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Research Article

Genotype by Environment Interaction and Yield Stability Studies on Medium Maturing Soybean Genotypes Tested in Northwest, Southern and Western Parts of Ethiopia for two Consecutive Years (2016-2017) Across Five Testing Locations

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Abstract

Soybean breeding program in Ethiopia has been actively involved in improving the genetic yield potential to meet the needs of farmers in different parts of the country. The study aimed to determine the presence of soybean production mega-environments and to evaluate the yield performance and stability of 17 soybean genotypes. Soybean yield performances were evaluated on five production centers in Ethiopia during 2016-2017 growing season. The experiment in each location was arranged in a randomized complete block design with three replications. Parameters observed included grain yield and yield components. The yield data were analyzed using GGE biplot and the yield components data were analyzed using analysis of variance. The results showed that the yield performances of soybean genotypes were highly influenced by genotype-environment interaction (GEI) effects. The yield components were significantly affected by GEI. The partitioning of the G + GE sum of squares showed that PC1 and PC2 were significant components which accounted for 48. 63% and 23.53% of G + GE sum of squares, respectively. Based on the GGE visual assessment, agro-ecology for soybean production in Ethiopia was divided into at least three mega-environments. Genotypes 8 and 5 were the best yielding genotypes in the most discriminating environment. Genotypes 8 and 5 were stable and had relatively high yield performances across test environments. And those genotypes were recommended to be released for production in Ethiopia as new soybean varieties.

Keywords: Soybean; Genotypes; Stability; Environments; Genotypes by Environment Interaction

Introduction

Soybean is one of the most important export oil crops next to sesame and recently interred in to the global market in Ethiopia. Soybean production is dealing with two issues, which are the decrease in total acreage and the increase in soybean consumption. On the other hand, the number of people who consume processed soybean products also increased, even the processed soybean products have already spread beyond the previlages of Ethiopia as cooking oil. The combination of the level of consumption per year and the increasing population triggers the increased domestic soybean demand, and so far is unable to be fully met soybean domestic demands. Hence, a key objective of soybean breeding in Ethiopia is increasing yields per unit area. In Ethiopia, soybean is grown in diverse agro ecological environments. The largest soybean area is in the lowland that cultivated in the rainy season (June/July–September/October) following the cropping pattern of cereal- cereal – soybean. Fertile land, mainly the low land such as paddy field, is the largest contributor of the national soybean production, i.e. 62% from the total 8.1 million hectares of lowland areas [1,2]. Soybean grain yield as a complex character is associated with some yield

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components and influenced by environmental fluctuations [3-5]. Soybean yield potential in various agro-ecological environments vary depending on the compatibility with the agro-ecosystem, biotic and abiotic stress magnitudes, and level of crop management [6,7]. Environmental variables such as soil type, growing season, planting pattern and elevation often become a determinant of suitability adaptation of soybean varieties in Ethiopia [8,9]. It also leads to the interaction between genotype and environment (GEI), which caused difficulties in selecting superior lines [10]. Optimization of such diverse environments can be achieved by the provision of high yielding and stable adaptation soybean varieties. So far, the Ethiopian Institutes of Agriculture released 26 soybean improved varieties. Superior/improved variety is recognized as a cultivation technology component which is inexpensive, easy to adopt and compatible with other technological innovations as well as safe for the environment [11]. Multi-environment yield trials are widely used for selecting superior soybean advanced lines to be released as a new variety for target environments in Ethiopia soybean breeding programs. Numerous methods for analyzing soybean multi-environment trial data have been developed to expose the patterns of GEI, for instance joint regression [12-14], AMMI model analysis [15], and the newest and most popular method of GGE biplot [16] GGE (genotype main effect plus genotype by environment interaction) shows visual examination of the relationships among the test environments, genotypes and the genotype by environment interactions [17]. The biplot tool is being increasingly used by plant breeders and agricultural researchers since its use in mega-environment investigation, genotype evaluation and test location evaluation [16]. A mega-environment is defined as a group of locations that consistently share the same best cultivar(s) [18]. The multi-environment analysis, especially GGE biplot, has been used in recent years for explaining GEI and quantifying the adaptability and stability of tested soybean genotypes [19,20]. However, the use of GEI study in Ethiopia has not been much adopted documented, particularly as a tool for determining the mega-environments and the best performing soybean genotypes in each location. The aims of this study were to determine the presence of soybean production mega-environments and to evaluate the yield performances and the yield stability of soybean genotypes tested for two years (2016-2017) across five testing locations.

