Selection for High Yield and Stability among Introduced Early Maturing Soybean Genotypes, Tested in Ethiopia for two qonsiquetive years across six testing locations

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Abstract – Soybean [Glysin max (L.) Merrill] is an important source of proteins, oil and micronutrients to small holder farmers in North East and Western parts of Ethiopia, but the biggest challenge on its production is climate change and most of our high yielding soybean were late in maturity and constrained by rain fall. Therefore to overcome such problem, 14 soybean genotypes were introduced from (IITA) and evaluated at three locations for two years using RCBD design in three replication to identify high yielding and stable early maturing variety. Yield performance data was subjected to analysis of variance (ANOVA) using SAS 9.3version and Meta-R version 4.0 to test the significance of genotype × environmental interactions and stability analysis using yield-stability statistic(YSi) and GGE biplot for selection of high yield and stability. Following the detection of significant genotype × environmental interactions, yield stability statistics (YSi) were used for simultaneous selection for high yield and stability. Yield-stability statistics (YSi) indicated that among 14 introduced genotypes (TGX-1990-21F and TGX-1990-55F) where identified as high yielding and stable compered to local check. These genotypes need to be assessed for farmer preferences/tastes and other quality traits in on-farm participatory trials before they can be recommended for release.

Keywords: yield- stability statistics, Soybean, Genotype×environment interaction, GGE Biplot, AMMI

1. 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 (Apio Ibedo, 2014). It is a rich source of proteins, cooking oil and micronutrients particularly it has highest protein (42%), oil (24%), rich in lysine, vitamins A and B and free from cholesterol Soybean is considered a 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). Soybean production in Ethiopia like much of Sub-Saharan Africa (SSA) still depends largely on late maturing and indeterminate varieties (Shanmugasundaram et al., 2009). However, shifts in rainfall patterns and seasons due to climatic change require the development of varieties that are early maturing. 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). Yield stability between genotypes is variable due to the wide occurrence of genotype × environmental interactions (G×E) i.e. the ranking of genotypes depends on particular environmental conditions where they are grown (Becker & Leon, 1988). Genotype × environment (G×E) interaction pauses a continuous challenge among plant breeders in making cultivar recommendations to farmers because of the associated consequences especially when selection is based on yield alone (Kang, 1993). This is due to lack of emphasis on both yield and stability in most breeding programs (Mekbib, 2002). Kang (1993) recently developed a statistic called yield-stability (YSi) that integrates both yield and stability in selecting genotypes tested across a range of environments. Recommendation of high yielding and stable Soybean genotypes is particularly important in western and North western parts of Ethiopia due to variations in environmental conditions, production is rain-fed and means of modifying the environment are unavailable. This study therefore aimed at identifying high yielding early maturing soybean varieties that have a stable performance across regions using the YSi selection criterion.

2. Materials and Methods

Fourteen early maturing soybean genotypes (12 introduced and two checks(one local and one standard checks) were evaluated in three locations for two different seasons. The locations were; Pawe/Mankush (at Benishangul Gumuze Regional states), Awassa (at SNNP) and Sirinka (at Amhara Regional States), located in Western, southern and north western part of Ethiopia from 2016-2017. These locations represent the major

Soybean growing areas in Ethiopia and are characterised by short growing and low rain fall conditions. All the genotypes except local check (control variety) used in the study were obtained from IITA (International Institutes of Tropical Agriculture/Nigeria) as shown in Table 1. In 2015 first season evaluations were conducted only in pawe while in 2016 and 2017 season, genotypes were evaluated in pawe (Mankush), Awassa and Sirinka. In all locations, genotypes were planted in Completely Randomized Block Design (RCBD) in three replications with 2.4 m × 4m plots size at spacing of 1.5m, 60cm, 40cm 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 based on the rate of 100kgha^{-1} fertilizers were applied. Data on Grain yield and Yield related traits collected on days to flowering 50%, days to maturity 95%, plant height (cm), Number of branch per plant, Number of pod per plant, Number of seed per pod, hundred seed weight(g), seed moisture content (%), stand count at harvest plot yield(g/plot) which was later extrapolated to yield per hectare. A combined analysis of variance to assess the significance of genotype × environment interactions was carried out before computing the yield and yield-stability statistics (YSi). Shukla's Stability Variance and Kang's Yield - Stability (Ys i) Statistics were calculated according to (Kang, 1993). All analysis was carried out using R version 3.1.2 (R Core Team, 2014).Meta R (GEA-R)

Table 1 List of IITA introduced Soybean Genotypes evaluated in the study over three locations for two years (2016-2017)

Cultivars	Specious	maturity	country	Year of introduction
TGX-1990-21F	*Glysin soja*	EARLY	IITA/Nigeria	2013
TGX-1990-55F	Glysin soja	EARLY	IITA/Nigeria	2013
GOZELLA	Glysin soja	EARLY	Standard check	
TGX-1989-49F	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1990-52F	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1990-3F	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1990-46F	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1989-40F	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1990-57F	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1989-68-FN	Glysin soja	EARLY	IITA/Nigeria	2013
AWASSA-04	Glysin soja	EARLY	Local check	
TGX-1990-40F	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1465-1d	Glysin soja	EARLY	IITA/Nigeria	2013
TGX-1989-68-FN	Glysin soja	EARLY	IITA/Nigeria	2013

Note: IITA International Institutes of Tropical Agriculture

1. Results

Combined analysis of variance

AMMI analysis of 14 soybean genotypes tested in 3 environments showed that Soybean grain yield was significantly ($P<0.05$) affected by environments (E), genotypes (G) and genotype×environment interaction (GEI) (Table2) indicating the presence of genetic variation and possible selection of stable genotypes. 65.45% of the total sum of squares was justified by environmental fluctuations exhibiting that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield (Table2). In multi environmental trial (MET), environment explains 80% or higher of the total yield variation (Yan, 2002). Only a small portion (25.46%) of the total sum of squares was attributed to genotypic effects. GEI significantly explained 9.05% of the treatments variation in grain yield. The magnitude of the GEI sum of squares was about 2 times smaller than that of genotypes, indicating reasonable differences in genotypic response across environments. As GEI was significant therefore we can further proceed and calculate phenotypic stability (Farshadfar, 2008). Analysis of variance (Table2) showed that genotype × environmental interactions were significant ($p<0.05$), therefore it was inappropriate to select genotypes on the basis of yield alone. The effect of genotype was also significant (at $p = 0.05$) though the interaction and environmental effects were significant (at $p<0.05$). There were differences in mean performance of genotypes at the different locations (Table 3).

