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Genotype by Environment Interaction and Grain Yield Stability Analysis of Medium Set Soybean (Glycine max (L.) Merrill) Genotypes in Parts of Western Oromia

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Abstract

The present study was aimed to identify and release stable, high yielding and medium maturing soybean varieties with better agronomic performance in parts of western Oromia. To this end, 13 soybean genotypes including the standard check, Billo, were evaluated at three locations (Bako, Uke and Billo) for two consecutive main cropping seasons (2020- 2021). The experiment was laid down in Randomized Complete Block Design in three replications. Additive Main Effect and Multiplicative Interaction (AMMI), Genotype, and Genotype by environment (GGE) interaction biplot and regression analysis were computed to identify stable genotypes across environments. The environment, genotype and genotype by environment interaction (GEI) effects were highly significant (p<0.001) based on combined analysis of variance and additive main and multiplication interaction (AMMI) models. The three models revealed similar result in that G7, G1 and G5 were stable and widely adapted genotypes. However, the genotypes G9, G10 and G12 had adapted low yielding environments. Hence, G7 followed by G1 was relatively stable and high yielding genotypes thus those genotypes were identified as candidate genotypes and recommended for further evaluation under variety verification trail at parts of western Oromia.

Keywords: AMMI; GGE biplot; Regression; Stability

Introduction

Soybean (Glycine max (L.) Merrill) is an important legume as good sources of inexpensive protein (40 %) and vegetable oil (26 %) worldwide (Pratap et al., 2012). It can be used directly for food in the household, or processed for soy-milk, cooking oil and a range of other products, including infant weaning food. The poultry industry also uses soybean for feed production. Soybean grain often has a good market demand. The crop residues are also rich in protein and are good feed for livestock or form a good basis for compost manure. The largest global oilseed crop production goes to soybean (53%), followed by rapeseed (15%), cottonseed (10%) and peanut (9%) (Pratap et al., 2012) [1].

It is used as food, nutritious animal feed and improves soil fertility through nitrogen fixation when used in crop rotation with cereal crops (Pratap et al., 2012). In the last five years soybean production in Ethiopia showed an increment, from 90,000 tons in 2015 to 126,000 tons in 2019 (FAO, 2019). The productivity of soybean in Ethiopia is 2.3 ton ha-1 and higher as compared to African average productivity (1.3ton ha-1), but below the world average (2.8 ton ha-1) in 2019 (FAO, 2019) [2].

The performance of a genotype is dependent on the genetic potential of the variety, the environment where the variety is grown, and the interaction between the genotype and the environment (Yan, 2001; Yan and Hunt, 2001). Breeders evaluate different genotypes across locations in order to develop high yielding, adaptable and stable cultivars over the testing environments or specific locations. A number of analytical tools and models have been used to assess the stability and adaptability of genotypes across environments. The regression model proposed by Eberhart and Russell (1966) allows for the computation of a complete analysis of variance with individual stability estimates and departure from linearity of a regression line [3]. The model considers a stable variety as the one with a high mean yield, bi=1 and s2 di=0. Similarly, genotypes with a high s2 di deviate significantly from linearity and have a less predictable response for the given environments. Additive Main effects and Multiplicative Interaction (AMMI) model involves correlation or regression analysis that also relates the genotypic and

environmental score derived from a principal component analysis of the genotype by environment interaction matrix to genotypic and environmental covariates. Genotype by Environment interaction studies were conducted for soybean by different researchers in different countries. Stability of a given genotype can also be determined by its response for diverse environments where soybean variety is grown. Research focusing on stability or genotype by environment interactions is necessary for plant breeders to develop genotypes that respond optimally and consistently across environments. Therefore, this experiment was initiated to determine the nature and magnitude of genotype by environment interaction and identify superior and stable soybean genotypes for the diverse environments [4].

Materials and Methods

Germplasm and study sites

Thirteen medium set soybean genotypes including the standard check (Billo) were tested at Bako, Uke and Billo for two consecutive main cropping seasons (2020-2021) (Table 1).

Experimental design and management

Thirteen medium set soybean genotypes were evaluated in a Randomized Complete Block Design with three replications. A plot consisted of four rows with the spacing of 0.6 m between rows and 0.1

Table 1: Environments used in the study and their main characteristics in Ethiopia.