Materials and Methods

The study materials used in this research includes 17 soybean promising lines which were introduced from IITA 2014 to obtain high yielding, stable and Medium maturing varieties, (table 1) and Gishama and Pawe-3 varieties were used as standard check that are high yielding and popular varieties. The field trials were conducted at five locations of soybean production centers in Ethiopia. Table 1, genetic materials used for soybean multi-location trials at five locations during main cropping season, June/July – October 2017. Genotype Pedigree, Source and Remark are indicated.

S.No.	Pedgree	Source	Remark
1	TGX 1989-11F	IITA	promissing
2	TGX 1989-42F	IITA	promissing
3	TGX 1989-45F	IITA	promissing
4	TGX 1989-53F	IITA	promissing
5	TGX 1989-75F	IITA	promissing
6	TGX 1990-106F	IITA	promissing
7	TGX 1990-107F	IITA	promissing
8	TGX 1990-110F	IITA	promissing
9	TGX 1990-111F	IITA	promissing
10	TGX 1990-114F	IITA	promissing
11	TGX 1990-87F	IITA	promissing
12	TGX 1990-80F	IITA	promissing
13	TGX 1990-95F	IITA	promissing
14	TGX 1993-4F	IITA	promissing
15	Pwe-3	IITA	Standard check
16	Gishama	PARC	Local check
17	korme	BARC	Released variety

Table 1: Genetic materials used for soybean multi-location trials at five locations during main season 2016-2017.

Description of each test location is presented in table 2. The study was conducted for two growing seasons from June/july2016 to September 2017. The study sites had different soil types, mean seasonal rainfalls and altitudes. The experiment in each of the five study sites was arranged in a randomized complete block design with three replications. Each variety was planted using 2.4 m × 4 m plot size, 60 cm and 5cm plant spacing, two seed per hill. Fertilizers used consisted of 100 kg ha–1 that were applied during sowing the seed. Weeds, pests and diseases were intensively controlled. Parameters observed included plant height, pod number per plant, branch number per plant, and total node number per plant, 100 grain weight, and grain yield per plot. Grain yield per plot was converted to quintal per hectare. Data were then analyzed using analysis of variance (ANOVA). GGE analysis was used to determine the effects of GEI on yields. The results were visualized in biplot graphs

[16,21]. The GGE model was as the following: Yijr = μ + ej + λk αik γjk+ εijr, Yijr = observation of the rth replicate of the ith genotype in the jth environment, μ = the overall means, ej = main effect of the j^{th} environment, $^{\chi}$ = matrix rank {gge}ij when {gge}ij = gi + geij, λk = the singular value for principal component k, αik = the eigenvector score for genotype i and component k, γjk = the eigenvector score for environment j and component k, and εijr = the error for genotype i and environment j and replicate r.

Location	Code	Land type	Altitude	Latitude	Longitude	RF (mm)	Soil types
Pawe	E1	Low land	1100 masl	11^0 18'N	036^0 24'E	1586 mm.	Nitisol
Areka	E2	Mid-land	1600masl	09^0 19'N	33^0 23E	1456mm	Sandy-clay
Bako	E3	Mid-land	1650	09°06'N	37°09'E	1431mm	Sandy-clay
Sirinka	E4	Mid-land	1500masl	11°49'00"N,	39°38'00"E	1850	Clay
Asossa	E5	Mid-low land	1650masl	10°02.922'N	34° 33.8'E	900 -1300 mm	loams and black clay

Table 2: Characteristics of the locations used for multi-environment trials study of soybean for two years (2016 -2017).

