Scientific Research and Essay Vol. 4 (11) pp. 1322-1330, November, 2009
Available online at http://www.academicjournals.org/SRE
ISSN 1992-2248 © 2009 Academic Journals

Full Length Research Paper

AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia

Asrat Asfaw[1]*, Fistum Alemayehu[1], Fekadu Gurum[1] and Mulugeta Atnaf[2]

[1]Awassa ARC, P. O. Box 6, Awassa, Ethiopia.
[2]Pawe ARC, P. O. Box 25, Metekle, Ethiopia.

Accepted 8 October, 2009

Matching soybean variety selection with its production environment is often challenged by the occurrence of significant genotype-by-environment interactions (GEI) in the variety development process. Several statistical models have been proposed for increasing the chance of exploiting positive GEI and supporting breeding program decisions in variety selection and recommendation for target set of environments. Additive main effects and multiplicative interactions (AMMI) and site regression (SREG) genotype plus genotype-by-environment interaction (GGE) models are among the models that effectively capture the additive (linear) and multiplicative (bilinear) components of GEI and provide meaningful interpretation of multi-environment data set in breeding programs. The objective of this study was to assess the significance and magnitude of GEI effect on soybean grain yield and exploit the positive GEI effect using AMMI and SREG GGE biplot analysis. Grain yield data of 11 genotypes evaluated at 4 sites for three cropping seasons (2002, 2003 and 2004) across the soybean production ecology in Ethiopia were used for this purpose. AMMI analysis showed that grain yield variation due to environments, genotypes and GEI were highly significant ($p<0.01$). Environments explained the greater proportion (61.08%) of total yield variation followed by GEI (34.13%) and genotypes (4.79%), indicating the necessity for testing soybean varieties at multi-locations and over years. The first five bilinear AMMI model terms were highly significant ($p<0.01$) and of which the first two terms explained 67.5% of the GEI. According to the AMMI and SREG GGE biplots models, no single variety has superior performance in all the environments. However, the genotype TGx-1892-10F was overall winner in combining high yield with relatively less variable yield across environments. Application of AMMI and GGE biplots facilitated visual comparison and identification superior genotypes for each target set of environments.

Key words: AMMI, GGE biplot, genotype-by-environment interaction, soybean, Ethiopia.

INTRODUCTION

Targeting variety selection onto its growing environments is the prime interest of any plant-breeding program. To realize this, breeding programs usually undertake a rigorous genotypes performance evaluation across locations and years mostly at the final stage of variety development process. In such type of multi-environment trials, the occurrence of genotype x environment interact-tion (GEI) is inevitable (Ceccarelli et al., 2006). GEI refers to inconsistent phenotypic performance of genotypes across environments. When it is associated with a significant genotypic rank change over environments, it potentially presents limitations on selection and recommenddation of varieties for target set of environments (Navabi et al., 2006). This is because in the presence of GEI, yield is less predictable and cannot be interpreted based on genotype and environmental means alone (Ebdon and Gauch, 2002b; Voltas et al., 2002). It is also one of the main causes for the failure of formal breeding to serve small resource-poor farmers in marginal fragile environ-

*Corresponding author. E-mail: asratasfaw@yahoo.co.uk. Tel: 251 913546737. Fax: 251462204521.

Abbreviations: AMMI, Additive main effects and multiplicative interactions; **GGE**, genotype plus genotype-by-environment interaction; **GEI**, genotype x environment interactions; **MS**, mean sum of squares; **PC**, principal component; **SREG**, site regression.

ments (Ceccarelli et al., 2006). Both biotic and abiotic factors are said to be the main contributors for GEI and yield instability in crops. However, these known factors not fully but can partly explain most of the GEI in multi-environment trials (Ferreira et al., 2006).

Several statistical models have been proposed for studying the GEI effect and exploiting its positive part in variety development process. The practical utility of different statistical models to explain GEI and facilitate variety release decision have been extensively reviewed and published elsewhere (Becker and Leon, 1988; Crossa, 1990; Ferreira et al., 2006; Flores et al., 1998; Hussein et al., 2000; Lin et al., 1986; Zobel et al., 1988). However, not all of them are always effective enough in analyzing the multi-environment data structure in breeding program (Navobi et al., 2006; Zobel et al., 1988). The additive main effects and multiplicative interactions (AMMI) and site regression (SREG) genotype plus genotype x environment interaction (GGE) biplot models are defined powerful tools for effective analysis and interpretation of multi-environment data structure in breeding programs (Ebdon and Gauch, 2002a; Samonte et al., 2005; Yan et al., 2000; Zobel et al., 1988). AMMI model analysis combines the additive parameters of traditional ANOVA (analysis of variance) with multiplicative parameters of PCA (principal component analysis). It has both linear and bilinear component of GEI and hence very useful in visualizing multi-environment data (understanding complex GEI and determining which genotype won which environment) and gaining accuracy (improving cultivar recommendation and accelerating progress) (Gauch, 2006). The SREG GGE model is a multiplicative model that absorbs the main effects of genotypes plus the environment interaction which are the two important factors in variety selection (Yan et al., 2000; Yan and Tinker, 2006). GGE biplots use the primary and secondary effects from SREG analysis and are useful in maga-environment analysis, test environments, and genotypes evaluation (Yan et al. 2007).

The application of these models for explaining GEI and analyzing the performance of genotypes and test environments have been very frequent among plant breeders in recent years (Gauch, 2006; Yan et al., 2007). Although the soybean breeding in Ethiopia was started with variety trials (Asrat et al., 2006), the uses of linear-bilinear models as well as the traditional statistical analysis models as a tool for analyzing multi-environment trials and interpreting GEI have not been very much documented. This paper therefore attempted to apply AMMI and SREG GGE biplot models to evaluate the significance and magnitude of GEI effect on soybean grain yield and determine the best performing varieties for selection environments.

