Yield stability of soybean promising lines across environments

A Krisnawati and M M Adie

Indonesian Legumes and Tuber Crops Research Institute, Jl. Raya Kendalpayak KM 8 Malang 65101, East Java, Indonesia

Email: my_ayda@yahoo.com

Abstract. Soybean is grown in the wide range of environments in Indonesia, hence the genotype and environment interaction is become one of major complication in the breeding programs. The objective of this study was to evaluate the stability performance of soybean promising lines in eight locations during the dry season 2015. A completely randomized block design with four replicates was used to arrange the experiment. An additive main effects and multiplicative interaction (AMMI) model was used to examine the performance of yield stability. Soybean seed yield was affected by genotype (9.23%), environment (45.23%) and their interaction (45.62%). The first two principal component axes (PCA 1 and PCA 2) were significant (p < 0.01) and cumulatively contributed to 77.41% of the total variation. Based on AMMI multivariate method, two genotypes (G511H/Anj-1-6 and G511H/Anj-1-4) with seed yield of 2.67 and 2.74 t/ha, respectively, were identified as high yielding and stable promising lines across environments.

Keywords: environment, genotype, soybean, yield stability

1. Introduction

Soybeans ([Glycine max (L.) Merr.] in Indonesia is grown over wide environments with different environmental conditions, such as soil characteristics, mean temperature, and rainfall. The large variation in soybean yield that appears as a result the genotype by environment interaction (GEI) [1,2]. The presence of significant GEI for quantitative traits such as yield will lead to the lack of consistency in genotype performance across environments, hence may limit the progress of selecting superior genotypes [3]. It is therefore important to study the GEI to identify the yield contributing traits and yield stability [4,5].

Various methods have been proposed to explore the performance of soybean genotypes and their interaction with the environment. Currently, the additive main effects and multiplicative interaction analysis (AMMI) have been widely used to quantify the genotypic effects of the GEI [6,7,8,9,10]. AMMI biplot analysis is defined as a useful tool to explore the GEI patterns [11] with simple graphic representation of genotypes and environments in a multivariate biplot [12]. Furthermore, it captures a large portion of the GEI sum of squares and cleanly separates main and interaction effects, and provides valuable interpretation of the data [13].

There are two basic AMMI biplots, i.e. AMMI 1 and AMM2 biplots. The AMMI1 biplot plots the main effects (genotype mean and environment mean) against IPCA1 scores for both genotypes and environments. The AMMI 2 biplot, e the scores of IPCA1 are plotted against IPCA2 scores [14]. The application of AMMI biplot has been widely used in soybean crops. Evaluation of soybean lines in five environments during three seasons in Uganda revealed the presence of a scale GEI for soybean
seed yield [15]. Similarly, a significant GEI also obtained for seed yield and stability of six soybean genotypes at ten locations in Nigeria [6]. Furthermore, an evaluation on combined yield of the 24 soybean genotypes across 15 environments in Ugandan mega-environments had found a genotype (Maksoy 3N) with the highest mean yield [16].

Multi-environmental trials (METs) are usually used to evaluate the varietal performance [17] and to identify the most superior genotype for wide or specific cultivated zones based on yield and stability [5]. A differential response of GEI is frequent in METs [18] and must be estimated and considered when indicating cultivars for breeding program [5]. Therefore, the study on GEI and identification of yield stability is important for breeding new cultivars. The objective of this study was to evaluate the stability performance of soybean promising lines.