Result and Discussion

Analysis of variance and GGE

The analysis of variance for grain yield and yield components of the 17 soybean genotypes tested in five environments showed that the mean squares of environments, genotypes and genotype × environment interactions (GEI) were highly significant (table 3), and the analysis of variance revealed that environments, genotypes and genotype × environment interactions accounted for 77.49%, 7.03% and 15.47% of sum of squares explained, respectively. A highly significant GEI indicates the necessity for further analysis for yield stability. In this present study, the Genotype was small in variation among them, whereas environment (E) and genotype by Environment Interaction (GEI) explained most of the variations. This indicated that Environment (E) and genotypes by Environment Interaction (GEI) are both important in governing for expression of this trait [22]. Another report demonstrated that GEI effects were higher than those shown by the genotypic and the environmental effects [20], and environmental effect was three times higher than the G and GE effects (Cravero., *et al.* 2010; Suwarto 2010), these is similar with the present study in which Environmental effect was ten times higher than Genotype effects and the interaction effect also two times higher than the Genotypes. The GGE analysis partitioned the sum of squares of GEI into five interaction principal components (PCs), of which the first two PC were significant (table 3). The partitioning of the G + GE sum of squares through GGE biplot showed that PC1 and PC2 were significant components that explained 47.63% and 23.53% of G + GE sum of squares, respectively. This result revealed that there were differential yield performances among soybean genotypes across testing environments due to the presence of GEI. The presence of GEI could complicate the selection process of superior genotypes and might reduce the selection efficiency in a breeding program According to Gauch [23].

Mean squares				
parameters	**Environment**	**Genotype**	**Gx E interaction**	**CV (%)**
DF 50%	4437.46	38.98**	16.29**	7.90
DM 95%	3162.29	1939.74**	2021.65**	36.26
PH(cm)	15944.10	88.47**	65.59**	12.25
Brch	127.48	2.19**	1.66**	19.66
ppp	24202.22	200.45**	233.26**	26.84
seed	4.92	0.028**	0.080**	12.05
Hsw(gm)	92.43	5.89**	2.79**	13.02
yield(kg/ha)	20610239.47	2487140.5***	208222.9**	22.80

Table 3: Analysis of variance for yield and yield components of 17 soybean genotypes tested in five environments in 2016-2017.

In the table above, where: **, ***=Indicates highly and strongly significance of genotype, Environ means and their interactions respectively.

Source of variation	Degree freedom	Sum of the squares (SS)	Explained ss % (δ)	Mean of the squares (MS)	p>F
ENV	4	82441128	77.49909	20610282	0.000
GEN	16	7478651.24**	7.03033	467415.7	<0.0001
ENV*GEN	64	16457118**	15.47058	257142.5	0.0008
PC1	19	5820085.66**	48.63086	306320.3	0.0005
PC2	17	2816030.44**	23.52989	165648.8	0.0094
Residuals	425	134801472		317179.9	
Pooled error	560				
Total Eigenvalue*			22.50*		

Table 4: Analysis of Variance for GGE Biplot.

PC = Principal component; * = total of Eigen values are equal with total of G +GE sum of squares; ** = significantly different at 1% level.

Which-won-where pattern and mega environment classification

The GGE biplot was used to effectively identify the existing GEI pattern of the grain yield data (figure 1). GGE biplot is an essential tool for addressing the mega environment issues, by showing which cultivar won in which environments, and it was effective for visualizing in mega-environment identification [16]. Polygon views the GGE biplot showing the mega-environments and their respective highest yielding cultivars (figure 1), and explicitly displays the "which-won-where pattern" as a concise summary of the GEI pattern derived from multi-environment yield trial data set for the five locations. In the present study, six lines in figure 1 divided the biplot into six sectors or six mega environments (I to IV) and the environments fall only into two of them (I, and II). The vertex genotypes in this study were genotypes G8, G5, G2, G3, G6 and G11. According to Yan and Tinker (2006), the vertex genotypes were the most responsive genotypes, as they have the longest distance from the origin in their direction.

