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Yield Stability Studys on Late Maturing Soybean genotypes tested in Ethiopia for two consiquetive years (2016-2017) across five testing locations using GGE Biplot analysis of data trial

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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 and market 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 11 soybean genotypes. Soybean yield performances were evaluated on five production areas 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 partitioning of the G + GE sum of squares showed that PC1, PC2 and PC3 were significant components which accounted for 80. 60% and 9.20 % and 7.44 % of G + GE explained sum of squares, respectively. Based on the GGE visual assessment, agro-ecology for soybean production in Ethiopia was divided into similar five mega-environments. Genotypes 11 and 7 were the best yielding genotypes in the most discriminating environments, but adapted to specific environment E1 and E4, thus highly recommended for that specific location. Genotypes 9 and 10 were stable and had relatively high yield performances across environments.

Keywords: Soybean, Genotypes, Genotypes by Environment Interaction, Stability, GGE

INTRODUCTION

Soybean [Glysin max (L.) Merrill] is one of the most important pulse crops widely grown by small holder farmers in the Eastern and North western parts of Ethiopia (Alghamdi SS. 2004). It rich source of proteins, cooking oil and micronutrients particularly it has highest protein (42%), oil (23%), rich in lysine, vitamins A and B and free from cholesterol. Soybean is considered as wonder crop among smallholder farmers due to its ability to tolerate and perform well under low amount of rainfall conditions, short maturity periods and ability to improve soil fertility through nitrogen fixation (Swaminathan et al., 2012) Late maturing and Indeterminate types of soybean variety are high yielding and expressing their genetic potentials than Early maturing and determinate types (Shanmugasundaram et al., 2009). Determinates types of soybean variety are characterised by having shorter in plant height and subjected to yield penalty due to soil moisture stress of their environments in line with shorter height and suffered for weedy problem at harvest .Therefore it was necessary to develop late maturing and indeterminate soybean variety that have high yielding potential and weedy problem free at harvest due to its height, provided that Such new varieties must show high performance for yield and other essential agronomic traits and their superiority should be consistent (stable) over a wide range of environmental conditions (Becker & Leon, 1988). Recommendation of high yielding and stable Soybean genotypes is particularly important in Ethiopia due to variations in environmental conditions and production is mainly depends on rain-fed and no means of modifying the environment are unavailable. Hence the present study was aimed at identifying high yielding and late maturing soybean varieties that have a stable performance across testing regions using the YSi selection and GGE analysis

Materials and Methods

Eleven late maturing soybean genotypes and two checks , were planted for evaluation in three replication on five locations for two consiquetive cropping seasons 2016-2017 in Ethiopia. All genotypes were obtained from IITA (International Institutes of Tropical Agriculture (Nigeria) in 2014/2015 as shown in Table1 except control varietys. The testing locations were; Pawe, Asossa (Benishangul Gumuze Regional States), Areka (SNNP) Regional State and Bako and Jimma (Oromia Regional States), located in Western, North Western and Southern parts of Ethiopia from 2016-2017.These locations represent the major Soybean growing areas of the country and are characterised by medium to long growing season with maximum rain fall . In all locations, genotypes were planted in Randomized. Completely Block Design (RCBD) in three replications with 2.4 m × 4m plots size at spacing of 1.5m, 60cm, 60cm and 5cm between block, plots, rows and plants respectively. In each season, experimental plots were kept free of weed following recommended agronomic practices with a fertilizer rate of 100kg/ha bases. Grain yield and Yield related traits. Data were collected on: Days to flowering (DF 50%), Days to maturity (DM 95%), Plant height (PH (cm)), Number of branch per plant (NBrch), Number of pod per plant (Npp), Number of seed per pod (NSpp), Hundred seed weight (HSW (g)), Seed moisture content (SMC (%)), Stand count at harvest (SCH) and plot yield (g/plot). A combined analysis of variance to assess the significance of GEI was carried out before computing the yield and yield-stability statistics (YSi). Shukla's Stability Variance and Kang's Yield - Stability (Ysi) Statistics were calculated according to (Kang, 1993). All analysis were carried out using, SAS 9.3 version, R- version 3.1.2 (R-Core Team, 2014), Meta R (GEA-R). Following the detection of significant GEI, YSi statistics for 11 G were calculated as described by Kang (1993)

Table1. List of IITA introduced soybean genotypes evaluated in the studies over three locations for two years (2016 – 2017)