Table 2 Gollob's test yield AMMI Analysis of variance for Genotype x Environment Interaction

	DF	SS	Explained SS%(δ)	MS
GENOTYPE	2	57786265	25.46833	28893133**
ENV	13	22474383	65.48433	1728799**
ENV*GEN	26	7983765	9.04733	307067.9**
PC1	14	12999405	87.78	928529**
PC2	12	1829168	12.22	152430.7
PC3	10	400500.3	2.62984	40050.03
Residuals	210	82592526		393297.7
Pooled error	287			

Where DF=degree of freedom, SS % (δ) =sum square percent of variance explained, MS= mean of the squares, PC1, PC2, PC3 are the first, second and third principal components

Table 3 The average mean yield in (kgha^{-1}) for 14 Early Maturing soybean genotypes tested for two years over three locations

Parameters/Season	2016			2017		
location	pawe	Awassa	Sirinka	pawe	Awassa	Sirinka
Mean yield(kg/ha)	2529.99	1368.51	1301.65	1979.6	804.267	2264.65
CV (%)	15.85	44.4727	30.1903	29.738	43.3767	23.8045
LSD	67.15	102.5	65.54	78.730	98.19	58.51

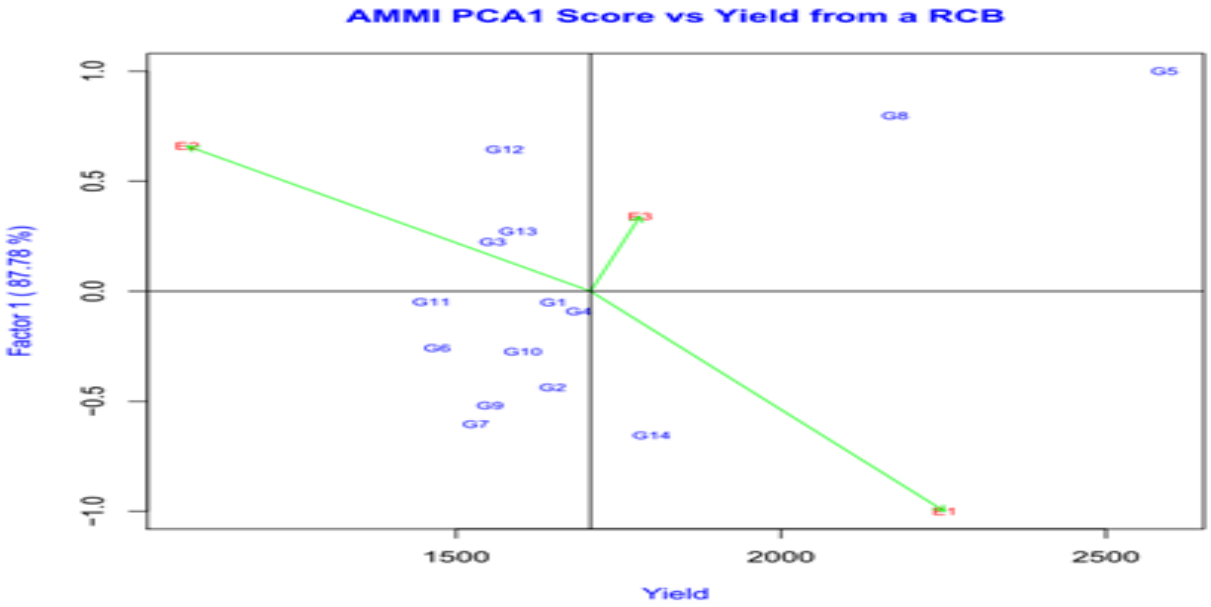
AMMI model and pattern analysis

In AMMI model, principal component analysis is based on the matrix of deviation from additivity or residual, while pattern analysis employs both classification and ordination techniques. In this respect both the results of AMMI analysis, the genotype and environment will be grouped based on their similar responses (Gauch, 1992; Pourdad and Mohammadi, 2008). GEI was further partitioned by principal component analysis (Table 2). Ordination technique using an approximate F-statistic (Gollob, 1968) revealed high significant differences for IPC1, IPC2 and IPC3. In this study, the first three multiplicative axis terms explained 87.78, 12.22 and 2.63% of GEI sum of squares, respectively. The first three interaction principal components (IPC1, IPC2 and IPC3) retained by Gollob's F-test accounted for 99.6 % of GE interaction. Corrected grain yield can be obtained by AMMI1, AMMI2 and AMMI3 for each environment and used as selection criteria in breeding programs. The three IPCAs accounted for 99.6% of the total interaction, the remaining 0.4% being the residual or noise, which is not interpretable and thus discarded (Purchase, 1997). The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments (Gauch and Zobel, 1996; Purchase, 1997; Martin and Alberts, 2004). The greater the IPCA scores, the more specific adapted is a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled.

Identifying high yielding stable genotypes

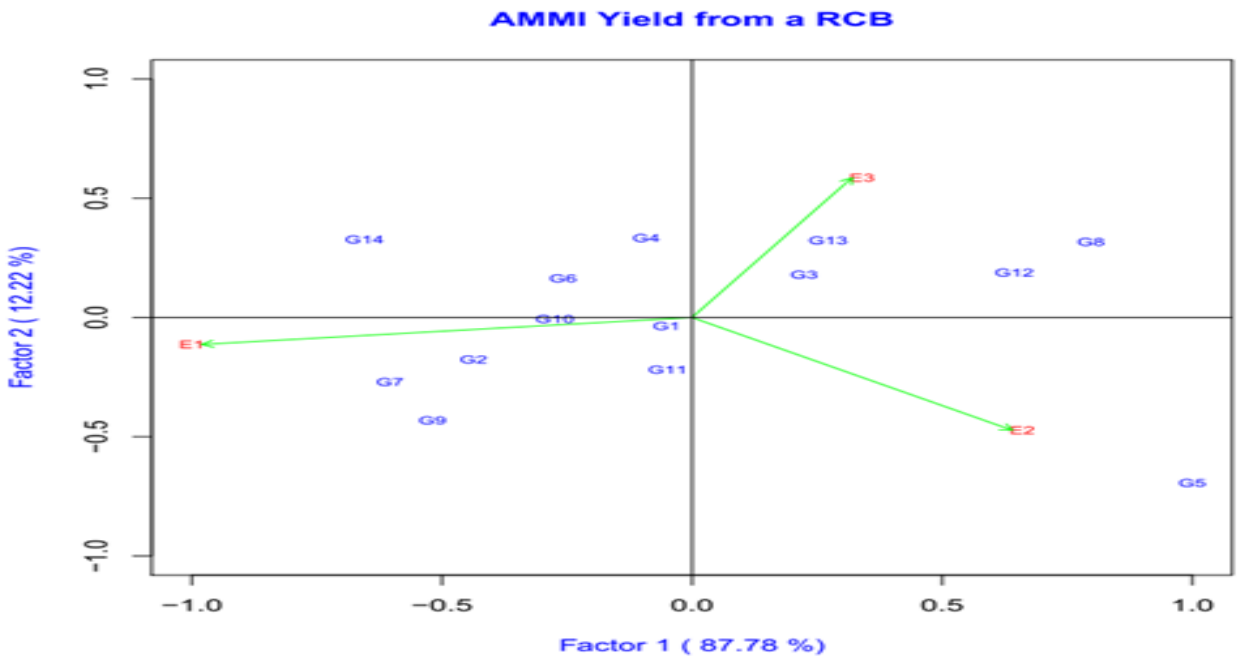
To investigate the main effects and interactions, AMMI1 biplot was constructed for yield. In Figure1, AMMI1 biplot of additive main effects or mean yield are shown along the abscissa and the ordinate represents the first IPCA or multiplicative interaction. The interpretation of a biplot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive; if different, their interaction is negative. Biplot space of Figure 1 is divided into 4 sections from low yielding environments in sections 1 (up left) and 4 (low left) to high yielding environments in sections 2 (up right) and 3 (low right). It is clear from the Biplot of Figure 1 that the points for environment are more scattered than the point for genotypes indicating that

