

The Relative Discriminatory Abilities of Techniques Measuring Genotype x Environmental Interaction in Soybean (*Glycine Max (L) Merr.*) in Semi-Arid and Rain Forest Environments of Nigeria

¹C.O. Aremu, ¹T.A Adebayo, ¹M. Oyekunle and ²O.J. Ariyo

¹Department of Agronomy, Ladoko Akintola, University of Technology, Ogbomoso, Nigeria

²Department of Plant Breeding and seed Technology, University of Agriculture Abeokuta, Nigeria

Abstract: The prediction and interpretation of quantitative traits complimenting the yield of crop genotype is a major problem in Genotype by Environment (G×E) interaction. Four different statistics were used. These are Regression models using Coefficient of determination and Mallows' statistics, Genotype-grouping technique, Ecovalence mean square and Additive Main effect and Multiplicative Interaction (AMMI) model. The Multiple Regression model, Mallows' statistics and Ecovalence mean square technique identified number of branch per plant and number of pods per plant as important components contributing meaningfully to the yield of soybean across environments. Genotype grouping-technique identified TG×1627-IF, TG×1448-DE and TG×1019-2E-N with above average yield to have stable performance across the environments. In addition to these three genotypes, (AMMI) model revealed TG×1519-1D, TG×1019-2EB and TG×1649-1F to show stable performance. AMMI model, Regression and Mallows' statistics gave wide and specific genotype adaptation where Ecovalence mean square and Genotype-grouping technique showed only wide genotype adaptation. But regression model and mallows' statistics deviated from AMMI model and genotype grouping technique in that while AMMI and Genotype grouping technique identified genotype adaptation with respect to yield character only, Regression and Mallows' statistics based genotype adaptation with respect to performance of other characters apart from yield. Regression and Mallows' statistics and AMMI model identified Ogbomoso environment to be most suitable for soybean adaptation. The use of Regression model, Mallows' statistics along side with AMMI model will reveal overall genotype performance better than only AMMI model which structures genotype performance based only on yield.

Key words: Adaptation, AMMI analysis, discriminative, ecovalence mean square, G×E interaction, mallows' statistics multiple regression

INTRODUCTION

Seed yield of soybean is difficult to improve directly because it is quantitatively inherited. Though a lot of progress has been made on improving the yield of soybean in humid agro-ecology using diverse statistics but, the problem of identifying appropriate characters influencing Genotype×Environment interaction across environments still remains a mirage (Sokal and Rohlf, 1995). Stability performance of crop genotypes in contrast environments are important as this ensures reliable selection of genotypes with high yield and consistent performance for wide and specific environments (Ariyo, 1990). To this effect several techniques have been employed to study the effect of yield and yield characters across environments. The discriminative use of statistical techniques becomes reliable in dis-entangling the genetic and environmental effect and get meaningful result.

Varma and Matura (1993) exploited the used of simple correlation analysis as important indicators of storage root yield in cassava. But the use of stability parameters was found to exploit the interaction effect of genotypes grown in diverse environments. According to Wricke (1962); Kang and Miller (1984), the stability parameters expose the adaptability of both yield and yield components of genotypes to specific environments. Some stability parameters have been successfully used. This include Ecovalence mean square (W-mean square) by Kang and Miller (1984) on okra, Unbiased estimator (δ^2i) by Shukla on wheat, Deviation mean square (S^2di) by Eberhart and Russel on rye, the Genotype-grouping technique by Francis and Kannernberg (1978) on rice. Other techniques include Coefficient of determination (R^2) by Gomez and Gomez and Mallows statistics (Cp). An alternative powerful approach to the analysis of G×E is called the Additive Main Effects and Multiplicative

Interaction (AMMI) model. This model with the bi-plot representation gives effective description of adaptation pattern (Nachit *et al.*, 1998; Gauch and Zobel, 1996). Thus understanding and easy interpretation is made on the effect of the environment on the genotypes. The discriminative use of stability parameters, regression statistics and AMMI model to reliably justify soybean adaptation based on their respective yield and yield components is yet utilized. This work is aimed therefore at investigating the overall performance of some genotypes and determine the relative discriminatory abilities of each of Ecovalence mean square by Kang and Miller, multiple regression technique of Weisberg, Mallows statistics, Genotype-grouping technique of Francis and Kannenberg and AMMI model of Gauch and Zobel (1996) in G×E interaction.

