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RESEARCH ARTICLE

Quantitative genetic variation, heritability and genetic advance in the segregating F₃ populations in Soybean (*Glycine max* (L.) Merrill.

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Abstract

Genotypes of soybean *Glycine max* (L.) Merrill were grown during the wet and dry seasons of 2011/ 2012 to study the variation and yield component among quantitative traits like; days to 50 percent flowering , plant height, seed dry weight, number of pods per plant, number of branches per plant, days to maturity, seed yield , number of seed per plant and 100-seed weight. The experiment was laid out in a randomized complete block design replicated three times. All the characters measured showed significant genetic variability with low heritable variation in plant height (3.92%) and number of pods per plant (5.91). Heritability was highest for five characters i.e. days to maturity, days to 50 per cent flowering, seed yield, seed dry weight and 100-seed weight. Seed yield showed significant and positive correlation with number of seed per plant (0.438) and seed dry weight (0.936) and also negative but highly significant correlation with days to 50 percent flowering (-0.786) and days to maturity (-0.396).

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INTRODUCTION

Annual wild soybean (*Glycine soja*), the ancestors of cultivated soybeans (*Glycine max*), are important sources of major genes for resistance to pests, diseases and environmental stresses. Genetic improvements could be accelerated if physiological attributes were used as selection criteria as reported by Pushpendra (1987). However, inheritance of quantitative characters is often influenced by variation in other characters which may be due to genetic linkage. Therefore, a measure of variability and understanding of genetic make-up of the crop are important constituents any crop improvement programme. In the early part of 20th century Johansson (1909) discussed the genetic and environmental components of variation of both heritable and non-heritable factors and the variation in a pure line to only environmental factors. The magnitude of variability and its genetic components are the most important aspect of breeding material; hence, basic understanding of the genetic variability is a pre-requisite for the planning of breeding programme. The focus of this research aims at evaluating yield and its components and to determine the degree of repeatability of quality traits among the segregating lines.

MATERIALS AND METHOD

The materials for the research were soybean lines from NACGRAB, National center for genetic resources and biotechnology in Ibadan, Nigeria. The crop is a sun loving crop that requires minimum moisture, therefore, the seed was sown in the late season of 2011 and early season of 2012 (September- December) and (March- June) respectively. The plots were laid out in a randomized complete block design replicated three times at a spacing of

30cm x 30cm row to row and plant to plant. Data collection starts immediately after germination on the following quantitative traits: Days to 50% flowering, plant height (cm), number of branches /plant, number of pods/plants, number of seed per plant, seed dry weight/plot, seed yield/plant (g), 100-seed weight (g) and days to maturity.

Days to 50% flowering is the number of days taken from the date of sowing to the day on which 50% of the plants in each of the genotype initiate first flower was recorded as days to flowering.

Plant height (cm) is height of the main stem from the ground level to the apical top of the main stem was measured in centimeters at the time of harvesting.

Number of braches per plant - This was recorded by counting the total number of braches present on main stem of each selected plant at the time of harvest.

Number of pods per plant - This was recorded by counting the total number of pods present on stem of each selected plant at the time of harvest.

Number of seeds per plant - Five plants was selected at random from each plot and the total number of seeds was counted, the average was calculated and recorded as the number of seeds per plant.

Days to maturity - This is number of days taken from date of sowing to physiological maturity of the plant.

Seed dry weight - This was determined in by the total weight of bulked seeds of selected five plants in each plot and recorded in grams.

100-seed weight - This was computed by weighing 100-seeds which are randomly chosen filled seeds from a complete sample made by mixing the seeds of all the five accession in each replication and recorded in grams.

Seed yield per plant - Was determined from seeds obtained from each selected plants, weighed in grams and recorded.

