

Prediction Of Grain Yield Through Heritability And Genetic Advance Of Yield Parameters In Soybeans [*Glycine Max* (L) Merr]

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ABSTRACT: Six soybean (*Glycine max* (L) Merr) genotypes were sown in two locations in Nigeria in 1996 and 1997 to obtain data for grain yield and six yield parameters. The data were subjected to analysis of variance and correlation analysis and were later used in the computation of heritability and genetic advance estimates for days to flowering, days to maturity, pod number per plant, pod weight per plant, number of branches per plant and 100 seed weight needed as possible predictors of grain yield. Highly significant effects were observed for genotypes, (g), year (y), location (l), g x l interactions. Whereas 100-seed weight was observed to have negative correlation, the five other parameters were positively and significantly correlated with grain yield. High heritability (H_B) (97.1-99.3%) and genetic advance (G.A.) estimates of 41.5%, 48.2% and 42.4% were observed for pod number, number of branches and pod weight per plant, respectively. The three other yield parameters gave genetic advance estimates of below 19.0%. Agreements that existed between H_B and G.A. estimates for pod number, number of branches and pod weight per plant suggested that selection for these traits could lead to substantial improvement in yield in a later generation of breeding as the three traits can be improved simultaneously in a selection programme. Number of branches per plant was observed the best predictor of yield in the current study.

Keywords: Correlation analysis, Genetic advance, Heritability, Tropical soybeans, Yield predictor.

INTRODUCTION

Soybean (*Glycine max* (L) Merr) is one of the most important grain legumes in the world today because it plays a key role in meeting the expanding needs for protein, edible oil and calories. Soybean is a good source of cheap dietary protein in Africa and the usefulness of this crop for human and animal protein particularly in Nigeria has led to increased research activities in recent years (Oyekun, 1985; IITA, 1989). Consequently, a number of soybean varieties with improved yield and good agronomic characteristics have been developed and recommended to farmers (FAO, 1999).

However, selection and subsequent recommendation for release of most of these varieties have been hitherto based on a subjective traditional analysis of yield data from a number of locations with little or no emphasis on predictive measurement of agronomic characters that contribute to grain yield. Borojevic (1990) reported that most quantitative traits are conditioned by a large number of genes that effect the expression of such traits in crop genotypes and that the heritability of a character measures the extent to which selection of crop genotypes can be based on phenotypic expression

of the character. Hence, the amount of gain expected from such a selection according to Borojevic (1990) is best given by the heritability, genetic coefficient of variation and selection differential of the character measured in terms of phenotypic standard deviation.

Allard (1990) also reported that genetic coefficient of variation and selection differential do provide information on the maximum effect of selection while heritability measures how closely that maximum can be approached. However, low estimates of heritability along with low genetic advance indicates the presence of non-additive components of variation and consequently, large effects of environmental factors (Kharb *et al.*, 1994).

Ketata *et al.* (1976) have reported earlier that the estimates of genetic advance and heritability of a character was very informative in genetic and breeding studies because unbiased estimates lead to substantial progress in the improvement of crop genotypes. Duvick (1984) and Troyer (1990) studied the genetic contributions of some traits to yield gains in hybrid maize and observed that the hybrid maize cultivars have traits with better defensive mechanism that reduces vulnerability to environmental stress and hence offer better adaptation.

No work has been found in literature in which the predictive approach has been used for the selection and recommendation of tropical soybean varieties for release. It would, therefore, be of interest to identify a faster and cost effective procedure for knowing the best single or multiple predictors of grain yield in tropical soybeans in order to reduce or eliminate the cost of conducting multilocational yield trials.

Thus, the objective of this work was to be able to predict grain yield using estimates of heritability and genetic advance of a few yield parameters as predictive criteria in tropical soybeans.

MATERIALS AND METHODS

Six soybean genotypes of three maturity groups obtained from the International Institute of Tropical Agriculture (IITA), Ibadan were sown in Zaria and Jos, Nigeria in 1996 and 1997. Immediately after land preparation, single phosphate and N.P.K., 15-15-15 fertilizers were applied and incorporated at the rate of 7.5kgN, 67.5kgP₂O₅ and 7.5kgK respectively.