MATERIALS AND METHODS

Soybean genotypes from the improved planting material of International Institute of Tropical Agriculture (IITA) evaluated in Northern (Abuja, Zaria, Kano) and Southern (Abeokuta, Ibadan, Ijebu-ode) ecologies of Nigeria and fifteen of the genotypes found as stable performers in these two ecologies were used. This work was designed among others to give an indication of the response of these fifteen different Soybean genotypes to environment and Agricultural conditions of Ogbomoso a non-soybean growing area of Nigeria. Ogbomoso lies in the northern guinea Savannah ecology of Nigeria.

The meteorology of these environments is as shown in (Table 1). The combination of a location in a year was considered a separate environment. A randomized complete block design with three replications was used in each location. Seed sowing was by drilling into four-row plots of 4 m² per row to give a total of 480 plants per plot. NPK compound fertilizer, (N.P.K: 15: 15: 15) were applied at recommended rate. Immediately after planting, a mixture of Galex (four liters) and Grammazon (one liter) in 20 liters of water was sprayed per hectare to control weeds. Subsequent weeds were controlled manually when necessary.

Data collection were from the central 5 m row for five agronomic characters including days to 50% flower,

number of branch per plant, number of pods per plant, number of seeds per pod and 100-seed weight. After harvesting, pods were threshed and data collected on seed yield and expressed in kilogram per hectare.

Data on yield and yield characters were obtained for each genotype grown in each location and for each genotype across the locations. Five statistical techniques were used. The first technique was use of multiple regression models by Weisberg. In this technique multiple regression analysis over locations was calculated to determine the most adequate and consistent variable that affect the yield of soybean. From the regression analysis, two statistical criteria of Mallows' statistics C (p), SAS (1988) and Coefficient of determination (R²) were used to choose the best regression equation. R² indicate how yield variation is explained by the linear function of the independent variables Gomez and Gomez where C (p) compares the different prediction models. The model with highest R² and lowest C (p) values can be said to best explain the linear function of the independent variables (Varma and Matura, 1993). The second technique is the use of stability parameter of Ecovalence mean square (W²i) by Wricke, (1962). A variable or genotype with a significant W-mean square is considered unstable. In this method W²i was calculated for each character in each genotype. The Ecovalence mean square for each genotype mean yield and yield component was calculated as follows:

$$W^2_i = \sum_{j=1}^q (X_{ij} - X_i - X_{.j} + X_{..})^2$$

Where:

- X_{ij} = Genotypes in ith and jth environment
- X_{i.} = Mean of genotype in ith environment
- X_{.j} = Mean of genotype in jth environment
- X_{..} = Grand mean

The third technique was the use of Genotype-grouping technique of Francis and Kannenberg (1978). In this technique mean yield of each genotype averaged over environments are plotted against its Coefficient of Variation (CV) with the following four groups:

Table1: Location, mean annual rainfall, temperature relative humidity and the climatic co-ordinates of the four environments used in growing soybean

Location	Rainfall (mm)		(mean)	Temperature (°C) humidity		Co-ordinates	
	Year	(mean)		Relative	Latitude	Longitude	
Abeokuta	(2002)	809.08	20.43	83	03°	24 E	07° N
Ibadan	(2002)	730.23	29.17	80	07°	54 E	3° 30 N
Ogbomoso	(2002)	1074.21	32.01	71	04°	10 E	08 10 N
Ogbomoso	(2004)	960.46	34.32	69	04°	10E	08 10 N

Group I: Genotype with above average mean yield but CV smaller than mean CV.

Group II: Genotype with below average mean yield and above average CV

Group III: Genotype with below average mean yield and below average CV.

Group IV: Genotype with below average mean yield but above average CV.

A genotype is considered stable if the mean yield is above average with below average CV.

The fourth technique was the use of Additive Main effects and Multiplicative Interaction (AMMI) model by a Gauch and Zobel (1996) as follows:

$$Y_{ger} = U + g + \sum_{n=1}^n \lambda_n Y_{gn} f_{en} + P_{ge} + E_{ger}$$

Where:

- Y_{ger} = Yield of genotype in jth environment
- U = ith genotype mean deviations (Genotype Mean-Grand mean)
- β_e = jth environment mean deviation
- n = number of PCA axes retained in the model
- λ_n = singular value for PCA axis n
- f_{en} = environment eigenvector values for PCA axis n
- p_{ge} = Residuals.
- E_{ger} = Error

The AMMI model gives a descriptive adaptation pattern with the aid of its bi-plots.

A mixed model was assumed. The genotype were fixed and the environments random.