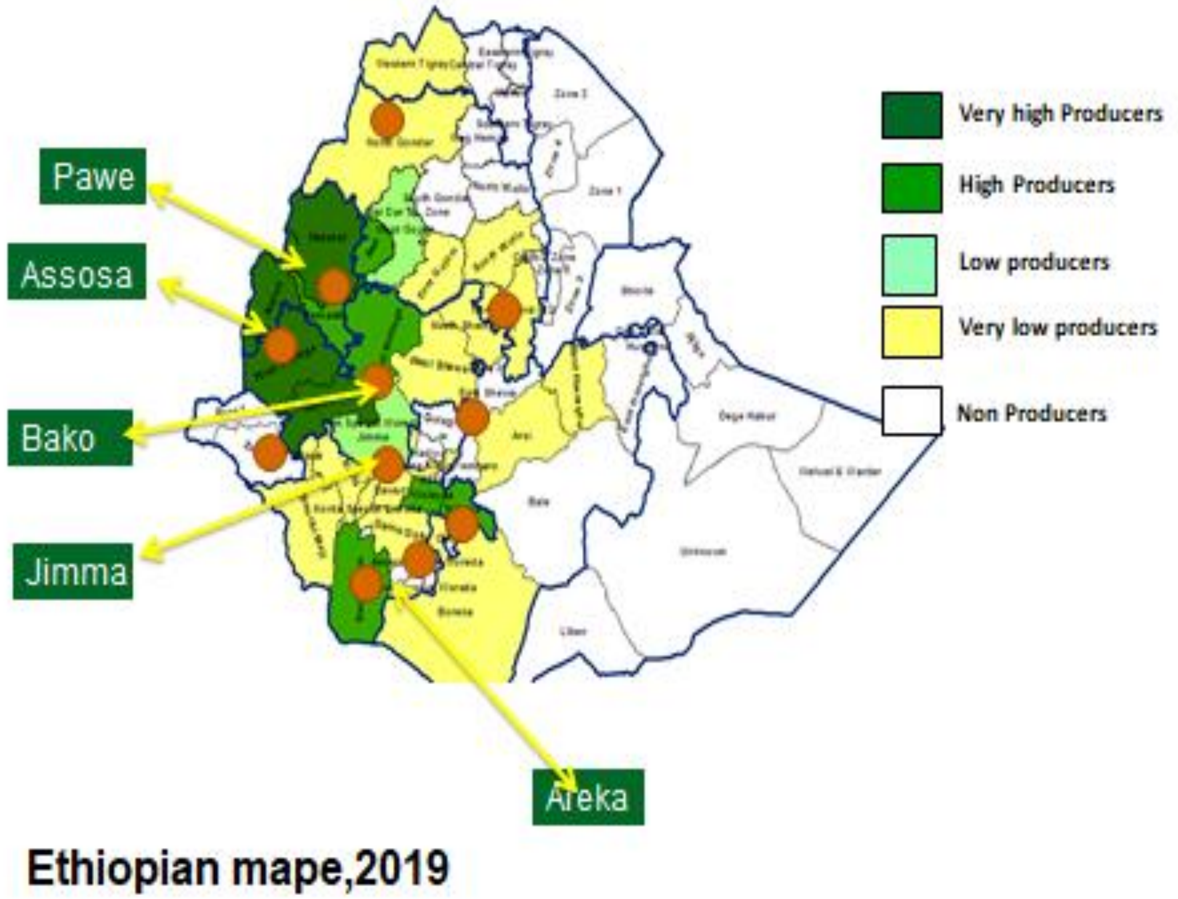
S.No	Variety	Specious	maturity	country	Year of introduction
1	PB-12-9	*Glysin soja*	Late	IITA/Nigeria	2013/14
2	PB-12-3	Glysin soja	Late	IITA/Nigeria	2013/14
3	PB-12-7	Glysin soja	Late	Standard check	2013/14
4	TGX-1904-6F	Glysin soja	Late	IITA/Nigeria	2013/14
5	PB-12-3	Glysin soja	Late	IITA/Nigeria	2013/14
6	P M12-62	Glysin soja	Late	IITA/Nigeria	2013/14
7	TGX-1990-128F	Glysin soja	Late	IITA/Nigeria	2013/14
8	TGX-1485-1D	Glysin soja	Late	IITA/Nigeria	2013/14
9	Paw-3	Glysin soja	Late	Standard chech	-
10	Belessa-95	Glysin soja	Late	local check	-
11	TGX-1990-59F	Glysin soja	Late	Local check	2013/14

Note: IITA International Institutes of Tropical Agriculture

Table2: Characteristics of the Multi Locations environments used for evaluation of Late maturing soybean genotypes tested for two consiquetive years (2016 -2017).

Location	Code	Land type	Altitude	Latitude	Longitude	RF (mm)	Soil types
Jimma	E1	Low land	1100 masl	11 0 18'N	036^{0} 24'E	1586 mm.	Nitisol
Bako	E5	Mid-land	1600masl	09 0 19'N	33^{0} 23E	1456mm	Sandy-clay
Areka	E4	Mid-land	1650masl	09°06'N	37°09'E	1431mm	Sandy-clay
Asossa	E3	Mid-low land	1650masl	10°02.922'N	34° 33.8'E	900-1300 mm	loam sandblack clay
Pawe	E2	Mid-land	1750masl	11'9''N	35^{0}23'E	1555mm	Loam black

Fig1. Showing the Location of the five potential test Environments for Soybean production in Ethiopian map and indicating the soybean suitability map in the country



RESULT AND DISCUSSIONS

Combined Analysis of Variance

AMMI analysis of 11 soybean genotypes tested in Five environments for two years showed that Soybean grain yield was significantly ($P<0.05$) affected by G, E and GEI. The presence of genetic variation and possible selection of stable genotypes were indicated table2 65.45% of the total sum of squares was justified by E fluctuations and exhibiting that the E were diverse and causes different grain yield (fig1 & Table2)

Table 3 Analysis of variance for GGE-Biplot

Source of variation	DF	SS	Explained ss% (δ)	MS
ENV	4	13116953.64	11.92	3279238.41
GEN	10	76400137.2	69.45	7640013.72
ENV*GEN	40	20481076.86	18.61	512026.922
PC1	13	4720520.151	80.60	363116.935
PC2	11	3862131.89	9.20	351102.899
PC3	9	1244550.648	7.44	400952.6
Residuals	275	61778382		224648.7
Pooled error	362			
Total Eigen values*			88.06*	

Fig2. GGE Biplot showing the first interaction Principal component axis (IPCA1) versus Second interaction principal component axis (IPCA2) for soybean genotypes