Loc.	Year	Longitude	Latitude	Altitude (m)	RF (mm) a.s.l.	Soil type
Bako	2020, 2021	37°09'E	09°06'N	1650	1431	Sandy-clay
Billo	2020, 2021	E:037000.165'E	N:09054.097'N	1649	1500	Reddish brown
Uke	2020, 2021	E:036032..391'E	N:09025.082'N	1319	NI	Sandy-loam
a.s.l.: above sea level mm: mile-meter m: meter E: east N: North NI: not indicated						

Table 2: Lists of experimental materials and their source used the experiments.

Pedigree	Source of materials	Remark
PB-12-2	IITA/Jimma ARC	Line
JM-ALM/H3-15-5C-1	IITA/Jimma ARC	Line
PB-12-3	IITA/Jimma ARC	Line
TGX 1989-45F	IITA/Jimma ARC	Line
PM-12-53	IITA/Jimma ARC	Line
JM-DAV/PAR142-15-5A	IITA/Jimma ARC	Line
TGX-1987-62F	IITA/Jimma ARC	Line
PI-12-55	IITA/Jimma ARC	Line
JM-Davs/PR142-15-5A	IITA/Jimma ARC	Line
PI-567061	IITA/Jimma ARC	Line
Korme	Bako ARC	Released variety
PM-12-56	IITA/Jimma ARC	Line
Billo	Bako ARC	Recent check

Table 3: Combined analysis of variance for13 Medium Set soybean varieties evaluated in Western Oromia.

Source Variation	DF	Mean Square
REP	2	87919.54ns
Genotype(G)	12	1447598.58**
Location(Loc)	2	34837374.79**
Year (Y)	1	1356361.01**
Genotype X Location (G X L)	24	444955.80**
Genotype x Year (G X Y)	12	330561.77**
Year x Location (Y X L)	2	81932.83ns
Genotype x Loc x Year(G*L*Y)	24	283248.65**
Grand mean: 1.89; CV (%): 10.12; ***: Significant at P P<0.01, ns: none significant		

m between plants. Fertilizer rate of 100 kg ha-1 NPS was applied at planting. Management practices were done for all experimental units across location and years according to the recommendations made for the crop and/or location. Two middle rows in each replication were harvested [5]. The grain was adjusted to 10% seed moisture content before weighing to record yield and converted to hectare basis before data analysis (Table 2).

Data analysis

The grain yield data collected at each site were subjected to analysis of variance (ANOVA) followed by combined analysis of variance for all the six sites using SAS statistical software.

Additive main effects and multiplicative interaction (AMMI)

The responses of the genotypes were evaluated with regression (Eberhart and Russel, 1966) and Additive Main-effect and Multiplicative Interaction (AMMI) models GenStat 16 edition software. The linear model proposed by Eberhart and Russell (1966) is:

$$Y_{ij} = \mu_i + b_i I_j + S^2 d_{ij}$$

Where Y_{ij} is the mean performance of ith variety (I=1, 2,…, n) environment; μ_i is the mean of ith variety over all the environments; b_i is the regression coefficient which measures the response of ith variety to varying environments; $S^2 d_{ij}$ is the deviation from regression of ith variety in the jth environment, I_j is the environmental index of jth environment [6].

AMMI model (Zobel and Gauch, 1996):

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_g \delta_e + \rho_g + \varepsilon_{ger}$$

Where Y_{ger} is the observed yield of genotype g in environment e for replication r; Additive parameters: μ the grand mean; α_g the deviation of genotype g from the grand mean and β_e the deviation of environment e; the multiplicative parameters: λ_n the singular value for interaction principal component axis (IPCA) n, γ_g the genotype eigenvector for axis n, and δ_e the environment eigenvector; ρ_g PCA residuals (noise portion) and ε_{ger} error term.

Results and Discussion

Combined analysis of variance

The combined analysis of variance for yield is presented in Table 3. The result revealed that the main effects, genotype (G), location (L) and Year (Y), and the interaction effect G × L, G × Y and G × L ×Y showed a highly significant (P ≤ 0.001) difference for grain yield [7].

