

Evaluation and Stability Analysis of Early Maturing Soybean (*Glycine Max* L.) Genotypes in Lowland Agro Ecologies of Ethiopia

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To cite this article:

Masreshaw Yirga, Yechalew Sileshi, Demelash Bassa. Evaluation and Stability Analysis of Early Maturing Soybean (*Glycine Max* L.) Genotypes in Lowland Agro Ecologies of Ethiopia. *Journal of Plant Sciences*. Vol. 11, No. 4, 2023, pp. 131-135.
doi: 10.11648/j.jps.20231104.14

Received: June 29, 2023; **Accepted:** July 24, 2023; **Published:** July 31, 2023

Abstract: Soybean is becoming the most important oil crops in Ethiopia. The national soybean breeding program is working to develop high-yielding, adaptable and stable varieties to increase production and productivity in the country. Breeding for early-maturing varieties is currently given due emphasis to overcome soybean production drawbacks in moisture deficit areas. Hence, performance evaluation of early maturing soybean genotypes across representative environments is essential to examine genotype \times environment (G \times E) interactions and identify the most stable and performed genotype. The trial was conducted using 10 soybean genotypes including checks in RCB design with four replications. The materials were evaluated over eight locations and G \times E interaction was assessed using GGE-biplot analysis to identify stable genotype across testing environments. Data on phenological, agro-morphological and reaction to important diseases were collected for the crop. The combined analysis of variances showed significant to highly significant ($P < 0.01$) difference among genotypes, environments and G \times E interactions for most of the studied traits. GGE-biplot models showed that the eight environments used for the study belonged to four mega-environments. According to the GGE results, G3 (JM-HAR/G99-15-SD-2), and G7 (JM-HAR/PR142-15-SB) were identified as ideal genotypes in terms of higher-yielding ability and stability, and hence these genotypes are recommended for mega environment production in the country.

Keywords: Soybean, Grain Yield, GGE Biplot, Stability

1. Introduction

Soybean (*Glycine max* L.) has been cultivated in eastern Asia since the 11th century [1]. The genus *Glycine* has assumed to be domesticated from the wild soybean progenitor, *Glycine soja* [2]. The crop is now grown under a wide range of climate conditions in Latin America and African countries. Until mid of 1940s, the major areas of soybean production were restricted to temperate regions of the world, after which production slowly to spread tropical and sub-tropical regions [3].

Soybean has the highest protein content (40%) as compared to other pulse crops. Moreover, it has high oil content (20%), together with numerous beneficial nutrients and bioactive factors. All of these quality parameters combine

to make soybean a highly desirable crop of choice with the potential to improve the diets of millions of people in the developing countries [4]. In low input farming systems, the crop is also known to improve and amend soil properties through nitrogen fixation and enhanced moisture retention. The combination of improved soil properties and the ability to break lifecycles of pests and diseases makes soybean an ideal crop in cereal rotation program [5].

Soybean was introduced to Ethiopia in 1950s and the introduced materials were evaluated to identify suitable varieties adaptable to different environmental conditions and at the same time to identify potential areas for soybean production in the country [6]. Based on their maturity period, soybean genotypes are classified into early, medium and late maturity groups. Early maturity genotypes are suitable for

moisture stress and moisture deficit areas and also suited for double cropping for long duration rain fall condition. Due to the effects of climate change, dry spell is increasing across soybean growing environments including in high rainfall areas in the past. Therefore, breeding for early maturing soybean genotypes with stable performance across growing environments has paramount importance.

Phenotypes are the manifestation of the genetic make-up (G), environmental effect (E) and their interaction (G x E). Multi-environment trials widely used by plant breeders to evaluate the relative performance of genotypes for target environments [7]. GGE biplot analysis is one of the most important methods to reveal the patterns of G x E interaction and can offer better varietal selection power. So, this research activity was conducted to evaluate and identify the performance and stability of early maturing soybean genotypes across growing environments of the country.

