

## Genotype x Environment Analyses and Selection for Yield Stability and Adaptation in Tropical Soyabean Genotypes

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### ABSTRACT

Six genotypes of soyabean (*Glycine max* (L.) Merr) were sown in six environments (site-year) in Nigeria. Yield data were subjected to the amended linear regression (LR) and the Additive Main Effect and Multiplicative Interaction (AMMI) analyses. AMMI biplot was used to determine stability of performance and adaptation of genotypes to specific environments. The LR and AMMI models captured 95.9% and 95.2% of the trial sum of square respectively. The first PCA axis of the AMMI model captured 62.3% while the joint regression component of the LR model captured only 10.5% of the interaction sum of squares. TGx 1448-2E and Bossier exhibited the least interactions while TGx 536-02D showed the largest interaction with the environments. TGx 1448-2E with above average mean yield and small interaction was highly consistent in all environments with specific adaptation to environments J2 and Z1. It has been recommended for a future breeding programme.

**Keywords:** AMMI model, Analysis of variance, Biplot, Genotype x environment interaction, LR model, Principal component axis, Soyabeans.

### INTRODUCTION

Stability of performance of a crop plant should be considered as a selection criterion in a breeding programme intended for the development of crop varieties to be grown in contrasting environments. Good knowledge of the existence and extent of genotype x environment (GxE) interaction is helpful to a breeder as a guide in his decision making with regards to which genotypes to select and eventually release to farmers. Ideally, varieties to be recommended for subsequent distribution to farmers should have good general adaptability in locations characterised by wide seasonal climatic factors. GxE interaction is said to occur when the relative performance of genotypes is not consistent from one environment to another and therefore the relative performance cannot be predicted with absolute confidence (Perkins and Jinks, 1968).

In the last two decades, soyabean varieties were recommended for release in Nigeria based on the results of uniform yield trials available from multilocational trials as a result of research efforts of IITA and the Nationally Coordinated Research on Soyabeans (IITA, 1983; 1984). The release method has been very subjective.

A number of statistical methods have been used for measuring the GxE interactions with practical implications for stability of performance in many crops. Simple analysis of variance (ANOVA) can, in most cases, detect the existence of GxE interaction. However, when and if the main effects account for a large percentage of the trial sum of square, ANOVA may fail to detect GxE interaction due probably to large degree of freedom of the GxE interaction component (Zobel *et al.*, 1988).

The Principal Components Analysis (PCA) is another statistical tool that shows the mean squares (MS) of the Principal Component axes but fails to identify GxE interaction as a source of variation (Gauch and Furnas, 1991). It is not a totally efficient tool for GxE analysis because it only makes use of a multiplicative model to produce a few PCA axes and a higher (noise) residual (Zobel *et al.*, 1988; Gauch and Furnas, 1991).

The linear regression (LR) technique in which the yield of a genotype is regressed on an environmental index is the most commonly used (Perkins and Jinks, 1968; Ariyo, 1987). The measure of adaptability of this technique is based on an assumption that a crop genotype responds linearly to environmental conditions (Finlay and Wilkinson, 1963). The

LR technique has been criticized (Zobel *et al.*, 1988; Ariyo, 1990) because the method could be misleading particularly when the proportion of GxE interaction due to linear regression is very small.

The amended Finlay-Wilkinson LR model which partitions the GxE interaction into joint regression (JR), genotype regressions (GRs), environment regressions (ERs) as well as the residual has been used to correct the peculiar problem of the traditional linear regression technique (Zobel *et al.*, 1988).

The Additive Main Effects and Multiplicative Interaction (AMMI) model has been proposed for general variety testing situations (Kempton, 1984; Gauch, 1990; Crossa *et al.*, 1989) because the traditional analysis of GxE interaction has laid emphasis on the analysis of stability rather than adaptation (Ariyo, 1998). AMMI analysis has been reliably used for better decision making with regards to selection of genotypes (Crossa *et al.*, 1991; Gauch, 1992). AMMI biplot has been particularly efficient because it provides additional insight into GxE interaction data beyond which is directly available in the various tables of analysis.