Statistical Analysis

The data collected on the quantitative traits was analyzed statistically using the analysis of variance (ANOVA) and coefficient of variation following the procedure of Parse and Sukhatine (1962). The procedure outlined by Steel and Torrie (1980) was used to estimate the yield components, as well as to determine the genotypic and phenotypic variances according to Chaudhary and Prasad (1968). The variance component was used to compute the genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) and expected genetic advance. Genotype coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance as percent of the mean were estimated by the formula as suggested by Johnson et al (1955). The genotypic correlation coefficient was estimated according to the procedure of Allard (1960).

Components of variance

The genotypic and phenotypic components of variance were computed according to formulae given by Lush (1940) and Chaudhary and Prasad (1968) for the observed characters.

$$\text{Genotypic variance } V_g = \frac{\text{Tr.m.s.s} - E.m.s.s}{r}$$

r

$$\text{Error variance } (V_e) = E.m.s.s.$$

$$\text{Phenotypic variance } (V_p) = V_g + V_e$$

$$\text{Number of replications } = r$$

Coefficient of variability

Genotypic and phenotypic coefficients of variability were computed according to Burton and Devane (1953).

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sqrt{V_g} \times 100}{x}$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sqrt{V_p} \times 100}{x}$$

Where V_g = Genotypic variance

And x = General mean of character

Heritability

Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson et al 1956).

$$\text{Heritability (h}^2\text{)} = V_g / V_p \times 100$$

Where V_g = genotypic variance

V_p = phenotypic variance

Genetic advance

Genetic advance was computed using the formula given by Johnson et al (1955).

$$\text{Genetic advance (GA)} = i h^2 \sqrt{V_p}$$

Where, i = selection differential (2.06) at 5 percent selection intensity.

h^2 = broad sense heritability

$\sqrt{V_p}$ = phenotypic standard deviation

Genetic advance as percent of mean (GAM) expressed in percentage was computed by the formula.

$$\text{GAM} = \frac{\text{GA} \times 100}{x}$$

x

Where, x = mean of the population.

Correlation matrixes were calculated between different pairs of traits in five genotypes of soybean accessions by Pearson correlation.

RESULTS

The results of the experiment conducted in Adekunle Ajasin University Akungba-Akoko in an open field beside the departmental screen house, to know the character expression and the genetic advance among 5 soybean accessions for yield and yield components are presented under the following headings.

- Analysis of variance and heritability estimates.
- Genetic variability studies.
- Correlation studies.

The mean sum of squares due to various source of variation for nine characters and heritability estimates on days to 50 percent flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seed per plant, seed yield, 100-seed weight and seed dry weight are presented in Table 1.

Table 1: Analysis of variance of heritability estimates four nine quantitative traits in soybean

S/N	Characters	Mean sum of squares.		Heritability Broad Sense (%)
		Genotypes	Error	
1	Days to 50% flowering	407.29**	1.503	98.90
2	Plant height(cm)	125.44**	111.76	3.92
3	Number of pods/plant	1129.38**	1356.60	5.91
4	Number of branches/plant	727.84**	139.58	58.42
5	Number of seed/plant	41527.80**	7335.05	60.84
6	Days to maturity	483.53**	1.20	99.26
7	Seed dry weight(g)	87257.49**	839.58	97.17
8	Seed yield(g)	55543.23**	249.64	98.66
9	100-seed weight(g)	59.96**	1.36	93.45

*Significant at 5% level of probability.

**Significant at 1% level of probability

The result of analysis of variance indicated that all the nine quantitative traits studied were highly significant whereas, there are variations in the heritability estimates with days to maturity having the highest heritability (99.26%) and lowest in plant height (3.92%) Table1. However, low CV values was recorded in days to 50% flowering (2.40%), days to maturity (1.00%) and hundred seed weight (6.89%) Table 2. There were no much significant differences between the PCV and GCV values except in plant height with a PCV (20.55) and GCV (4.07) and number of pods per plant with PCV (44.74) and GCV (10.83). The genetic advance for plant height (0.87) and number of pods per plant (4.36) was very low as well as their corresponding genetic advance as percent of mean (GAM) compared to the other traits.

Table 2: Estimation of mean and different genetic parameters for different characters in five accessions of soybean.