2. Materials and Methods

The experiment was conducted at eight environments, namely, Jimma (Tiro-Afeta), Areka (Gofa), Humera for two cropping seasons (2018 and 2019) while Mehoniin and Sirinka for one year in 2018 and 2019 cropping season, respectively.

Table 1. Description of experimental locations.

Testing sites	Altitude (m.a.s.l)	Annual rainfall (mm)	Temperature (°C)	
			Min	Max
Mehoni	1571	300-750	18	25
Tiro-afeta	2200	1592-1275	18	26
Gofa	1774	1298	13	28
Sirinka	1749	680-1200	18	27

Most of the tested soybean genotypes were introductions from USA while the four genotypes namely, JM-HAR/G99-15-SD-2, JM-PR142/G99-15-SB, JM-HAR/PR142-15-SB, and JM-DAV/PR142-15D are recombinant inbred lines developed by JARC. The other two genotypes, Gazale and Nova were released varieties in Ethiopia included as checks in the present study (Table 2). The field trial was arranged using RCB design in four replications. Planting was done in a plot of four rows with 4m length and with regular spacing of 5 cm between plants and 40cm between rows. Planting was done with two seeds per hill and later thinned to one plant per hill at 2-3 weeks after emergence. Fertilizer NPS (19%Nitrogen, 38% Phosphorus, 7% Sulfur; and the rest filler) at the rate of 122kg/ha rate was applied at planting. And, the rest agronomic management practices were done as per the recommendations.

Agronomic characters; like Days to flowering, days to maturity, Plant Height (cm), Number of Pod per plant, Number of seeds per plant; hundred seed weight (gm) and grain yield per plot were recorded. All the data including grain yield were collected from the middle two harvestable rows. Prior to proceeding with the analysis of variance (ANOVA), homogeneity test was made for each variable and all the data were subjected to combined analysis of variance (ANOVA)

over environment for RCB design using the SAS program software. GGE analysis was used to determine the effects of GEI on yields. The results were visualized in biplot graphs [8, 9]. The GGE model was as the following: $Y_{ijr} = \mu + e_j + \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ijr}$. While, Y_{ijr} = observation of the r th replicate of the i th genotype in the j th environment, μ = the overall means, e_j = main effect of the j th environment, λ_k = matrix rank $\{g_{ge}\}_{ij}$ when $\{g_{ge}\}_{ij} = g_i + g_{ej}$, λ_k = the singular value for principal component k , α_{ik} = the eigenvector score for genotype i and component k , γ_{jk} = the eigenvector score for environment j and component k , and ϵ_{ijr} = the error for genotype i and environment j and replicate r .

Table 2. Descriptions of soybean genotypes used in the study.

GID	Genotype Name	Origin/Source
G1	Gazale (C2)	Released variety
G2	PI200488	USA
G3	JM-HAR/G99-15-SD-2	RIL by JARC
G4	PI417116	USA
G5	JM-PR142/G99-15-SB	RIL by JARC
G6	PI506764	USA
G7	JM-HAR/PR142-15-SB	RIL by JARC
G8	Nova (C1)	Released variety
G9	JM-DAV/PR142-15D	RIL by JARC
G10	Delsoy 4710	USA

GID (Genotype code/ID), RIL (recombinant inbred line).

3. Results and Discussion

The result from the combined analysis of variance is presented in Table 3. The pooled analysis of variance revealed that the mean square due to location and genotype were highly significant ($P \leq 0.01$) for all the traits, indicating the distinct nature of the test locations. Mean square due to years differed significantly with respect to all the traits, meaning that there was a change on weather condition during the study. Mean squares due to location x genotype were significant for most of traits, implying that genotypes exhibited different relative performance under each location. Significant genotype x year was observed for most of the traits. Location x year interaction revealed significant effect for all traits except for hundred seeds weight. Mean squares due to Genotype x location x year interaction found significant effect for most of the traits except for days to flowering. The result for yield and related traits indicated that phenotypic variability for these traits is dependent on genetic factors, environmental variables and the interaction between them (Table 3).