2. Materials and Methods

2.1. Genetic materials

The genetic materials consisted of seven soybean promising lines and two check varieties (Table 1). The check varieties (Anjasmoro and Grobogan) are high yielding and large seeded size.

| Code | Genotype  | Pedigree                   |
|------|-----------|----------------------------|
| G1   | MYT-11-2  | G511H /Anjasmoro //Anjasmoro / //Anjasmoro |
| G2   | MYT-1-6   | G511H /Anjasmoro           |
| G3   | MYT-7-1   | G511H /Anjasmoro //Anjasmoro //Anjasmoro |
| G4   | MYT-5-1   | G511H /Anjasmoro //Anjasmoro |
| G5   | MYT-2-1   | G511H /Argomulyo //Argomulyo |
| G6   | MYT-1-4   | G511H /Anjasmoro           |
| G7   | MYT-1-2   | G511H /Anjasmoro           |
| G8   | Anjasmoro | -                          |
| G9   | Grobogan  | -                          |

2.2. Field trials

The field trials were conducted at eight locations of soybean production centers with different soil types, mean seasonal rainfall, and altitude. The detail description of test locations is presented at Table 2. The study was conducted during the dry season 2015. The first dry season was started from February to May 2015, and the second dry season was started from June to September 2015.
Table 2. Location, code and characteristics of the multi-environment trials, 2015

| No. | Location                        | Code | Soil Type       | Land Type | Climatea | Altitude (masl)b |
|-----|---------------------------------|------|-----------------|-----------|----------|------------------|
| 1.  | Jati Kampir, Bagor, Nganjuk, East Java | E2   | Regosol         | Lowland   | E        | 58               |
| 2   | Kedunguneng, Bangsal, Mojokerto, East Java | E3   | Gray Grumosol   | Lowland   | C3       | 72               |
| 3   | Binangun, Binangun, Blitar, East Java | E4   | Alluvial        | Upland    | C3       | 355              |
| 4   | Sumber Banteng, Kejayan, Pasuruan, East Java | E5   | Brown Mediteran | Upland    | E        | 124              |
| 5   | Sumber Banteng, Kejayan, Pasuruan, East Java | E6   | Brown Mediteran | Lowland   | E        | 124              |
| 6   | Budeng, Jembrana, Jembrana, Bali| E8   | Alluvial        | Lowland   | D2       | 174              |
| 7   | Berabah, Kediri, Tabanan, Bali | E9   | Latosol         | Lowland   | D3       | 20               |
| 8   | Segara Anyar, Pajut, Central Lombok, West Nusa Tenggara | E10  | Regosol         | Lowland   | C3       | 24               |

aClimate type based on Oldeman (1974) climate classification system: C3 = 5-6 wet months and 4-6 dry months, D2 = 3-4 wet months and 2-3 dry months, D3 = 3-4 wet months and 4-6 dry months, E = < 3 wet months
bmasl = meter above sea level.
cPlanted during the first dry season
dPlanted during the second dry season

2.3. Experimental design and plant cultivation

The experiment was arranged in a completely randomized block design with four replicates in each location [2]. Each line was planted using 2.0 m × 4.5 m plot size, 40 cm × 15 cm plant spacing, two seeds per hill. Plants were fertilized with 50 kg ha⁻¹ Urea, 100 kg ha⁻¹ SP36 and 75 kg ha⁻¹ KCl which applied prior sowing the seeds. Weeds, pests and diseases were intensively controlled. Irrigation was made to keep the optimum soil moisture.

2.4. Observation and Data Analysis

Parameters observed included plant height, days to flowering, days to maturity, number of branch per plant, number of node per plant, number of filled pod, 100 seed weight, and seed yield (t ha⁻¹) [14]. The data were subjected to combined analysis of variance (ANOVA). SAS ver. 9.1.3 [19] was used to perform stability analysis on seed yield by using AMMI method.

3. Result and Discussion

The analysis of variance for seed yield and yield components of the seven soybean promising lines and two check varieties tested in eight environments revealed that environment, genotype, and genotype × environment interactions (GEI) were highly significant for most all of the observed traits, except for the number of branches per plant and number of empty and filled pods (Table 3). The seed yield of nine genotypes were significantly affected by environment, genotype, and GEI. The coefficient of variation (CV) for seed yield was 12.34%, indicating the precision of experimental research and control of environmental factors [8]. The highly significant genotype indicates the different performance of genotypes across environments [5]. A research which evaluated for seed yield and stability of six soybean genotypes at ten sites also obtained significant GEI [6].
Table 3. Analysis of variance for yield and yield components of seven soybean promising lines and two check varieties tested in eight environments. 2015