Significant differences were observed for grain yield among genotypes in all environments (Table 3). This indicated the presence of genetic variability among the genotypes. Environment for grain yield (averaged across genotypes) ranged from 1.09 ton ha-1 at Billo in 2020 to 2.66 ton ha-1 at Uke in 2020. Mean grain yield across environments ranged from 1.41 ton ha-1 (JM-PR142/CLR-15-5C-2) to 2.49 ton ha-1 (TGX-1987-62F) with grand mean of 1.89 ton ha-1. Five genotypes (TGX-1987-62F), (PB-12-2), (PM-12-53), (TGX 1989- 45F) and JM-ALM/H3-15-5C-1 gave yield above grand mean (1.89 ton ha-1) and the remaining eight genotypes including old and newly released check Korme and Billo gave below the average yield. The mean grain yield combined over location and years showed that genotype TGX-1987-62F was the top ranking in performance [8].

AMMI model analysis

An output of the AMMI model analysis of variance for grain yield is presented in Table 4. This analysis also revealed the presence of highly significant (P< 0.01) differences among medium set soybean genotypes for grain yield. From the total treatment sum of squares, the largest (72.2%) portion was due to environments main effect followed by genotypes main effect (18.6%) and genotype by environment interaction (11.34%). A large yield variation explained by environments indicated the existence of both spatial and temporal diversity in test-environments, with large differences among environmental means causing most of the variation in grain yield [9]. In line with this result, Tolessa and Gela (2014) reported large yield variation of common bean genotypes due to environments. This also indicates the existence of a considerable amount of deferential response among the evaluated soybean genotypes to changes in growing environments and the differential discriminating ability of the test environments. Substantial percentage (74.36%) of G × E interaction was explained by IPCA1 followed by IPCA-2 (25.66%) and, therefore, used to plot a two-

Table 4: Mean Seed Yield (ton ha^{-1}) of Soybean Genotypes evaluated in western Oromia across Locations and Years.

No.	Genotypes	Mean seed yield in ton h^{-1}						Mean
		2020			2021			
		Bako	**Billo**	**Uke**	**Bako**	**Billo**	**Uke**	
1	PB-12-2	3.03	1.37	2.73	2.34	1.00	2.58	2.26
2	JM-ALM/H3-15-5C-1	1.19	0.87	2.94	1.61	1.41	2.55	1.94
3	PB-12-3	2.02	1.01	2.55	1.10	1.18	2.28	1.75
4	TGX 1989-45F	1.82	1.38	2.67	1.71	1.60	2.34	2.00
5	PM-12-53	2.44	0.97	2.67	1.98	1.6	2.55	2.11
6	JM-DAV/PAR142-15-5A	2.15	0.98	3.09	1.7	1.32	1.71	1.89
7	TGX-1987-62F	2.48	1.29	2.62	3.12	2.05	2.81	2.49
8	PI-12-55	1.86	1.18	2.11	1.84	1.48	1.96	1.80
9	JM-Davs/PR142-15-5A	1.53	0.69	1.63	1.34	1.01	1.92	1.41
10	PI-567061	1.64	0.70	2.96	0.88	1.01	1.90	1.52
11	Korme	1.95	1.52	2.95	1.43	0.96	2.45	1.80
12	PM-12-56	1.46	0.89	2.90	1.35	1.20	2.28	1.74
13	Billo	1.84	1.33	2.80	1.57	0.87	2.07	1.81
	MEAN	*2.01*	*1.09*	*2.66*	*1.69*	*1.28*	*2.26*	*1.89*
	LSD	*0.16*	*0.58*	*0.16*	*0.24*	*0.15*	*0.27*	*0.13*
	CV%	*3.6*	*31.7*	*6.4*	*8.4*	*7.1*	*7.1*	*10.3*
	P value	**	*	**	**	**	**	**

dimensional GGE biplot. Amare and Tamado (2014) and Temesgen et al. (2014) suggested that the most accurate model for AMMI could be predicted by using the first two IPCA [10].

AMMI biplot analysis

AMMI biplot graph (Figure 1) with X-axis plotting IPCA1 and Y-axis plotting IPCA2 scores illustrate stability, adaptability and high yielding of soybean genotypes to the testing environments. It has been reported that the IPCA1 scores of a genotypes in AMMI analysis are an indication of the stability or adaptation over environments (Alberts, 2004) (Table 5).

