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Relative Discriminating Powers of GGE and AMMI Models in the Selection of Tropical Soybean (*Glycine max* L. Merr.) Genotypes

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ABSTRACT

Six genotypes of soybean (*Glycine max* L. Merr.) were evaluated at ten locations in Nigeria for grain yield and stability. The field experiment was carried out using a randomized complete block design with three replicates. Data on grain yield were evaluated for analysis of variance and the discriminatory abilities of additive main effects and multiplicative interaction (AMMI) and genotype plus genotype by environment (GGE) biplot were used to evaluate the stability performance of the genotypes. The analysis of variance revealed significant ($p = 0.05$) GEI effect. Mean grain yield of the soybean genotypes ranged from 1148 kg ha⁻¹ for genotype M-351 to 1584 kg ha⁻¹ for TGx1448-2E. Ilorin in the southern guinea savanna of Nigeria was the most variable with a high Interaction Principal Component Axes (IPCA) while Bauch in the northern guinea savanna was identified as more stable location in evaluating the soybean genotype. Mega-environments and the best yielding soybean genotypes in each mega-environment were revealed by the GGE biplot analysis. Furthermore, TGx1448-2E and TGx1440-1E, were established as the most promising and stable genotypes across the test locations. Stability model of GGE biplot was more superior, effective and informative in mega-environment analysis compared to AMMI analysis.

Key words: Additive main effects, multiplicative interaction, genotype plus genotype by environment, interaction principal components analysis, mega-environment, soybean

INTRODUCTION

Soybean (*Glycine max* L. Merr.) is a legume grows in tropical, subtropical and temperate climates. It is a crop with essential amino acid pattern that come close to satisfying the needs of the human diet (Osho *et al.*, 1995). In Africa, the high cost of protein-rich food stuffs (meat, fish, eggs and milk) has resulted in increased soybean utilization as an alternative source of inexpensive protein (Ogundipe and Weingartner, 1992).

Traditionally, evaluation of genetic diversity in soybean has been based on the differences in morphological and agronomic characters (Bernard *et al.*, 1998). However, individual genotypes of soybean are only well adapted to certain regions and the phenotypes are highly influenced by many environmental factors. This phenomenon is referred to as Genotype by Environment Interactions

(GEI) which is a routine occurrence in plant breeding programmes. Both the genotype and the environment determine the phenotype of an individual. The effects of these two factors, however, are not always additive because of the interaction between them. The presence of significant GE Interaction (GEI) makes it necessary to partition a cultivar development program with different objectives for different regions and for different weather conditions (Busey, 1983).

The additive main effects and multiplicative interaction (AMMI) analysis has been reliably used for better decision making with regards to selection of genotypes (Crossa *et al.*, 1991; Gauch, 1992). However, there is need to perfectly incorporate Genotype (G) and genotype by environment (GEI) in cultivar evaluation and plant breeding programme in Multi-Environment Trials (MET). The objective this research is to examine the relative discriminatory abilities of AMMI and GGE stability models in selection for grain yield and stability among tropical soybean genotypes.

MATERIALS AND METHODS

Experimental site: The MET study was carried out for three years at ten different locations in Nigeria. The locations cut across three ecological zones of Nigeria. Abeokuta (7°11'N, 3°18'E) in the derived Savanna region with transitional forest Savanna vegetation, Ikenne (6°52'N, 3°41'E) and Ile-Ife (7°49'N, 4°07'E) in rain forest zone, Ilorin (8°30'N, 4°32'E), Mokwa (9°18'N, 5°04'E) Bida (9°05'N, 6°00'E) and Yandev (7°23'N, 9°05'E) in Southern Guinea Savanna, Samaru (11°17'N, 4°18'E), Zaria (11°02'N, 7°43'E) and Bauchi (10°21'N, 9°52'E) in Northern Guinea Savanna vegetation (Agro-climatology stations, Nigeria).