| Parameter                              | Mean Square Replication| Environment (E) | Genotype (G) | G × E | CV (%) |
|----------------------------------------|------------------------|-----------------|--------------|-------|--------|
| Days to flowering (day)                | 0.68ns                 | 4.01**          | 129.88**     | 0.01**| 2.18   |
| Days to maturity (day)                 | 1.67*                  | 81.26**         | 126.27**     | 3.39**| 1.21   |
| Plant height (cm)                      | 68.01                  | 2589.54**       | 2352.82**    | 127.32**| 10.72  |
| Number of branches/plant               | 0.09                   | 0.58**          | 0.52**       | 0.06ns| 16.78  |
| Number of node/plant                   | 7.869ns                | 54.88**         | 72.36**      | 12.75*| 22.68  |
| Number of filled pod/plant             | 90.12ns                | 1029.63**       | 632.07**     | 134.06ns| 21.25  |
| Number of empty pod/plant              | 0.28**                 | 2.18**          | 0.20ns       | 0.15ns| 25.57  |
| 100 seed weight (g)                    | 4.28**                 | 51.63**         | 98.05**      | 4.65**| 7.71   |
| Seed yield (t/ha)                      | 0.19**                 | 2.32**          | 0.54**       | 0.37**| 12.34  |

CV = coefficient of variation
* = significant at 5 % probability level (p < 0.05) ** = significant at 1 % probability level (p < 0.01), ns = not significant

The AMMI analysis of variance of seed yield showed that 45.23% of the total sum of squares was due to environmental effects, 9.23% to genotypic effects, and 45.62% to GEI effects (Table 4). This result revealed that the environment and GEI were the most important source of yield variation, due to their large contribution to the total sum of squares. Similar findings were also obtained in previous studies [20,21], which showed environments has greater proportion of total yield variation followed by GEI and genotypes. However, another research by [22] on twenty soybean genotypes tested at six environments found the GEI as the most important source of variation.

Through AMMI model, the GEI had partitioned into the first two significant IPCAs with contributions of IPCA1 (58.29%) and IPCA2 (19.12%). The remaining residuals were not significant (Table 4). The IPCA1 and IPCA2 cumulatively captured 77.41% of the total GEI sum of square, thus the interaction of the nine genotypes in eight environments can be predicted by the first two principal components of genotypes and environments. This result is in agreement with previous study [23] which stated that the most accurate model for AMMI can be predicted using the first two IPCAs. Furthermore, the overall pattern of genotypes interaction with environments was interpreted using AMMII1 and AMMII2 biplot.

Table 4. Additive main effects and multiplicative interactions analysis of variance for seed yield of the soybean genotypes across environments. 2015

| Source of variation       | Degree of freedom | Sum of Squares | Mean Square | Explained (%) |
|---------------------------|------------------|----------------|-------------|---------------|
| Total                     | 287              | 77.18          | 0.48**      | 9.15          |
| Treatment                 | 95               | 46.46          | 0.48**      | 45.23         |
| Genotype (G)              | 8                | 4.25           | 0.53**      | 58.29         |
| Environment (E)           | 7                | 21.01          | 3.00**      | 19.12         |
| G × E                     | 56               | 21.19          | 0.37**      | 58.29         |
| *IPCA1                    | 14               | 12.35          | 0.88**      | 19.12         |
| IPCA2                     | 12               | 4.05           | 0.33*       | -             |
| IPCA3                     | 10               | 2.78           | 0.27ns      | -             |
| Residual                  | 20               | 1.99           | 0.33ns      | -             |
| Pooled error              | 192              | 0.15           | 0.15        | -             |