variability due to environments is higher than that due to genotypes difference which is in complete agreement of ANOVA (Table 2). On the biplot, the points for the generally adapted genotypes would be at right hand side of grand mean levels (this suggests high mean performance) and close to the line showing IPCA= 0 and (this suggests negligible or no G × E Interaction). According to the AMMI model, the genotypes which are characterized by means greater than grand mean and the IPCA score nearly zero are considered as generally adaptable to all environment. However, the genotype with high mean performance and with large value of IPCA score are consider as having specific adaptability to the environments. According to Figure 1: G12, G13and G3 (adaptive group 1) exhibited specific adaptability for environments: E2 with grain yield less than mean. Genotypes G14 (adaptive group 2) revealed specific adaptation for E1 with high grain yield more than mean yield and positive interaction. The accessions G1 and G4 (adaptive group 3) on the IPCA= 0 showed general adaptability with grain yield close to mean yield and negligible interaction, whereas G2, G6, G7, G9, G10 and G11 are exhibits specific adaptability with grain yield less than the mean. The entries G5 and G8 (adaptive group 4) were identified with in E3 positive interaction and screened with general adaptability for high grain yield more than mean yield and negligible interaction. AMMI Analysis was also conducted and the stability of genotypes was predicted on the basis of mean performance and the magnitude of IPCA1 scores in soybean (Zobel et al. 1988) maize and wheat (Crossa et al.1990), sorghum (Zavala-Garcia et al.1992), barley (Romagossa et al. 1993) and chickpea (Zali et al., 2011)



Scaling =0, centered = 2, SVD =1, transformation = 0

Figure 1 AMMI1 Biplot Additive main effect that shows mean yield along the abscissa and the first PCA1 along the ordinates of multiplicative interactions



Scaling =0, centered = 2, SVD =1, transformation = 0

Figure 2 Biplot of the first interaction Principal component axis (IPCA1) versus Second interaction principal component axis (IPCA2) for soybean genotypes

In Figure 2 genotypes and environments are depicted as points on a plane. The position of the point for genotype i is given by the estimates for the genotypic scores, similarly, the point coordinates for environment j originate from the estimates for the environmental scores. Distances from the origin (0,0) are indicative of the amount of interaction that was exhibited by either genotypes over environments or environments over genotypes (Thangavel et al., 2011). For example, the genotypes G14, G7, G9, G8 and G5 and environments E1 and E2 displayed a highly interactive behavior, whereas the environments E3 exhibited low interaction. In a vector representation, the genotype and environment points determine lines starting at the origin (0,0). The interaction effect of genotype i in environment j is approximated by projecting the genotype point onto the line determined by the environmental vector, where distance from the origin provides information about the magnitude of the interaction. The angle between the vectors of genotype i and environment j tells us something about its nature: the interaction is positive for acute angles, negligible for right angles, and negative for obtuse angles. Genotypes G6, G14 and G4 showed acute angle with the vectors of E1 and obtuse angles with the vectors of environments E3 and E2. Genotypes G2 and G7, G9, G1 and G11 exhibited acute angle with environments E1, and E2, while obtuse angle with environments E3. The accessions G5 revealed acute angle and positive interactions with vectors E2 and E3. Whereas obtuse angle and negative interaction with the vectors of environment E1. The entries G13, G3, G12 and G8 displayed acute angle with the vectors of environment E2, while showed negative interaction and obtuse angle with environments E1. As the length of the vectors of genotypes G3, G1, G6, G10 and G11 is shorter than the other ones hence they are more adapted to their specified environments, while G7, G9, G12, G8, G14 with longer vectors indicated more deviation from their specified environments.

AMMI 2 biplot

The IPCA 1 versus IPCA 2 biplot (i.e. AMMI 2 biplot) (Figure 2) explain the magnitude of interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors (Osiru et al., 2009). A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and is therefore best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environment and it helps to identify genotypes best suited for specific

environmental conditions. However, for the AMMI 2 model, IPCA2 scores was considered in interpreting GEI that captured 12.6% of the interaction sum of squares as suggested by Gauch and Zobel (1996). A biplot is generated using genotypic and environmental scores of the first two AMMI components (Vargas and Crossa, 2000). Furthermore, when IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the genotypes score to the center of the biplot (Figure 2), the more stable they are. Figure 2 gives the AMMI2 biplot for yield. The IPCA1 component accounted for 87.78% of G×E interaction, while IPCA 2 accounted for only 12.22 % (Table2). Distribution of genotype points in the AMMI 2 biplot revealed that the genotypes, G1, G10, and G11 scattered close to the origin, indicating minimal interaction of these genotypes with E1. The remaining 11 genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. Interaction of genotypes with specific environmental conditions was judged by projection of genotype points on to environment spokes. On this basis, the genotypes G4, G6 and G14 had negative interaction with environments E2, hence exhibited specific adaptation environments Genotypes G3, G12, G8 and G13 indicated specific adaptability and positive interaction with environments E3. The accessions G5 showed specific adaptability and positive interaction with environments E2

