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Genotype x Environment Interaction and Grain Yield Stability Analysis of Soybean (*Glycine max* (L.) Merrill) Genotypes in Western Ethiopia

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Abstract

The performance of the genotypes depends on the genetic potential of the crop and the environment in which the crop is grown. The present study was aimed to identify and release of stable high yielding and medium maturing soybean variety with better agronomic performance in western Ethiopia. To this end, seventeen soybean genotypes including the standard check, Korme, were evaluated at three locations (Bako, Gute and Boshe) for two consecutive main cropping seasons (2017-2018). Additive main effect and multiplicative interaction (AMMI), Genotype and Genotype by environment (GGE) interaction biplot and regression analysis were computed using R- statistical software to identify stable genotype across locations in both years. The environment, genotype and genotype x environment interaction (GEI) effects were highly significant ($p < 0.001$) based on combined analysis of variance and additive main and multiplication interaction (AMMI) model. The three models revealed similar result in that PM-12-20, PM-12-32, PM-12-18 and PM-12-39 were stable and widely adapted genotypes. However, the genotypes PM-12-31, PM-12-45 and PM-12-43 had higher regression coefficient (b_i) value showing that these genotypes were sensitive to changes in environmental conditions and tend to give high yield at a favorable environment. Genotype PM-12-37, now named as Billo-19, was relatively stable and high yielding thus released for the western Ethiopian and other areas with similar agro-ecologies.

Keywords: AMMI, GGE biplot, Regression, Stability

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1. 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 has the highest protein content of all field crops and second only to groundnut in terms of oil content among the food legumes (Gurmu *et al.*, 2009). The largest global oilseed crop production goes to soybean (53%), followed by rapeseed (15%), cottonseed (10%) and peanut (9%) (Pratap *et al.*, 2012). It is used as food, nutritious animal feed and improves soil fertility through nitrogen fixation when used in crop rotation with cereal

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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). Ethiopia's soybean productivity in 2019 is 2.3 tons ha⁻¹, which is higher than the average productivity compared to Africa (1.3 tons ha⁻¹) but lower than the global average (2.8 tons ha⁻¹) (FAO, 2019).

The performance of a genotype is dependent on the genetic capacity 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 over the testing environments or specific locations. Genotype x environment interactions are said to exist when the responses of two genotypes to different level of environmental factors fail to be parallel (Allard and Bradshaw, 1964). In this case, selection of specifically adapted genotypes for a specific location, while the GEI is non-significant important when selecting widely adapted genotypes (absence of cross over) (Kaya *et al.*, 2006).

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. The model considers a stable variety as the one with a high mean yield, $b_i=1$ and $s^2d_i=0$. Similarly, genotypes with a high s^2d_i deviate significantly from linearity and have a less predictable response for the given environments (Eberhart and Russell, 1966). Additive Main effects and Multiplicative Interaction model (AMMI) involves correlation or regression analysis that also relates the genotypic and environmental score derived from a principal component analysis of the genotype x environment interaction matrix to genotypic and environmental covariates (Zobel *et al.*, 1988).

Genotype x Environment interaction studies were conducted for soybean by different researchers in different countries (Akande *et al.*, 2009; Gurmu *et al.*, 2009; Carter *et al.*, 2018; Mwiinga *et al.*, 2020). Stability of a given genotype can also be determined by its response for diverse environments where soybean variety grown. Research focusing on stability or genotype x 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 x environment interaction and identify superior and stable soybean genotypes for the different environments.

2. Materials and Methods

2.1. Germplasm and Study Sites

Seventeen soybean genotypes including the standard check (*Korme*) were tested at Bako, Gute and Boshe for two cropping seasons (2017-2018). All the genotypes were medium maturity group (mean 120–150 days for physiological maturity).

2.2. Experimental Design and Management

The 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 m between plants. Fertilizer rate of 50 kg ha⁻¹ NPS was applied at planting. Management practices were done according to the recommendations for the particular crop and/or location the two middle rows in each replication were harvested. The grain yield adjusted to 10% seed moisture content before data analysis.

3. Data Analysis

3.1. Analysis of Variance

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 R (2016) statistical software.

3.2. Regression and 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 with R Software (2016). The linear model proposed by Eberhart and Russell (1966) is:

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

where Y_{ij} is the mean performance of i^{th} variety ($I=1, 2, \dots, n$) environment; m_i is the mean of i^{th} variety over all the environments; b_i is the regression coefficient which measures the response of i^{th} variety to varying environments; $S^2 d_{ij}$ is the deviation from regression of i^{th} variety in the j^{th} environment, I_j is the environmental index of j^{th} environment.

