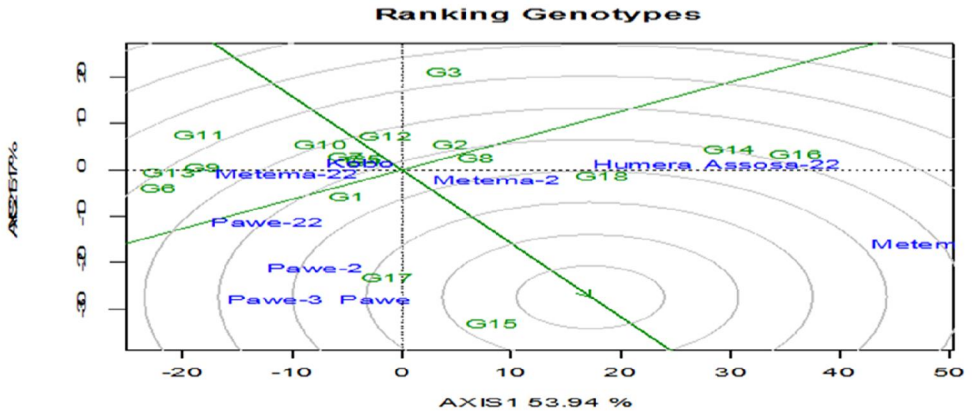

Fig. 4: GGE-biplot based on genotype focused scaling for comparison of the genotypes with the ideal genotype. Grean and blue stand for genotypes and environments, respectively

4. Conclusions

Genotype x environmental interaction is a very crucial role to lower the genotype means in various environments. Breeders must continuously work on this task due to the fluctuating environmental conditions over time and across different locations. It serves as a gauge of how adaptable genotypes are to the expression of phenotypes in various environments. For estimating variance components associated with various sources of variation, such as genotypes, environment, and GxE, in multi-environment trials, combined analysis of variance is essential. The result of the present study revealed very high variation in grain yield across environments. From the 10 test environments, three distinct mega-environments were identified. The first mega environment consists of three locations (seasons) Kobo, Metema-22, and Pawe-22 the winning genotype was G6, 2nd Pawe, Pawe-3, and Pawe with a winning genotype was G17 and G15, and the third mega environment was consisting of four environments Metema-2, Metema, Assossa-22, and Humera with the winning genotype G16. According to AMMI and the GGE results, G12, G10, G2, and G7 were low productive and stable genotypes, G14(TGx 1935-10E), and G16 (PC-4) high productive and unstable genotypes whereas G1, G8, G17(TGx 1988-5E) and G15 (TGx 1989-40F) were high yielder and stable genotypes. Hence, in regarded most productivity in grain yield and relative stability, we recommended G17 (TGx 1988-5E), and G15 (TGx 1989-40F) for the test environments.

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