S/N	Characters	Mean	V p	V g	PCV	GCV	GA	Coeff of variation	GAM
1	Days to 50% flowering	51.10	136.76	135.26	22.89	22.76	23.82	2.40	46.62

2	Plant height(cm)	52.49	116.32	4.56	20.55	4.07	0.87	20.14	1.66
3	Number of pods/plant	80.39	1280.85	75.74	44.74	10.83	4.36	45.82	5.42
4	Number of branches/plant	46.64	335.67	196.09	39.28	30.02	22.05	25.33	47.28
5	Number of seed/plant	187.23	18732.64	11397.58	73.10	57.02	171.54	45.74	91.62
6	Days to maturity	109.92	161.98	160.78	11.58	11.54	26.02	1.00	23.68
7	Seed dry weight(g)	84.12	29645.55	28805.97	204.68	201.76	344.65	34.45	409.71
8	Seed yield(g)	63.45	18680.84	18431.20	215.41	213.97	277.80	24.9	437.82
9	100-seed weight	16.94	20.90	19.53	26.99	26.09	8.80	6.89	51.95

The result of genotypic correlation coefficient for the nine quantitative characters studied were presented in Table 3; days to 50% flowering showed negative but highly significant correlations with plant height (-0.124), number of seeds per plant (-0.316), seed dry weight (-0.707), seed yield (-0.786) and hundred seed weight (-0.582), however, it only shows positive and highly significant correlation with days to maturity (0.521).

Plant height had positive and highly significant correlations with number of pods per plant (0.392), number of branches per plant (0.369), number of seeds per plant (0.385), seed dry weight (0.270) and seed yield (0.215).

Number of pods per plant had positive and highly significant correlations with number of branches plant (0.292) and number of seeds per plant (0.893).

Number of branches per plant only had highly positive significant correlation with number of seeds per pod (0.317) and negative significant correlation with days to maturity (-0.326).

Number of seeds per pod showed positive and highly significant correlations with seed dry weight (0.428) and seed yield (0.438).

Table 3: Genotypic correlation coefficients among nine quantitative characters in soybean.

Charactes	DF	PH	NOP	NOB	NOS	DM	SDW	SY	100_SW
DF	-	-0.124**	-0.063	-0.068	-0.316**	0.521**	-0.707**	-0.786**	-0.582**
PH		-	0.392**	0.369**	0.385**	-0.132	0.270**	0.215*	-0.019
NOP			-	0.292**	0.893**	0.098	0.157	0.124	-0.105
NOB				-	0.317**	-0.326**	0.140	0.137	0.146
NOS					-	-0.063	0.428**	0.438**	0.111
DM						-	-0.304**	-0.396**	-0.627**
SDW							-	0.936**	0.292**
SY								-	0.393**

100_SW									-
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Key: DF- days to 50% flowering; PH- plant height; NOP- number of pods per plant; NOB- number of branches per plant; NOS- number of seeds per plant; DM- days to maturity; SDW- seed dry weight; SY- seed yield; 100_SW- hundred seed weight.

Days to maturity had negative and highly significant correlations with seed dry weight (-0.304), seed yield (-0.396) and hundred seed weight (-0.627).

Seed dry weight correlates significantly with seed yield (0.936) and hundred seed weight (0.292).

Seed yield had positive and highly significant correlation with hundred seed weight (0.393).

DISCUSSION

Crop improvement programmes generally commence with the collection of germplasm from diverse origin as possible, followed by its proper evaluation and characterization. This requires careful analysis of variability present in the material by computing various parameters like the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance as percent of mean.

Seed yield being a complex quantitative trait is influenced by different yield contributing traits. Therefore, it is necessary to measure the association among these traits. Association measures only neutral relationship between two or more variables. The nature and extent of genetic variability observed in the population largely depend on the diversity existing between the parents and the coefficient of variability has been used as a quantitative measure of genetic variability among the soybean accessions.