The aims of this study were to compare the amended LR and the AMMI models in the analysis of soyabean yield data obtained from six environments (site-year) in Nigeria and to determine the stability of performance and adaptation of genotypes to the different environments.

## MATERIALS AND METHODS

Six soyabean genotypes obtained from the International Institute of Tropical Agriculture (IITA), Ibadan were sown in six different environments (site-year) in Nigeria in 1996 (year 1) and 1997 (year 2). Mokwa and Zaria are in the Southern and Northern Guinea Savanna ecologies respectively while Jos is in a pseudo-savanna ecology. Genotypes were sown in a randomized complete block design with three replications in four-row plots of 6m long. Rows were 75cm apart leaving a plot size of 18m<sup>2</sup>. Plots were sown by drilling. On emergence, seedlings were thinned to plant-to-plant spacing of 5cm with about 480 plants per plot.

Single super-phosphate and NPK, 15:15:15 were applied and incorporated at the rate of 67.5kg P2O5 and 7.5kgN respectively during land preparation. At harvest maturity yield data were collected from the central 4m of

the two middle rows and seed yield was expressed in kilograms per hectare.

Analysis of variance of seed yield was carried out to estimate and test for significance of GxE interaction. The GxE interaction mean square was also partitioned according to the amended LR model to determine the relative proportion of variances due to JR, GRs and ERs using the equation

$$Y_{ge} = \mu + \alpha_g + \beta_e + K\alpha_g\beta_e + \gamma_g\beta_e + \alpha_g\delta_e + \theta_{ge}$$

Where  $Y_{ge}$  is the yield of genotype  $g$ , in environment  $e$ ;  $\mu$  is the grand mean;  $\alpha_g$  is the genotype mean deviation;  $\beta_e$  is the environment mean deviation;  $K$  is the concurrent or joint regression constant;  $\gamma_g$  is the genotype slope on environment mean;  $\delta_e$  is the environment slope on genotype mean; and  $\theta_{ge}$  is the residual. The AMMI analysis of yield data was also examined according to the equation:

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

Where  $\lambda_n$  is the eigen value of the PCA axis  $n$ ;  $\gamma_{gn}$  and  $\pi_{en}$  are the genotype and environment PCA scores respectively, for PCA axis  $n$ ;  $N$  is the number of PCA axes retained in the model and  $\theta_{ge}$  is the noise or residual portion. For any genotype-environment combination, the main effects equal the genotype mean plus the environment mean minus the grand mean. The interaction is the product of genotype and environment PCA scores.

The AMMI biplot was used to provide a graphical view of the transformed GxE interaction (Kempton, 19884) for easy interpretation. Genotypes or environments that occur almost on perpendicular line have similar means and those that fall almost on a horizontal line have similar interaction patterns. Genotypes or environments with large first principal components axis (PCA1) scores either positive or negative gave high interactions whereas those with PCA1 scores of zero or nearly zero have small interactions. Genotypes or environments with the same sign on the PCA axis have positive interaction, if different, their interaction is negative (Crossa *et al.*, 1990). The percentages of GxE interaction SS accounted for the JR, GRs and ERs of the LR model and the interaction PCA1 of the AMMI model were used to compare the effectiveness of the two models.

Table 1: Analysis of variance of grain yield of six soyabean genotypes in six environments.

Source	df	SS	MS
Trials	35	5,264,355.33	150,410.15**
Rep (Env)	12	517,655.12	43,137.93
Genotype (G)	5	1,871,443.87	374,288.77**
Env (E)	5	2,721,243.74	544,248.75**
G x E	25	672,436.14	26,897.44
Error	60	4,146,202.65	69,103.38

\*\* = Significant at 1% probability level.

Table 2: Analysis of variance including Finlay-Wilkinson regressions of soyabean yield.