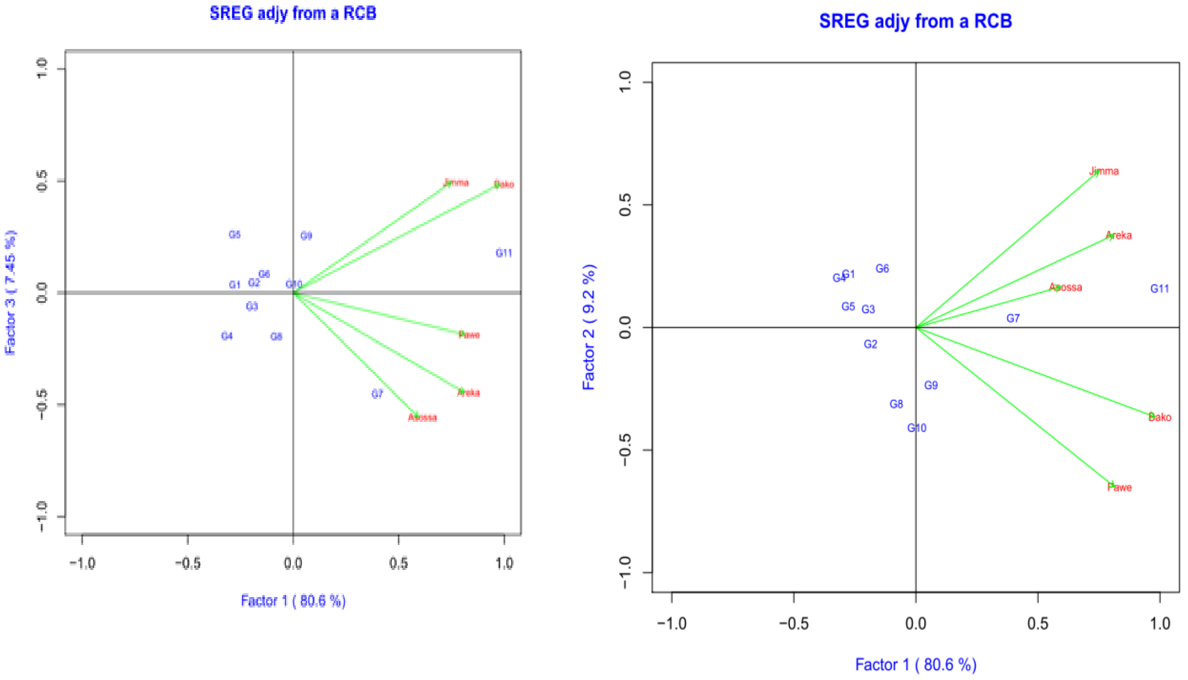


Table4 ANOVA table showing the significance of interaction among genotypes and test environment using mean squares of yield contributing traits in soybean tested across five location in2016-2017 cropping season in Ethiopia

Source of Variation	df	Mean squares							
		DF (50%)	DM (95%)	PH(cm)	Brch(No.)	POD(No.)	SEED(No.)	HSW(gm)	YLD(gm)
Y	1	1876.875**	2077.52	964.61**	4659.39 **	86.343 **	0.22936**	35.5027**	8087482.59**
L	4	29902.1**	27662.28**	24664.27**	84.68**	2371.00**	4.901**	189.462**	3279238.4**
R (Y*L)	12	38.703ns	2748.8*	400.17**	24.90**	117.710ns	0.180ns	0.477ns	4358.52ns
G	11	294.64**	849.49*	331.53**	73.355**	763.98**	0.28549**	41.66**	7640013.7**
Y*G	11	120.90**	682.0*	151.84ns	74.63***	149.48ns	0.18**	28.39**	738213.98**
L*G	44	90.69**	872.08*	270.55**	26.745**	372.81**	0.1818**	8.1148**	512026.92**
Y*L*G	44	298.48***	1150.03*	581.87**	27.72**	592.08**	0.094**	8.064**	654569.7**
Error		42.03	911.08	89.2258	15.6691	106.834	0.07384	2.90541	80270.5
CV (%)		9.75	23.39	14.52	7 .61	20.45	12.09	12.8	15.55

Where, Y=year, L=Loc, R= replication= for Genotypes, CV (%), Coefficient of variations, DF (50%)=Days to flowering, df=degree of freedom, DM(95%)=Days to physiological Maturity, PH= Plant height, Brch=Branch, Pod=Pod number per plant, Seed=seed number per plant, HSW= Hundred seed weight, YLD=plot yield

Table5. The location mean grain yield of the candidates and the standard check with indicating yield advantages over the standard check (%) at five locations in 2016-2917

Test years	Test Location	Candidate-1 (TGX-1990-59F)			Candidate-2 (TGX-1990-128F)	
		Grain yield of the first Candidate (TGX-1990-59F) (Kg/ha)	Yield of the standard (Pawe-3) (Kg/ha)	Yield advantage of the first candidate over the standard check (%)	Grain yield of the second Candidate TGX-1990-128F(PM-12-7) (Kg/ha)	Yield advantage of the second candidate over standard (%)
2016-2017	**Pawe**	3419.7	1886.7	81.2	2244.9	18.9
	Bako	3807.2	2260.2	68.4	2521.8	11.5
	Areka	2834	1657.2	71	2457.2	48.2
	Asossa	2615.7	1599.7	63.5	2500.9	56.3
	Jimma	3419.7	1886.7	81.2	2044.9	8.3
Mean		**3219.26**	**1858.1**	**73.1%**	**2353.94**	**28.7%**

Table6 Combined and summarized Protein content advantage of soybean candidates over the standard check tested in Ethiopia for two consiquetive years (2016-2017) across five testing location

Candidate-1 (TGX-1990-59F)			**Candidate-2 (-1990-128F)**	
Protein content of the 1st candidate (%)	Protein content of the standard check (Pawe-3)	Protein content advantage of the candidate over standard check (%)	Protein content of the 2nd candidate (%)	Protein content advantage of the 2nd candidate over the standard (%)
35.35	32.35	9.29 %	33.3	2.93%