Visualization of mean performance and stability for mean yield

Visualization of which won where patterns of MEYTs data is important for studying the possible existence of different mega environment (ME) in the region (Gauch and Zobel, 1997; Yan et al., 2000, 2001).The polygon view of a GGE-biplot explicitly displays the which-won-where pattern, and, hence, is a succinct summary of the GEI pattern of a MEYT data set (Fig 1). By connecting the markers of the genotypes and the rays as depicted, the rays in Figure 1 are lines that are perpendicular to the sides of the polygon or their extensions. Ray 1 is perpendicular to the side that connects genotype numbers G14 and G5. These 7 rays divide the biplot into 8 sectors, but environments fall into two of them, so the genotype(s) vertex in these sectors may have higher or the highest yield compared to other parts in all environments (Yan, 2002). The two environments (E3 and E2) fell into sector2 but environment (E1) has a joint point between sector 2 and the vertex genotype for this sector was G5, suggesting a higher yielding genotype for this environment. Two environments, E3, and E2 (normal environments), fell into sector 2, which was delineated by Rays 1 and 2, and the vertex genotype for this sector was G5 through G8, suggesting that this is a higher yielding genotype for this 3 environments. Whereas G1, G3, G7, G4, G2, G9, G10 and G14 all fell in to sectors that contained none of the locations tested. The yield stability of genotypes was evaluated by an average environment coordination (AEC) method (Yan, 2001; Yan and Hunt, 2000; Yan, 2002). In this method, the average principal components will be used in all environments, as depicted in (Fig 2). A line is then drawn through this average environment and the biplot origin; this line is called the average environment axis and serves as the abscissa of the AEC. Unlike the AEC abscissa, this has one direction, with the arrow pointing to a greater genotype main effect; the AEC ordinate and either direction away from the biplot origin. Following the detection of significant genotype × environmental interactions, YSi statistics for the fourteen genotypes were calculated as listed below as described by Kang (1993) to give results in Table 4.

1) Determine the contribution of each genotype to Genotype × Environmental interaction by calculating σ^2 (Shulka, 1972) as follows:

$$\sigma^2 = [1/(s\text{-}1)\ (t\text{-}1)\ (t\text{-}2)] \times [t\ (t\text{-}1) \sum_{ij}\ (\mu ij - \overline{\mu i})^2 - \sum i \sum j (\mu ij - \overline{\mu i})^2]$$

Where, $\mu_{ij} = x_{ij - x_j^-}$ *Xij* = observed yield value of the ith genotype in jth environment, x_j^- = mean of all genotypes in jth environment, $\overline{\mu i} = \sum_j \mu ij / S$, s = number of environments and t = number of genotypes. Shukla's Stability Variance and Kang's Yield Stability (YSi) statistics were computed using Agricolae package in R (Felipe de Mendiburu, 2014). (2) Arrange genotypes from highest to lowest yield and assign yield rank (Y'), with the lowest yielding genotype receiving the rank of 1. (3) Calculate protected LSD α (2) for mean yield comparisons [α (2) refers to a two-tailed test] as t α (2), v (2EMS/s × r 1/2), where EMS = error mean square, v = Degree of freedom associated with EMS, and r = number of replications. (4) Adjust Y' according to LSD, and determine adjusted yield rank (Y) [as shown in Table 4]. (5) Assign respective stability-variance statistic (values to genotypes and determine whether or not is significant at α (2) = 0.10, 0.05, 0.01, using an approximate test with (s - 1), v df [a significant indicates that genotype performance across environments was unstable]. (6) Assign stability rating (S) as follows: -8, -4, and -2 for significant at α= 0.01, 0.05, and 0.1, respectively; and 0 for non-

significant [The stability ratings of - 8, - 4, and - 2 were chosen because they changed genotype ranks from those based on yield alone (Y') (Kang, 1993). (7) Sum adjusted yield rank (Y) and stability rating (S) for each genotype to determine YSi statistic. (8) Calculate mean YSi as ΣYS i /t. Select genotypes with YSi > the mean YSi.

Table4. Yield-stability statistic (YS i) for simultaneous selection for yield and stability in Soybean trials tested at three location for two years

Note. YS i = yield-stability statistic; + Genotypes selected on the basis of YS i.

Genotypes Nammes	Mean yield	Rank	Adjustment to rank	Adjusted yield rank	Stability variance	Stability rating(S)	YSi
TGX-1990-21F	2589.7778	14	3	17	219931.75**	-4	13
TGX-1990-55F	2175.4889	13	3	16	123761.53**	-4	12
GOZELLA	1801.0611	12	3	15	84822.67**	-4	11
TGX-1989-49F	1689.3333	11	-3	8	5196.25**	-4	4
TGX-1990-52F	1650.1222	10	-3	7	3682.49**	-4	3
TGX-1990-3F	1648.7833	9	-3	6	34201.00**	-4	2
TGX-1990-46F	1602.7778	8	-3	5	10056.85**	-4	1
TGX-1989-40F	1595.4333	7	-3	4	17216.15**	-4	0
TGX-1990-57F	1574.8222	6	-3	3	77142.26**	-4	-1
TGX-1989-68-FN	1556.3833	5	-3	2	7568.78**	-4	-2
AWASSA-04	1552.2167	4	-3	1	60157.90**	-4	-3
TGX-1990-40F	1530.5667	3	-3	0	70249.12**	-4	-4
TGX-1465-1d	1470.9944	2	-3	-1	10295.90**	-4	-5
TGX-1989-68-FN	1462.5333	1	-3	-2	-425.99**	-4	-6
Mean	**1707.16**						**+1.14**
LSD(0.05)							

* Adjustment for +1 for mean yield > overall mean yield (OMY); +2 for mean yield ≥ 1LSD above OMY; +3 for mean yield ≥ 2LSD above OMY; -1 for mean yield < OMY; -2 for mean yield ≤1LSD below OMY; and -3 for mean yield ≤ 2LSD below OMY,** Significant at α = 0.05

Table Comparison among the yield stability statistics and GGE Biplot techniques showing mean yield of selected genotypes in the parenthetic

S.No	GGE Biplot	YSi
1	TGX-1990-55F, G8 (2175.5)	TGX-1990-21F G5 (2589.8)
2	GOZELLA G14 (1801.1)	TGX-1990-55F G8 (2175.5)
3		GOZELLA G14 (1801.1)
4		TGX-1989-49F G1 (1689.33)
5		TGX-1990-52F G13 (1650.12)
6		TGX-1990-3F G12 (1648.8)
Mean	**1988.3**	**1925.77**

The YSi labels a genotype as being high yielding and stable if it YSi is above average (6.33) thus V2, V7, V3, V5, V 1 and V4 that met therequirement were selected ($) (Kang and Magari, 1995). Though V2 was identified as an uns table genotype, it was still selected by the YSi.The mean of the genotypes selected by the YSi was 17.64. Twelve introduced soybean genotypes in addition to one local and one standard check were tested in three locations for two years and among this two variety had yield-stability statistic (YS i) values greater than the mean YSi value (+1.14) (Table 4,Table2 Fig 4). These genotypes gave high mean yield values with low genotype × environment interaction (an indicator of wide adaptability and are therefore preferred since they can express high yield potential in varied environments. Therefore these genotypes are both stable and high yielding and are suitable for cultivation in Ethiopian environments in which they were tested. These genotypes will be subjected to farmer preference assessment and other quality parameters in on-farm participatory trials before they can be submitted for release and subsequent production.