Source	df	SS	MS
Trials	35	5,264,355.33	150,410.15**
Rep (Env)	12	3,521,005.91	293,417.16**
Genotype (G)	5	1,872,280.15	374,456.03**
Env (E)	5	2,720,023.41	544,004.68**
G x E	25	672,051.76	26,882.07
Joint Regr	1	70,479.45	70,479.45
Env Regrs	4	119,637.28	29,909.32
Gen Regrs	4	263,591.29	65,897.82*
Residual	16	218,343.75	13,646.48
Error	60	1,141,408.90	19,023.48
Total	107	9,926,770.14	92,773.55

\*, \*\* = Significant at 5% and 1% probability levels respectively.

## RESULTS

The analysis of variance (ANOVA) of seed yield of 6 genotypes of soyabean in six environments is presented in Table 1. Effects of genotype and environment were significant while those of the GxE interaction were not. Table 2 presents the ANOVA of seed yield including the amended LR model. The entire LR model captured about 95.9% while the GxE interaction captured 12.8% of the trial SS. The JR, ERs and GRs contained 10.5%, 17.8% and 39.2% of the interaction SS respectively; leaving 32.5% in the residual. Only the GRs portion of the GxE interaction showed a significant MS. The interaction MS of the model was about 2 times the residual MS.

The AMMI analysis of seed yield is presented in Table 3. Differences between genotypes and environments accounted for 35.5% and 51.7% of the trial SS respectively, while the GxE interaction component captured only

12.8%. The PCA1 axis captured 62.3% of the interaction SS compared with the JR of the LR model which captured only 10.5%. The MS of the PCA1 was about 3 times the MS of the residual.

Table 4 shows the means as well as the PCA1 scores of genotypes and environments. M2 produced the highest yield of 785.6kg per hectare whereas J1 produced the least yield of 293.4kg per hectare. Average yield ranged from 447.3kg per hectare for genotype 737p to 789.6kg per hectare for TGx 923-2E. Genotypes TGx 923-2E, TGx 1448-2E and TGx 536-02D yielded above average whereas the other three yielded below average. Mean yield of all genotypes were lower in year 1 than in year 2 in all environments.

The AMMI biplot presents a graphical information of the main effects and the first interaction PCA (IPCA1) axis in Figure 1. It shows the main effects on the abscissa and the IPCA1 scores as the

Table 3: AMMI analysis of variance for soyabean seed yield.

Source	df	SS	MS
Trials	35	5,264,355.33	150,410.15**
Rep (Env)	12	3,521,005.91	293,417.16**
Genotype (G)	5	1,872,280.15	374,456.03**
Env (E)	5	2,720,023.41	544,004.68**
G x E	25	672,051.76	26,882.07
PCA1	9	418,931.86	46,547.98*
Residual	16	253,119.91	15,819.99
Error <sup>60</sup>	1141	408.90	19.023.48
Total	107	9,926,770.14	92,773.55

\*, \*\* = Significant at 5% and 1% probability levels respectively.

Table 4: Yield kg/ha of six soyabean genotypes grown in six environments (site-year) mean values and the first PCA scores.

Genotype	Environment) <sup>e</sup>				M1	M2	Mean scores	First PCA
	J1	J2	Z1	Z2				
Bossier	183.0	383.9	515.7	530.6	619.0	744.5	496.2	-1.1
TGm 737p	161.3	392.5	504.8	555.5	507.3	562.7	447.3	3.6
TGx 536-02D	211.3	772.6	720.5	765.6	1042.1	1027.3	756.6	-15.4
TGx 849-313D	400.7	447.4	378.8	594.0	607.3	687.9	519.4	10.3
TGx 1448-2E	298.3	680.1	668.0	575.4	777.2	786.7	661.3	-1.2
TGx 923-2E	505.8	910.0	719.2	860.6	837.5	904.3	789.6	3.8
Mean	293.4	597.7	584.5	677.4	731.8	785.6	611.7*	
	First PCA scores							
	15.7	-1.7	-2.6	3.0	-9.0	-5.4		

e: J = Jos; Z = Zaria; M = Mokwa

1 & 2 denote year 1 and year 2 respectively

\*Grand mean is 611.7kg/ha

ordinates. AMMI biplot accounted for 95.2% of the trial SS. TGx 1448-2E and Bossier exhibited the least interaction while TGx 536-02D showed the largest positive interaction with the M<sub>1</sub> & M<sub>2</sub> environments. The values of interactions were least in J2 and largest in J1. Whereas J1 had the largest positive interaction effect, M1 had the largest negative interaction effect. Genotype TGx 849-313D and Bossier had similar means while TGx 1448-2E and Bossier had similar interactions. Although both TGx 1448-2E and Bossier showed stability of

performance and were adapted to J2 and Z1 environments, TGx 1448-2E had above average while Bossier had below average mean yield. Environments J2 and Z1 had near similar interaction in the current study.