MATERIAL AND METHODS

Eleven genotypes grown in national variety trials during 2002-2004 cropping season were used for this analysis. The trials were executed at four sites: Awassa, Abobo, Bako and Pawe. These sites represented the major soybean production ecologies of the country. The genotypes were TGx-1185-10, TGx-1835-10F, TGx-1892-10F, TGx-1895-23F, TGx-1897-17F, TGx-1876-4E, TGx-1895-4F, TGx-1805-8F and TGx-1895-22F obtained from International Institute for Tropical Agriculture (IITA) as test material, and Davis and Cocker-240 as a check. All the genotypes belonged to medium maturity group (mean 120 – 150 days for physiological maturity). The treatment design was a randomized complete block replicated three times at each site per year. The plots were six rows of 4 m long with between row and plant spacing of 60 and 5 cm, respectively. The central four rows were harvested for grain yield measurement. The grain yield was adjusted for 10% seed moisture before conversion to kgha^{-1} for the analysis.

The grain yield data were subjected to AMMI and SREG model analysis in SAS version 9.1 (SAS Institute Inc., 2003) using a SAS program written by Hermandez and Crossa (2000). In the analysis, each combination between the four locations and three years was considered as an environment, making a total of 12 environments. The AMMI model used for the data was:

$$\bar{y}_{ij.} = \mu + \tau_i + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \bar{\varepsilon}_{ij.}$$

and the SREG linear-bilinear model was:

$$\bar{y}_{ij.} = \mu + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \bar{\varepsilon}_{ij.}$$

Where; $\bar{y}_{ij.}$ is the mean of the ith genotype in the jth environments; μ is the overall mean; τ_i is the genotypic effect; δ_j is the environment effect; $\lambda_k (\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_t)$ are scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for genotypes, $\boldsymbol{\alpha}_{ik} = (\alpha_{1k}, \ldots, \alpha_{gk})$ and environments, $\boldsymbol{\gamma}_{jk} = (\gamma_{1k}, \ldots, \gamma_{ek})$, such that $\sum_i \alpha_{ik}^2 = \sum_j \gamma_{jk}^2 = 1$ and $\sum_i \alpha_{ik} \alpha_{ik'} = \sum_j \gamma_{jk} \gamma_{jk'} = 0$ for $k \neq k'$; α_{ik} and γ_{jk} for k=1,2,3,… are called “primary,” ”secondary,” “tertiary,”. . . etc effects of genotypes and environments, respectively; $\bar{\varepsilon}_{ij.}$ is the residual error assumed to be normally and independently distributed $(0, \sigma^2/r)$ (where σ^2 is the pooled error variance and *r* is the number of replicates). Least squares estimates of the multiplicative (bilinear) parameters in the kth bilinear term are obtained as the kth component of the deviations from the additive (linear) part of the model. In the AMMI model, only the GEI term is absorbed in the bilinear terms, whereas in the SREG model, the main effects of genotypes (G) plus the GEI are absorbed into the bilinear terms.

The results of the AMMI model analysis were interpreted on the basis of three AMMI graphs: (a) the graph that showed the main and first multiplicative axis term (PC1) of both genotypes and environments, (b) the graph that showed nominal yield (expected yield from the AMMI model equation without environmental deviation) of genotypes across PC1 scores of environments, and (c) the biplot that used scores of environments and genotypes PC1

Table 1. AMMI analysis of variance for grain yield (kgha^{-1}) of 11 soybean genotypes grown at 12 environments (combination of four locations and three years).

Source of variation	DF	SS	MS	F value	Explained % of GEISS
Treatments	131	155856296.09	1189742.718		
Replications (E)	24	3735457.99	155644.08	2.12**	
Environments (E)	11	95197867.84	8654351.62	118.122**	
Genotypes (G)	10	7462423.38	746242.34	10.185**	
GEI	110	53196004.87	483600.04	6.601**	
AMMI 1	20	20591452.17	1029572.61	14.0525**	38.71
AMMI 2	18	15315319.42	850851.08	11.613**	28.79
AMMI 3	16	7087576.19	442973.51	6.0461**	13.32
AMMI 4	14	3709491.69	264963.69	3.6164**	6.97
AMMI 5	12	3070563.70	255880.31	3.4925**	5.77
Residual	30	3421601.7	114053.39	1.556ns	6.43
Pooled error	240	17583942.2	73266.4		
CV=19.12 R^2=0.9					

** Significant at the 0.01 probability level; ns= non significant; DF = degree of freedom; SS = sum of squares; MS = mean sum of squares; CV = coefficient of variation, R^2 = coefficient of determination.

against scores of environments and genotypes of the second multiplicative axis term (PC2). The GGE biplots were constructed from the first two principal components (PC1 and PC2) derived by subjecting the environment-centered yield data (which contains G and GE) to singular valued composition (SVD) (Yan, 2002; Yan et al., 2000). GGE biplots were used to compare the performance of different genotypes at an environment, compare performance of a genotype at different environments and to compare the performance two genotypes at all environments. Both AMMI and GGE biplots were constructed using a SigmPlot version 10.0 software (SYSTAT Software Inc., 2006).