4. Discussion

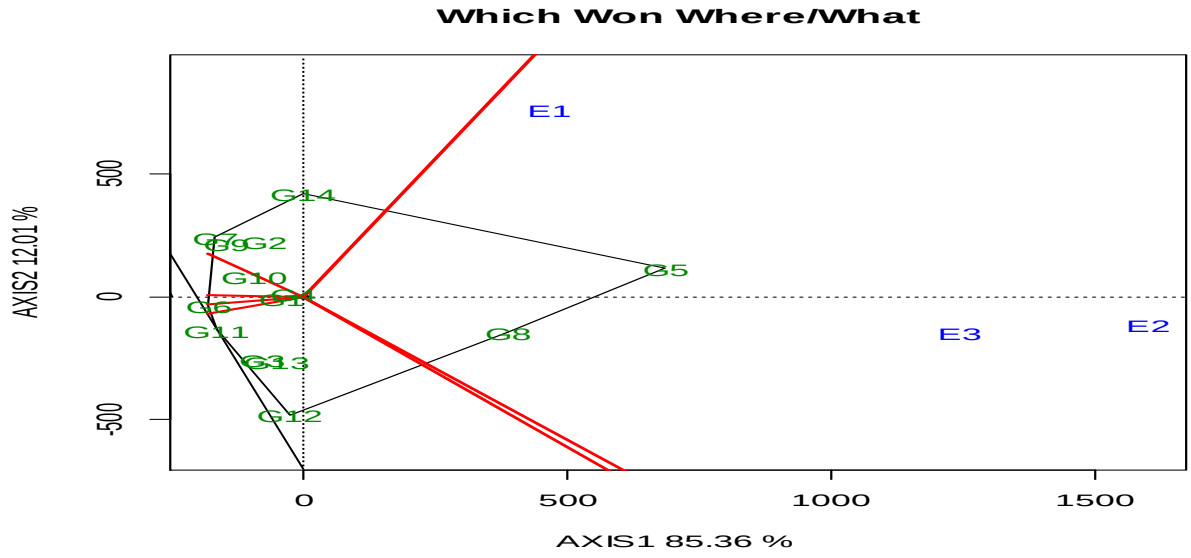
The presence of Genotype × Environmental interactions pause a challenge to plant breeders because it implies that the behavior of the genotypes in the trial depends upon the particular environment in which they are grown (Ceccarelli, 1989; Hill, 1975). Thus the performance of any one of the genotypes relative to the remaining genotypes grown in the same environment will be in consistent, such in consistencies resulting either in alteration to the ordering of the genotypes from one environment to the next, or to changes in the absolute differences between genotypes which leave the rank order unchanged. Such interactions make utilizing data from multi-environmental trials complex (Tukamuhabwa et al., 2012). When there are Genotype × Environmental interactions, they can be dealt with through; 1) ignoring them (by using genotypic means across environments); 2) avoid them (by grouping similar environments together) or 3) exploit them in breeding objectives by analyzing and interpreting genotypic and environmental differences (Eisemann et al., 1990). The first approach pauses a great risk to growers (Kang, 1993) while with the second approach, useful information about environments may be lost especially if broad adaptation were the goal (Kang, 1997). Third approach enables researchers to identify the causes of genotype × environmental interactions and provides opportunities to address them through genetic or environmental manipulations to enhance productivity. In order to conserve resources, genotypes that are widely adaptable and with reliable performance across environments need to be identified through analysis and utilization of genotype × environmental interactions. In order to analyze genotype × environmental interactions, it is important to integrate both yield and stability of genotype performances across environments using reliable stability statistics (Kang, 1993). A yield-stability statistic (YSi) that uses Genotype × Environmental interaction with great emphasis on stability component has been recommended in identifying high yielding and stable genotypes (Kang, 1993). In this study, YSi was used in studying the performance of introduced Greengram and Blackgram genotypes in different growing areas in Uganda.

The results in this study showed that genotype × environmental interactions were significant, therefore it was inappropriate to select genotypes on the basis of mean yield alone as is conventionally done (Kang, 1993) but instead both genotype yield and stability of performance were needed to evaluate genotype performance. Kang (1993) highlighted the fact that researchers who emphasize stability of performance than currently done in the selection process would benefit farmers. Farmers would have a greater risk of suffering yield losses when a variety is chosen only on the basis of mean yield alone than when selection is based on yield and stable performance. It is a fact that farmers would prefer to use a high-yielding cultivar that exhibits temporal adaptation and might be willing to sacrifice some yield if they are guaranteed, to some extent, that a cultivar would produce consistently from year to year (Kang et al., 1991). Breeding for stability of performance under variable conditions is a complex and difficult task because selection pressure is variable and unpredictable. Therefore, evaluation of varieties under different environments and adoption of simultaneous selection for yield and stability is a reliable selection criterion that has to be used in any plant breeding programme (Mekbib, 2002). The finding that the local check commonly grown by farmers gave a stable yield performance across the test environments is not surprising since farmers especially in marginal areas always grow landraces that are suitable to their environments as well as those that meet their needs and preferences (Vernooy, 2003). The mean yield values for the genotypes evaluated in this study are still below those required for an ideal variety (> 2 tons/ha) (Shanmugasundaram et al., 2009) and therefore more needs more research is needed in breeding as well as crop agronomy in order to raise yield so as to enhance returns to farmers. In addition to the stable performance of the two genotypes identified in this study, other traits need to be considered as these may be useful to farmers through on-farm participatory trials. This is because it enables researchers to take advantage of

farmers' knowledge and experience thus allowing a quick identification of promising genotypes and eventually contributing to the improvement of a breeding program (Abidin et al., 2005).

Which-won-where

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 five sectors with cultivars G7, G14, G12, G6, G7 and G5 as the corner or vertex cultivars. Environments E1, E2 and E3 fell in the sector in which G5 was the vertex cultivar. While G12 had the lowest yield, similarly genotypes G1, G4, G8, G3, and G13 performed above average mean yield. This means that G5 was the best cultivar for E1, E2 and E3. While G14, G9, G7 and G2 had the lowest yield. In the case of E1 in sector1 for which vertex genotype G5 through G8 also among the testing locations E1 have the highest mean performance environment in sector 1 followed by E3 and E2 are normal environment fall into sector2. No environments fell into sectors with G9, G6, G12 and G7 as the vertices, indicating that these cultivars were not the best in any of the environments.