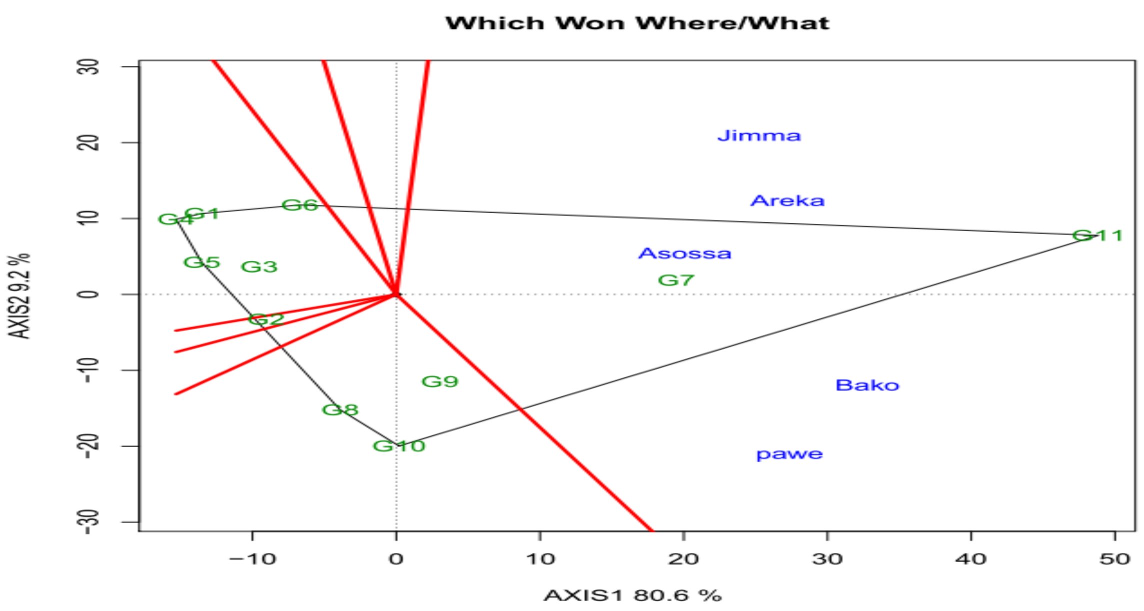
Table7. Combined and summarized Oil content advantage of Soybean candidates over the standard check tested in Ethiopia for two consiquetive years (2016-2017) across five testing location

Candidate-1 (TGX-1990-59F)			**Candidate-2 (-1990-128F)**	
Oil content of the 1st candidate (%)	Oil content of the standard check (Pawe-3)	Oil content advantage of the candidate over standard check (%)	Oil content of the 2nd candidate (%)	Oil content advantage of the 2nd candidate over the standard (%)
23.5	23.0	2 %	23.12	0.52 %

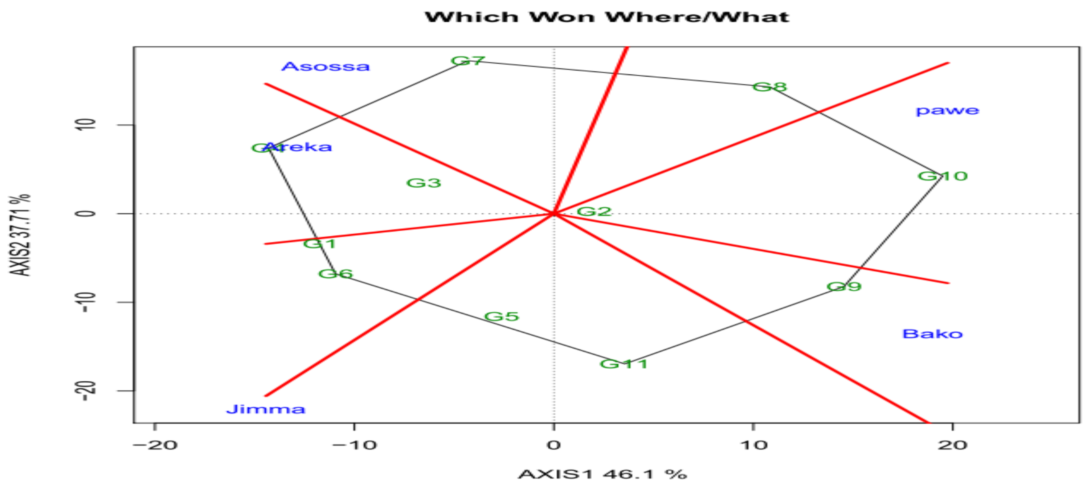
Which-won-where pattern and mega environment classification

The GGE biplot which is based on a "Tester-centered (G + GE)" table, without any scaling and it is row metric preserving. The polygon is formed by connecting the markers of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. Figure 3 also contains a set of lines perpendicular to each side of the polygon. These perpendicular lines divide the biplot into several sectors.The winning genotype for each sector is the one located at the respective vertex. Genotypes located at the vertices of the polygon reveal the best one on the test environment Yan and Tinker (2006). There are seven sectors with cultivars G11, G10, G4, G6 and G1 as the corner or vertex cultivars. Environments Pawe, Bako, Asossa, Areka and Jimma, fall in the sector in which G11, G10 and G4 was the vertex cultivar. While G4 had the lowest yield folowed by G10 of the vertex genotype, similarly genotypes G11, G7and G9 performed above average mean yield. This means that G11 and G7 was the best cultivar for Pawe, Bako, Areka, Asossa and Jimma. While G10 yeald equal to the average mean yield, but G8, G5, G2, G1 and G3 had the lowest yield below the average mean. In the case of environment Asossa in sector 1 for which vertex genotype G11 through G5, G8, G2 and G6 also have the lowest mean performance environment in sector 1 followed by environment Pawe, Bako, Areka and Jimma are normal environment fall into the same sector. No environments fell into sectors with G10, G4, and G6 as the vertices genotypes through G5, G8, G1 and G2, indicating that these cultivars were not the best in any of the environments.