RESULTS

Seed yield of the genotype were significantly different. The wide variations were in number of pods per

lant, number of branch per plant and number of seeds per pod (Table2). This is an indication that these characters contributed differently to the yield of the genotypes. Differences in the genotypes may be attributed to the wide genetic variability.

The multiple regression values of the five soybean characters as affecting yield of soybean in each location and for the combined data over the locations and years are presented in Table 3. The regression value varied in each location, indicating the influence of the location environment on the seed yield of soybean. However, number of branch per plant and number of pods per plant were found to best fit the model at all locations. These suggest that the two characters are important in the seed yield determination for soybean. Number of branch performed relatively the same in the four environments. Meanwhile, the best model for Ogbomoso location with optimum rainfall and least relative humidity recorded the highest R^2 and relatively low C (p) value (0.94 and 2.81) giving a fitting equation with days to flower, number of branch per plant, number of pods per plant, number of seeds per pod and 100-seed weight. All these characters also fitted the model for Ogbomoso. At Abeokuta location, the model fitted the regression equation with all the characters except weight of seeds while only days to 50% flower did not fit the model for Ibadan location. The combined model gave same R^2 value with Abeokuta (0.70) while retaining all the characters in the model except weight of seeds.

The stability parameter for the fifteen soybean genotypes and the five characters as measured by Ecovalence mean-square of Kang and Miller (1984) are detailed in Table 4. TG×1519-ID and TG×1649-IF were most stable and responsive with respect to all the characters even as TG×536-OD and TG×1448-DE were stable with respect to days to 50% flower, number of branch per plant and number of pods per plant. But TG×1456-2E and TG×1497-ID-2E were most unstable with respect to the characters.

The Genotype-grouping technique by Francis and Kannembert (1978) classified the genotypes into four

Table 2: Mean squares in the analysis of variance of five soybean characters from fifteen soybean genotypes

Source of variation	Df	Days to flower	Number of branch/plant	Number of pods/plant	Number of seeds/pod	300-seed wt	Seed yield (kg ha ⁻¹)
Block	2	0.24	6.51**	1.06*	4.33**	2.75*	7291.52**
Genotype	14	2.72*	30.46**	0.79*	9.07**	18.55*	6901.19

Table 3: AMMI analysis of variance for soybean yield across four environments

Source	df	SS	Ms	% ISS
Treatment	59	53751.32	9063.58*	38.46
Genotype	14	256630.57	256902.14**	43.54
Environment	3	232852.04	17761.35*	18.00
G×E	42	939670.16	223723.09*	71.77
IPCA	16	284491.22	277780.70**	
Residual	26	41357.74	1590.68	
Error	123	339246.70	2758.09	
Total	182	210589.12	1157.08	

Table 4: Multiple Regression of five characters from soybean genotypes grow in four environments

Location	Character	Regression values	S.E	Prob.
Abeokuta (2002)	Intercept	0.37	0.62	0.73
	Days to 50% flower	-0.06	0.04	**
	Number of branch/plant	0.32	0.01	**
	Number of pod/plant	4.01	0.07	*
	Number of seeds/pod	0.03	0.002	*
	300seed weight (g)	-0.09	0.03	NS
	R2	0.61		
Ibadan (2002)	C(p)	4.81		
	Intercept	-0.56	0.67	0.64
	Days to 50% flower	0.40	0.02	NS
	Number of branch per plant	0.61	0.007	**
	Number of pods per plant	2.47	0.06	**
	Number of seeds per pod	0.19	0.06	*
	300 seed-weight (g)	0.43	0.05	*
Ogbomoso (2003)	R2	0.71		
	C(p)	5.93		
	Intercept	-0.71	0.74	0.55
	Days to 50% flower	0.94	0.003	*
	Number of branch per plant	0.26	0.09	**
	Number of pods per plant	1.79	0.01	*
	Number of seeds per pod	-0.51	1.03	*
Ogbomoso (2004)	300 seed weight (g)	0.07	0.08	*
	R2	0.89		
	C(p)	2.96		
	Intercept	-0.82	0.83	0.43
	Days to 50% flower	-0.27	0.09	*
	Number of branch per plant	-0.29	0.04	*
	Number of pods per plant	2.36	0.92	**
Combined	Number of seeds per pod	0.13	0.006	*
	300 seed weight (g)	0.41	0.023	*
	R2	0.94	0.023	
	C(p)	2.81		
	Intercept	0.46	0.62	0.66
	Days to 50% flower	0.02	0.08	*
	Number of branch per plant	0.13	0.07	**
	Number of pods per plant	2.08	0.63	*
	Number of seeds per pod	0.34	0.09	*
	300 seed weight (g)	-0.03	0.02	NS
	R2	0.70		
	C(p)	4.56		