Based on the combined data analysis, the performance of the genotypes ranged widely for days to flowering (40.8 – 47.9), days to maturity (85.5 – 102), total plant height (29.5–56.5 cm), number of pods per plant (23.5–50.2), number of seeds per plant (56.8–129.2), hundred seeds weight (12.9–19.1g) and grain yield per hectare (1.1–2.11 t/ha). Among important traits, highest ranges were obtained for the number of seeds per plant followed by number of pods per plant, plant height, days to maturity, hundred seeds weight and grain yield, which played important role in the total variability of the test genotypes. The

maximum yield was recorded from genotype JM-HAR/PR142-15-SB (2.11t/ha) followed by JM-HAR/G99-15-SD-2 (1.98 t/ha) and JM-PR142/G99-15-SB (1.97 t/ha), which exhibited a yield advantage of 16.6% and 26.3%; 9.4% and 18.56%; and 8.8% and 17.9%) over the standard checks; Gazale (2.1t/ha) and Nova (1.67t/ha), respectively (Table 4). In terms of maturity period, all genotypes exhibit early

physiological maturity that ranged between 86 and 102 days. The outstanding genotypes identified were, JM-HAR/PR142-15-SB (98 days), JM-HAR/G99-15-SD-2 (97 days) and JM-PR142/G99-15-SB (101 days) had relatively shorter maturity period than the standard check Gazale (102), which is a positive trait in breeding for earliness. Similar finding was reported by the research [8-10].

Table 3. Mean squares of the combined analysis of variance for yield and related characters of soybean genotypes.

Source	df	DTF	DTM	PH	NPP	NSP	HSW	YLD
Yr	1	168.38**	1439.97**	6252.23**	630.99*	10959.23**	989.88**	47.12**
Loc	4	5606.67**	25332.09**	3308.69**	26758.66**	234009.86**	1341.13**	47.73**
Rep	3	14.45ns	45.0ns	5.85**	94.05ns	1188.44ns	14.87ns	0.09ns
Geno	9	155.27**	1097.53**	2414.33**	1678.83*	14029.06**	90.99**	2.88**
Yr*Loc	2	2562.86**	4763.41**	524.31**	4360.06**	29124.59**	11.58ns	23.81**
Loc*Geno	36	57.35**	188.89**	392.85**	500.88**	4920.31**	40.93**	1.36**
Yr*Geno	9	14.89*	154.55**	82.79**	319.85*	2668.00*	15.38*	1.25**
Yr*Loc*Geno	18	11.23ns	222.01**	178.16**	316.18**	2647.59*	21.15**	0.623**
Error	226	7.95	23.81	38.94	134.33	1330.79	8.41	0.16

Where, * = significant at ($P \leq 0.05$) and ** = significant at ($P \leq 0.01$), Yr = year, Loc = location, Geno = genotype, df = degree of freedom, DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = Number of pods per plant, NSP = Number of seeds per plant, HSW=hundred seeds weight, YLD = Seed yield per ha.

Table 4. Mean yield and yield components of early maturing soybean genotypes based on over location mean values.