3.3. AMMI model (Zobel and Gauch, 1996)

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

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_{gn} the genotype eigenvector for axis n , and δ_{en} the environment eigenvector; ρ_{ge} PCA residuals (noise portion) and ε_{ger} error term.

4. Results

4.1. Combined Analysis of Variance

The combined analysis of variance for yield is presented in Table 1. The result revealed that the main effects, genotype (G), location (L), and Year (Y), G x L, G x Y, L x Y and G x L x Y showed a highly significant ($p < 0.001$) difference for grain yield.

Table 1: Combined Analysis of Variance of 17 Soybean Varieties Evaluated in Western Ethiopia			
Source of Variations	Degree of freedom	Sum Squares	Mean Squares
Replication	2	0.08	0.04ns
Genotype(G)	16	16.38	1.02***
Location(L)	2	41.08	20.54***
Year(Y)	1	16.10	16.10***
G x L	32	12.08	0.38***
G x Y	16	5.55	0.35***
L x Y	2	13.70	6.85***
G x L x Y	32	11.23	0.35***
Residuals	198	3.40	0.02

Note: Grand mean = 1.97; CV (%) = 6.62; ***=Significant at $P < 0.001$, ns=not significant

Significant differences were observed for grain yield among the genotypes in all of environments (Table 2). This indicated the presence of genetic variability among the genotypes. Environment grain yield (averaged across genotypes)

Table 2: Mean Seed Yield (ton ha ⁻¹) of Soybean Genotypes Across Locations and Years								
No.	Variety	Mean seed yield in ton h ⁻¹						Mean
			2017			2018		
		Bako	Gute	Boshe	Bako	Gute	Boshe	
1.	PM-12-31	3.29	1.97	1.60	2.65	1.98	1.42	2.15
2.	PM-12-25	3.43	1.70	2.19	1.86	1.33	1.26	1.96
3.	PM-12-43	3.69	1.91	1.72	1.96	1.85	1.17	2.05
4.	PM-12-32	2.86	2.00	1.75	1.88	1.53	1.91	1.99
5.	PM-12-21	2.61	1.67	1.42	1.82	1.41	1.56	1.75
6.	PM-12-37	4.02	2.43	1.52	2.39	1.88	2.64	2.48
7.	PM-12-38	3.02	1.69	1.80	1.80	1.53	1.80	1.94

Table 2 (Cont.)								
No.	Variety	Mean seed yield in ton h ⁻¹						Mean
			2017			2018		
		Bako	Gute	Boshe	Bako	Gute	Boshe	
8.	PM-12-22	3.26	1.40	2.18	1.37	1.23	1.20	1.77
9.	PM-12-20	3.09	1.94	2.92	2.47	2.05	1.85	2.39
10.	PM-12-18	3.02	2.10	2.03	2.07	2.07	1.74	2.17
11.	PM-12-44	2.0	1.57	2.02	1.75	1.39	1.37	1.68
12.	PM-12-39	3.14	1.82	1.53	2.65	1.40	2.17	2.12
13.	PM-12-35	2.71	2.10	1.52	1.19	1.81	1.29	1.77
14.	PM-12-30	2.86	1.44	1.62	1.78	2.36	1.24	1.88
15.	PM-12-45	3.08	1.29	1.23	2.22	1.53	1.56	1.82
16.	PM-12-29	2.61	2.06	1.15	1.33	1.46	1.09	1.62
17.	Korme	2.46	1.88	1.63	2.01	1.82	1.48	1.88
	MEAN	3.01	1.82	1.75	1.95	1.68	1.57	1.97
	LSD	0.28	0.18	0.18	0.21	0.20	0.21	
	CV%	5.56	5.93	6.20	6.40	7.20	8.20	
	<i>p</i> -value	***	***	***	***	***	***	
Note: LSD = Least Significant Difference; CV = Coefficient of Variations.								

ranged from 1.57 ton ha⁻¹ at Boshe in 2018 to 3.01 ton ha⁻¹ at Bako in 2017. Mean grain yield across environments ranged from 1.62 ton ha⁻¹ (PM-12-29) to 2.48 ton ha⁻¹ (PM-12-37) with grand mean of 1.97 ton ha⁻¹. Seven genotypes (PM-12-37, PM-12-20, PM-12-18, PM-12-31, PM-12-39, PM-12-43 and PM-12-32) gave yield above the grand mean (1.97 ton ha⁻¹) and the remaining 10 including the standard check, *Korme*, were below the average yield. The mean grain yield combined over location and years showed that genotype PM-12-37 was the top ranking (Table 3).