Genotypes were sown by drilling in four-row plots in randomized complete block design with three replications. Rows were 75cm apart. On emergence, seedlings were thinned to a plant-to-plant spacing of 5cm leaving a population of about 480 plants per plot.

Pre-emergence herbicides of a mixture of Galex and gramoxone at the rate of 5 and 3 litres per hectare, respectively, was applied immediately after sowing. Subsequent hand weeding was employed as required. At harvest maturity (when seeds attained 13-15% moisture content), yield data were collected from the two 4m middle rows and grain yield was then expressed in kilograms per hectare.

Data were also collected for six yield parameters: days to first flowering, days to maturity, number of pods per plant, pod weight per plant, 100-seed weight and number of branches per plant. Data for yield and yield parameters were also subjected to analysis of variance while correlation analysis was conducted to know the degree of associations between each parameter and yield on one hand and pairs of parameters on the other. Broad sense heritability estimates (H_B) were obtained for each character according to the formula of Allard (1960), viz:

$$H_B = \sigma^2_g / \sigma^2_{ph}$$

Where σ^2_{ph} = phenotypic variance of means of genotypes

σ^2_g = genotypic variance

σ^2_c = environmental or error variance

$$\sigma^2_{ph} = \sigma^2_g + \sigma^2_c$$

Genetic advance (G.A.) was calculated following Borojevic (1990) given as

$$G.A. = H_B K \sigma_{ph}$$

Where

H_B = broad sense heritability estimate.

σ_{ph} = phenotypic standard deviation of genotype means.

K = selection differential expressed in phenotypic standard deviation with a value of 2.06 which is the expectation in the case of 5% selection in a large sample of a normally distributed population.

Soybean genotypes used were Bossier, TGm 737p, TGx 536-02D, TGx 849-313D, TGx 1448-2E and TGx 923-2E.

RESULTS

Mean squares (MS) from analysis of variance (ANOVA) of yield data from six soybean genotypes sown in two locations over two years is presented in Table 1. Highly significant effects of year (Y), location (L), genotype (G), Y x L and L x G were observed. However, Y x G and Y x G x L interactions were reduced to non-significance.

Table 1: Means squares from analysis of variance of grain yield of six soybean genotypes sown in two locations in Nigeria in 1996 and 1997.

Source	df	Mean square
Year (Yr)	1	14,687.74**
Location (Loc)	1	74,236.92**
Yr x Loc	1	18,946.70**
Rep (Y x L)	8	15,395.99**
Genotype (Gen)	5	66,724.65**
Yr x Gen	5	3,371.74
Loc x Gen	5	54,598.73**
Yr x Loc x Gen	5	8,999.48
Error	40	7,360.33

Mean values, ANOVA means squares, coefficient of variation (CV) and estimates of heritability and genetic advance of yield and yield parameters are presented in Table 2. Mean yield across environments was 611.7kg/ha. On the average, soybean genotypes flowered 48 days and matured 101 days after sowing. Mean pod weight per plant was 47.4g and mean 100-seed weight was 11.3g. Highly significant MS were observed for all parameters evaluated except 100-seed weight. Coefficient of variation was highest for grain yield (13.9) and lowest for days to flowering (1.8).

* This is correlating with the selected parameters in prediction of grain yield.
J.G. 2000

Table 2: Mean value, mean squares (MS), coefficient of variation (CV), estimates of heritability (H_B) and genetic advance (GA) for yield and yield parameters of six soybean genotypes sown in four environments.

Trait	Mean value	MS	CV(%)	H_B (%)	GA(%)
Yield (kg/ha)	611.70	66.72465**	13.9	97.83	48.70
Dayfl. (d)	47.78	220.84**	1.8	98.93	14.36
DayMat. (d)	101.40	930.80**	0.6	99.27	12.14
Podno./plt.	114.10	18,160.00**	12.6	97.87	41.45
100-seed wt (g)	11.31	23.74	2.9	97.80	18.56
Pod wt./plt	47.36	1,545.10**	10.4	97.07	42.35
Branch no./plt	5.60	615.52**	13.2	97.18	48.24

Table 3: Combined correlation matrix of soybean grain yield and yield parameters in four environments.