Plant materials: Six soybean cultivars TGx1440-1E, TGx1448-1E, TGx1448-2E, TGx1455-1D, Samsay-2 and M 351 that were released for cultivation in Nigeria and other tropical countries (Ojo, 2003) were obtained from Genetic Resource Unit of International Institute for Tropical Agriculture (IITA), Nigeria for the study. The experimental design was a Randomized Complete Block Design with three replicates at each site under rain-fed conditions. Each plot consisted of 480 plants in 4 plant rows. Each row was 6 m long with 75 cm inter-row spacing. Spacing between plants was 5 cm. Weeding was done when necessary.

Data collection and analysis: At maturity, data on grain yield was collected from the inner rows leaving 1 m on either sides as borders. The data was subjected to combined analyses of variance using the GLM procedure of Statistical Analysis System (SAS Institute, 1999) to determine the magnitude of the main effects and interactions. The GGE Biplot methodology which is composed of two concepts, the Genotype (G) concept (Gabriel, 1971) and the genotype plus Genotype by Environment Interaction (GGE) concept (Yan *et al.*, 2000), was applied for visual examination of the genotype by environment interaction (GEI) (GGE-biplot software). The GGE biplot was constructed using first two principal components (PC1 and PC2) derived from subjecting environment centered yield data. The Additive Main Effect and Multiplicative Interaction (AMMI) analysis using MATMODEL (version 2.0) was also utilized to analyze the data.

The AMMI model is stated below:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum \lambda_n Y_{gn} \pi_{en} + \theta_{ge}$$

Where:

- Y_{ge} is the yield of genotype
- g , in environment e

- μ is the grand mean
- α_g is the genotype mean deviation
- β_e is the environment mean deviation
- λ_n is the eigenvalue of the PCA axis n
- Y_{gn} and π_{en} are the genotype and environment PCA scores for the PCA axis n
- N is the number of PCA axes retained in the model
- θ_{ge} is the residual error

RESULTS

The result of Table 1 revealed that genotypes, environments and genotype by environment interaction (GEI) effects were significantly different ($p \leq 0.01$). The genotype effect accounted for about 3.7% of the total variation while the environmental effect contributed about 61.8%, over fifteen times that of genotype. This indicated that environment effect was the predominant source of variation followed by GEI which accounted for 14.9% of the total variation. The importance of GEI component over genotype gives opportunity for specific breeding (adaptation).

The grain yield (kg ha^{-1}), average over three years, of the six soybean genotypes grown at ten locations is presented in Table 2. Genotype TGx1448-2E recorded the highest grain yield of $1593.19 \text{ kg ha}^{-1}$ while genotype M-351 had the least mean grain yield of $1141.96 \text{ kg ha}^{-1}$. The location effect on the production of grain yield in soybean showed that the highest grain yield of $1706.95 \text{ kg ha}^{-1}$, average of three years, was recorded in Ilorin (Table 3). There were no significant differences ($p = 0.05$) in grain yield observed at Zaria ($1591.98 \text{ kg ha}^{-1}$), Yandev ($1589.19 \text{ kg ha}^{-1}$), Ikenne ($1485.5 \text{ kg ha}^{-1}$) and Mokwa ($1443.41 \text{ kg ha}^{-1}$). Abeokuta had the least mean yield of $1001.76 \text{ kg ha}^{-1}$. The grain yield at each test location, average over three years, was used for the evaluation of GEI.

AMMI analysis of variance for grain yield of six soybean genotypes evaluated in ten locations across three years showed significant differences ($p \leq 0.01$) for all the sources of variation (Table 4). Over 50% of the total sum of square was attributed to environmental effect, 11% to

Table 1: Combined analysis of variance for grain yield of six soybean genotypes evaluated at thirty environments in Nigeria

| Source of variation | df | Sum of squares | Mean squares | Total variation (%) |
|----------------------------------|-----|----------------|---------------|---------------------|
| Replication (within environment) | 60 | 1,589.16 | 264,860.8** | |
| Genotype (G) | 5 | 1,204.03 | 2,408,058.4** | 3.70 |
| Environment (E) | 29 | 20,129.85 | 6,934,430.9** | 61.80 |
| G×E | 145 | 4,850.96 | 336,872.3** | 14.89 |
| Error | 293 | 4,817.53 | | |