Fig3. Biplot of which won where /what of soybeans tested at five locations for two consiquetive years years 2016-2017



Tester centered with symmetric preservation



Double cent

Yield and yield component performances and yield stability

Means versus stability

The biplot was based on genotype focused singular value partitioning SVP = 1 and therefore appropriate for visualizing the similarities among genotypes. It explained 89.8% of the total variation due to GGE. The two lines that passed through the origin are the ordinate lie with double arros and the abscissa single arrowed of the Average Environment Coordinate (AEC). The AEC itself represented by the small circle close to the abscissa is the mean PC1 and PC2 scores of the environment (Yan and Kang, 2003). The ordinate divides the genotypes into those that yielded above average genotypes on the right and those that yielded below average genotypes on the left. Thus the abscissa arrow points indirection of increasing yield performance. The best performer across five locations based on yield is G11 followed by G7. In the bottom half in the coordinate direction genotypes were below the average mean descending order to the left hand side of the polygon performance are G1, G3, G5, G2 G4, G6 and G9. The projections on to the ordinate are measures of variability or Instability of the genotypes, the longer the vector irrespective of the direction, the more unstable is the associated genotype. Thus, short vector implies high stability (Yan and Kang, 2003). G9 has the shortest vector and therefore identified as the most stable, folowed by G7, while G11 with the longest vector length is less stable, but high yielder than G11. While G7 is fairly stable compered to G11 and high yielder compered to G9, G6, G1, G3, G6, G8, G4 and G5 as below the average mean yields

Figure 4. GGE biplot showing the comparison among eleven soybean genotypes for grain yield and stability

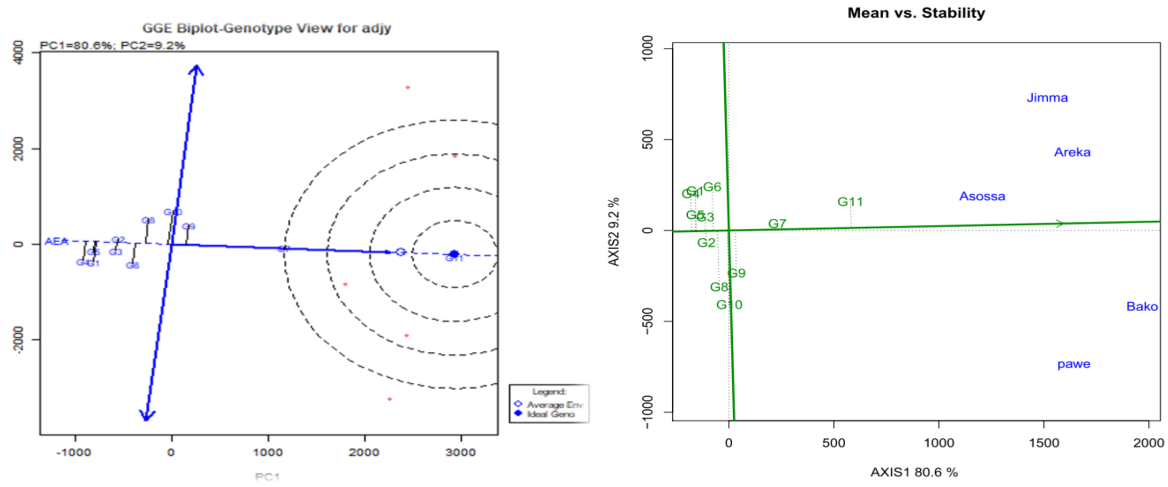


Table 8 Stability prediction using stability models for eleven late maturing Soybean genotypes tested across five testing locations for two consiquetive years 2016-2017

