COMPARISON OF JOINT REGRESSION ANALYSIS (JRA) AND ADDITIVE MAIN EFFECT AND MULTIPLICATIVE INTERACTION (AMMI) MODEL IN THE STUDY OF G x E INTERACTION IN SOYBEAN ACROSS TWO AGROECOLOGICAL ZONES IN NIGERIA

Aremu, C. O.[1], Ojo, D. K.[2], *Oduwaye, O. A.[2] and Amira, J. O.[2]
[1]Agronomy Department, Faculty of Agriculture, Ladoke Akintola University of Technology, Ogbomoso Nigeria
[2]Department of Plant Breeding and Seed Technology, University of Agriculture, Abeokuta, Nigeria

ABSTRACT

Ten each of early-maturing and late-maturing genotypes of soybean were evaluated in four environments. The yield data were subjected to joint regression (JRA) and additive main effect and multiplicative interaction (AMMI) analyses to determine the effectiveness of the two models in G x E interaction yield trials. The heterogeneity of regression (HR) and deviation from concurrence (DC) portions of the Genotype x Environment interaction of the JRA were not significant in both early and late-maturing genotypes, suggesting that genotype response was not a linear function of the environment. The JRA also gave large residuals of about 50.0 and 81.0% respectively, in the early and late-maturing genotypes. The G x E interaction in the AMMI model was highly significant in the early-maturing genotypes only. However, the first Principal Components Axis (IPCA) of 50.68 and 49.68% AMMI model accounted for 93.64 and 83.97% of the interaction sum of squares with comparatively low residuals for the early and late-maturing genotypes, respectively.

INTRODUCTION

The improvement of grain yield in soybean (*Glycine max* (L) Merr.) depends on thorough understanding of the influences of genotypes, environment and the interaction between genotype and environment (G x E) as this interaction limits the genetic advancement of plant breeding programmes (Helms, 1993). It is therefore important to quantify such interaction before a reliable genotype selection is made. A number of techniques have been used to study the sensitivity of a genotype to different environments. These include the joint regression technique and the additive main effect and multiplicative interaction (AMMI) technique.

The joint regression analysis (JRA) is a technique used in determining genotype response to different environments. The technique quantifies each environment by the means of all the genotypes tested. The sensitivity of a genotype to different environments is determined by the magnitude of its regression coefficient and the deviation from linearity (Wescott, 1986; Ariyo, 1995). However, the major objective of G x E analysis is to explain as much as possible, the structural variability in the G x E interaction and also interpret the variability biologically. The joint regression technique

has been widely used for soybean (Ariyo 1995) for cowpea, (Ntare and Aken'Ova, 1985) and for maize (Eberhert and Russell, 1966).

The AMMI estimate of genotype performance removes G x E 'noise' that is intrinsic to estimates from data of genotype performance in specific environments thereby producing estimates that may be more predictive of future performance of genotype. The model has also been used in multilocation yield trials for maize (Crossa *et al.*, 1990) wheat (Mclaren and Chaudhary, 1994) and soybean (Ariyo 1998). AMMI model explains more of the variations in the interaction sum of squares (SS) than the joint regression analysis as the environment or location increases (Nachit *et al.*, 1992). However, as the environmental diversities are restricted, it is proposed that JRA and AMMI could both explain the variations in the interaction sum of square (Acciaresi *et al.*, 1997)

Ojo (2000) compared various methods of G x E analysis on six genotypes of soybean sown in three contrasting tropical field ecologies. The findings of this study needs further clarification making use of larger number of entries, in order to obtain results with clearer agronomic meaning. The objectives of this study were; to

determine the effectiveness of JRA and AMMI models in the G x E interaction studies of early and late-maturing genotypes of soybean. To indicate the adaptability of each soybean genotype to each of the two agroecological zones using the two techniques.

MATERIAL AND METHOD

Ten each of early-maturing and late-maturing soybean genotypes obtained from the Crop Improvement Division (CID) of International Institute of Tropical Agriculture, Ibadan, were grown in four environments, Abeokuta (derived savanna) in 1999 and 2000 and Ogbomoso (guinea savanna) in 2001 and 2002 planting seasons.