RESULTS AND DISCUSSION

The AMMI analysis of variance of grain yield (kg ha^{-1}) of 11 soybean genotypes tested in 12 environments is presented in Table 1. The analysis showed that soybean grain yield was significantly ($p<0.01$) affected by environments (E), genotypes (G) and genotype x environment interaction (GEI). Environment significantly explained about 61.08% of the total sum of squares due to treatments (G + E+ GEI). A large yield variation explained by environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. Environment grain yield (averaged across genotypes) ranged from 733.4 kgha^{-1} at Awassa in 2004 to 2592.2 kgha^{-1} at Abobo in 2003 (Table 2). Only the small portion that is, 4.79% of the total sum of squares due to treatments was attributed to genotypic effects. Genotype grain yield (averaged across environments) ranged from 1187.6 kgha^{-1} (TGx-1185-10) to 1718.8 kgha^{-1} (TGx-1892-10F) (Table 2). GEI significantly explained 34.13% of the treatments variation in grain yield. The magnitude of the GEI sum of squares was about 7 times larger than that for genotypes, indicating that there were sizeable dif-ferences in genotypic response across environments. The GEI was a crossover type as revealed by differential yield ranking of genotypes across environments (Table 2). Genotype TGx-1892-10F was the top ranking geno-type at four environments while TGx-1876-4E at three environments. TGx-1892-10F recorded the top yield 3767.3 kgha^{-1} at the highest yielding environment (Abobo in 2003) whereas the released cultivar Davis was the highest yielder (1515.6 kgha^{-1}) at the lowest yielding environment (Awassa in 2004).

The application of AMMI model for partitioning of GEI (Table 1) revealed the first five terms of AMMI were significant using an approximate F-statistic (Gollob, 1968). The Gollob's test most often retains the multiplicative axis terms of little practical relevance that is, axis with a low proportion of explained GE variation (Voltas et al., 2002). In this study, the first and second multiplicative axis terms explained 38.71 and 28.79% of GEI sum of squares, respectively. The adequacy of the multiplicative terms containing the real structure of GEI was inspected by estimating the amount of noise present in the interaction from the pooled error and comparing it with the sum of squares retained in consecutive AMMIn models (Voltas et al., 2002). Accordingly, the GEI con-tained 73266.4 (pooled error mean square) x 110 (degree of freedom for GEI) = 8059304 noise sum of square (15.2%) and 55196004.87 - 8059304= 45136700 pattern sum of square (84.8%). This last percentage was larger than that retained by the first two multiplicative terms that together accounted for 67.50% of GEI sum of squares. Moreover, the first two terms had sum of squares greater than that of genotypes and were highly significant ($p<0.01$). This suggested the AMMI model with first and second multiplicative terms was adequate for cross-validation of the yield variation explained by GEI in the present data set since it excludes most of its actual noise. Further

Table 2. Mean grain yield (kgha^{-1}) of the genotypes across environments.

Genotypes		Environments†												
Code	**Name**	**BK02**	**PW02**	**AB02**	**AW02**	**BK03**	**PW03**	**AB03**	**AW03**	**BK04**	**PW04**	**AB04**	**AW04**	**Mean**
G1	TGx-1185-10	1305.7	1233.3	1024.0	1001.2	784.1	1784.9	2676.7	889.8	371.2	566.0	1596.3	1017.4	1187.6d
G2	TGx-1835-10F	1594.3	1297.9	1478.0	650.6	1489.3	1977.9	2360.0	1126.0	1312.3	657.8	3144.4	244.0	1444.4bc
G3	TGx-1892-10F	2080.3	1242.7	1833.7	1265.5	1660.0	1531.5	3767.3	1338.6	1345.8	1025.0	2198.3	1336.4	1718.8a
G4	TGx-1895-23F	1625.0	1387.2	1385.1	590.6	1722.7	2072.9	2050.3	1005.3	1353.3	1113.3	1595.6	187.2	1340.7cd
G5	TGx-1897-17F	1828.7	1733.3	1255.0	740.0	986.0	1785.1	2152.3	1090.1	1497.8	1503.0	1952.6	625.6	1429.1bc
G6	TGx-1876-4E	1869.7	2322.2	975.3	825.1	1436.0	1858.9	2545.0	1303.3	2295.1	1803.4	1184.9	564.3	1581.9ab
G7	TGx-1895-4F	1893.0	1626.1	1380.3	393.4	1246.0	1886.0	3055.0	1428.7	932.8	1098.6	2128.6	120.7	1432.4bc
G8	TGx-1805-8F	1509.3	1703.8	1233.8	782.6	493.7	1869.5	3010.0	1185.6	1422.4	713.1	2842.2	407.0	1431.1bc
G9	TGx-1895-22F	1265.0	1839.6	1254.2	1056.8	1389.7	1608.5	2759.0	1164.9	1085.4	1085.9	1388.7	777.4	1389.6bcd
G10	Davis	1767.7	1044.4	961.2	959.1	1701.7	1440.2	2285.3	948.6	886.7	761.4	1841.9	1515.6	1342.8cd
G11	Cocker-240	1733.0	1212.1	1418.2	1169.3	1593.7	1768.7	1853.0	1123.6	902.3	578.1	559.0	1272.2	1265.3cd
	Mean	1679.2bc	1513.0cd	1290.8ed	857.7gh	1318.4ed	1780.4b	2592.2a	1145.9ef	1218.6e	991.4fg	1857.5b	733.4gh	1414.9

†Abbreviations: BK02 = Bako in 2002; PW02 = Pawe in 2002; AB02 = Abobo in 2002; AW02 = Awassa in 2002; BK03 = Bako in 2003; PW03 = Pawe in 2003; AB03 = Abobo in 2003; AW03 = Awassa in 2003; BK04 = Bako in 2004; PW04 = Pawe in 2004; AB04 = Abobo in 2004; AW04 = Awassa in 2004.
Mean followed by similar letters are not significantly different at the 0.05 probability level based on Tukey's Studentized Range (HSD) test; underlined values are highest yields at each test environments.

actual noise. Further AMMI axes (3rd, 4th, 5th and residuals) captured mostly noise and therefore did not help much for cross-validation of the yield variation explained by the GEI in soybean. Zobel et al. (1988) stated AMMI with the first two multiplicative terms was the best predictive model. Thus, the approximation of factual interaction pattern of the 11 soy-bean genotypes with 12 environments was best cross-validated with the first two multiplicative terms of genotypes and environments that easily visualized with the aid of a biplot (Figure 3).