## DISCUSSION

According to IITA (1990), significant progress had been made in the improvement of genetic backgrounds of tropicalized soyabean varieties with multiple resistance characteristics in terms of superior seed storability and promiscuous nodulation for

Africa (IITA, 1983; 1984). A number of high-yielding genotypes had also been released in Nigeria, Ghana, Uganda and Zaire (IITA, 1994; FAO, 1999). However, selection and subsequent release of soyabean varieties for yield stability and adaptation has been based on the traditional but subjective analysis of the genotype x environment yield data rather than the use of modern statistical tools and procedures. Consequently, the effectiveness of the release method had been questionable and as such was not necessarily reliable.

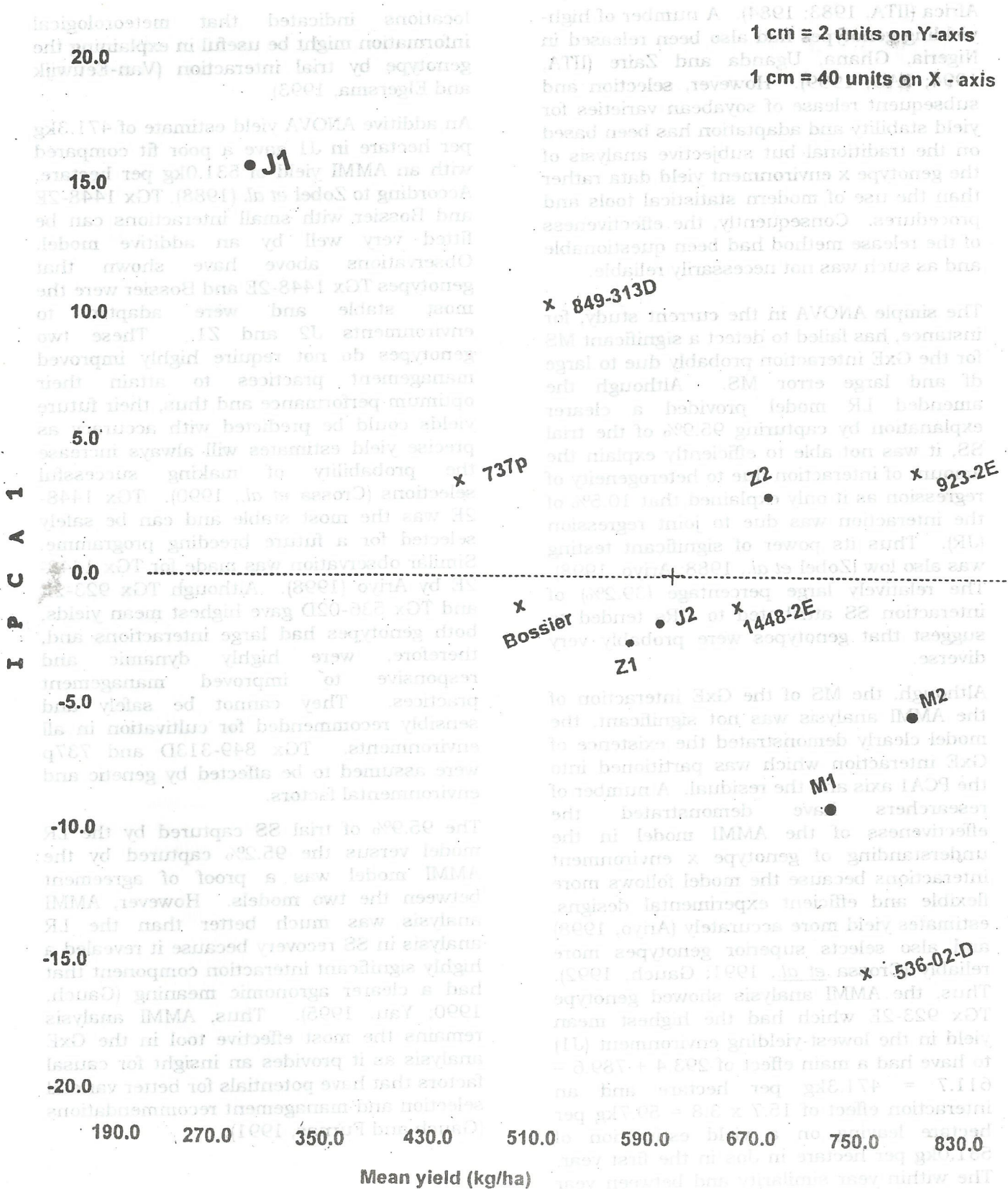
The simple ANOVA in the current study, for instance, has failed to detect a significant MS for the GxE interaction probably due to large df and large error MS. Although the amended LR model provided a clearer explanation by capturing 95.9% of the trial SS, it was not able to efficiently explain the amount of interaction due to heterogeneity of regression as it only explained that 10.5% of the interaction was due to joint regression (JR). Thus its power of significant testing was also low (Zobel *et al.*, 1988; Ariyo, 1998). The relatively large percentage (39.2%) of interaction SS attributed to GRs tended to suggest that genotypes were probably very diverse.