	Yield	Dayfl.	Daymat	Podno/plt	100-seed wt.	Podwt/plt
Dayfl.	0.649*					
Daymat.	0.949**	0.915**				
Podno/plt	0.777**	0.567	0.543			
100-seedwt	-0.188	-0.550	-0.479	0.244		
Podwt/plt	0.811**	0.658*	0.559	0.699*	-0.531	
Branchno/plt	0.763**	0.848**	0.756**	0.676*	-0.425	0.805**

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

while heritability (H_B) estimates ranged from 97.1% for pod weight per plant to 99.3% for days to maturity. Genetic advance (G.A.) of yield parameters ranged from 18.56% for 100-seed weight to 48.24% for number of branches per plant. However, G.A. for grain yield was not significantly different from that of branch number per plant.

The correlation matrix of soybean grain yield and yield parameters in the four environments used for the study is shown in Table 3. With the exception of 100-seed weight which was negatively correlated, all other parameters were positively and significantly correlated with grain yield. Days to maturity, pod number per plant, pod weight per plant and number of branches per plant were positively correlated with days to flowering while number of branches per plant was also positively and significantly correlated with days to flowering, days to maturity, pod number and pod weight per plant.

DISCUSSION

It has been reported long ago (Miller et al., 1958) that progress from selection would be realized only when superior crop genotypes in a population are identified and good genotype testing procedures are designed to

maximize genetic effects relative to environmental and interaction effects. Thus, significant MS for genotypes, year and location in the current study indicated the presence of sufficient genetic variability among the genotypes evaluated and that locations varied over the two years of the experiment. Highly significant year x genotype interaction also indicated that genotypes performed differently in each year. Thus, the three replications used for the study was quite adequate because error variance was relatively low compared with treatment mean squares.

Highly significant means squares obtained for each character evaluated suggested that a lot of variations exist among genotypes and environments used for the evaluation. This further indicates that substantial amount of improvement could be provided by selecting superior genotypes for each of the character evaluated. High heritability and low genetic advance estimates obtained for days to flowering, days to maturity and 100-seed weight partially explains the adequacy of selecting for these three parameters as good predictors of yield in tropical soybeans. According to Kharb et al. (1994), the partial adequacy of this selection procedure suggests the presence of non-additive (epistasis, dominance and interaction) components of variation as well as the negative influence of some environmental

factors. Hence, very little improvement would be made when days to flowering, days to maturity and 100-seed weight are used as selection criteria for grain yield in soybeans.

However, high heritability and relatively high genetic advance estimates obtained for pod number per plant (41.5%), pod weight per plant (42.4%) and branch number per plant (48.2%) indicated that these characters are a reliable and good predictors of yield over and above all other characters evaluated, because environmental effects were probably very minimum on the former three characters. Heritability estimates that are close to the theoretical limit of 100% has been ascribed to several causes such as sampling errors and differential response of genotypes to environmental variables. Ketata *et al* (1976) has reported that non-allelic interactions could result in an upward bias in heritability estimates. Thus, high H_B and relatively high G.A. obtained for pod number per plant, pod weight per plant and branch number per plant in this study as well as the positive and significant association between the three and grain yield have confirmed the reliability and applicability of using the three traits as good predictors of yield and the three can thus be improved simultaneously in a selection program (Hayes *et al.*, 1955). The genetic advance of 41.5, 42.4 and 48.2 as predicted improvement for pod number per plant, pod weight per plant and branch number per plant, respectively, over the means of all genotypes for these three characters were very encouraging. However, these amount of superiority will be better realized only if most of the genetic effects are additive because according to Ketata *et al.* (1976) non-additive effects may decrease the amount of genotypic superiority that are available for a future breeding programme.

It can, therefore, be safely concluded that selection for increased pod number, pod weight and branch number per plant in later generation of breeding could lead to a substantial improvement in the yield of tropical soybeans because of the strong agreement that exist between heritability and genetic advance estimates for the three yield parameters. Estimation of both heritability and genetic advance is more informative in genetic and breeding studies than reporting either of them alone. Evaluation of G x E interaction is thus suggested to be used to reduce biases associated with heritability and genetic advance estimates.

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