Each of the four-row plots of 3 m x 6 m in size was planted in a randomized block design with three replications. The between and within-row spacing were 75 and 5 cm, respectively. Seed yield data were collected from the two inner competitive rows and expressed in kilogramme per hectare (kg/ha). Statistical analysis was performed, separately, on the early and late-maturing genotypes. The data were subjected to combined analysis of variance, joint regression (JRA) and AMMI analyses.

The procedure of Freeman (1973) was used for the JRA in which case a mixed model was assumed where the genotypes are fixed and the environments random using the procedure,

$$Y_{ijk} = \mu + G_i + E_j + b_iE_j + d_{ij} + S_{jk} + e_{ijk}$$

Y_{ijk} = Yield (kg/ha) of the ith genotype in the kth replicates of the jth environment

μ = Grand mean

G_i = Additive effect of the ith genotype

E_j = Additive effect of jth environment

b_iE_j = Linear regression coefficient of ith genotype in j^{th} environment

d_{ij} = Deviation from regression

S_{jk} = Effect of the kth replicates of the jth environment

e_{ijk} = Average of the errors associated with i^{th} genotypes and j^{th} environment

For the AMMI model, the procedure given by Yau (1995) was used. This model takes into account the additive effect and the interaction (multiplicative effects) in the genotype x environment interaction studies.

$$Y_{ij} = \mu + a_g + \beta e + \Sigma n \, \lambda n \, Ygn \, \delta en + Pge - \Sigma ger$$

Where

Y_{ij} = Seed yield (kg/ha)

μ = Grand mean

a_g = Grand mean of the genotype

βe = Grand mean of the environment

λ = Eigen value of the principal component analysis (PCA) axis.

Ygn and δen = The genotype and environment PCA scores for the PCA axis, respectively

Pge = Residual from the AMMI

Σger = Error term

The JRA and AMMI statistical analyses were performed by MAT MODEL Version 2.0 (Gauch, 1986). The PCA scores were used in the AMMI biplots.

The criteria to compare the two models were based on:

1. The significant value obtained in the heterogeneity of regression in JRA and the first PCA axis in AMMI, respectively. (Yau, 1995).

2. The effectiveness of the two models measured through the values of the percentage sum of squares (% SS).

3. The significance of the concurrence of regression, deviation from concurrence and the AMMI biplot structure (Kempton, 1981).

RESULTS

The mean seed yield for both early and late-maturing soybean genotypes are presented in Table 1. The mean yield of late-maturing genotypes was higher than that of the early-maturing genotypes. Three genotypes, TGX 1636-7F, Samsoy-2 and TGX 1849-1E yielded below average in the early-maturing genotypes. Similarly, genotypes TGX 1440-1E, TGX 596-1D and TGX 1448-2E had below average seed yield in the late-maturing genotypes.

Genotype TGX 1485-1D had the lowest positive PCA score with the least interaction whereas TGX 1456-2E recorded the largest negative interaction among the early-maturing genotypes. However, the least interaction among the late-maturing group was observed in genotype TGX 1410-1D.

The mean performance of the early and late-maturing genotypes across the locations and IPCA from AMMI analysis are presented in Table 2. The highest yield of 1097.51 kg/ha among the early-maturing genotypes was obtained at Ogbomoso in 2002. Among the late-maturing genotypes, the highest mean yield (1139.73 kg/ha) was obtained in 1999 at Abeokuta. The first PCA score was least for Abeokuta environments in the early and late-maturing genotypes.

The regression coefficients (b) and deviation from regression (S^2d) of the genotypes are presented in Table 3. TGX 1485-1D, TGX 1019-2EN and TGX 1627-1F among the early-maturing genotypes and TGX 925-2C, TGX 1410-1D, TGX 1445-3E and TGX 596-1D among the late-maturing genotypes were the most responsive as these genotypes had regression coefficients that were significantly higher than 1.0 with high mean yields. The deviation mean squares for all the genotypes, whether early or late-maturing, were significantly greater than zero.

The genotype, environment and G x E interaction mean squares were highly significant ($P < 0.01$) in respect of the early and late-maturing genotypes except for genotype x environment interaction that was not significant in the late-maturing genotypes (Table 4).