Figure 1: Polygon views of the GGE-biplot of grain yield for the which-won-where pattern for genotypes and environments. PC1 = first principal component, PC2 = second principal component, I =1st sector, II = 2nd sector, III = 3rd sector, IV= 4th sector, V= 5th sector and VI=6th sector of the biplots and testing locations are Areka, Bako, Asossa and Sirinka.

Two environments (Areka and Bako) fell into the first sector (mega-environment) with vertex genotype for this mega-environment was G8 through the standard chech (G15) also performed well in those two environments. Three environments (Pawe, Asossa, and Sirinka) fell into the second sector (mega-environment) and the vertex genotype for this mega-environment was G5, suggesting that this is the most responsive genotype and performed well for these three environments. None of the environment fell in to sector VI, V, IV and III in which the vertex genotypes for these sectors are G11, G6, G3 and G2. This vertex genotype for this sector suggesting that these genotypes are classified as a winning genotype for this sector and none of them are falling into the testing environment and yields below the average mean yield. Genotypes G4, G12, G17, G7, G1, G9, G14, G11, G6, G2 and G3 fell in sectors where there were no testing locations at all, showing that those genotypes were poorly adapted in all of the five tested environments.

Yield and yield component performances and yield stability

Yield performance and yield stability of the tested soybean genotypes were graphically visualized through GGE biplot (figure 2). This can be evaluated by the average environmental coordinate (AEC) method [24,25]. In this method, a straight line passing through AEC with the biplot origin is as AEC abscissa, and a straight line through the origin and perpendicular biplot is as AEC ordinate. Directions to the AEC ordinate that move away from the origin biplot showed increased stability. AEC ordinate splitted the genotypes under and above the general yield average. Referring to figure 2, four high yielding soybean genotypes (G 16, G15, G8 and G5) performed over the general yield average. Genotype 5 demonstrated the highest yield and adapted to the three test environments of the lowland areas of Ethiopia, which are receiving high rain fall amount anualy like Pawe**,** Asossa and Sirinka that could be cultivated in the area up to 1650 masl with the soil type of Regosol or association of Alfisol and Inceptisol, such as in pawe or Asossa.

Figure 2: Average environment coordinate (AEC) of the GGE biplot based on symmetrical scaling.
On the fig. above where: AEC: indicates Average environment coordinate, GGE: Genotypes, Genotypes by Environment interaction, PC1=the first Principal Components and PC2: the second Principal components.

Other high yielding genotypes which also adapted to specific environments were genotypes G16 and G15. These results showed a number of similarities with the previous reports showing that three top high yielding genotypes out of twenty soybean genotypes tested were unstable when evaluated across different locations, and hence such genotypes were recommended for a specific environment [26]. In this study, genotypes G8 showed the highest yield stability and relatively high yield. The poorest yield performance and also the unstable genotype was genotype G11, G6. G12, G3, G17, G10, G2, G4 and G13. Numerous studies have been conducted to investigate soybean yield stability. Atnaf (2013) found three ideal soybean genotypes as it exhibits both high mean yield and high stability performances across the test environments. Another study reported that soybean genotype was reported as an ideal genotype with high yield and high stability as demonstrated by low GEI [20,27,28].

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Asfaw., *et al.* (2009) also reported that GEI was an important source of soybean yield variation. The use of biplots was effective to graphically visualize the GEI pattern of genotypes and environments, and to determine the stability and adaptability of the genotypes. Table 5 presents the grain yield of each soybean genotype in each location. Average of 17 genotypes, the grain yields across five environments ranged from 2.621 ton/ha in environment (Sirinka) to 2.317ton/ha in Pawe, suggesting that there was almost 0.3 ton/ha difference between these two environments.