*IPCA = Interaction Principal Component;
* = significant at 5 % probability level (p < 0.05) ** = significant at 1 % probability level (p < 0.01), ns = not significant
AMMI1 biplot shows the mean seed yield performance and adaptability of nine soybean genotypes across environments (Fig. 1). In this biplot, the abscissa represents the main effects (mean) and ordinate represents the effects of the interaction (IPCA1). In this figure, the vertical line in the middle of biplot represents the grand mean ($\bar{X} = 2.64$ t ha$^{-1}$). Right side of the line showed genotypes with higher yield than the grand mean, and the left side were genotypes with lower yield than the grand mean. Based on those description, thus G7, G6, G5, and G2 were generally high yielding (2.70 t ha$^{-1}$, 2.74 t ha$^{-1}$, 2.68 t ha$^{-1}$, 2.67 t ha$^{-1}$, respectively) with G6 being the overall best yield of 2.74 t ha$^{-1}$. In contrast, G3 G4, and two check varieties (G8 and G9) were generally have low yield.

The genotypes with IPCA1 scores close to zero exhibit general adaptation, meanwhile a more specific adaptation was represented by a larger scores IPCA1 [24]. Furthermore, the relative magnitude and direction of genotypes along the abscissa and ordinate axis in biplot is useful to describe the response pattern of genotypes across environments and also to differentiate high yielding and adaptable genotypes [4,25]. Accordingly, G3 and G5 were the most unstable and contributed the most toward GEI. Furthermore, 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 [26]. In this study, G9, G7, G2, and G1 were over the grand mean and located near the zero point of IPCA1, indicate those four genotypes have good adaptation across environments.

The AMMI1 biplot also describe the presence of two mega-locations [27,28]. Accordingly, three environments (E3, E6, and E7) with similar IPCA1 scores had constructed one mega-environment, meanwhile another five environments had constructed another mega-environment. However, the mega-environment classification can be explored in detail through AMMI2 biplot [28].

![Figure 1](image1.png)

**Figure 1.** Biplot AMMI1 (means yield vs PC1) for seed yield of seven soybean promising lines and two check varieties tested in eight environments. 2015

In AMMI2 biplot, which created using scores of genotypec and environment of the first two AMMI components (IPCA1 and IPCA2), explain the magnitude of interaction of each genotype and environment [4,26,29]. Genotypes which located near biplot origin were more stable (less interaction) compared to genotypes positioned further away (30). In Figure 2, based on distribution of genotype points in the AMMI2 biplot, it revealed that soybean promising lines G2 and G6 scattered close to the origin, indicating less interaction (showed high stability) of these genotypes with environments. The remaining seven genotypes scattered away from the origin of the biplot showing that the genotypes were more responsive to environmental interactive forces (lower stability or large interaction).
Another research on Indonesian soybean promising lines had found four stable genotypes [2]. Similarly, a study by using AMMI had found a stable and high yielding promising line which recommended to be released as new improved soybean variety [31]. Interaction of genotypes with specific environmental conditions can be reflected by projection of each genotype to environment spokes [14,32]. For instances, the G8 had positive interaction with environments E7 and specifically adapted to this environment, whereas G3 and G9 indicated specific adaptability with E5 and E8 (Fig. 2).

**Figure 2.** Biplot AMMI2 (PC1 vs PC2) for seed yield of seven soybean promising lines and two check varieties tested in eight environments. 2015

The mean yield of the nine genotypes grown in eight environments was presented in Table 4. Mean yields ranged from 2.44 t ha\(^{-1}\) (G4) to 2.74 t ha\(^{-1}\) (G6). Five of the genotypes showed higher yield than the mean average yields. Among the environments, four environments (E2, E4, E5, and E8) below the mean average yields. The highest yields were recorded in environments E1 followed by E6 with mean yields of 3.03 t ha\(^{-1}\) and 2.87 t ha\(^{-1}\), respectively.