Table 3: Stability Analysis in Soybean Grown in Western Part of Ethiopia			
Genotypes	Regression Slope (b _i)	Deviation from Linearity (S ² d _i)	Mean Grain Yield (ton ha ⁻¹)
PM-12-31	1.6277	-0.014	2.15
PM-12-25	1.2881	-0.014	1.96
PM-12-43	1.5369	-0.021	2.05
PM-12-32	0.7209	-0.059	1.99
PM-12-21	0.8987	-0.067	1.75
PM-12-37	1.4023	-0.066	2.48
PM-12-38	0.8841	-0.029	1.94
PM-12-22	0.9936	0.045	1.77

Table 3 (Cont.)			
Genotypes	Regression Slope (b_i)	Deviation from Linearity (S^2d_i)	Mean Grain Yield (ton ha ⁻¹)
PM-12-20	0.7138	0.039	2.39
PM-12-18	0.7425	-0.058	2.17
PM-12-44	0.3654	-0.038	1.68
PM-12-39	1.4712	0.003	2.12
PM-12-35	0.4061	0.069	1.77
PM-12-30	0.8876	0.011	1.88
PM-12-45	1.5971	-0.058	1.82
PM-12-29	0.7486	0.100	1.62
<i>korme</i>	0.7153	-0.040	1.88
Mean			1.97

4.2. Regression Analysis Based On Eberhart and Russell Model

The mean performance, regression coefficient (b_i) and squared deviation (s^2d_i) from the regression values are presented in Table 4. According to Eberhart and Russell (1996) genotypes with high mean yield and regression coefficient (b_i) equal to unity and deviation from regression (s^2d_i) approach to zero. Therefore, genotypes PM-12-20, PM-12-32, PM-12-18, PM-12-39 and PM-12-37 have mean yields higher than the average, (b_i) did not differ from unity and (s^2d_i) approaching zero. However, the PM-12-44 and PM-12-35 performed poorly in all of the environments because its mean grain yield was lower than the average and its coefficient of regression was less than unity. On the other hand, the genotypes PM-12-31, PM-12-45 and PM-12-43 had higher b_i value showing that these genotypes were sensitive to changes in environmental conditions.

Table 4: Analysis of Variance for Additive Main Effects and Multiple Interaction (AMMI)			
Source of Variation	Df	Mean squares	% G x E interaction Explained
Environments	5	14.18***	
Reps within Env.	12	0.04**	
Genotype	16	1.02***	
Genotype x Env.	80	0.36***	
IPCA 1	17	0.20ns	56.4
IPCA2	15	0.18ns	43.6
Residual	192	0.02	
Note: ***=Significant at $p < 0.001$, **=Significant at $p < 0.01$, ns = not significant.			

4.3. Additive Main Effects and Multiplicative Interaction (Ammi) Model

Analysis of variance for AMMI revealed that highly significant difference ($p < 0.001$) among environments, genotypes and genotype x environment were observed (Table 4). The percentage of G x E interaction explained by IPCA 1 and IPCA 2 and was 56.4% and 43.6%, respectively of the G x E interaction sum of squares. The AMMI analysis result revealed that PM-12-20 was the most stable genotype having IPCA score closer to zero (Table 5). Whereas, PM-12-35, PM-12-39 and

Table 5: IPCA1 Scores and Mean Grain Yield of Genotypes and Environments			
Designation of Genotypes	Genotype	IPCA 1 Score	Mean Grain Yield (tonha ⁻¹)
A	PM-12-31	0.2269	2.15
B	PM-12-25	0.2635	1.96
C	PM-12-43	0.1857	2.05
D	PM-12-32	-0.1074	1.99
E	PM-12-21	-0.0446	1.75
F	PM-12-37	0.2335	2.48
G	PM-12-38	0.0306	1.94
H	PM-12-22	0.1555	1.77
I	PM-12-20	0.0013	2.39
J	PM-12-18	-0.1836	2.17
K	PM-12-44	-0.2589	1.68
L	PM-12-39	0.3778	2.12
M	PM-12-35	-0.4932	1.77
N	PM-12-30	-0.1928	1.88
O	PM-12-45	0.3645	1.82
P	PM-12-29	-0.3288	1.62
Q	Korme	-0.2300	1.88
Environments			
A	Bako	0.7720	2.48
B	Boshe	-0.0925	1.66
C	Gute	-0.6795	1.75

PM-12-29 with IPCA score deviate from zero are suitable for specific adaptation. Environment Bako gave high environmental mean yield.