The greater the IPCA scores, negative or positive, the more specific adapted is a genotype to certain environments. According to AMMI biplot, Environments Bako and Uke relatively showed high IPCA scores and contributed largely to GEI. Bako and Uke environments were conducive for best performing soybean genotypes. Genotypes JM DAVS/ALM-15-5A, PI 567061and PM-12-56 was intended to low yielding environment (Figure 1). Based on the IPCA score, PI-12-55 and PB-12-3 were not stable genotypes and as well performed under low yielding environments. TGX-1987-62F and PM-12-53genotypes revealed more static performance across environments in comparison to other medium set soybean genotypes in the trial. PB-12-3 performed to low yielding environments and also was relatively stable (Figure 1). PM-12-53, PB-12-2 and TGX-1987-62F genotypes have relatively lower IPCA by virtue of which they proved to give best grain yield and stability than other genotypes (Figure 1). TGX-1987-62F genotype had the highest grain yield followed by PB-12-2 and PM-12-53 genotypes. Similar results were also reported by Temesgen et al. (2014) on linseed and Niger seed and Adane et al., (2020) on soybean (Table 6).

GGE biplot analysis

In GGE biplot (Figure 2), IPCA1 and IPCA2 explained 76.31 and 14.74 %, respectively of soybean genotypes by environment interaction and made a total of 91.05 %. In a study conducted on groundnut by Amare and Tamado (2014) and white lupines by Atnaf et al. (2017), IPCA1 and IPCA2 explained an interaction of 81.8 and 63.4%, respectively, extracted from IPCA1 and IPCA2. An ideal genotype

Table 5: Partitioning of the explained sum of square (SS) and mean square (MS) from AMMI analysis for grain yield of seven soybean genotypes.

Source	df	SS	Explained SS (%)	MS
Total	233	112675210		483585
Treatments	38	96463093		2538502**
Genotypes	12	17556356	**18.6**	1463030**
Environments	5	68194844	**72.2**	34097422**
Interactions	24	10711893	**11.34**	446329***
Block	6	277093		46182
IPCA 1	13	7963145	**74.34**	612550***
IPCA 2	11	2748749	**25.66**	249886***
Residuals	0	0		*
Error	189	15935024		84312

ns: non- significant, **: significant at 1% and *: significant at 5% probability level. SS: sum of square, DF: degree of freedom

is defined as a genotype which has the greatest IPCA1 score (mean performance) and with zero GEI, as represented by an arrow pointing to it (Figure 2). A genotype is more desirable if it is located closer to the ideal genotypes. Thus, using the ideal genotype as in the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important [11].

In this study, TGX-1987-62F and PB-12-2 genotypes which fell closest to the ideal genotype were identified as the most desirable genotypes as compared to the rest of the tested medium set soybean genotypes in the trials (Figure 2). Similarly, Dabessa et al. (2016) identified ideal genotypes based on the genotype-focused scaling that assumes stability and high mean yield of studied genotypes. Ideal test environment is an environment which has more power to discriminate genotypes in terms of the genotypic main effect as well as being able to represent the overall environment. But such a type of environment may not exist in real conditions. Therefore, by assuming a small circle which is located in the center of concentric circles and an arrow pointing on it as the ideal environment (Figure 2), it is possible to identify desirable environments which are found closer to the ideal environment (Yan and Rajcan, 2002). Hence, among the testing environments, Bako,

Table 6: Average Yield AMMI-estimates per environment.