No.	**Variety**	**2016**								**2017**				**Over all Mean**
		Bako	**Areka**	**Assosa**	**Pawe**	**Sirinka**	**Mean**	**Bako**	**Areka**	**Assosa**	**Pawe**	**Sirinka**	**Mean**	
1	TGX 1989-11F	1760.8	1262.7	1550.9	1337.4	1913.4	1565.0	1372.3	1491.7	1393.1	2563.8	2771.5	1918.5	1741.8
2	TGX 1989-42F	1969.4	1312.5	1105.9	1590.0	1753.8	1546.3	1994.1	1618.4	1676.1	2830.0	2233.3	2070.4	1808.3
3	TGX 1989-45F	1810.7	1454.0	927.0	1035.9	1782.7	1402.1	1696.9	1661.4	1512.3	2545.3	2442.7	1971.7	1686.9
4	TGX 1989-53F	2076.7	1567.5	1582.1	980.6	1771.1	1595.6	1437.3	1588.5	1860.6	1981.3	2621.8	1897.9	1746.7
5	TGX 1989-75F	2374.0	2275.4	1605.7	2473.9	2403.0	2226.4	1958.1	2184.4	2415.0	2570.5	2506.7	2326.9	2276.7
6	TGX 1990-106F	1545.5	1391.2	1449.9	963.6	1727.1	1415.5	1148.1	2283.0	1289.0	2479.5	2585.3	1957.0	1686.2
7	TGX 1990-107F	1778.0	1682.0	1411.6	1441.0	1870.4	1636.6	1395.6	1748.0	1902.3	2320.2	2460.9	1965.4	1801.0
8	TGX 1990-110Fn	2142.6	1743.6	1961.5	1966.7	2497.3	2062.3	1475.4	1984.4	2371.0	2665.0	3074.7	2314.1	2188.2
9	TGX 1990-111F	1474.0	1320.4	1600.8	1231.3	2432.5	1611.8	1859.9	1689.2	1531.8	2314.4	2660.7	2011.2	1811.5
10	TGX 1990-114F	2008.9	1246.8	1388.5	1385.3	2050.8	1616.0	1630.4	1466.5	1055.1	2461.8	2732.0	1869.2	1742.6
11	TGX 1990-87F	1921.0	1858.2	1517.5	1486.2	1861.1	1728.8	2258.2	1565.8	1829.0	2319.2	2489.3	2092.3	1910.5
12	TGX 1990-80F	1688.4	1220.2	1326.2	1297.5	1646.4	1435.7	1564.0	1711.0	1058.1	1674.9	3016.7	1804.9	1620.3
13	TGX 1990-95F	1707.9	1396.2	1338.5	1486.2	2051.6	1596.1	2006.5	1084.7	1394.8	1839.9	2591.9	1783.6	1689.8
14	TGX 1993-4F	2009.5	1129.2	1341.1	1353.8	1646.8	1496.1	1713.5	1695.2	1328.4	2392.3	2655.7	1957.0	1726.6
15	Pawe-03	1626.4	1184.8	1346.0	1551.3	1785.3	1498.8	1455.4	1518.4	1710.3	2195.7	2609.1	1897.8	1698.3
16	Gishama	1928.4	1918.7	1650.4	1556.5	1925.2	1795.9	2637.9	1752.4	1572.5	2051.3	2525.4	2107.9	1951.9
17	korme	1765.4	1349.0	1249.5	1447.7	1740.9	1510.5	1860.5	1573.4	1862.5	2195.3	2582.6	2014.9	1762.7
	Mean	1858.1	1489.0	1432.4	1446.2	1932.9	1631.7	1833.2	1683.3	1632.0	2317.7	2621.2	1997.7	1814.7
	CV (%)	23	21	37	28	32		12	20	29	29	10		
	LSD	710.6	512.7	875.3	663.8	101.6		350.0	571.5	794.7	110.2	425.8		
	Loc*Treat	**	**	**	**	**		**	**	**	**	**		
	Loc*Treat*year	**	**	**	**	**		**	**	**	**	**		

Table 5: Average Grain yield of 17 soybean genotypes tested for two years over five locations.

Where: loc = is stand for locations, LSD: Least Significant Difference at 5% and1%level of probability values and CV (%) Coefficient of variation.

In the presents study table 6, the grain yield and yield components of 17 soybean genotypes tested in five environments indicates that Genotype 5, as unstable genotype, but it shows the highest yield and medium maturing comparable to Genotype 8 stable the stable one. Genotype 8 also had medium grain size compared to Genotype 5 having medium to large seed size and furthermore the stable genotypes 8, with high perse performances (over the general mean) demonstrated medium maturity and medium grain size.