The JRA gave a non significant heterogeneity of regression (HR) which accounted for 7.04% and deviation from occurrence (DC) that accounted for 13.73% in the early-maturing genotypes. In the late-maturing genotypes, HR accounted for 6.46% and DC 15.61% of the total sum of squares. However, the concurrence from regression (CR) was significant in the two locations and accounted for 14.43 and 13.73% of total variation, respectively. Deviation from regression (DR) accounted for 14.26% of total sum of squares and about 50.0% of the G x E sum of squares in the early-maturing genotypes.

Differences between JRA and AMMI model became evident when the interaction sum of squares (SS) were partitioned. On the other hand, AMMI analysis (Table 5) recorded highly significant IPCA mean squares which accounted for 50.68% of the G x E interaction sum of squares with 11 degree of freedom (df) in the early-maturing genotypes. Also the late-maturing genotypes gave a significant IPCA axis, accounting for 49.68% of the G x E sum of squares with 11 degree of freedom.

The biplots for the early and late-maturing genotypes are presented in Figures 1 and 2, respectively. The ten soybean genotypes from each maturity group are coded as TGX 1 to TGX 10 in the Figures. The Y-axis showed the main effects (seed yield) while the ordinate showed the IPCA axis. The AMMI biplot as a whole accounted for 93.64% and 83.97% with residuals of 6.36 and 16.03% of the total sum of squares for the early and late-maturing genotypes, respectively.

In Figure 1, (early-maturing genotype) all the ten genotypes except Samsoy-2 and TGX 1849-1E were found adaptable to Ogbomoso environment. Among the late-maturing genotypes, TGX 1410-1E, TGX 996-22E and TGX 1019-2EB were adaptable to environmental conditions in Abeokuta while TGX 925-2E, TGX 1445-3E and M351 were adaptable to Ogbomoso location. The other genotypes had below average mean yield and were, therefore, not promising.

DISCUSSION

The enormous usefulness of soybean as a source of protein, fats and oil has gradually made this crop popular in Nigeria especially in the transitional humid and Guinea savanna agroecological zones where animal protein is insufficient. The productivity of soybean crop in diverse environment is determined, among others by its adaptability and interaction with the environment.

The comparative advantage of AMMI over the joint regression analysis (JRA) in sum square recovery has been revealed in the current study and elsewhere (Yau, 1995; Gauch, 1990; Ojo, 2000). This is because the former reveals a highly significant interaction component that has clearer

agronomic meaning. The fact that the G x E and its two components, HR and DR were not significant suggests total absence of G x E interaction and larger residual effects. The non-significance of GR in particular, indicated that the correlation coefficient (r) could not be a response parameter. This, according to Helms (1993), explained that the genotype response was not a linear function of the environment and hence regression coefficient was not a true index of testing genotype adaptability.

Although, the significance of concurrence of regression in the two evaluations especially in the late-maturing genotypes indicated the existence of a high correlation between the regression coefficients and the genotype means in the four environments (Nachit *et al.*, 1992), the non-linearity in the G x E interaction for both early and late-maturing genotypes in the current study revealed the ineffectiveness of JRA in determining genotype response to a given environment.

On the other hand, the AMMI model clearly demonstrated the existence of a significant G x E interaction which was partitioned into the first PCA axis in the two evaluations. Also the mean squares for the first PCA axis were larger than the mean square from the residuals. Wheareas the complete AMMI

model recorded greater proportion of interaction sum of square with smaller residual in the two locations, the JRA gave larger residuals relative to the interaction sum of squares.

Therefore, the AMMI model is seen to have explained, as much as possible, the structural variability in the genotypes interaction (Mclaren and Chandhary, 1994). The AMMI biplots in particular, identified the adaptable and high yielding genotypes in each location and also quantified the contribution of each genotype to interaction with the environment (Yau, 1995). In the early-maturing genotypes, TGX 1566-2E, TGX 1636-7F and TGX 1456-1D apart from recording above average yield, also gave low PCA values. Therefore the three genotypes can be recommended for the Ogbomoso (Guinea savanna) agroecology. Genotype TGX 1410-1D in the late-maturing group was able to combine above average yield with low interaction and thus was adaptable to Abeokuta (derived savanna) agroecology.