AMMI biplot analysis

Figure 1 is AMMI biplot where genotypes and environments are depicted as points on a plane. The abscissa showed the main effects and the ordinate showed the first multiplicative axis term (PC1). The horizontal dotted line showed the interaction score of zero and the vertical dotted lines indicated the grand mean yield. Displacement along the vertical axis indicated interaction differences between genotypes and between environments, and displacement along the horizontal axis indicated difference in genotype and environment main effects. The solid line connecting environment markers indicated the year-to-year variation within individual location. The AMMI biplot illustrated 79.08% of treatments SS (155856295.65), with 4.79% due to G SS (7462423.38), 61.08% due to E SS (95197867.84), and 13.21% due to PC1 SS (20591452.17). The genotypes with PC1 scores close to zero expressed general adaptation whereas the larger scores depicted more specific adaptation to environments with PC1 scores of the same sign (Ebdon and Gauch, 20-02a).

Therefore, genotypes like G2 (TGx-1835-10F) and G8 (TGx-1805-8F) with larger PC1 score were better adapted to Abobo in 2004 with larger and same sign PC1 score (Figure 1) which combination results in a larger positive interact-tion. In contrast, genotype G11 (Cocker-240), was adapted to Awassa in 2002 and 2004 with larger negative PC1 scores. The relative magnitude and direction of genotypes along the abscissa and ordinate axis in biplot is important to understand the response pattern of geno-types across environments. The best genotype should combine high yield and stable per-formance across range of production environ-ments. For example, the two high yielding (averaged over environments) genotypes G3 (TGx-1892-10F) and G6 (TGx-1876-4E) can best judged based on their stability. G3 (TGx-1892-10F) combined low absolute PC1 score and high yield would be

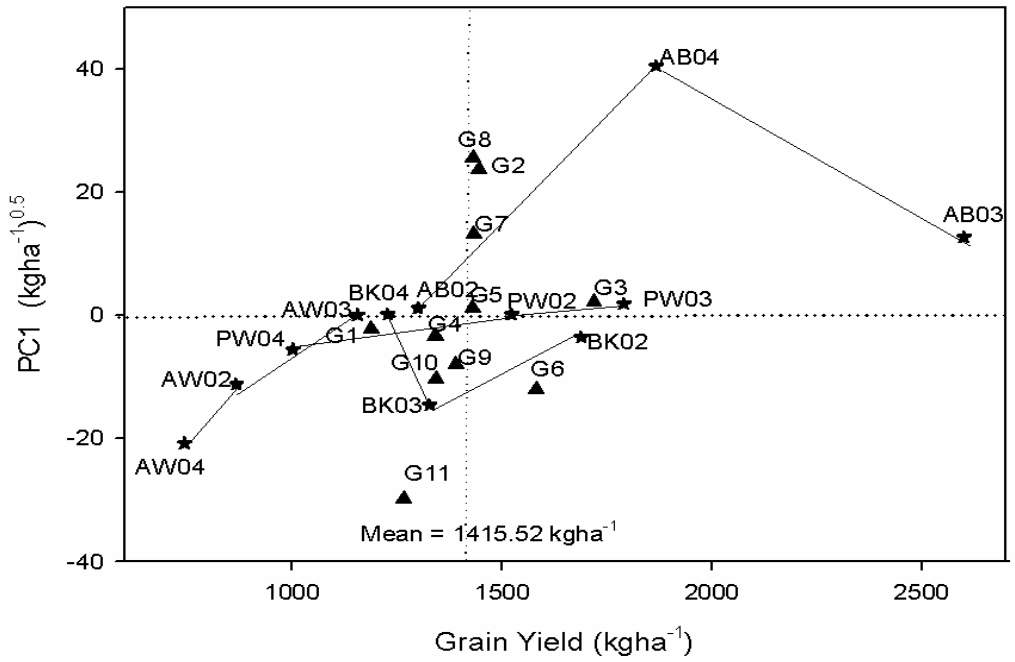

Figure 1. AMMI biplot showing the main and interaction (PC1) effects of both genotypes and environments on grain yield. An estimate of the GE interaction effect for a specific genotype–environment combination is the product of their corresponding interaction PC1 scores. **AMMI**, Additive main effects and multiplicative interaction; **PC**, Principal component analysis axis. Abbreviations of environments and genotypes are as given in Table 2.