**Table 5.** Seed yield of seven soybean promising lines and two check varieties tested in eight environments. 2015

| Code\(^a\) | E1  | E2  | E3  | E4  | E5  | E6  | E7  | E8  | Mean     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|----------|
| G1        | 2.88| 2.17| 3.40| 2.60| 2.26| 3.01| 2.62| 2.26| 2.65a    |
| G2        | 2.89| 2.44| 2.79| 2.90| 2.46| 2.75| 2.78| 2.34| 2.67a    |
| G3        | 2.74| 2.35| 2.27| 2.60| 2.12| 2.31| 2.64| 2.55| 2.45b    |
| G4        | 3.23| 2.20| 2.09| 2.96| 2.01| 2.35| 2.25| 2.41| 2.44b    |
| G5        | 3.12| 2.29| 3.18| 1.73| 2.02| 3.57| 2.92| 2.65| 2.68a    |
| **G6**    | 3.39| 2.40| 2.54| 2.94| 2.55| 2.89| 2.59| 2.63| **2.74a**|
| G7        | 3.14| 2.36| 2.77| 2.78| 2.14| 3.58| 2.59| 2.21| 2.70a    |
| G8        | 2.75| 2.07| 2.52| 1.91| 2.20| 2.98| 2.63| 2.68| 2.47b    |
| G9        | 2.65| 2.33| 2.48| 2.26| 2.52| 2.43| 2.43| 2.47| 2.45b    |
| **Mean**  | 3.03| 2.35| 2.70| 2.51| 2.25| 2.87| 2.72| 2.64| 2.64     |
The performances of agronomic characters of seven soybean promising lines and two check varieties tested in eight environments were presented in Table 6. The average of days to flowering was 33 days. Seven tested genotypes have early days to maturity (< 80 days), and the rests have medium maturity (G5 and G7). The seed size of nine genotypes was categorized as large, ranged from 15.36 to 21.11 g.

**Table 6. Agronomic characters of seven soybean promising lines and two check varieties tested in eight environments. 2015**

| Code | Agronomic characters |   |   |   |   |   |   |
|------|----------------------|---|---|---|---|---|---|
|      | DTF<sup>a</sup> | DTM<sup>b</sup> | PH<sup>c</sup> | NOB<sup>d</sup> | NON<sup>e</sup> | NFP<sup>f</sup> | NEP<sup>g</sup> | SW<sup>h</sup> |
| G1   | 34b                  | 79c                      | 49.82d        | 1.92          | 12.79bcd        | 47.85          | 1.85          | 15.63d         |
| G2   | 33c                  | 77f                      | 59.50b        | 2.39          | 13.72bc         | 45.71          | 1.67          | 17.02b         |
| G3   | 32d                  | 76g                      | 46.19c        | 1.77          | 10.73e          | 42.12          | 1.64          | 16.35c         |
| G4   | 32d                  | 78e                      | 56.48b        | 1.49          | 12.36cd         | 41.36          | 1.95          | 17.15b         |
| G5   | 35a                  | 80b                      | 69.28a        | 2.60          | 15.23a          | 50.89          | 2.12          | 15.74cd        |
| G6   | 34b                  | 79cd                     | 53.31b        | 2.25          | 13.65bc         | 50.93          | 1.55          | 16.33c         |
| G7   | 35a                  | 78de                     | 68.70a        | 2.64          | 15.22a          | 51.57          | 2.04          | 15.36d         |
| G8   | 35a                  | 82a                      | 68.84a        | 2.15          | 14.00ab         | 48.53          | 1.91          | 15.92cd        |
| G9   | 29e                  | 76g                      | 52.99c        | 1.97          | 11.84e          | 40.08          | 1.30          | 21.11a         |
| Mean | 33.13                | 78.31                    | 58.91         | 2.13          | 13.28           | 46.56          | 1.78          | 16.73          |

<sup>a</sup>Days to flowering (days); <sup>b</sup>Days to maturity (days); <sup>c</sup>Plant height (cm); <sup>d</sup>Number of branches per plant; <sup>e</sup>Number of node per plant; <sup>f</sup>Number of filled pod per plant; <sup>g</sup>Number of empty pod per plant; <sup>h</sup>100 seed weight (g)

In this study, G2 and G6 exhibit higher stability than other genotypes. The agronomic characters both of G2 and G6 were having early days to maturity (77 and 79 days, respectively), and large seed size (17.02 g and 16.33 g, respectively). Considering the mean yield, the stable promising line G6 had the highest yield (2.74 ha<sup>-1</sup>). Similarly, G2 also showed a high yield (2.67 ha<sup>-1</sup>) which was not significantly different to G6. Thus, those two genotypes may be recommended to be released as new improved soybean variety, or may be used as parents in crosses on breeding program.