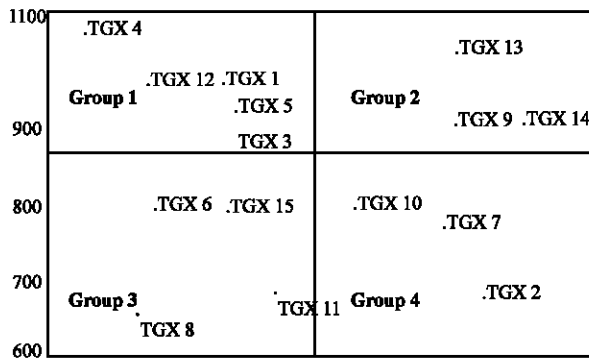


Fig. 1: Mean yield of 15 genotypes against coefficient of variation using genotype grouping technique of Francis and kannenbert (1978)

groups according to their means and CV's as shown in Fig. 1. By this method, only TG×1448-DE, TG×536-OD, TG×1627-1F and TG×1019-2EN could be regarded as showing consistent above average performance.

Although, TG×1556-2E, TG×1636-IF, TG×923-2E and TG×1497-ID-2E were stable by having below average CV but their yields were also below average. Tg×1649-IF, TG×1660-15F and TG×1637-3Fhad above average mean yield but their respective CV's were large. This is an indication of their sensitivity to environmental changes. Tg×1456-2E TG×1019-2EB and TG×1485-IB were most undesirable as they combined above average CV with below average yield.

The AMMI model of variance for soybean genotypes and environment are presented in Table 5. The genotype, environment and G×E interaction were significant, each accounting for 38.43%, 43.3% and 18.00% of the total sum of squares (TSS %). The IPCA was also very important in explaining the interaction and it accounted for 71.77% of the G×E interaction. Ogbomoso environment with least interaction was most stable but Abeokuta was structured as most interactive and hence unstable. TG×1448-DE, TG×1019-2E-N, TG×1519-ID and TG×1649-1F are adaptable to Ogbomoso environment, even as TG×1627-IF with low PCA score is adaptable to Ibadan

Table 5: Stability variance of five soybean characters for each of the 15 soybean genotypes grown in four environments as measured by Ecovalence mean square of Kang and Miller (1984); Wricke (1962)

Genotype	Days to flower	Number of branch/plantt	Number of pods/plant	Number of seeds/plant	300-seed weight
Tg×536-OD	1.96	0.51	2.13	1.20	2.34
TG×1456-2E	5.71 ^a	2.31 ^a	0.62	14.09 ^a	0.97
TG×1627-1E	0.03	0.31	3.56 ^b	13.24 ^a	3.29 ^a
TG×1448-DE	-0.44	0.53	1.75	0.87	0.22
TG×1019-2E-N	2.52	0.97	0.16	2.15	1.01
TG×1556-2E	3.27 ^a	1.04 ^a	1.27	10.05 ^a	1.74
TG×1485-1B	4.16 ^a	0.13	0.91	8.19 ^a	0.19
TG×1636-1F	15.39 ^a	2.43 ^a	0.63	14.22 ^a	2.06
TG×1660-15F	3.74 ^a	0.59	2.43	2.05	3.26
TG×1019-2EB	4.26 ^a	0.05	6.21 ^a	7.56	3.19 ^a
TG×923-2E	5.20 ^a	0.51	5.01 ^a	10.39 ^a	4.07 ^a
TG×1519-1D	1.21	0.31	0.71	2.13	1.37
TG×1649-1F	0.35	0.71	0.52	1.33	0.42
TG×1637-3F	3.77 ^a	0.98	3.06 ^a	0.92	1.81
Tg×1497-1D-2E	5.08 ^a	2.11 ^a	4.11 ^a	16.01 ^a	4.30 ^a

environment. Even though, Tg×1637-3F and TG×1497-ID-2E had below average mean yield, under improved cultural practices, they may still be adaptable to Abeokuta environment.