**Significant at $p \leq 0.01$ probability level

Table 2: Grain yield of six soybean genotypes evaluated at ten locations in Nigeria for three years

| Genotypes | Mean yield (kg ha^{-1}) |
|------------|------------------------------------|
| Tgx1440-1E | 1,537.66 |
| TGx1448-1E | 1,424.24 |
| TGx1448-2E | 1,593.19 |
| TGx1455-1D | 1,271.97 |
| Samsay-2 | 1,405.97 |
| M-351 | 1,141.96 |
| LSD | 172.32 |

Table 3: Mean yield (kg ha⁻¹) of soybean varieties in ten locations in 2005, 2006 and 2007

| Location | Yield (kg ha ⁻¹) | | | |
|----------|------------------------------|----------|----------|----------|
| | 2005 | 2006 | 2007 | Mean |
| Ikenne | 1,083.33 | 1,398.17 | 1,975.00 | 1,485.5 |
| Abeokuta | 119.06 | 1,095.6 | 1,790.61 | 1,001.76 |
| Ife | 1,456.44 | 1,097.94 | 1,218.22 | 1,257.53 |
| Ilorin | 88.89 | 1,515.28 | 3516.67 | 1,706.95 |
| Mokwa | 1,610.06 | 1,695.83 | 1,024.33 | 1,443.41 |
| Bida | 1,559.72 | 1,166.72 | 495.56 | 1,074.00 |
| Samaru | 723.11 | 1,791.56 | 1,207.28 | 1,240.65 |
| Yandev | 1,061.56 | 1,886.56 | 1,819.44 | 1,589.19 |
| Bauchi | 1,755.67 | 609.55 | 1,536.78 | 1,300.19 |
| Zaria | 2,041.72 | 1,624.94 | 1,109.28 | 1,591.98 |
| LSD | | | | 236.33 |

Table 4: Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of six soybean genotypes evaluated in ten locations across three years

| Source | df | Sum of squares | Mean squares | Total variation (%) | G×E (%) |
|-------------|-----|----------------|----------------|---------------------|---------|
| Environment | 9 | 60,678,514.71 | 6,742,057.19** | 53.50 | |
| Block | 20 | 6,092,115.60 | 304,605.78** | | |
| Genotype | 5 | 12,579,255.97 | 2,515,851.19** | 11.09 | |
| G×E | 50 | 20,494,849.00 | 409,896.98** | 18.07 | |
| IPCA 1 | 12 | 9,239,434.44 | 769,952.87** | | 45.08 |
| IPCA 2 | 10 | 6,695,125.40 | 669,512.54** | | 32.67 |
| Residual | 28 | 4,587,757.72 | 163,848.49 | | 22.38 |
| Error | 95 | 17,646,598.65 | 185,753.67 | | |
| Total | 179 | 113,423,042.12 | 633,648.28 | | |

**Significant at p≤0.01 probability level

Table 5: Means and first principal component analysis (PCA) scores from AMMI analysis of grain yield for six soybean genotypes evaluated at ten locations

| Genotypes | Ikenne | Abeokuta | Ife | Ilorin | Mokwa | Bida | Samaru | Yandev | Bauch | Zaria | Mean | IPCA1 |
|------------|---------|----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-------|
| Tgx1440-1E | 1916.67 | 1025.11 | 1279.34 | 2163.89 | 1668.22 | 1063.45 | 1181.78 | 1695.89 | 1490.56 | 1889.78 | 1537.47 | 43.31 |
| TGx1448-1E | 1940.78 | 802.67 | 902.89 | 2072.22 | 1361.22 | 1199.56 | 1142.11 | 1848.89 | 1437.67 | 1523.22 | 1423.12 | 46.37 |
| TGx1448-2E | 1879.66 | 1063.56 | 1204.22 | 2086.11 | 1580.67 | 1097.33 | 1437.33 | 1960.67 | 1545.56 | 2050.89 | 1590.60 | 40.62 |
| TGx1455 | 1106.44 | 838.44 | 1372.33 | 1983.33 | 1500.11 | 1033.89 | 1173.56 | 1555.33 | 1429.33 | 1245.33 | 1323.81 | 31.33 |
| Samsøy-2 | 1037.00 | 1376.22 | 1533.33 | 1717.67 | 1439.00 | 1182.89 | 1303.33 | 2076.89 | 1233.55 | 1523.11 | 1442.30 | 29.32 |
| M-351 | 939.89 | 934.22 | 1252.89 | 1819.43 | 1200.11 | 866.89 | 1204.33 | 1249.33 | 688.56 | 1319.56 | 1147.52 | 26.58 |
| Mean | 1470.07 | 1006.70 | 1257.50 | 1973.78 | 1458.22 | 1074.00 | 1240.41 | 1731.17 | 1304.20 | 1591.98 | 1410.80 | |
| IPCA1 | 4.80 | -10.73 | -4.40 | 16.02 | 1.69 | -8.18 | -4.13 | 6.32 | -1.33 | 6.19 | | |

