

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

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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.

Keywords: AMMI and Joint Regression Analysis, Savanna Ecology, Tropical soybean

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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 (Eberherth 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 (McClaren 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,

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

Y_{ijk} = Yield (kg/ha) of the i^{th} genotype in the k^{th} replicates of the j^{th} environment

μ = Grand mean

G_i = Additive effect of the i^{th} genotype

E_j = Additive effect of j^{th} environment

$b_i E_j$ = Linear regression coefficient of i^{th} genotype in j^{th} environment

d_{ij} = Deviation from regression

S_{jk} = Effect of the k^{th} replicates of the j^{th} 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.

$$Y_{ij} = \mu + a_g + \beta e + \sum n \lambda_n Y_{gn} \delta_{en} + P_{ge} - \sum g_{er}$$

Where

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

μ = Grand mean