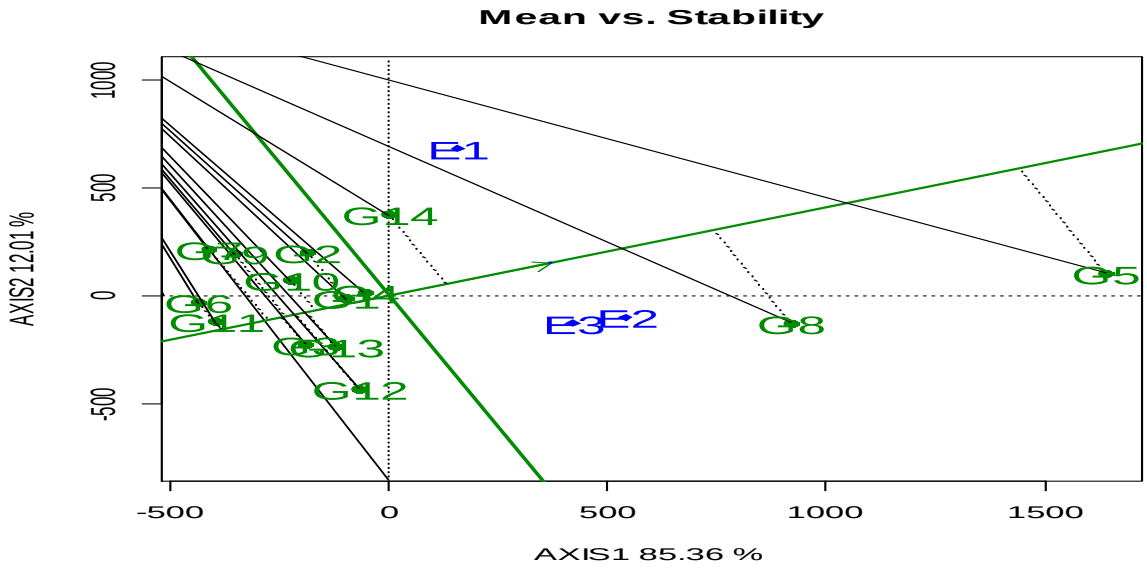


Scaling =0, centered = 2, SVD =1, transformation = 0

Figure 3 Biplot of which won where /what of soybeans tested at three locations for two years 2016-2017

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 97.5% 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 three locations based on yield is G5 followed by G8. 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 G12, G9, G7, G6 G4 and G14. 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). G8 has the shortest vector and therefore identified as the most stable. It is closely followed by G5 fairly stable while G7, G6, G11, G12, G6, G1, G4 and G14 are unstable with yield below the average mean yields

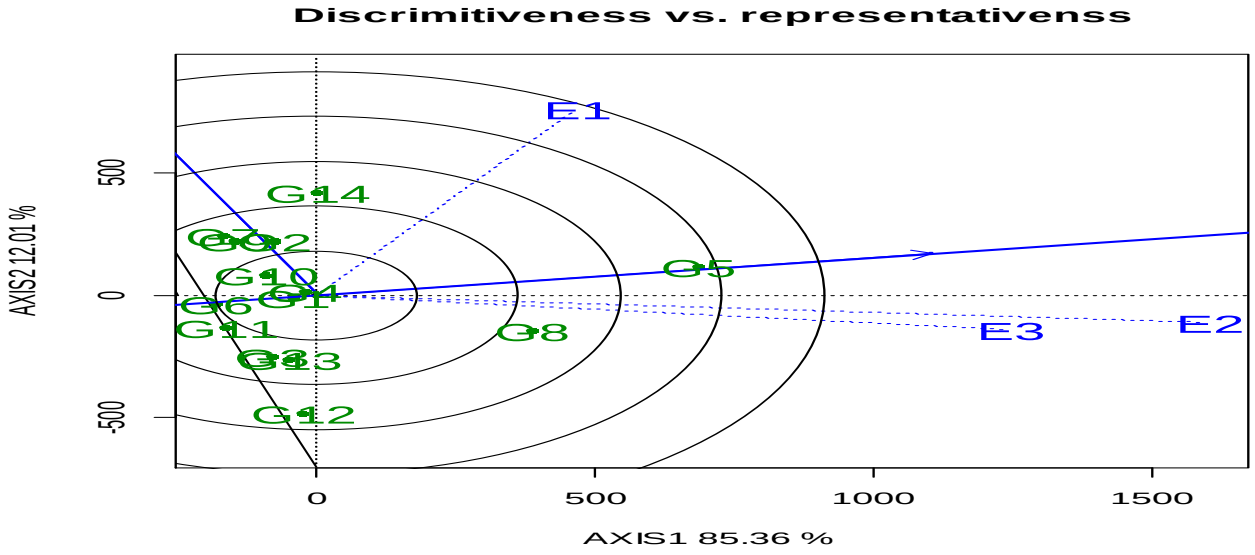


Scaling =0, centered = 2, SVD =1, transformation = 0

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

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 E1 as the most representative since its vector formed the shortest angle with the AEC abscissa. It was followed by E3 while E2 with the largest angle is the least representative. E2 also has the highest discriminatory power due to its possession of the longest vector, followed by E3 and then E1 with the least (Fig 5). The small circle close to the arrow of the AEC abscissa delineates the ideal environment and the location closest to it is adjudged the best (Yan and Kang, 2003). From the biplot E1 was the closest to ideal environment and therefore the best among the three testing locations

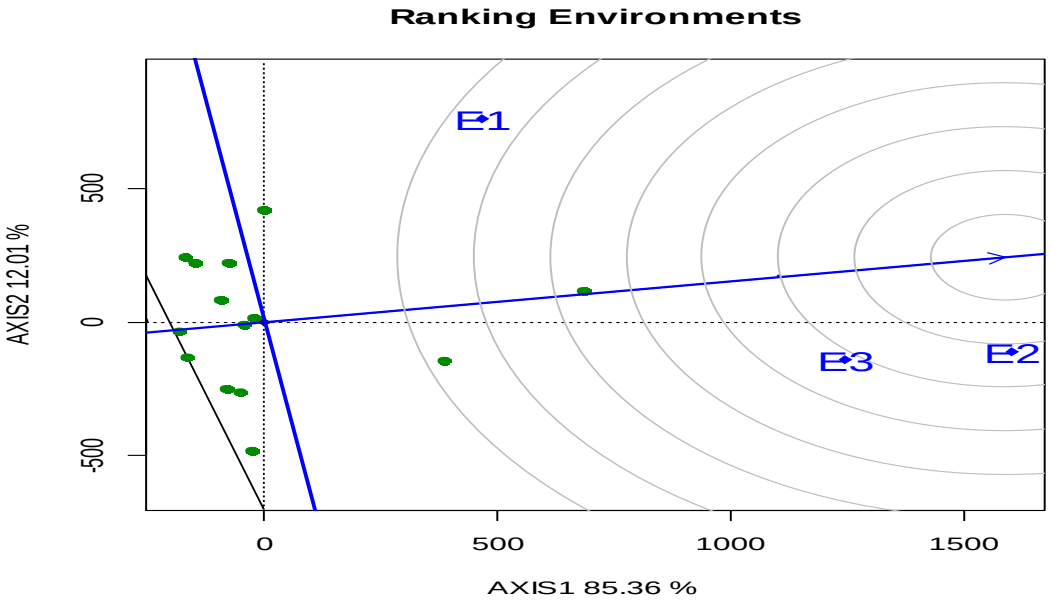


Scaling =0, centered = 2, SVD =1, transformation = 0

Fig. 5: GGE biplot showing the discriminatory ability and representativeness of the test environments