GID	Combined value of seed yield (t/ha)									Combined value of yield related traits					
	Y1L1	Y1L2	Y1L3	Y1L4	Y2L1	Y2L2	Y2L3	Y2L5	Combined	DTF	DTM	PH	NPP	NSP	HSW
G1 (C1)	1.35	1.35	0.53	0.80	4.08	3.65	1.17	1.38	1.81	48	102	53.9	43.4	113.0	18.3
G2	1.33	1.05	0.66	0.85	3.98	1.38	0.20	1.53	1.41	43	87	38.4	31.5	80.0	18.2
G3	2.18	2.60	0.58	0.50	4.65	3.23	0.77	1.08	1.98	45	97	45.4	34.0	94.1	18.2
G4	1.35	0.70	0.53	0.28	2.30	1.83	0.43	1.33	1.11	42	86	30.8	26.2	57.2	19.1
G5	1.73	2.35	0.83	0.85	4.23	3.4	0.80	1.30	1.97	48	101	54.5	38.8	104.5	17.3
G6	0.98	0.60	1.15	0.10	1.68	1.45	1.03	1.58	1.30	41	89	29.6	23.5	56.8	18.4
G7	1.90	2.45	0.80	0.85	4.45	3.83	0.40	1.45	2.11	45	98	56.5	43.5	113.4	15.7
G8 (C2)	1.58	2.45	0.83	0.48	4.13	2.23	0.33	1.05	1.67	44	86	54.5	50.2	129.2	12.9
G9	1.73	1.75	1.03	0.88	4.38	2.35	0.83	1.13	1.79	46	96	41.3	40.7	100.2	17.3
G10	1.45	2.00	1.03	0.38	2.60	2.28	0.23	1.20	1.43	41	88	41.7	34.9	95.2	16.0
Mean	1.56	1.73	0.80	0.60	3.65	2.56	0.62	1.30	1.66	44	93	44.7	36.7	94.4	17.1
CV (%)	22.36	14.54	14.7	14.57	8.96	23.65	44.99	14.54	24.36	6.4	5.3	14	31.6	38.7	16.8
LSD (0.05)	0.5	0.36	0.17	0.13	0.47	0.88	0.48	0.36	0.78	5.5	9.6	12.2	22.7	71.5	5.7

L1= Tiroafeta; L2 =Gofa; L3 =Humera; L4 = Mehoni; L5= Sirinka; Y1= year 1, Y2 = year 2; DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP =pod per plant, NSP= seed per plant, HSW=hundred seed weight

The GGE biplot is important to visualize the genotype by environment interaction. The polygon view of soybean genotypes tested at eight environments is presented in figure 1. Results of the GGE biplot analysis indicates that the first two principal components IPCA 1 and IPCA 2 accounted for 72.6% and 12.9% of the sum of squares, respectively explained about 85.5% of the total variation for seed yield. Genotypes at the vertex of the polygon are either the best or poorest in one or more environments [11]. The genotypes found at the vertex of the polygon perform best in the environments within the sector [12, 13]. Six rays divide the biplot into six sectors and the eight environment fall into four different mega-environments (Figure 1). Genotypes, G1, G2, G3, G6, and G7 were the vertex genotypes, and G1 is best performer at Y2L3 on the first environment. The second environment comprises the higher yielding environment Y2L2 with a winner genotype G7. The third environment includes Y1L4, Y1L1 and Y1L2 with a vertex genotype G3

while the fourth environment includes Y2L5 and Y1L3 with the winner genotype G6. Furthermore, the figure displayed that G2 though it is on the vertex, there was no environment representing it (Figure 1). This indicates that genotypes in vertex without environment performed poorly in all of the testing sites [14].

Figure 2 indicates the ranking of the genotypes based on their mean performance and stability. The line passing through the Biplot origin and the average environment indicated by a circle is called the average environment coordinate (AEC) axis, which is defined by the average PC1 and PC2 scores of all the environments. By using the average principal components in all environments, the AEC method was employed to evaluate yield stability of the genotypes. A line drawn through the average environment and the Biplot origin, having one direction pointed to a greater genotype main effect. Moving in either direction away from AEC ordinate and from the Biplot origin indicates the greater GEI

effect and reduced stability. From this study, genotypes performing above average mean includes G3, G5, G7 and G1. An ideal genotype is the one with the highest mean performance and be absolutely stable (i.e. the best performer under all environments). Accordingly, genotype G9 had yield performance greater than the mean yield. While genotype on the right of the ordinate line had yielded less than the average mean. Hence, G2, G10, G4 and G6 showed lower yield performance as compared to the mean yield of the most stable genotypes such as G3, G7 and G5. On the other hand, G2 is the lowest stable among the test genotype (Figure 2).