genotypic effects while GEI effects capture 18%. The GEI was partitioned into two Interaction Principal Components Analysis Axes (IPCA). IPCA1 and IPCA2 of the AMMI model captured 45 and 33% of the GEI Sum of Squares (SS), respectively. Table 5 shows the mean yield of six soybean genotypes grown at ten locations and the value of the first IPCA scores. Tgx1448-1E had the highest IPCA score (46.37) while the smallest value (26.58) was recorded for M-351. This showed the stability of M-351 across the test locations. Also, IPCA value of 1.33 was recorded for Bauchi while the highest IPCA value was observed for Ilorin. This indicated low interaction of the climatic conditions in Bauchi and high interaction in Ilorin. Bauchi is therefore more stable in evaluating the performance of the soybean genotypes.

The GGE biplots of the first two interaction principal component (PC1 and PC2) accounted for 86.6% of the total variation with PC1 and PC2 explaining 67.5 and 19.1%, respectively (Fig. 1). The polygon view was drawn to join TGx1448-1E, TGx1448-2E, Samsay-2 and M-351 which were the genotypes located farthest from the biplot origin such that the other genotypes, TGx1455-1D and TGx1440-1E were within this polygon. Figure 1 also shows that all the test locations used in the study can be grouped into three mega-locations. Ilorin in one sector and Ikenne, Bida, Mokwa, Samaru, Bauchi, Zaria and Yandev in another sector. Abeokuta and Ife were also group together in another sector.

Figure 2 shows the mean grain yield and stability performance of the soybean genotypes. The genotypes were ranked along the Average-Environment Co-ordinate (AEC x-axis) with an arrow pointing to a greater value based on their mean performance across all locations. The

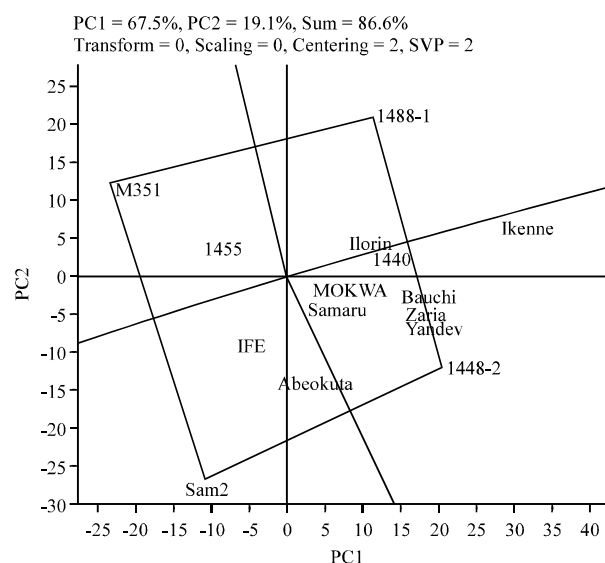


Fig. 1: The “which-won-where” view of the GGE biplot showing which soybean genotypes best in which location