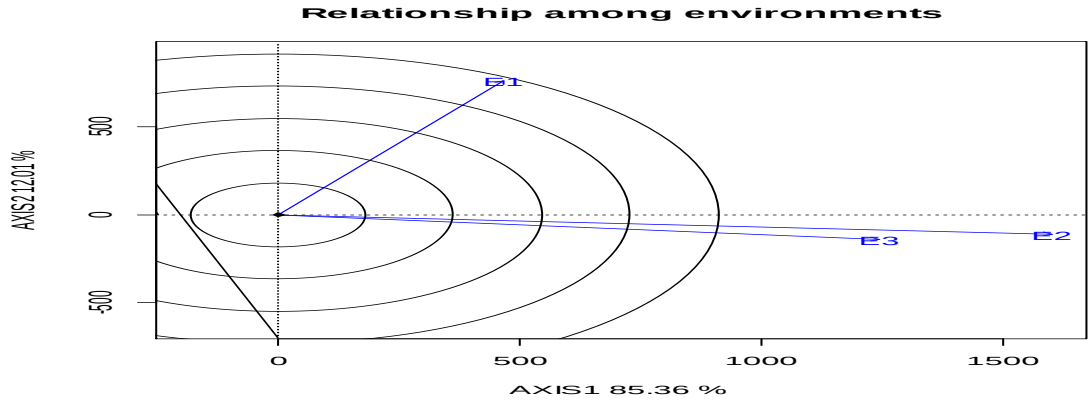
Environment ranking

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 representative), with a distance to the biplot origin equal to the longest vector of all environments (most informative)Yan and Tinker (2006).E1 is closest to this point and is, there-fore, best, whereas E3 and E2 were poorest for selecting cultivars adapted to the whole region. Figure 6 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). Figure 6 shows that environment E1 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 three environment, results showed that G5 has greater stability and high yielding in this environment, and that G11,G6 and G14 was a low yielding genotype (Fig 6).



Scaling =0, centered = 2, SVD =1, transformation = 0

Fig 6 GGE biplot showing the relation among the testing environments

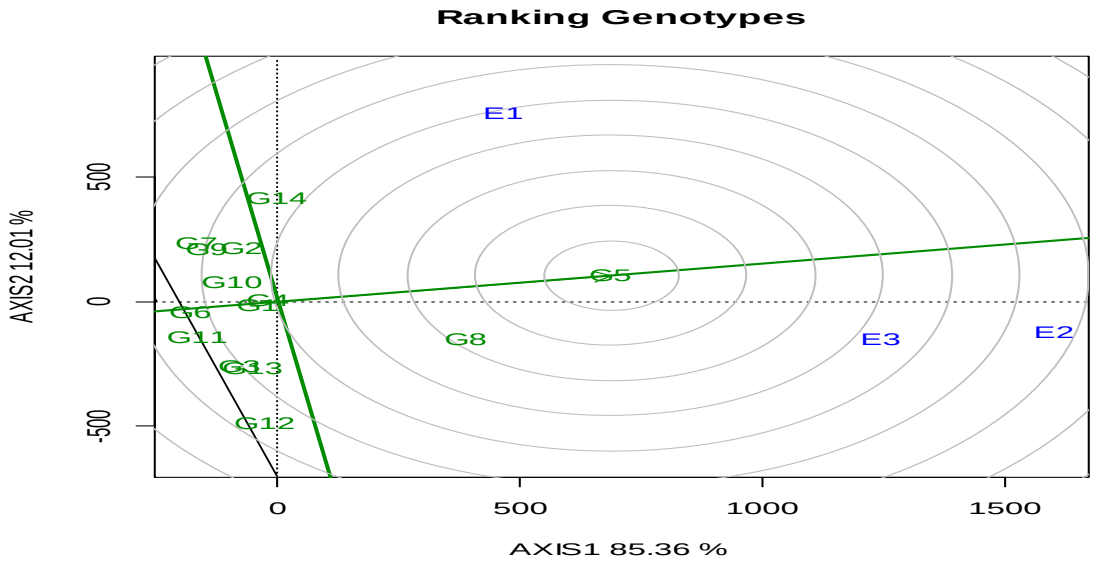


Scaling =0, centered = 2, SVD =1, transformation = 0

Fig 6 GGE biplot showing the relation among the 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 G14,G8 and G5, while genotypes with below-average means were G12,G2,G9,G10,G11,G6,G7,G3,G and G13. Genotypic stability is quite crucial in addition to genotype yield mean; genotypes G5 is more stable followed by G8 were more stable as well as having appropriate yield, while, conversely, G14,G1,G2 ,G10 and G3 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 (Fig 7). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI. 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 G5, which fell into the center of the concentric circles, was ideal in terms of higher yielding ability and stability. The remaining genotypes, like G8, were situated in the next grades. Based on these results, cultivar G5 was identified as having a main role in producing adaptable genotypes.