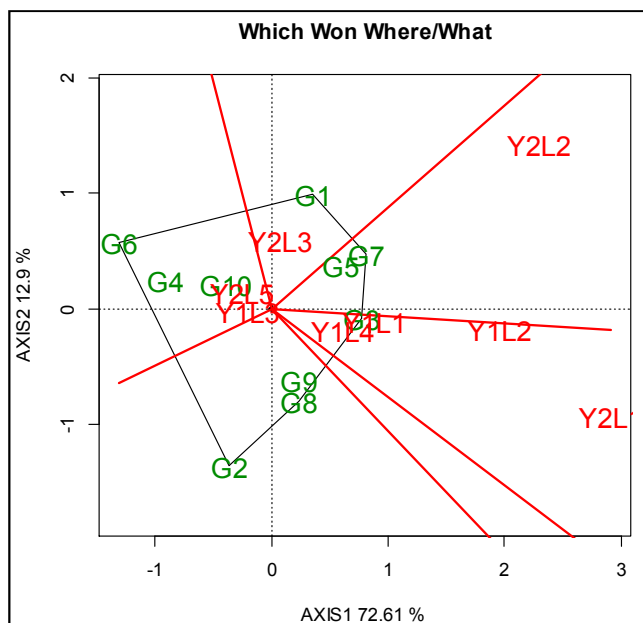


Figure 1. Polygon view of which won where.

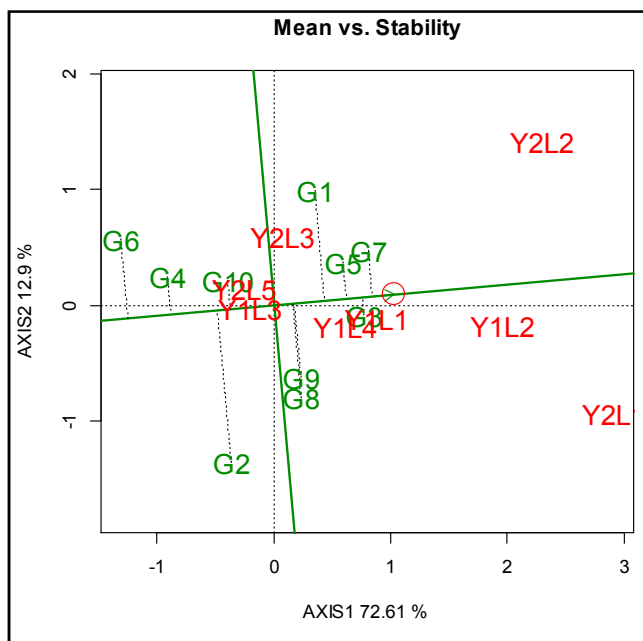


Figure 2. Ranking of the genotypes based on their mean performance and stability.

The ideal genotype is the one that with the highest mean

performance and absolutely stable [15] and to be in the center of the concentric circles is an ideal genotype. If a given genotype is located closer to an ideal genotype, it is the most desirable genotype. Hence, genotypes G3 and G7 were ideal in terms of higher-yielding ability and stability as compare. While genotypes G6, G2, and G4 were located distant from the first concentric circle and are low yielding and unstable genotypes (Figure 3).