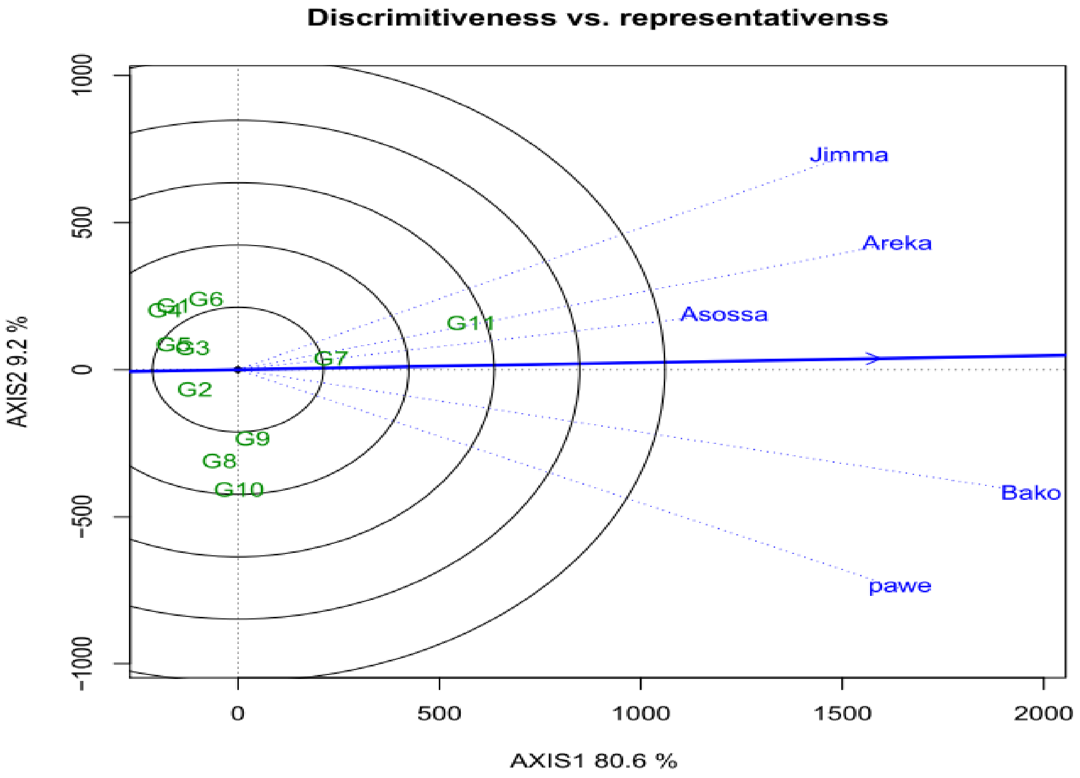
GEN	Mean	δ^2	CV (%)	bi	S^2	R^2	ri^2	Bi	DJi	Wi^2	Pi
G1	1471.19	227.6092	15.4711	0.4176	-18939.1	0.1672	63847.75	-0.5824	57523.41	239988.2	1414128
G10	1797.643	491.22	27.3258	1.3685	121201.4	0.3856	179955.8	0.3685	197664	619978.1	967967.3
G11	3115.183	486.4963	15.6169	1.8958	1000.873	0.7545	110261.8	0.8958	77463.43	391888.6	0
G2	1574.543	300.745	19.1005	1.2948	-66931.9	0.921	4532.448	0.2948	9530.626	45865.4	1232153
G3	1587.463	312.3324	19.6749	0.9258	-3179.68	0.4366	58027.97	-0.0742	73282.88	220941.6	1259124
G4	1434.457	150.7252	10.5075	-0.0824	-46621.3	0.0148	89015.99	-1.0824	29841.24	322357	1522629
G5	1445.113	375.6461	25.9942	1.5061	-38579.4	0.7987	40796.27	0.5061	37883.14	164547	1408563
G6	1648.717	272.0304	16.4995	0.6683	-7386.89	0.2999	60517	-0.3317	69075.67	229087.6	1121649
G7	2368.023	183.818	7.7625	-0.1996	-34050.5	0.0586	116787.6	-1.1996	42412.1	413246	419890.5
G8	1715.227	374.8931	21.8568	0.9277	53915.71	0.3043	110348.8	-0.0723	130378.3	392173.5	1105554
G9	1873.51	519.5908	27.7335	2.2773	-60069.6	0.9545	104624.6	1.2773	16392.95	373439.7	806022.1

In the presents study table 6, the grain yield and yield components of 11 soybean genotypes tested in five environments indicates that G11, as unstable genotype, but it shows the highest yield and late maturing comparable to G7 which is stable and high yielder than G10,G9, but low yielder, but more stable than G11. Genotype 11 also had larger seed size compared to Genotype 7, having medium to large seed size and furthermore stable than genotypes 11, with high perse performances (over the general mean) demonstrated late maturity and medium grain size. Average of 11 genotypes, the grain yields across five environments ranged from 2834kg/ ha in environment (Areka) to 3807.2kg/ ha in environment (Bako), for first candidate, while 2044.9 kg/ha (Jimma) to 2521.8kg/ha (Bako) for the second candidates suggesting that there was almost 0.9 tons ha^{-1} and 0.48 tons ha^{-1} difference between these two environments respectivily for the first and second candidates across location due to environmental variation

Discrimitiveness versus representativeness

The length of the environment vectors (which approximates the standard deviation with in each environment) from the biplot origin and the angle formed with the abscissa of the AEC reveals the discriminatory ability and the representativeness of the test locations (Yan and Kang, 2003). The longer the vector the higher the discriminatory ability of the associated environment and the shorter the angle formed the more the representative the associated environment (Yan et al., 2007).The biplot identified Asossa as the most representative since its vector formed the shortest angle with the AEC abscissa. It was followed by Pawe, Jimma, and Areka while Bako with the largest angle is the least representative. Bako also has the highest discriminatory power due to its possession of the longest vector, followed by Areka and then Asossa with the least discriminator (Fig 5). The small circle close to the arrow of the AEC abscissa delineates the ideal environment, then Asossa is the ideal env't and the location closest to it is adjudged the best (Yan and Kang, 2003). From the biplot Asossa was the closest to ideal environment and therefore the best folowed by pawe among the five testing locations.

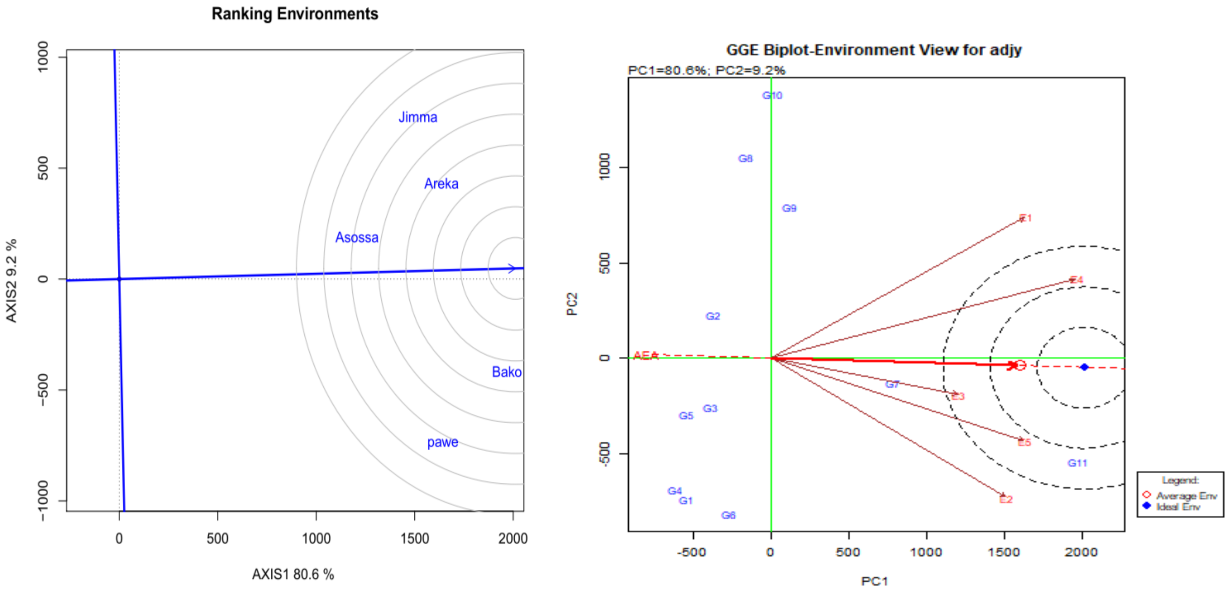
Fig5. GGE biplot showing the discriminatory ability and representativeness of the five test environments