| Genotype designation No	Pedigree name	AMMI yield estimate per Environments (kg ha^{-1})			Ranks of genotypes per environment		
		Bako	Billo	Uke	Bako	Billo	Uke
13	Billo	1782	1102	2542	8	10	7
2	JM DAVS/ALM-15-5A	1502	850	1873	11	13	13
6	JM- DAV/PR142-15-5A	2034	1166	2481	4	8	10
2	JM-ALM/H3-15-5C-1	1835	1204	2849	7	6	2
11	Korme	1561	1459	2387	10	3	11
5	PB 12-3	1614	1261	2528	9	5	8
1	PB-12-2	2798	1183	2783	2	7	3
8	PI 12-55	1943	1164	2133	5	9	12
10	PI 567061	1301	854	2525	13	12	9
5	PM-12-53	2310	1288	2738	3	4	4
12	PM-12-56	1471	1043	2700	12	11	5
4	TGX 1989-45f	1850	1593	2625	6	2	6
7	TGX1987-62F	2954	1671	2854	1	1	1
Environments 1: Bako, Environment 2: Billo and Environment 3: Uke							
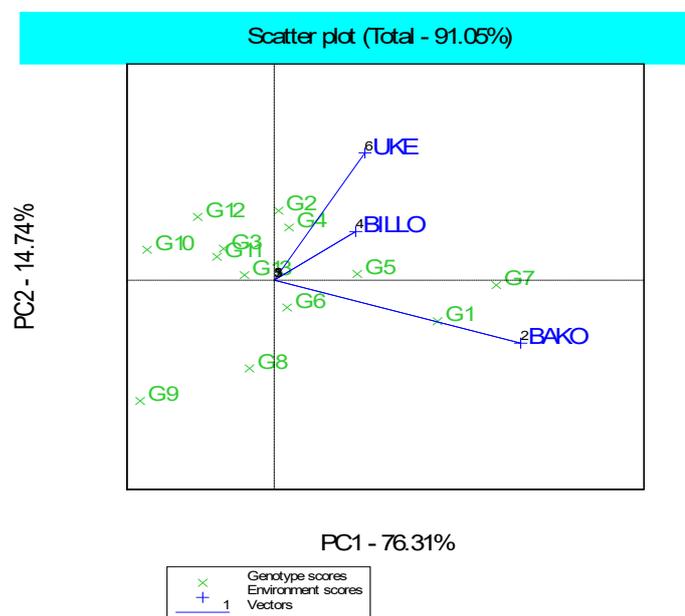
Figure 1: AMMI biplot showing "which won where" and stable soybean genotypes evaluated at six environments in western Oromia.

located near to this ideal environment was identified as the best desirable testing environment in terms of being the most representative of the overall environments and powerful to discriminate medium set soybean genotypes in the trial [12].

Conclusion and Recommendations

Combined analysis of variance indicated that grain yield performance of the tested medium set soybean genotypes is highly influenced by environment, genotypes, and GEI. This indicates that a particular genotype does not exhibit uniform performance under different environmental conditions or different genotypes may respond differently to a specific environment. The varieties and environment main effects and genotype-by-environment interaction effects are highly significant for medium set soybean genotypes in the trial. The environment contributed most to the variability in grain yield. Genotype TGX-1987-62F was close to the ideal genotype and could thus be used as bench mark for the evaluation of medium set soybean genotypes in western Oromia. Considering mean grain yield and
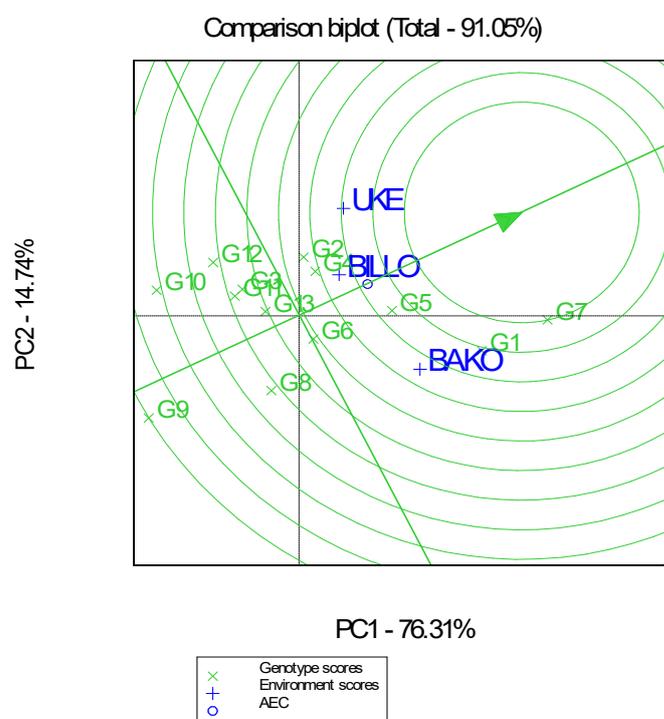

Figure 2: GGE-biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype.

stability simultaneously, PB-12-2 was the best medium set soybean genotype in the trial and is recommended for further evaluation under variety verification trial.

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