4. Conclusion
AMMI biplot is a useful technique that was able to effectively reveal the existence of a significant GEI between nine soybean genotypes across eight environments. The stability analysis using AMMI method had successfully identified the G2 and G6 as high yielding and stable soybean promising lines across environments.

Acknowledgment
This research was supported by the Indonesian Agricultural Agency for Research and Development (IAARD), Ministry of Agriculture. We thank Arifin for his assistance during the field research.

References
[1] Susanto GWA and Adie MM 2010 Adaptability of promising soybean lines at different environmental conditions. *Penelitian Pertanian Tanaman Pangan* **29** (3): 166-170.
[2] Adie MM and Krisnawati A 2015 Soybean yield stability in eight locations and its potential for seed oil source in Indonesia. *Energy Procedia* **65**: 223–229.
[3] Fan XM, Kang M, Chen H, Zhang Y, Tan J and Xu C 2007 Yield stability of maize hybrids
evaluated in multi-environment trials in Yunnan, China. Agron J 99:220–228.

[4] Sanni KA, Ariyo OJ, Ojo DK, Gregorio G, Somado EA, Sanchez I et al 2009 Additive Main Effect and Multiplicative Interaction Analysis of grain yield performances in rice genotypes across environments. Asian J of Plant Sci 8 (1): 48-53.

[5] Roshandel M, Pourmohammad A, Babaei HR and Shekari F 2016 Grain yield stability analysis of soybean genotypes by AMMI method. Azarian J of Agric 3(6): 119-128.

[6] Amira JO, Ojo DK, Ariyo OJ, Oduwayne OA et al 2013 Relative discriminating powers of GGE and AMMI models in the selection of tropical soybean (Glycine max L. Merr.) genotypes. Afr Crop Sci J 21: 67-73.

[7] Bose L, Jambhulkar NN and Singh ON 2014 Additive Main Effect and Multiplicative Interaction (AMMI) analysis of grain yield stability in early duration rice. J of Animal and Plant Sci. 24: 1885-1897.

[8] Sousa L.B. Hamawaki O.T. Nogueira APO, Batista RO, Oliveira VM and Hamawaki RL 2015 Evaluation of soybean lines and environmental stratification using the AMMI, GGE bipolt, and factor analysis methods. Gen and Mol Res 14: 12660-12674.

[9] Satoto, Rumanti IA and Widyawastuti Y 2016 Yield stability of new hybrid rice across locations. Agrivita 38 (1): 33-39.

[10] Bhartiya A, Aditya JP, Singh K, Pushpendra, Purwar JP and Agarwal A 2017 AMMI & GGE bipolt analysis of multi environment yield trial of soybean in North Western Himalayan state Uttarakhand of India. Legume Research 40 (2): 306-312.

[11] Kaya Y, Palta C and Taner S 2002 Additive Main Effect and Multiplicative Interaction Analysis of yield performances in bread wheat genotypes across environments. Turk J Agric For 26: 275-279.

[12] Yokomizo GK, Duarte JB, Vello NA and Unfried JR 2013 AMMI analysis of grain yield in soybean lines selected for resistance to Asian rust. Pesq Agropec Bras 48: 1376-1384.

[13] Gauch HG 1992 Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier Science Pub. Amsterdam, Netherland.

[14] Akter A, Hassan MJ, Kulsum MU, Islam MR, Hossain K and Rahman MM 2014 AMMI bipolt analysis for stability of grain yield in hybrid rice (Oryza sativa L.). J of Rice Res 2 (2): 126-129.