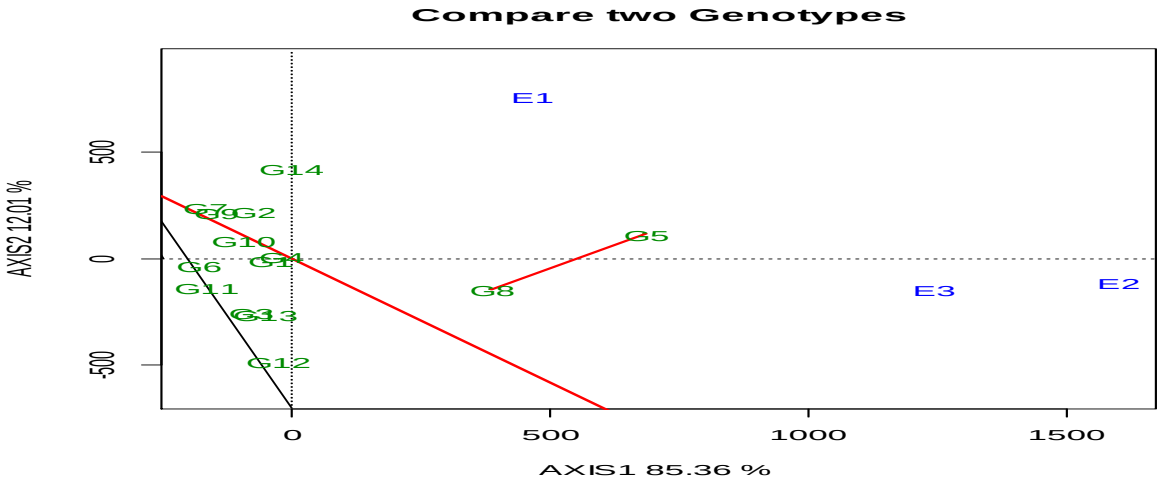


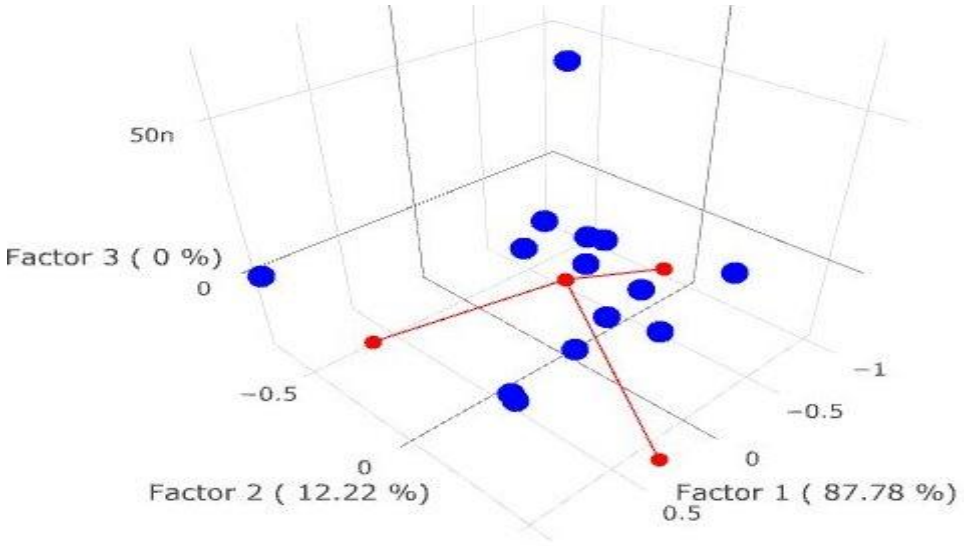
Scaling =0, centered = 2, SVD =1, transformation = 0

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

Scaling =0, centered = 2, SVD =1, transformation = 0

Fig 8 GGE biplot showing the comparesion among soybean genotypes in relation to their testing environments





Scaling =0, centered = 2, SVD =1, transformation = 0

Fig 9 GGE biplot showing the 3D of soybean genotypes with their testing location

5. Conclusion

High Genotype × Environmental 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 YSi, it was possible to identify two genotypes (TGX-1990-21F and TGX-199055F) that are both high yielding and stable among the introduced genotypes that would be beneficial to farmers if they are released for production.

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References

1. Abidin, P. E., Eeuwijk, F. van, Stam, P., Struik, P. C., Malosetti, M., Mwanga, R. O., & Carey, E. E. (2005).
2. Adaptation and stability analysis of sweet potato varieties for low-input systems in Uganda. Plant Breeding, 124(5), 491-497. http://dx.doi.org/10.1111/j.1439-0523.2005.01149.x Apio Ibedo, S. (2014).
3. Analysis of the Greengram value chain in Uganda (Thesis). Makerere University. Retrieved from http://dspace.mak.ac.ug/handle/10570/3242
4. Becker, H. C., & Leon, J. (1988).Stability analysis in plant breeding. Plant Breeding, 101(1), 1-23.http://dx.doi.org/10.1111/j.1439-0523.1988.tb00261.x Ceccarelli, S. (1989). Wide adaptation: How wide? Euphytica, 40(3), 197-205.
5. Eisemann, R. L., Cooper, M., & Woodruff, D. R. (1990). Beyond the analytical methodology, better interpretation and exploitation of GE interaction in plant breeding. Felipe, de M. (2014). Agricolae: Statistical Procedures for Agricultural Research (R Package Version 1, pp. 1-8).Retrieved from http://CRAN.R-project.org/package=agricolae Hill, J. (1975). Genotype-environment interactions − A challenge for plant breeding. J. Agric. Sci., 85, 477-493. http://dx.doi.org/10.1017/S0021859600062365

6. http://dx.doi.org/10.1017/S0021859602001946 Plant Variety Protection Bill. (2010).Bill No. 2 (p.37). Ministry of Agriculture, Animal Industry and Fisheries (MAAIF).
7. Kang, M. S. (1993). Simultaneous selection for yield and stability in crop performance trials: Consequences for growers, Agronomy Journal, 85(3), 754-757. http://dx.doi.org/10.2134/ agronj 1993.00021962008500030042x
8. Kang, M. S.(1997).Using Genotype by Environment Interaction for Crop Cultivar. Advances in Agronomy, 62,199. http://dx.doi.org/10.1016/S0065-2113 (08)60569-6
9. Kang, M. S., Gorman. D. P., & Pham, H. N. (1991).Application of a stability statistic to international maize yield trials. Theor: Appl. Genet., 81, 162-165. http://dx.doi.org/10.1007 /BF00215718
10. Mekbib F. (2002). Simultaneous selection for high yield and stability in common bean (Phaseolus vulgaris) genotypes. The Journal of Agricultural Science, 138(03), 249-253.
11. R Core Team. (2014). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. Retrieved from http://www.R-project.org
12. Shanmugasundaram, S., Keatinge, J. D.,& Hughes, d'Arros J. (2009).The mungbean transformation: Diversifying crops, defeating malnutrition. IFPRI, 00922.
13. Shukla, G. K. (1972). Some statistical aspects of partitioning genotype-environmental components of variability. Heredity, 29, 237-245. http://dx.doi.org/10.1038/hdy.1972.87
14. Swaminathan, R., Singh, K., & Nepalia, V. (2012). Insect Pests of Greengram Vigna radiata (L.) Wilczek and Their Management. In G. Aflakpui (Ed.), Agricultural Science (p. 252). In Tech. http://dx.doi.org/10.5772/35176
15. Tukamuhabwa, P., Oloka, H. K., Sengooba, T., & Kabayi, P. (2012). Yield stability of rust-resistant soybean lines at four mid-altitude tropical locations. Euphytica, 183, 1-10. http://dx.doi.org/10.1007/s10681-011-0404-3
16. Vernooy, R. (2003).In focus: Seeds that give participatory plant breeding. International Development Research Centre, Ottawa, Canada.