Environment ranking

The ideal test environment should be most discriminating (informative) and also most representative of the target environment. Figure 6 defines an ideal test environment, which is the center of the concentric circles. This is a point on the AEA in the positive direction (most representatives), with a distance to the biplot origin equal to the longest vector of all environments (most informative) Yan and Tinker (2006). Bako (E5) is closest to this point and is there-fore; best, folowed by Areka (E4) and pawe (E2), whereas Jimma (E1) and Asossa (E3) were poorest for selecting cultivars adapted to the whole region. Figure6 is based on a "Tester-centered (G+GE)" table, without any scaling and it is row metric preserving. An environment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan et al., 2000; Yan and Rajcan, 2002). Figure6 shows that environment Bako (E5) was an ideal test environment in terms of being the most representative of the overall environment, based on mean yield performance and comparison among genotypes for the five environment, results showed that G11 has greater stability and high yielding in this environment, and that G7,G9 and G10 was a low yielding genotype respectivily compared to G11.

Fig6. GGE biplot showing the relation among the five testing environments



Ranking Genotypes

The AEC ordinate separates genotypes with below-average means from those with above-average means. Genotypes with above average means were G10, G9, G7 and G11, while genotypes with below-average means yield were G2, G3, G94, G5, G8, G6 and G1. Genotypic stability is quite crucial in addition to genotype yield mean performance; genotypes G11 is more stable followed by G7 were more stable as well as having appropriate yield, while, conversely,G3,G1,G2,G10 and G6 were more variable. The ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2003), which is represented by the dot with an arrow pointing to it (Fig7). Such an ideal genotype then G11, is defined by having the greatest vector length of the high yielding genotypes and with zero GEI (Yan et al., 2007). Concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype; a genotype is more desirable if it is located closer to the ideal genotype, so genotype number G11, which fell into the center of the concentric circles, was ideal in terms of higher yielding ability and stability folowed by G7. Based on these results, cultivar G11 was identified as having a main role in producing adaptable genotypes.

Fig 7. GGE biplot showing the rank of eleven soybean genotypes refering to the ideal testing environments

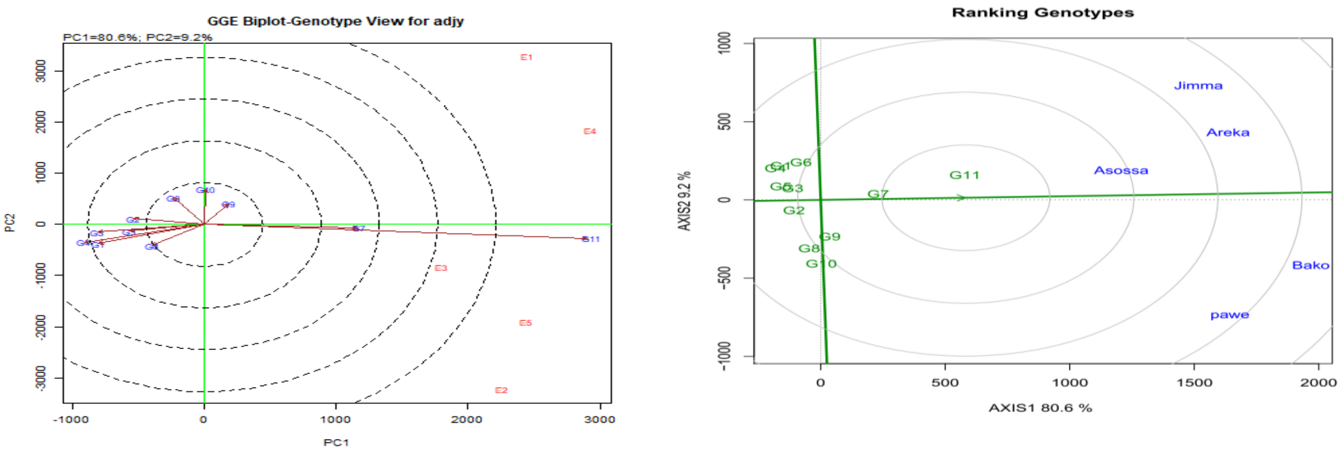


Fig 8. GGE biplot showing the Adaptation maps of soybean genotypes tested at five environments and ideal testing environments where genotypes are adapted