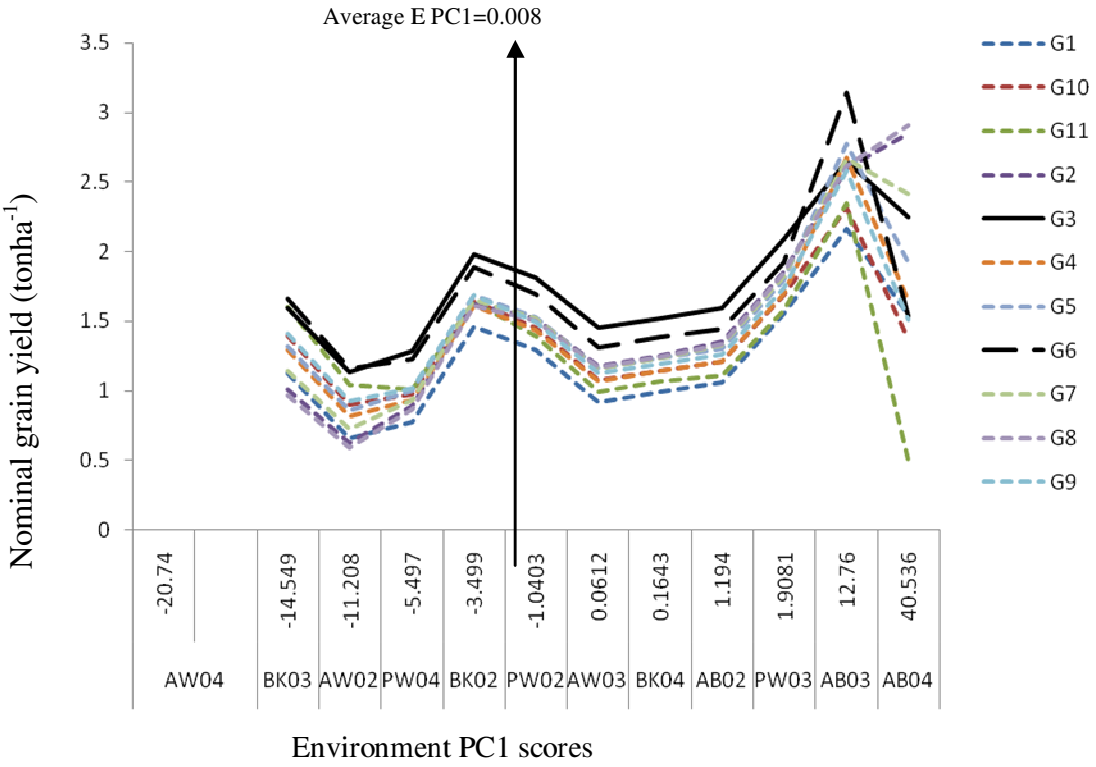

Figure 2. Nominal grain yield of 11 soybean genotypes based on AMMI model equation without environmental deviation, across environment PC1 score. Abbreviations of environments and genotypes are as given in Table 2.

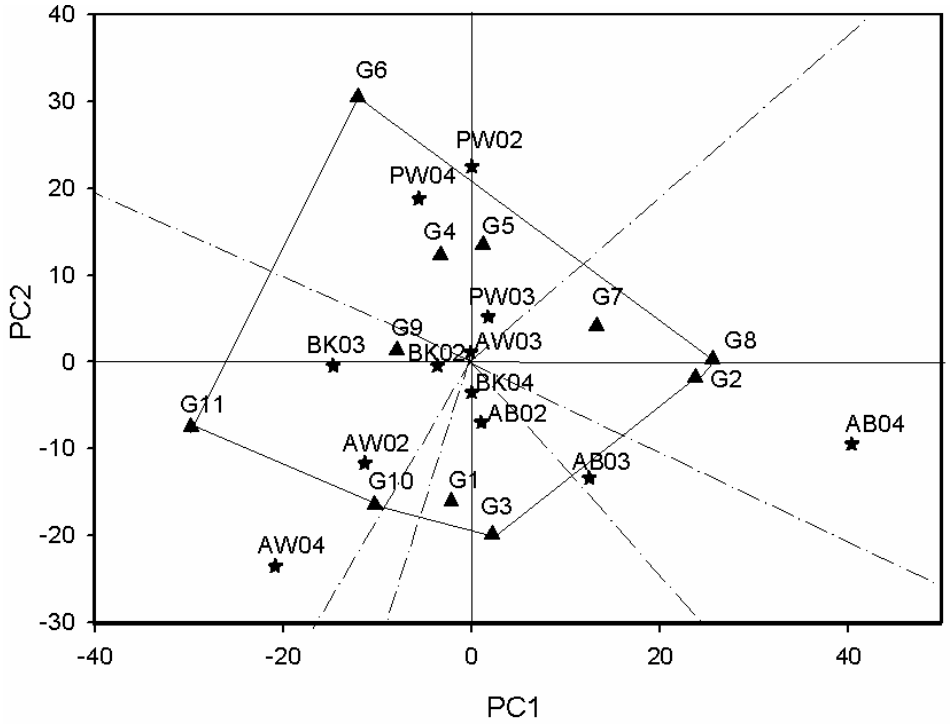

Figure 3. AMMI biplot analysis showing the mega-environments and their respective high yielding genotypes. Abbreviations of environments and genotypes are as given in Table 2.

best overall winner with relatively less variable yield across environments. The stability ranking of genotypes based on lower absolute PC1 scores was G5 (1.19), G3 (2.12), G1 (2.20), G4 (3.32), G9 (7.97), G10 (10.35), G6 (12.1), G7 (13.22), G2 (23.73), G8 (25.53) and G11 (29.84).

Pawe and Bako had the relatively smaller variation in the interaction (PC1 score) from year to year while Abobo had the largest (Figure 1). This indicated that the relative ranking of genotypes were stable at Pawe and Bako than at Abobo. Abobo was described as a location that combined larger main effects with larger interaction effects making it less predictable location for soybean variety evaluation.

The performance of the genotypes was also evaluated with nominal yields (Figure 2) estimated based on the AMMI model equation without the environmental deviation (that is, based on G and GEI PC1 effects only) across environment PC1 scores. Such analysis helps in targeting genotypes onto its growing environments (Samonte et al., 2005). Therefore, the adaptation patterns of the genotypes were assessed based on average environment PC1 score (which was 0.008). G3 (TGx-1892-10F) had the highest nominal grain yield at majority the test environments with environment PC1 score greater than 0.008. This genotype also recorded highest nominal yield in majority of the test environments with environment PC1 score below 0.008. Based on the frequency that genotypes were expected to yield highest in a location TGx-1892-10F best qualified for national recommendation for cultivation by growers.