4.4. GGE Biplots

In the which-won-where view of the GGE biplot (Figure 1) based on the data in Table 1, the six environments fell into two sectors with different winning cultivars. Specifically, PM-12-20 was the highest yielding cultivar in Gute 2018 and Boshe 2017, and PM-12-37 was the highest yielding cultivar at Bako in 2017 & 2018, at Gute in 2017 and at Boshe in 2018.

The discriminativeness vs representativeness was indicated (Figure 2). Bako and Gute 2018 was representative of mega-environment, while Boshe could not represent the mega-environment. Bako with longer vector and smaller angle to the axis it is regarded as ideal testing location and important to select superior genotypes such as PM-12-20 and PM-12-37, whereas, Gute is with short vector and provide little information. Environments like Boshe have long vectors and large angles with the AEC abscissa they cannot be used in selecting superior genotypes, but are useful in culling unstable genotypes. Boshe 2017 with long vector is most discriminating and Bako 2008 near AEC abscissa is most representative environments.

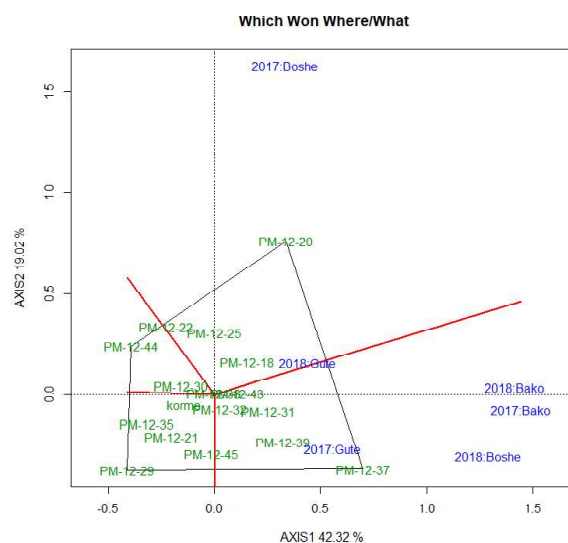


Figure 1: The “Which-won-Where” View of the GGE Biplot Based on the $G \times E$ Soybean Data

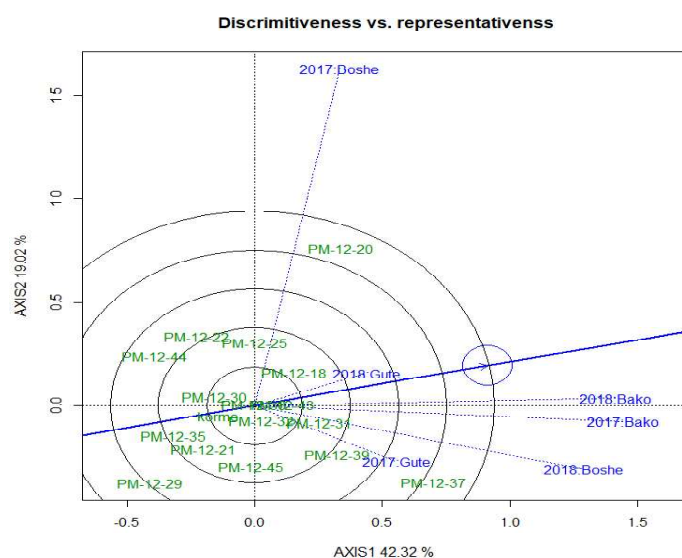


Figure 2: Discriminating Power and Representativeness of Testing Environments

5. Discussion

The combined ANOVA showed that the genotype (G), environment (E) and genotype by environment interaction (GEI) were highly significant indicating that the genotypes had significantly different mean performances and ranking in the test environments Table 1. The existence of significant GEI effects on grain yield suggests the existence of difference among soybean genotypes tested and genotype performance varies across seasons and locations. The occurrences of GEI necessitate the need for regression and stability analysis (Yan and Tinker, 2006). In agreement to this study different authors reported the presence of significant differences for GEI in different traits of soybean (Asfaw et al., 2009; Gurmu et al., 2009; Carter et al., 2018; Mwiinga et al., 2020). On the contrary Jandong et al. (2019) reported non-significant GEI for most soybean traits.