Average of 17 genotypes, the grain yields across five environments ranged from 2621.2 kg/ ha in environment (Sirinka) to 2317.7kg/ ha in environment (Pawe), suggesting that there was almost 0.3tons ha-1 difference between these two environments due to environmental variation.

T.N.	Varieties	DF50 %	DM95 %	PH (cm)	Br NPP	NPPP	NSPP	HSW (g)	Adjyld (q/ha)
1	TGX 1989-11F	64.8	122.2	72.4	4.9	64.3	2.4	12.9	1741.8
2	TGX 1989-42F	63.6	122.3	66.5	3.0	64.5	2.3	12.7	1808.3
3	TGX 1989-45F	61.9	121.6	73.8	5.1	64.7	2.4	12.7	1686.9
4	TGX 1989-53F	63.7	121.9	69.6	5.2	64.3	2.4	12.6	1746.7
5	TGX 1989-75F	62.8	122.5	69.1	5.0	66.8	2.4	13.0	2276.7
6	TGX 1990-106F	64.7	122.2	70.9	5.0	70.5	2.3	12.7	1686.2
7	TGX 1990-107F	64.2	122.8	72.4	4.9	67.2	2.3	13.3	1801.0
8	TGX 1990-110Fn	61.4	121.8	67.1	5.3	64.3	2.4	12.9	2188.2
9	TGX 1990-111F	64.5	121.4	68.6	3.2	62.9	2.4	12.7	1811.5
10	TGX 1990-114F	65.1	122.2	74.3	3.5	67.6	2.3	13.0	1742.6
11	TGX 1990-87F	62.4	122.6	71.9	5.4	64.9	2.4	13.1	1910.5
12	TGX 1990-80F	64.9	156.4	66.1	5.0	63.1	2.2	13.4	1620.3
13	TGX 1990-95F	67.0	122.3	69.6	3.4	66.2	2.3	12.6	1689.8
14	TGX 1993-4F	63.9	122.9	71.6	3.2	64.8	2.4	12.8	1726.6
15	Pawe-3	65.0	123.0	72.0	5.2	62.4	2.4	12.7	1698.3
16	Gishama	64.4	121.9	71.5	4.0	64.6	2.3	12.5	1951.9
17	korme	63.2	122.6	73.7	4.9	66.7	2.4	12.9	1762.7
Mean		64.0	124.3	70.7	5.1	65.3	2.3	12.9	1814.7
CV (%)		8.2	2.2	14	13	14	16	10	24
LSD (5%)		2.7	1.6	5.1	2.4	4.5	0.2	0.64	226.2
Sign		**	**	**	**	**	**	**	***

Table 6: The Means yield and agronomic characters performance of Soybean National variety trial in five locations for two years (2016-2017).

Where: DF50%=days to flowering at 50%, DM 95%=days to physiological Maturity at 95%, PH (cm) Plant height at harvest, BrNPP=Branch Number per plant, NPPP=Number of pod/plant, NSPP=Number of seed /pod, HSW(g)=Hundred seed weight, Adjyld (q/ha)=Adjusted yield in quintal/ha, CV(%)=Coefficient of variation, LSD: The list significant difference among treatments tested across five location at 5% level of significance.

Conclusion

High Genotype × Environmental interaction complicates breeding work because it makes difficult to predict how genotypes selected under a given set of conditions will perform in a different set of environmental conditions. By exposing a number of genotypes to a set of contrasting environments, it is possible to identify genotypes with a high average yield and low G × E interaction. Such genotypes are commonly referred to as widely adapted genotypes and they possess characteristics, such as resistance to pests and tolerance to environmental stress that enhance their performance and makes yield fluctuation over year and across the divers test environments of the Genotypes by Environment Interaction and yield stability study, in the present shows that, two genotypes (TGX-1989-75F and TGX-1990-110FN) were identified as both high yielding and stable over the test location and those variety among the introduced genotypes were considered as having wide adaptation and they would be beneficial to farmers if they are released and it recommended for seed production.

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