

GENETIC VARIABILITY STUDIES OF SOME TRAITS IN SOYBEAN (*GLYCINE MAX* (L) MERR) IN SAVANNA AND HUMID ENVIRONMENTS.

C. O. AREMU, O. J. ARIYO, AND D.K .OJO

* *Dept. of Agronomy, Lautech, Ogbomoso*

***Dept of Plant Breeding And Seed Technology Unaab, Abeokuta*

ABSTRACT

Fifteen improved soybean genotypes were evaluated in two locations in four years. The result showed location (Loc.), year (Yr.), genotype (Gen.) effects to be significant. Also Loc x Yr and Gen x Yr interactions were significant for all the characters. Gen x Yr x Loc interaction effects were significant only with days to flower, number of branches per plant, number of pods per plant and seed yield. This indicated year and Gen x Yr interaction effects to be more important in soybean performance and that year and location effects could be exploited in soybean improvement. Gen x Loc interaction was not significant for all the characters except with number of seeds per plant. Genotypic coefficients of variation were higher for number of branches per plant, number of pods per plant and seed yield in Ogbomoso location than the phenotypic coefficient of variation.. All the characters correlated positively with seed yield in Ogbomoso a guinea savanna agro-ecology. Whereas, number of pods per plant did not show genotypic correlation with seed number and seed yield in Abeokuta a humid agro-ecology. Path coefficient analysis revealed that seed yield was affected by days to flower, number of branch per plant and number of seeds per pod in Ogbomoso location. Only days to flower directly affected seed yield in Abeokuta location. The high broadsense heritability estimates for branch number and number of seeds per pod ensures successful selection for these traits in Ogbomoso specific location for maximum yield performance. The results of this study revealed that soybean cultivation should be encouraged in Ogbomoso a guinea savanna agro-ecology where branch and pod number per plant exhibited high potential performance for high yield and reliable selection.

Keywords: character, variability, genotype, location, year, interactions, soybean, yield

* For all correspondence.

INTRODUCTION

The knowledge of genetic variability and the heritability estimates of characters is necessary in plant improvement programmes.

Such knowledge helps to determine the nature and amount of heritable and non-heritable variations. This ensures effective breeding procedure. However, variety selection and subsequent recommendation for release are

based on yield data analysis, and measurement of agronomic characters that contribute to grain yield (Araujo and Coulman, 2002).

The degree of phenotypic and genotypic variance is usually measured by the coefficient of variability. As such, the expected genetic response to selection is determined by heritability and the variability of the traits for which selection is to be made (Burton, 1989; Osiketa *et al.*, 2000).

Heritability which measures the genetic variation in a population relative to the total phenotypic variation of a trait is highly influenced by the genotypes method of determination and environment to which the genotypes are subjected (Saleh *et al.*, 1995).

Inter-character relationship is very important in plant breeding for character selection and to determine most effective breeding procedure. As the number of independent characters, affecting a dependent character increases, there is bound to be some amount of interdependency. Correlation may be purely genetic or environmental. Genetic correlations arise from linkages that have not reached equilibrium and from pleiotropy (Simmonds 1979) and therefore important in crop improvement. Singh and Ram (1986) reported high heritability estimates for days to flower, number of pods per plant and number of branch per plant in soybean. According to Karb *et al.* (1994), estimates of both heritability and genetic advance are more informative in genetic and breeding studies than only genetic advance. According to Ojo (2000), characters with high broadsense heritability estimates and low genetic advance are said to serve as good predictors of yield in tropical soybean. But Rao *et al.* (1997) reported the use of path coefficient analysis as most informative in identifying cause and effect relationship in grains. In crop improvement programmes, knowledge of seed yield is insufficient until relationships among

various quantitative characters with seed yield are known. This knowledge enhances meaningful character selection in plant breeding. This present study evaluated the character variation, and relationship as well as heritability of six soybean traits in guinea and humid savanna agro-ecologies.

MATERIALS AND METHODS

Fifteen soybean varieties obtained from the International Institute of Tropical Agriculture (IITA) Ibadan, were grown in two locations of Ogbomoso (Guinea savanna) and Abeokuta (Humid savanna) in the late seasons of 1999, 2000, 2001 and 2002. The trial locations are as described in Table 1.

Following land preparation, 7.5kg N, 7.5kg, P₂O₅ and 7.5kg K single phosphate as NPK 15:15:15 Compound fertilizer was applied into the soil. The varieties were grown in a randomized complete block design with three replications. Seed sowing was by drilling in four-row plot of 3m x 6m. On emergence seedling spacing was 75cm between rows and 5cm within rows to give a total of 242,000 plants per hectre. Immediately after planting a mixture of Galex (four litres) and Grammazone (1 litre) were sprayed per hectare to control weeds. This was followed by manual weeding as at when necessary.

Data from the two inner rows consisting of 242 plant stands were used and characters measured were days to flower, number of branches per plant, numbers of pods per plant, numbers of seeds per pod, 300-seed weight and seed yield. These characters were subjected to combined analysis of variance for locations and years to obtain the variance components. The mean square for a source of variation was equated to its expectation and the unknown solved for according to the method of Rasmusson and Lambert (1961) as follows:

$$\sigma_x^2 = \sigma_g^2 + (\sigma_g^2/l) + (\sigma_g^2/y/y) + (\sigma_{gly}^2/ly) + (\sigma_e^2/rlly)$$