[15] Tukamuhabwa P, Asimwe M, Nabasirye M, Kabayi P and Aphosa M 2012 Genotype by environment interaction of advanced generation soybean lines for grain yield in Uganda. African Crop Sci J 20: 107-115.

[16] Obua T, Maphosa M, Tusiime G and Tukamuhabwa P 2013 Genotype main effects and genotype by-environment bipolt analysis for soybean grain yield in Uganda. African Crop Sci Conference Proc 11: 537 – 541.

[17] Li T, Ali J, Marcaida M III, Angeles O, Franje NJ, Revilleza JE et al 2016 Combining limited multiple environment trials data with crop modeling to identify widely adaptable rice varieties. PLoS ONE 11(10): e0164456. https://doi.org/10.1371/journal.pone.0164456

[18] Rodrigues PC, Malosetti M, Gauch HG and Van Eeuwijk FA 2014 A weighted AMMI algorithm to study genotype-by-environment interaction and QTL by-environment interaction. Crop Sci 54 (4): 1555-1570.

[19] SAS Institute 2011 SAS/STAT 9.3 User's Guide. SAS Institue Inc: Cary, NC, USA.

[20] Bertoia LM and Aulicino MB 2014 Maize forage aptitude: Combining ability of inbred lines and stability of hybrids. The Crop J 2 (6): 407-418.

[21] Asfaw A, Alemayehu F, Gurum F and Atnaf M 2009 AMMI and SREG GGE bipolt analysis for matching varieties onto soybean production environments in Ethiopia. Sci Res Essays 4: 1322-1330.

[22] Gurmu F, Hussein M and Alemaw G 2009 Genotype × environment interactions and stability of soybean for grain iyeld and nutrition quality. African Crop Sc J 17 (2): 87 – 99.

[23] Gauch HG and Zobel RW 1996 AMMI analysis of yield trials. In Kang MS, Gauch HG, editors. Genotype-by-Environment Interaction. CRC Press, Boca Raton. New York, United States of
[24] Ebdon JS and Gauch HG 2002 Additive Main Effect and Multiplicative Interaction Analysis of national turfgrass performance trials: I. Interpretation of genotype × environment interaction. *Crop Sci* **42**: 489-496.

[25] Samonte SO, Wilson LT, McClung AM and Medley JC 2005 Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analyses. *Crop Sci* **45**: 2414–2424.

[26] Rashidi M, Farshadfar E and Jowkar MM 2013 AMMI analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments. *Intl J of Agric and Crop Sci* **5**(3): 253-260.

[27] Oliviera RL, Pinho RGV, Balestre M and Ferreira DV 2010 Evaluation of maize hybrids and environmental stratification by the methods AMMI and GGE biplot. *Crop Breeding and App Biotech* **10**: 247-253.

[28] Zeleke AA and Berhanu FA 2016 AMMI and GGE models analysis of stability and GEI of common bean (*Phaseolus vulgaris* L.) lines in Ethiopia. *J of Biol Agric and Helathcare* **6**(9): 127-135.

[29] Vargas M and Crossa J 2000 The AMMI analysis and graphing the biplot. Biometrics and Statistics Unit, CIMMYT.

[30] Pržulj N, Miroslavijevic M, Canak P, Zoric M and Bocanski J 2015 Evaluation of spring barley performance by biplot analysis. *Cereal Res Communication* **43**(4): 692-703.

[31] Krisnawati A, Basunanda P, Nasrullah and Adie MM 2016 Genotype stability analysis of soybean using Additive Main Effect and Multiplicative Interaction (AMMI) methods. *Informatika Pertanian* **25**(1): 41-50.

[32] Osiru MO, Olanya OM, Adipala E, Kapinga R and Lemaga B 2009 Yield stability analysis of *Ipomoea batatus* L. cultivars in diverse environments. *Aust J Crop Sci* **3**(4):213-220.