Although, the MS of the GxE interaction of the AMMI analysis was not significant, the model clearly demonstrated the existence of GxE interaction which was partitioned into the PCA1 axis and the residual. A number of researchers have demonstrated the effectiveness of the AMMI model in the understanding of genotype x environment interactions because the model follows more flexible and efficient experimental designs, estimates yield more accurately (Ariyo, 1998) and also selects superior genotypes more reliably (Crossa *et al.*, 1991; Gauch, 1992). Thus, the AMMI analysis showed genotype TGx 923-2E which had the highest mean yield in the lowest-yielding environment (J1) to have had a main effect of  $293.4 + 789.6 - 611.7 = 471.3\text{kg}$  per hectare and an interaction effect of  $15.7 \times 3.8 = 59.7\text{kg}$  per hectare leaving on a yield estimation of 531.0kg per hectare in Jos in the first year. The within year similarity and between year variation in genotype performance across

locations indicated that meteorological information might be useful in explaining the genotype by trial interaction (Van-Eeuwijk and Elgersma, 1993).

An additive ANOVA yield estimate of 471.3kg per hectare in J1 gave a poor fit compared with an AMMI yield of 531.0kg per hectare. According to Zobel *et al.* (1988), TGx 1448-2E and Bossier with small interactions can be fitted very well by an additive model. Observations above have shown that genotypes TGx 1448-2E and Bossier were the most stable and were adapted to environments J2 and Z1. These two genotypes do not require highly improved management practices to attain their optimum performance and thus, their future yields could be predicted with accuracy as precise yield estimates will always increase the probability of making successful selections (Crossa *et al.*, 1990). TGx 1448-2E was the most stable and can be safely selected for a future breeding programme. Similar observation was made for TGx 1448-2E by Ariyo (1998). Although TGx 923-2E and TGx 536-02D gave highest mean yields, both genotypes had large interactions and, therefore, were highly dynamic and responsive to improved management practices. They cannot be safely and sensibly recommended for cultivation in all environments. TGx 849-313D and 737p were assumed to be affected by genetic and environmental factors.

The 95.9% of trial SS captured by the LR model versus the 95.2% captured by the AMMI model was a proof of agreement between the two models. However, AMMI analysis was much better than the LR analysis in SS recovery because it revealed a highly significant interaction component that had a clearer agronomic meaning (Gauch, 1990; Yau, 1995). Thus, AMMI analysis remains the most effective tool in the GxE analysis as it provides an insight for causal factors that have potentials for better varietal selection and management recommendations (Gauch and Furnas, 1991).



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