Figure 3 cross-validated the interaction pattern of the 11 soybean genotypes with 12 environments. The distances from the origin (0, 0) are indicative of the amount of interaction that was exhibited by genotypes either over environments or environments over genotypes (Voltas et al., 2002). With the present data set, the genotype G6, G8, G2, G3, G10 and G11 expressed a highly interactive behaviour (positively or negatively), whereas the environment Awassa in 2003 exhibited low interaction. The nearly additive behaviour of Awassa in 2003 indicated that genotypic yield in that environment was highly correlated with the overall genotypic means across environments. Among the extreme genotypes, G2 and G8 are located in pairs indicating their similar response pattern. Connecting the extreme genotypes on a GE biplot forms a polygon and the perpendiculars to the sides of the polygon form sectors of genotypes and sites (Hernadez and Crossa, 2000). The genotypes at vertex are the winners in the sites included in that sector (20). In the AMMI biplot (Figure 3), seven sectors of which six had environments were observed. Pawe in both years clustered in one sector indicating repeatable performance of the genotypes observed in this location and it could be considered as separate mega-location for soybean variety evaluation and recommendation. Bako in all the test years relatively closer to biplot origin and hence less interactive location and could be good enough location for

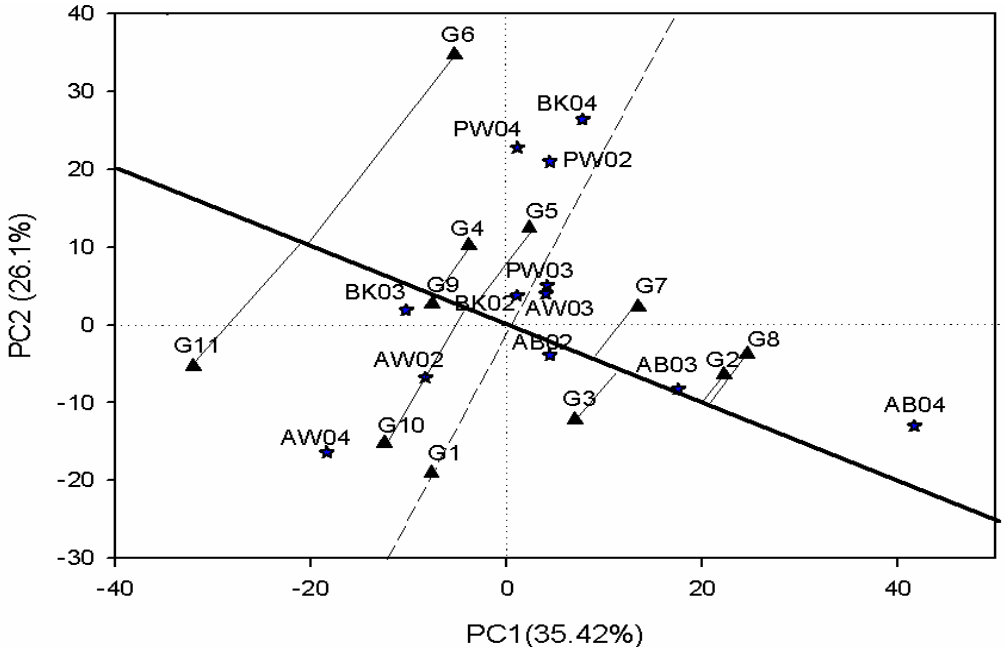

Figure 4. GGE biplot obtained from sites regression (SREG) analysis showing the performance of different genotypes at Abobo in 2003. Abbreviations of environments and genotypes are as given in Table 2.

selection of genotypes with average adaptation.

SREG GGE biplot analysis

The GGE refers to the genotype main effect (G) plus the genotype-by-environment interaction (GE), which are the two sources of variation of the site regression (SREG) model (Yan et al., 2000, 2007). GGE biplot best fits for which-won-where pattern analysis, genotype, and test environment evaluation (Yan et al., 2007). The biplot from the SREG model is used for assessment of ideal genotype and test location in multi-environment data provided that a given data set has a high correlation between PC1 and G main effects (Crossa et al., 2002; Yan et al., 2000). However, the requirement for a near-perfect correlation between genotype PC1 scores and genotype main effects was not happened with the present data set (In this case r = 0.45). This precondition restricts the utility of the GGE biplot for visualization of the yielding ability and stability of the genotypes, and the discriminating ability and the representativeness of the test environments (Gauch, 2006). This weakness was better captured with AMMI analysis in previous sections.

The GGE biplots of SREG analysis results were used to show the relative performance of all genotypes at a specific environment (Figure 4), relative adaptation of a specific genotype across environments (Figure 5) and comparison of two genotypes in different environments (Figure 6). In Figure 4, the highest yielding environment among the 12 environments, Abobo in 2003, was used to evaluate the genotypes. Apparently, a line that pass through the biplot origin and the environment marker of AB03 (Abobo in 2003) and a broken lines drawn from each genotypes marker perpendicular to the AB02 axes was used to compare the relative yield of genotypes. The genotypes were ranked based on length of their projections from AB02 axis and a broken line that is perpendicular to the AB03 axis and that pass through the origin separates the genotypes with higher than average yield from those with lower than average yield (Yan et al., 2000). Hence, G2, G8, G3 and G7 yielded above average yield at Abobo in 2003 and the rest genotypes yield performance was below average.