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REFERENCES

Acciaresi, H. A., H. O. Chidichimo and Y. C. B. Fuse 1997. Study of genotype x environment interaction for forage yield in oat (*Avena sativa* L.) with joint linear regression and AMMI analysis. *Cereal Research Comm* 25(1): 55-62.

Ariyo, O. J. 1995. Performance of soybean genotypes as evaluated by joint regression analysis. *Crop Res.* 9(2): 296-302.

Ariyo, O. J. 1998. Use of Additive main effect and multiplicative interaction model to analyse multilocation soybean varietal trials. *J. Genet. and Breed.* 53: 129-134.

Crossa, A. J., H. G. Gauch and R. W. Zobel 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. *Crop Sci.* 30: 493-500.

Eberhert, S. T. and W. A. Russell 1966. Stability parameters for comparing varieties. *Crop Sci.* 6: 36-40.

Freeman, G. H. 1973. Statistical methods for the analysis of genotypes – environment interaction. *Heredity* 31: 339-354.

Gauch, H. G. 1986. MATMODEL, a Fortran 77 program for AMMI analysis microcomputer power. Itchaca, N. Y.

Gauch, H. G. 1990. MAT MODEL version 2.0. AMMI and related analyses for two-way data matrices. Microcomputer Power, Ithaca, New York.

Helms, T. C. 1993. Selection for yield and stability among oat lines. *Crop Sci.* 33: 423-426.

Kempton, R. A. 1984. The use of biplots in interpreting variety by environment interactions. *J. Agric. Sci. Cambride* 103: 123-135.

Mclaren, C. G. and R. C. Chandhary 1994. Use of additive main effects ad multiplicative interaction model to analyse multilocation variety trials Proceedings of the FRCSSP Conference, Palawan, Phillipines. Aug. 1994 pg. 19-25.

Nahit, M. N., G. Nachit, H. Ketata, H. G. Gauch Jr., and R. W. Zobel 1992.

Use of AMMI and regression models to analyses genotype x environment interaction in durum wheat. *Theo Appl. Gent.* 98(3): 597-601

Ntare, B. R. and M. E. Aken' Ova 1988. Yield stability in segregating populations of cowpea. *Crop Sci.* 25: 208-211

Ojo, D. K. 2000. Genotype x environment analysis and selection for yield stability and adaptation in tropical soybean genotypes *Nigerian Journal of Ecology* 2: 49-55.

Westott, B. 1986. Some methods of analysis genotype-environment interaction. *Heredity* 56: 243-253.

Yau, S. K. 1995. Regression and AMMI analysis of genotype x environment interactions. An empirical comparison. *Agron. J.* 87: 121-126.

Table 1. Mean seed yield (kg/ha) and first PCA values from AMMI analysis for 10 soybean genotypes grown in four environments

| | Early-maturing genotypes | | | Late-maturing genotypes | |
	Mean yield	IPCA axis		Mean yield	IPCA axis
Genotype			**Genotype**		
TGX 1566-2E	1022.34	-8.01	TGX 925-2E	1101.35	-10.22
TGX 1636-7F	998.22	7.42	TGX 1447-1D	1038.13	-11.89
TGX 1019-2EN	1065.41	-7.26	TGX 996-22E	1121.27	10.57
TGX 1456-2E	1180.11	-13.28	TGX 1410-1D	1097.56	4.82
TGX 1485-1D	1097.54	2.30	TGX 1445-3E	1141.27	-15.07
Samsoy-2	849.68	6.50	TGX 1440-1E	960.43	-0.94
TGX 536-02D	1028.37	12.50	TGX 596-1D	1011.14	-6.42
TGX 1649-11F	1153.71	-12.76	M 351	1181.41	-4.92
TGX 1849-1E	898.43	-14.07	TGX 1448-2E	938.45	-7.2
TGX 1627-1F	1227.56	-10.79	TGX 1019-2EB	1155.17	9.65
Grand mean	1052.14			1026.50	
Environment			**Environment**		
Abeokuta 1999	858.75	1.27	Abeokuta 1999	1131.73	7.92
Abeokuta 2000	663.34	-7.39	Abeokuta 2000	948.25	9.37
Ogbomoso 2001	974.93	-13.21	Ogbomoso 2001	998.42	-10.81
Ogbomoso 2002	1097.51	-18.44	Ogbomoso 2002	1072.14	-8.01
Grand mean	999.06		Grand mean	972.00	