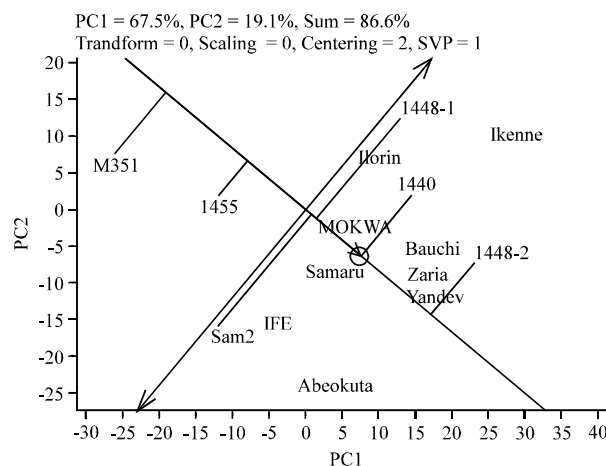


Fig. 2: The mean yield and stability of soybean genotypes across ten locations in Nigeria

double-arrowed line separates entries with below-average means. Genotypes TGx1448-2E, TGx1440-1E, Samsoy-2 and TGx1448-1E were placed above the double-arrowed line while the remaining genotypes were located below the double-arrowed line. Genotype TGx1448-2E was the leading genotype on the AEC (x-axis). Genotypes TGx1448-1E and Samsoy-2 had longer projections on the ATC (y-axis) while genotypes TGx1448-2E and TGx1440-1E had shorter projections on the AEC (y-axis).

DISCUSSION

The final selection of specific crop genotypes in plant breeding is often preceded by multi-location testing in which the relative performance of the test genotypes is determined. The presence of Genotype×Environment Interaction (GEI) makes it difficult for breeders to decide which genotypes should be selected. Therefore, it is important to decompose the interaction in order to determine the yield potential and stability of the soybean genotypes (Yan *et al.*, 2001; Setimela *et al.*, 2007). According to Finnah and Mark (1980), there is need to select for stability whenever such interactions assume a practical importance in a testing programmes. The mean yield of soybean genotypes used in this experiment over a three year period across the ten locations differed substantially. This is indicative of the wide genetic background of the genotypes.

The AMMI analysis provided a clear picture of the G×E interaction. As a result of its low interaction, TGx1455-1D could be considered stable in any environment. Genotype TGx1448-2E, TGx1440-1E and Samsoy-2, with above average grain yield, can only be recommended for all the test locations provided that improved management practices and optimum climatic factors are in place. The three genotypes were responsive to changes in the environments and thus, not stable.

GGE biplot was also used to compare the performance of the soybean genotypes at the test locations. In the “which-won-where” polygon view, the vertex cultivar in each sector represents the highest yielding cultivar in the location that falls within that particular sector (Yan *et al.*, 2007). A line drawn from the origin of the biplot and perpendicular to the side of the polygon effectively divided the test locations into three sectors. This indicates that a single genotype had the highest yield in each mega-location and each mega-location provided similar information about the genotypes. TGx1448-1E performed best in Ilorin while TGx1448-2E can be selected for grain yield production in Ikenne, Mokwa, Bida, Samaru, Bauchi, Zaria and Yandev. In Ife and Abeokuta, Samsoy-2 had the best performance while genotypes M-351 did not perform well in any of the locations.

According to Yan *et al.* (2000), the average yield of the cultivars is approximated by the projections of their markers on the AEC x-axis while the stability of the cultivars is measured by their projection onto the double-arrow line (AEC y-axis). TGx1448-2E and TGx1440-1E, were identified as high yielding and more stable genotype which was in disagreement with the result of AMMI analysis.

CONCLUSION

The selection of crops is preceded by multilocal testing in plant breeding, however, it becomes difficult for breeders to determine which genotypes should be selected in the presence of GEI. In the current study, GGE biplots and AMMI were used to compare the performance of different genotypes at different environments. The AMMI analysis was able to explain the GEI, however, investigation of GEI was observed to be more meaningful when used with Genotype (G). The methodology of GGE biplot was a useful tool because the concept of the analysis considers both

and only G plus GE and not all of the phenotypic variation which may be misleading. Environmental component is irrelevant in making selection decision. Genotype plus Genotype×Environment (GGE) biplot was able to identify which genotype performs best in a given environment and also which genotype had the highest stability in the test locations. GGE biplot view, therefore, is more effective and informative than AMMI in mega-environment analysis and GEI evaluation.

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