In Figure 5, the relative adaptation of G3 (TGx-1892-10F) which was identified as best genotype with AMMI analysis was assessed. This was done by drawing a line that pass through the biplot origin and G3 marker and a broken line drawn from each environment marker perpendicular to the G3 axis. The length of environment projections onto G3 axis assessed the performance of G3 at different environments, relative to other genotypes. Hence, G3 would yield highest at Abobo in all years (2004, 2002 and 2003) followed by Awassa in all years (2004, 2002 and 2003), Pawe in 2003, Bako in 2002 and in 2003, Pawe in 2002, Bako in 2004 and Pawe in 2004. The broken perpendicular line to the TGx-1892-10F axis and pass through the origin divided the environments where TGx-1892-10F would yield above average and below average. Hence, its yield performance was above average at Abobo in all the test years and at Awassa in 2004 and 2002.

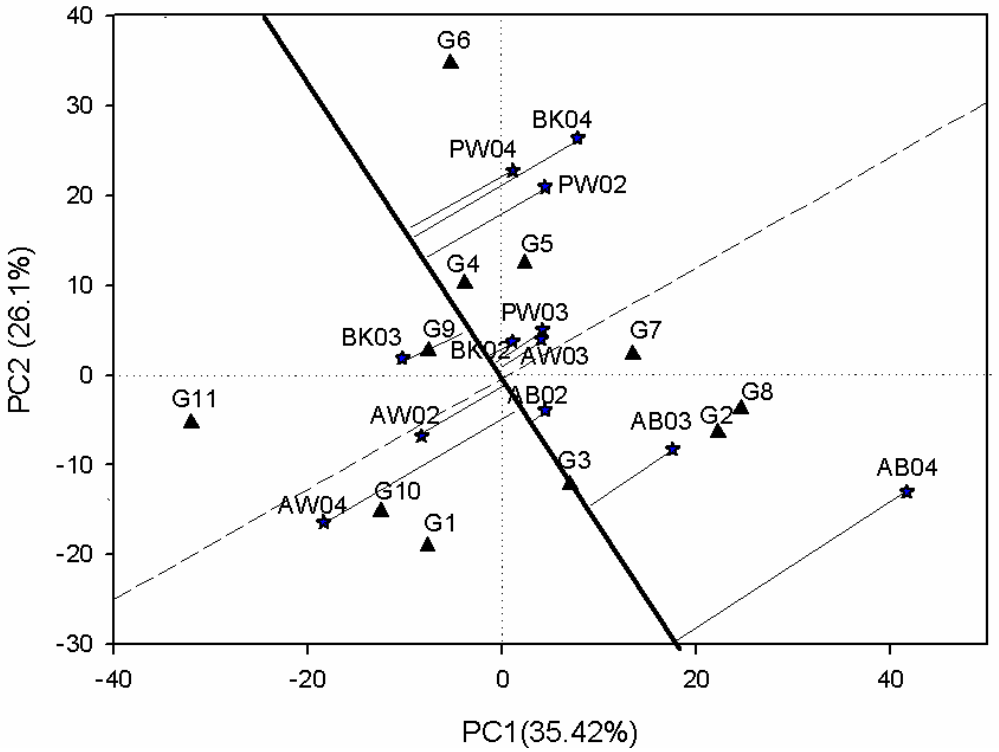

Figure 5. GGE biplot obtained from site regression (SREG) analysis showing the performance of G3(TGx-1892-10F) at different locations. Abbreviations of environments and genotypes are as given in Table 2.

The performance of the top two yielding genotypes (G3 and G6) compared in GGE biplot by a straight line connecting the markers of the two genotypes and a broken perpendicular line passing plot origin (Figure 6). This perpendicular divided the environments into two groups; each of these genotypes would yield better than the other at environments with markers on its side of the perpendicular, and vice versa (Yan et al., 2000). Thus, G3 (TGx-1892-10F) would yield better than G6 (TGx-1876-4E) at Abobo (in 2002, 2003 and 2004) and at Awassa in 2002 and 2004 whereas TGx-1876-4E would yield better than TGX-1892-10F at the rest 11 environments that is, at both Pawe and Bako in all the years and at Awassa in 2003.

Conclusion

Needless to mention, GEI is a common phenomenon in variety trials and its presence usually complicates variety selection and release decision. This paper demonstrated the AMMI and SREG GGE models were very effective for studying the pattern of GEI and interpreting of soybean grain yield data from multi-environment trials. AMMI model provided the relative magnitude and importance of the effects of GEI and its interaction terms related with genotype and environmental effects. It revealed that the GEI was an important source of soybean yield variation and its biplots were effective enough for visualizing the response patterns of genotypes and environments. The GGE model aided in determination of the relative performance of genotypes at a specific environmental comparison of the performance of genotypes at different environments and identification of genotypes suitable for groups of environments.

ACKNOWLEDGEMENTS

The authors would like to acknowledge the financial support provided by Ethiopian Institute of Agricultural Research via soybean national project for conducting the field trials. The authors also highly appreciate and acknowledge the efforts of soybean national project co-operators at Awassa, Pawe, Bako and Abobo agricultural research centres for managing the field trials and collecting data.

REFERENCES

Asrat A, Abush T, Sintayehu A, Mulugeta A (2006). Soybean genetic improvement in Ethiopia. In: Food and Forage Legumes of Ethiopia: Progress and Prospects. Kemal A, Gemechu K, Sied A, Malhotra R, Beniwal S, Makkouk K, Halila, M H (eds) . Proceedings of the