The knowledge of genetic variability is basic to improve any character by adopting selection based on variation present in the population, therefore, the analysis of variance for nine traits revealed highly significant variation among the genotype/accessions. The high variability observed might be attributed to their genetic makeup and the environment in which the accessions were evaluated.

In the present study, the phenotypic coefficient of variation was higher than genotypic coefficient of variability for all the nine characters. All the five accessions showed wide range of variation for the traits viz; days to 50 % flowering, plant height, number of branches per plant, numbers of pod per plant, number of seeds per plant, seed dry weight, seed yield and 100_seed weight. This variation indicated the scope for selection of these traits for further breeding work. The characters viz; days to 50 percent flowering, plant height, days to maturity and hundred seed weight showed low values of PCV and GCV. Similar results were obtained by Amaranath et al (1991).

The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. The result of heritability estimate were high for all the characters under study i.e days to 50 percent flowering, number of branches per plant, number of seed per plant, days to maturity, seed dry weight, seed yield and hundred seed weight. This finding is in line with the observations of the research work carried out by Chaudhary and Singh (1987).

But low heritability estimates were observed in plant height and number of pods per plant suggesting that selection for improvement would be focused on these traits. The high heritability coupled with high genetic advance as percent of mean observed for the seven traits listed above indicated lesser influence of environments in expression of characters and prevalence of additive gene action in their inheritance, since they are amenable for single selection. High genetic advance was observed for seed dry weight, number of seeds per plant, and seed yield and where as low estimates were recorded for plant height, number of pods per plant, hundred seed weight, number of branches per plant, days to maturity and days to fifty percent flowering, similar results were recorded by(mehetre et al 1997). The character days to maturity showed highest heritability but low genetic advance as percent of mean, thereby indicating that expression of these characters may be due to non-additive gene action. Similar results were obtained by Agarwal et al (2000).

Yield being a complex quantitative character governed by large number of genes and highly influenced by environment, hence the selection of superior genotypes based on yield as such is not effective for a rational approach towards improvement of yield; selection has to be made based on the components of yield. Association of yield components and yield then assumes special importance as the basis for indirect selection. Genetic correlation between different characters of plants often arises because of linkage or pleiotropy (Harland, 1939).

In the present study seed yield was positive and highly significant with number of seeds per plant, seed dry weight, plant height but with negative and highly significant association with days to maturity and days to 50 percent flowering. The trait with negative association does not need to be emphasized while selecting for improvement of seed yield. The findings of Shah (2003) confirmed the above results, similar results were also obtained by Choudry (1999); Rajanna et al (2000).

CONCLUSION

The analysis of variance revealed the prevalence of significant difference among the genotypes for all the nine traits/characters studied. Phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation in respect to all the characters. The characters seed yield, seed dry weight, number seeds per plant showed high PCV and GCV, while days to 50% flowering, number of branches per plant and hundred seed weight had moderate PCV and GCV values whereas, days to maturity, and plant height had low PCV and GCV.

Heritability in broad sense and genetic advance as percent of mean were higher for days to 50 percent flowering, number of branches per plant, number of seeds per plant, seed dry weight, seed yield and hundred seed weight.

Higher heritability and moderate genetic advance as percent of mean was observed for only days to maturity. Low heritability and genetic advance as percent of mean was observed for plant height and number of pod per plant. Number of seed per plant, seed dry weight and plant height showed positive and significant correlation with seed yield whereas days to 50 percent flowering and days to maturity was significant and negatively correlated with seed yield.

Variability studies indicated that the character days to 50 percent flowering, plant height, number of pods per plant, number of branches per plant, number of seed per plant, days to maturity, seed dry weight, seed yield and hundred seed weight had high genetic variability. These characters can be exploited by direct selection for yield improvement in subsequent hybridization work.

The correlation analysis pointed out that number of seeds per plant, seed dry weight and plant height had significant and positive association with seed yield. It might be emphasize that the importance of these characters should be considered in selection programs aimed at yield improvements.

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