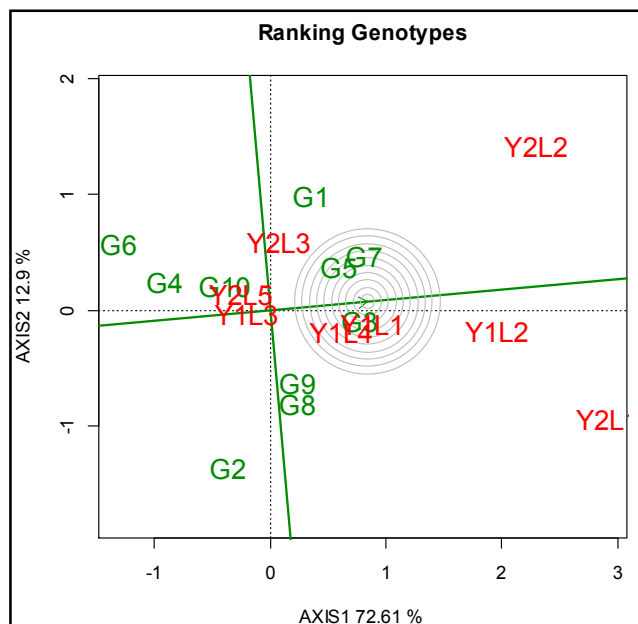


Figure 3. Ranking of the genotypes based on the ideal genotype.

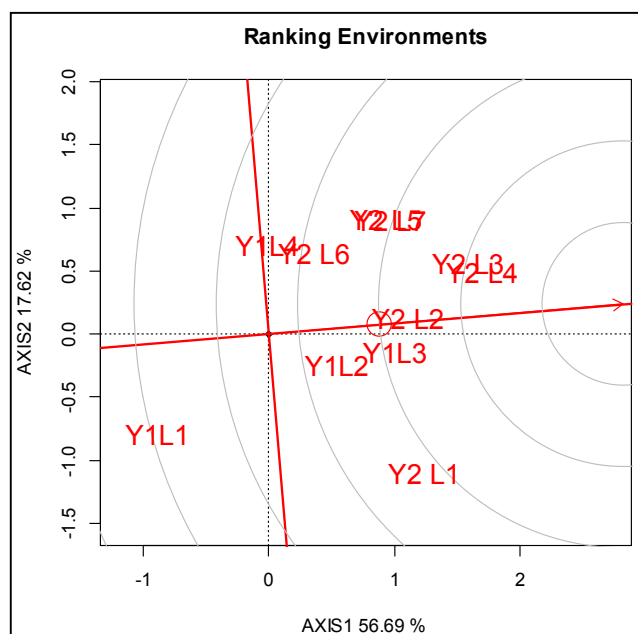


Figure 4. Ranking of the environments based on the ideal environments.

Similar to the ideal genotype, an ideal environment is also important as a reference for genotype selection. The ideal environments had the longest vector with small IPCA, which fell into the center of the concentric circles. The ideal environment is the most representative of the overall

environments and is the most powerful to discriminate among the test genotypes. Accordingly, Y2L2 and Y1L3 represent ideal environments in the present study. Environments Y1L1 on the other hand was found far from the ideal environment and hence, considered as less powerful to discriminate among genotypes (Figure 4).

4. Conclusions

Evaluation of early maturing soybean genotypes is becoming an important component of soybean improvement program targeting moisture stress growing areas in Ethiopia in view of the current climate change scenarios. The present study revealed that the tested genotypes significantly differed for most of the studied traits. The maximum seed yield was recorded from genotypes JM-HAR/PR142-15-SB (2.11t/ha) followed by JM-HAR/G99-15-SD-2 (1.98 t/ha) and JM-PR142/G99-15-SB (1.97 t/ha). According to GGE biplot analyses, G3 (JM-HAR/G99-15-SD-2), and G7 (JM-HAR/PR142-15-SB) were ideal genotypes in terms of higher-yielding ability and stability among the test genotypes. Hence, these two genotypes which are well performed over years and locations are potential genotypes. On the other hand, Y2L2 (Gofa) and Y1L3 (Humera) are identified to represent ideal environments for soybean production in the country.

Acknowledgements

We thank the Ethiopian Institutes of Agricultural Research and soybean innovation laboratory (SIL) for the financial support.

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