Table 2. Mean yield of soybean genotypes and IPCA from AMMI analyses in four environments

	Early-maturing		Late-maturing	
Environment	Mean yield (kg/ha)	IPCA	Mean yield (kg/ha)	IPCA axis
Abeokuta 1999	858.75	1.27	1131.73	7.92
Abeokuta 2000	663.34	-7.39	948.25	9.37
Ogbomoso 2001	974.93	-13.21	998.42	-10.81
Ogbomoso 2002	1097.51	-18.44	1072.14	-8.01
Grand mean	999.06		972.00	

Table 3. Regression coefficients (b) and deviation from regression for the early and late-maturing soybean genotypes

Early-maturing genotypes			Late-maturing genotypes		
Genotype	Regression coefficient (b)	Deviation (s^2d)	Genotype	Regression coefficient (b)	Deviation (s^2d)
TGX 1566-2E	0.92	52, 405.21	TGX 925-2E	1.21	14, 525.41
TGX 1636-7F	0.84	5, 882.34	TGX 1447-1D	0.92	127, 107.22
TGX 1019-2EN	1.22	40, 327.31	TGX 996-22E	0.21	178, 974.53
TGX 1456-2E	0.99	118, 453.22	TGX 1410-1D	1.16	37, 229.40
TGX 1485-1D	1.01	14, 533.40	TGX 1445-3E	1.24	8, 471.07
Samsoy-2	1.00	212, 525.40	TGX 1440-1E	1.06	9, 866.29
TGX 536-02D	0.81	7, 831.44	TGX 596-1D	1.28	13, 588.24
TGX 1649-11F	0.49	106, 458.39	M 351	0.47	7, 443.25
TGX 1849-1E	0.69	19, 281.47	TGX 1448-2E	0.82	153, 683.41
TGX 1627-1F	1.10	16, 397.63	TGX 1019-2EB	0.67	199, 461.27

Table 4. Joint regression analysis of yield (kg/ha) for early- and late-maturing soybean genotype.

Source	df	SS	MS	% SS	df	SS	MS	% SS
	Early-maturing genotypes				Late-maturing genotypes			
Treatment	39	7, 122, 024.44	18, 261.01		39	6, 241, 110.21	178, 317.44	
Genotype (G)	9	1, 652, 855.25	183, 650.58**	23.20	9	1, 144, 361.81	143, 045.23**	18.34
Environment (E)	3	1, 024, 310.40	3, 414, 36.8**	14.38	3	1, 233, 512.25	127, 151.31**	19.75
G x E	27	3, 124, 307.43	115, 715.09**	28.26	27	1, 840, 013.11	76, 667.21	29.48
H.R	9	498, 469.96	55, 385.55	7.04	9	402, 21.253	50, 290.41	6.46
CR	1	977, 88.46	97, 788.46*	14.30	1	892, 691.20	892, 691.20**	13.73
DC	8	101, 572.23	12, 696.53	13.73	8	974, 291.83	11, 347.12	15.61
DR (Residual)	18	1, 544, 367.97	85, 798.19	14.26	18	1, 489, 946.32	93, 121.65	23.87
Error	80	3, 895, 349.50	48, 691.87		80	291, 683.22	3, 646.43	

*, ** significant at 5% and 1% probability levels, respectively

Table 5. AMMI analysis of yield (kg/ha) for early- and late-maturing soybean genotype