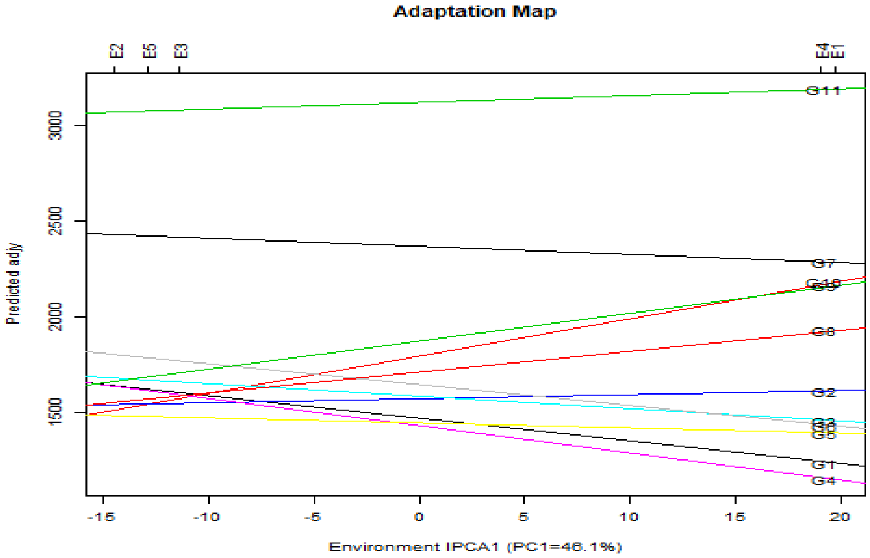


Fig 9. GGE biplot showing the the responses of soybean yield performance across five testing location and responses of each soybean genotypes across five testing locations

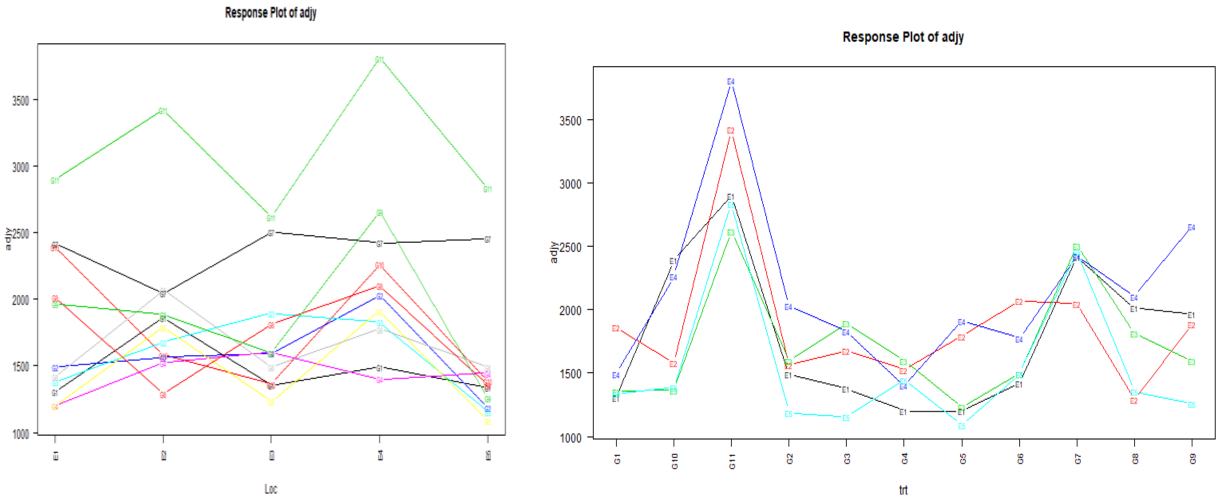
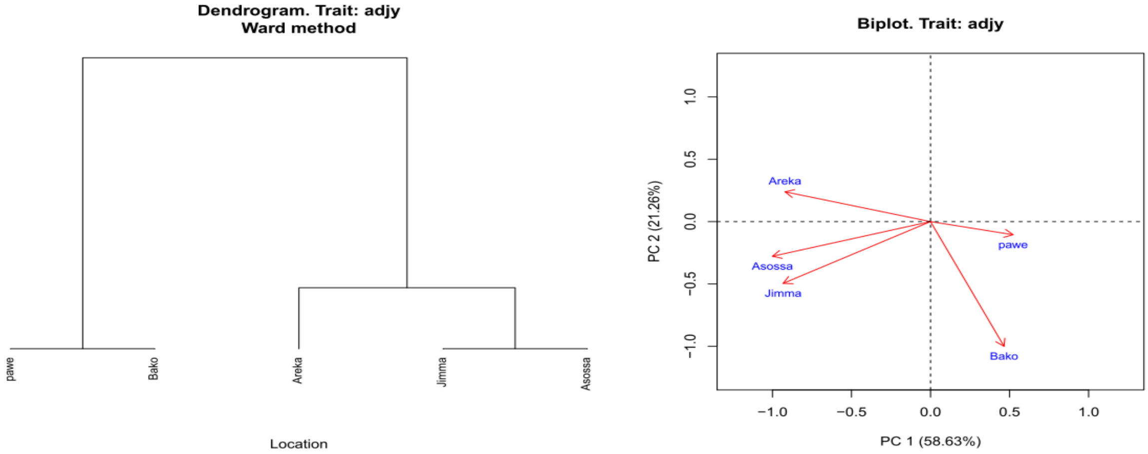


Fig 10. GGE biplot showing the soybean genotypes to yield, fig at right side and the dendrogram showing location clastered based on trait by yield ward method to the left side



Conclusion

High Genotype×environment interaction complicates breeding work because it makes it difficult to predict how genotypes selected under a given set of conditions will perform in a different set of 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 (factors) that enhance their performance. With the help of GGE, it was possible to identify and visualize two genotypes (TGX-1990-59F and TGX-1989-128F) that are both high yielding and stable among the introduced genotypes that would be beneficial to farmers if they are released and registered for production.

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