According to Allard and Bradshaw (1964) GEI are said to exist when genotypes response is different in different environments (locations and year). In this case, selection of genotype depends on specific location performance, while

the GEI is non-significant important when selecting widely adapted genotypes (absence of cross over) (Kaya *et al.*, 2006). The ideal, genotypes must present both high grain yield and stable performance across the growing environments (Dalló *et al.*, 2019).

In the present study regression analysis based on Eberhart and Russell Model identified genotypes PM-12-20, PM-12-32, PM-12-18, PM-12-39 and PM-12-37 have mean yields higher than the average, (b_i) did not differ from unity and (s^2di) approaching zero. These genotypes relatively stable across environments. Gurmu *et al.* (2009) identified three stable genotypes for yield based on regression analysis among twenty soybean tested at five locations in Ethiopia. Jandong *et al.* (2019) reported two stable soybean genotypes after evaluating 20 genotypes and 5 improved varieties in two locations and seasons in Nigeria.

The AMMI IPCA scores were used to classify the genotypes based on stability. AMMI analysis result revealed that PM-12-20 was the most stable genotype having IPCA score closer to zero (Table 5). Whereas, PM-12-35, PM-12-39 and PM-12-29 with IPCA score deviate from zero are suitable for specific adaptation. Environment Bako gave high environmental mean yield. This indicates that the varieties perform well in this environment due to proper agronomic practices and favorable environment to grow soybean varieties. In agreement to the current study, Mwiinga *et al.* (2020) recommended one soybean line using AMMI analysis and AMMI's stability value (ASV) for release based on highest grain yield performance among twenty elite soybean lines and five commercial checks in Zambia, Malawi, Mozambique and Zimbabwe. While Nassiuma and Wasike (2002) reported 5 stable soybean varieties from ten genotypes in four locations and 5 seasons at Kenya.

The genotype main effect and genotype x environment interaction (GGE) biplot methods are considered superior because provides graphic images and effective overview of the results (Dalló *et al.*, 2019). In this study, which-won-where view of the GGE biplot (Figure 1) based on the data in Table 1, PM-12-20 was the highest yielding cultivar in Gute2018 and Boshe2017, and PM-12-37 was the highest yielding cultivar in the other four environments. The graph helps to identify the winning genotype across the testing location. According to discriminativeness vs representativeness (Yan *et al.*, 2007) reported that test environments that have small angles with AEC abscissa is the "average-environment axis," is more representative of the mega-environment than those that have larger angles. Therefore, Bako and Gute 2018 are representative of mega-environment, while Boshe could not represent the mega-environment. Bako with longer vector and smaller angle to the axis it is regarded as ideal testing location and important to select superior genotypes such as PM-12-20 and PM-12-37 While, Gute is with short vector provide little information. Environments like Boshe have long vectors and large angles with the AEC abscissa they cannot be used in selecting superior genotypes, but are useful in culling unstable genotypes. Boshe 2017 with long vector is most discriminating and Bako 2008 near AEC abscissa is most representative environments.

6. Conclusion and Recommendations

According to Eberhart and Russell Model (regression analysis) genotypes PM-12-20, PM-12-32, PM-12-18, PM-12-39 and PM-12-37 were relatively stable and widely adapted. Whereas, PM-12-37 was high yielder in most of the test locations. The two models regression analysis and Additive Main effects and Multiplication Interaction (AMMI) revealed similar result that PM-12-20 stable and widely adapted genotypes. However, genotypes, PM-12-35, PM-12-39 and PM-12-29 with IPCA score deviate from zero are suitable for specific adaptation and sensitive to change of environmental conditions. Based on which-won-where view of the GGE biplot genotypes PM-12-20 and PM-12-37 were high yielder and discriminativeness vs representativeness analysis, PM-12-20 and PM-12-37 were superior genotypes. Generally, genotype PM-12-20 and PM-12-37 were the relatively stable and high yielding genotype and proposed candidate varieties. However, PM-12-37 named *Billo-19* variety released for western and similar agro-ecologies.

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