Source	df	SS	MS	% SS	df	SS	MS	% SS
	Early-maturing genotypes				Late-maturing genotypes			
Treatment	39	7, 122, 024.44	18, 261.01		35	6, 241, 110.21	178, 317.44	
Genotype (G)	9	1, 652, 855.25	183, 650.58**	23.20	9	1, 144, 361.81	127, 151.31**	18.34
Environment (E)	3	1, 024, 310.40	3, 414, 36.8**	14.38	3	1, 233, 512.25	411, 179.75**	19.75
G x E	27	3, 124, 307.43	115, 715.09**	28.26	27	1, 840, 013.11	76, 667.21	29.48
IPCA I	11	928, 230.35	84, 384.58**	50.68	11	914, 210.11	83110.11**	49.68
Residual	16	453, 186.19	28, 324.14		16	952, 207.81	59, 512.99	
Error	80	3, 895, 349.50	48, 691.87		80	291, 683.22	3, 646.43	

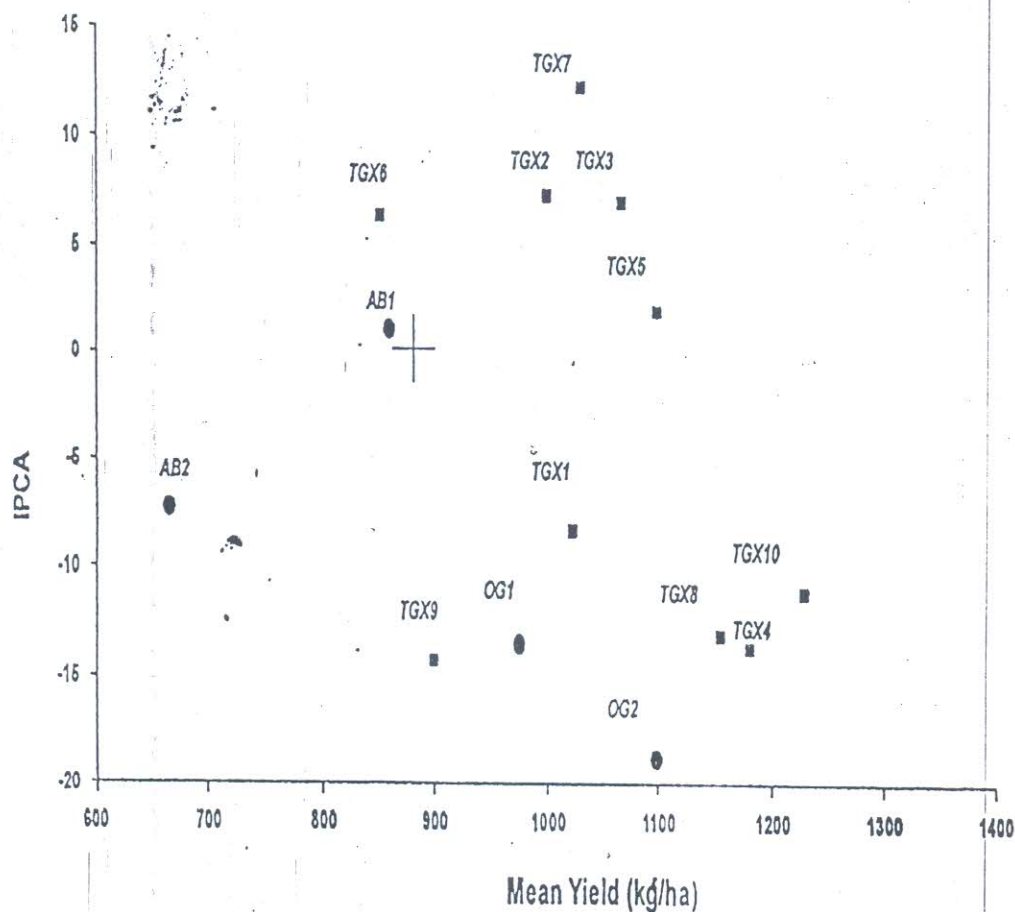*, ** significant at 5% and 1% probability levels, respectively