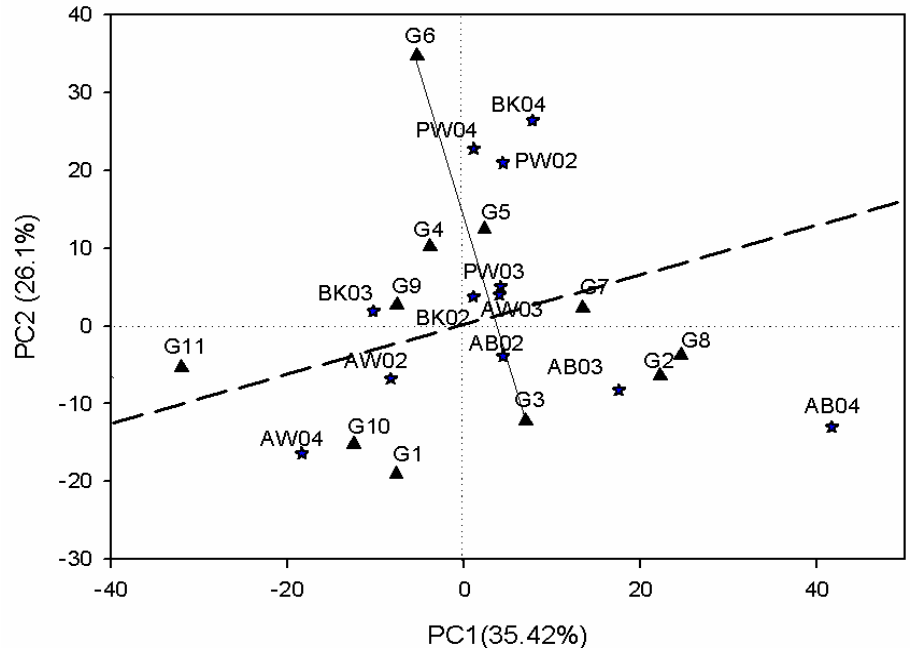

Figure 6. GGE biplot obtained from site regression (SREG) analysis that clusters the environments into those where G3 (TGx-1892-10F) out-yields G6 (TGx-1876-4E) (below the broken line) and where TGx-1876-4E out-yields TGx-1892-10F (above the broken line). Abbreviations of environments and genotypes are as given in Table 2.

workshop on food and forage legume, 22-26 September 2003, Addis Ababa, Ethiopia. ICARDA, Aleppo, Syria.

Becker H B, Leon J (1988). Stability analysis in plant breeding. Plant Breed. 101: 1-23.

Ceccarelli S, Grando S, Booth RH (2006). International breeding programmes and resource-poor farmers: Crop improvement in difficult environments. Available at www.icarda.cgiar.org/oldsite/parti-cipatory/PDF/Papers/1%20FORMAL.pdf (verified 10 November, 2007). The International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria.

Crossa J (1990) Statistical analysis of multi-location trials. Adv. Agron. 44: 55-85.

Crossa J, Cornelius PL, Yan W (2002). Biplots linear-bilinear model for studying cross over genotype x environment interaction. Crop Sci. 42: 619-633

Ebdon JS, Gauch HG (2002a). Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype x environment interaction. Crop Sci. 42: 489-496.

Ebdon JS, Gauch HG (2002b). Additive main effect and multiplicative interaction analysis of national turfgrass performance trials II: Cultivar recommendations. Crop Sci. 42: 497-506.

Ferreira DF, Demetrio CGB, Manly BFJ, Machado AA, Vencovsky R (2006). Statistical model in agriculture: biometrical methods for evaluating phenotypic stability in plant breeding. Cerne, Lavras 12 (4): 373-388.

Flores F, Moreno MT, Cubero JJ (1998). A comparison of univariate and multivariate methods to analyze G x E interaction. Field Crops Res. 56: 271-286.

Gauch HG (2006). Statistical analysis of yield trials by AMMI and GGE. Crop Sci. 46: 1488-1500.

Gollob HF (1968). A statistical model that combines features of factor analysis and analysis of variance techniques. *Psycrometrika* 33: 73-115.

Hermandez MV, Crossa J (2000). The AMMI analysis and graphing the biplot. CIMMYT, INT. Mexico. [Online]: Available at http://www.cimmyt.org/biometrics/biplots.exe; verified 8 November 2007.

Hussein MA, Bjornstad A, Aastveit AH (2000). SASG x ESTAB: A SAS program for computing genotype 3 environment stability statistics. Agron. J. 92: 454-459.

Lin CS, Binns MR, Lefkovitch LP (1986). Stability analysis: Where do we stand? Crop Sci. 26: 894-900.

Navabi A, Yang RC, Helm J, Spawer DM (2006). Can spring wheat-growing megaenvironments in the northern great plain be dissected for representative locations or niche-adapted genotypes? Crop Sci. 46: 1107-1116.

Samonte SOPB, Wilson LT, McClung AM, Medley JC (2005). Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. Crop Sci. 45: 2414-2424.

SAS Institute Inc. (2003). Version 9.1. SAS Institute Inc., Cary, NC.

SYSTAT Software Inc. (2006). SigmaPlot Version 10.0.

Voltas J, Van EF, Igartua E, García del Moral LF, Molina-Cano JL, Romagosa I (2002). Genotype by environment interaction and adaptation in barley breeding: Basic concepts and methods of analysis. In Slafer GA, Molina-Cano J L, Savin R, Araus J L, Romagosa I (eds.) Barley Science: Recent Advances from Molecular Biology to Agronomy of Yield and Quality. The Harworth Press Inc., New York, pp. 205-241.

Yan W (2002). Singular-value partitioning in biplot analysis of multi-environment trial data. Agron. J. 94: 990-996

Yan W, Hunt LA, Sheng Q, Szlavnics Z (2000). Cultivar evaluation and mega-environment investigation based on GGE biplot. Crop Sci. 40: 597-605.

Yan W, Kang MS, Ma B, Wood S, Cornelius PL (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci. 47: 643-655.

Yan W, Tinker NA (2006). Biplot analysis of multi-environment trial data: Principles and applications. Can. J. Plant Sci. 86: 623-645.

Zobel RW, Wright MJ, Gauch HG (1988). Statistical analysis of a yield trial. Agron. J. 80: 388-39.