DISCUSSION

Several statistics have been employed to assess G×E interaction. The stability parameters have been suggested by workers but methods that assign stability variance to each genotype such as Ecovalence mean square (W-mean square) have been considered useful. Other statistics that have proved reliable include Multiple Regression analysis Weisberg, Sokal and Rohlf (1995). The most recent and even more reliable tool in G×E analysis is the AMMI model. The common fit of number of branch per plant and number of pods per plant in all the four environments using the multiple regression technique revealed importance of these two characters in soybean seed yield determination. However, all the characters retained in the linear model contributed significantly to the variation in the yield. That the two environments in the Ogbomoso location recorded highest coefficient of variation indicated that soybean seed yield was relatively well predicted in these locations. Moreover, the equation models equally fitted the characters in the two Ogbomoso environments of 2003 and 2004. It could be implied therefore that year effect was not important in determining the performance of soybean genotypes. This is in agreement with the findings of Ariyo and Ayo-Vaughan that year effect did not contribute significantly to pod yield in okro. Better still, the Ecovalence means square stability parameter also found number of branch and number of pods per plant to be most stable thus confirming the reliability of these two statistic tools in evaluating individual genotype performance. Kang and Miller (1984), Ariyo (1990) also found Ecovalence mean square and unbiased estimator stability parameters to be reliable in okro. The ecovalence mean square and genotype-grouping

techniques produced similar results with few discrepancies in that genotype-grouping technique identified TG×536-OD, TG×1448-DE and TG×1519-ID as stable genotypes with above average mean yield and below average CV. Also the Ecovalence mean square identified in addition to these genotypes TG×1649-1F to be stable. AMMI model however, revealed TG×1019-2EN and TG×923-2E genotypes to have stable performance across environments in addition to those identified by Ecovalence and Genotype-grouping techniques. AMMI model gave a more visible variability in the performance of these stable genotypes. Only TG×536-OD was found to have consistent performance and therefore adaptable to Ogbomoso environments. According to Gauch and Zobel (1996), genotypes and environments with PCA values near zero are stable. Better still, AMMI model structured the stability of the genotypes in specific environments. Ogbomoso, a semi arid environment was structured to have least interaction and most condusive environment to grow TG×1019-2E-N, TG×1519-ID and TG×1649-1F. R² and C (p) Multiple Regression models also found Ogbomoso environment to be the best for the performance of the soybean genotypes with respect to the characters (Table 6). This could be due to the optimal rainfall and temperature with least relative humidity prevalent in Ogbomoso environment. The use of Regression and AMMI models were more reliable in revealing the effect of each environment than the other stability parameters. But the superiority of the AMMI model over the Multiple Regression model was more evident in the fact that Multiple Regression model did not reveal individual genotype performance. The fact that more genotypes had high interaction and therefore unstable with AMMI model, further justify the effective descriptive and adaptation patterns in the use of AMMI model. Nachit *et al.* (1992), described AMMI model as most effective in G×E analysis. However, overall genotype performance is assessed using character performance. Therefore, the stability parameters of Ecovalence mean square and Multiple Regression models revealed genotypes

Table 6: Mean yield, PCA scores and coefficient of variation (CV) of 15 soy bean genotypes

Genotype	Mean yield kg ha ⁻¹	PCA score	CV
Tg×536-OD	950	5.26	11.50
TG×1456-2E	795	4.01	34.65
TG×1627-1E	870	-2.16	12.13
TG×1448-DE	1050	0.31	11.00
TG×1019-2E-N	900	-0.26	16
TG×1556-2E	793	4.02	75
TG×1485-1B	815	-3.00	10.50
TG×1636-1F	650	2.16	25.20
TG×1660-15F	902	1.36	12.50
TG×1019-2EB	780	4.01	31.50
TG×923-2E	670	-0.73	21.20
TG×1519-1D	943	0.16	18.40
TG×1649-1F	970	-0.22	11.60
TG×1637-3F	785	-2.08	31.31
TG×1497-1D-2E	798	3.20	33.20
E1	720.51	3.05	
E2	860.38	-1.71	
E3	935.28	0.43	
E4	1020.74	-0.20	

Grand mean = 864.25 ; Mean CV = 18.71

stability based on character performance explained the uncompromising importance and reliability of the Ecovalence mean square technique and Multiple Regression model in the analysis of G×E interaction studies. This work therefore recommend that apart from AMMI model, the complementary use of Ecovalence mean square along side with Multiple Regression model would produce reliable result in G×E studies.

ACKNOWLEDGMENT

The authors are grateful to Mr Tayo Oyelakin of grain legume unit of International Institute of Tropical Agriculture (IITA), for the data analysis.

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