FIGURE 1. AMMI biplots of 10 early-maturing soybean genotypes grown in the four environments
+ = Grand mean yield
AB1 & AB2 = Abeokuta 1999 and Abeokuta 2000, respectively.
OG1 & OG2 = Ogbomoso 2001 and Ogbomoso 2002, respectively.
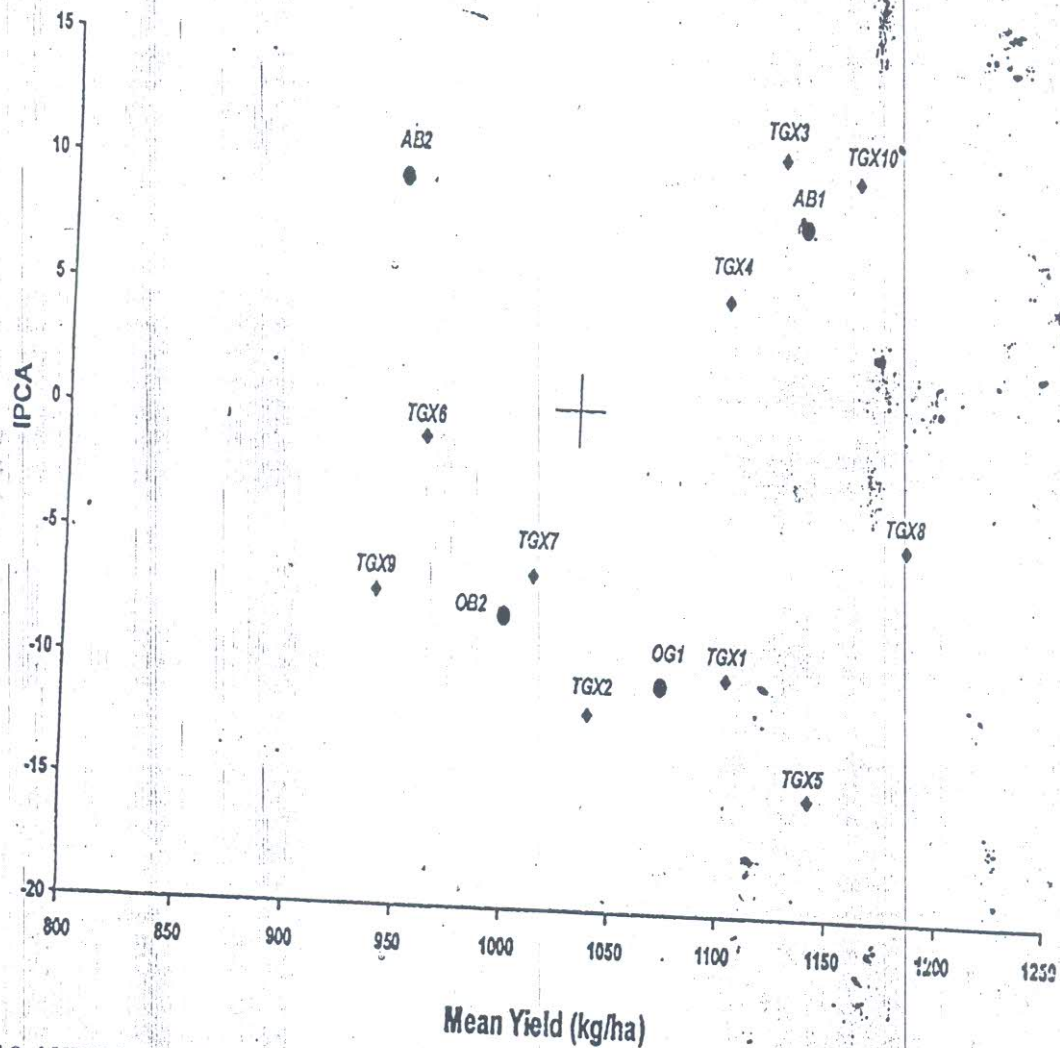Tax1 - Tax10 are the ten soybean genotypes as listed in Table 1

FIGURE 2. AMMI biplots of 10 late-maturing soybean genotypes grown in four environments

+ = Grand mean yield
AB 1 & AB 2 = Abeokuta 1999 and Abeokuta 2000, respectively
OG 1 & OG 2 = Ogbomoso 20001 and Ogbomoso 2002, respectively.
Tax 1 – Tax 10 are the ten soybean genotypes as listed in Table 1