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Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.)

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A study with 20 soybean genotypes was conducted in 2015 and 2016 to determine the genetic variability, heritability and genetic advance for some agronomic and yield traits in some soybean genotypes for selection criteria in a breeding programme. The field experiments were laid out in a randomized complete block design (RCBD) and replicated three times. Analysis of variance (ANOVA) revealed significant variation among the genotypes indicating that the planting materials were genetically divergent from each other. The estimates of genetic variability showed that phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the traits. Portraying the importance of environmental factors in the variations shown. High value of PCV and GCV were observed for traits such as plant height, number of leaves, number of pods and seed yield indicating the presence of sufficient genetic variation for selection in these traits. High heritability coupled with high genetic advance observed for plant height and number of pods suggests that selection could be effective for these traits.

Key words: Genetic advance, heritability, soybean, traits, variability.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is one of the most valuable and most widely cultivated crops among the grain legumes. It has the highest protein content (38-42%) and edible oil (18-25%), therefore generally viewed to be one of the most foremost pulses and oil seed crops. Soybean occupies a pivotal place in Nigeria and Sub-Saharan Africa agriculture as a result of the insatiable demands for cheap source of protein from food and fodder. Soybean as a leguminous crop also has the

capacity for soil fertility replenishment particularly in the Guinea Savanna (Yusuf et al., 2006), since it is able to fix approximately 300kg Nha⁻¹ of nitrogen from the atmosphere into the soil (Keyser and Li, 1992). Soybean leftovers such as haulms so obtained also help in improving the soil condition of the farm, as on decay it supplies nutrients to subsequent crops more especially in a crop rotation system.

The improvement of genetic architecture of any crop is

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determined by the magnitude of genetic differences in a population ready to be taken advantage of and the extent to which the desirable traits are passed from one generation to the other (Tiwari et al., 2011). Variability can be defined as the availability of differences among the individuals of plant population. Variation usually arises as a result of differences either in genetic makeup of the individuals of a plant population or in the environment in which the plants are grown (Kavera, 2008). The existence of genetic variability is essential for performance of selection in any breeding programme. Selection as a breeding method will be meaningful if there is an appreciable quantity of genetic differences within the various genotypes used in the breeding programme. The selection of potential candidates among a particular germplasm, making use of them in the hybridization programme and subsequently picking the outstanding segregants in the segregating population is the usual breeding method in a highly self-pollinating crop like soybean.

Heritability estimates reveal the extent of transmission of quantitative traits such as plant height and seed yield from one generation to the other, as continuity in performance of selection is based on the transmittable aspect of the differences. Estimate of heritability help the breeder to effectively assign the necessary strategies to be adopted for a successful selection of the desired traits and to achieve the highest genetic gain within the shortest possible time and resources (Patil et al., 2015). Broad sense heritability is estimated using the total genetic variance. Researchers have observed that traits with higher heritability can be more easily manipulated by selection and breeding compared to traits with lower heritability. In the same manner, genetic advance is also a useful tool in forecasting the gain to be in a specified selection intensity. However, when genetic advance is considered along with heritability, it becomes a more important measure in predicting responses to selection than the heritability estimates alone (Johnson et al., 1955). Grain yield is the most important trait in breeding soybean, depending on both the phenotypic potential and environmental conditions. Grain yield being a complex trait comprised of aspects of quantitative characters, whose expression is measured by the interaction of the genetic and environmental factors. This means that variability of quantitative trait is caused by genetic variability, environmental variability and variability of their interactions (Bos and Caligari, 1995; Soldati, 1995). Therefore, this study was undertaken to estimate the extent of genetic variability and heritability in soybean for effective selection in a breeding programme.

MATERIALS AND METHODS

The experimental material for the study comprised of twenty (20) soybean genotypes: Five (5) from the International Institute for

Tropical Agriculture (IITA), Ibadan and fifteen (15) from various locations in Nigeria. The research was conducted during a two-year period (2015 and 2016) from July to November of each year at the experimental field of the Department of Crop Science, University of Nigeria, Nsukka (Lat. 06° 52' N, long. 07°24' E and 447.26 masl) which is located in a derived Guinea Savanna Zone. The soil type of the study area was sandy clay loam and of acidic pH (4.9). The experiment was laid out in a randomized complex block design (RCBD) in three replications on a plot size of 4m² and the soybean seeds were planted at the spacing of 15cm between stands and 30cm between rows. Acceptable management and cultural practices of soybean were carried out as required in each year of the trial. Data were collected in five plants that were randomly selected on days to 50% flowering, plant height, number of leaves, number of pods, number of branches, pod weight (g) and seed yield (g). The data collected were subjected to analysis of variance (ANOVA) using the generalized linear model (GLM) procedure of Statistical Analysis System (SAS) and significant means were compared using Least Significant Difference (LSD) at 5% level of probability. Phenotypic and genotypic coefficients of variation were estimated as per the formula prescribed by Burton and Devane (1952).

$$GCV = [\delta^2g / \bar{X}] \times 100$$

$$PCV = [\delta^2p / \bar{X}] \times 100$$

Where; GCV = genotype coefficient of variation; PCV = phenotype coefficient of variation; δ^2g = genotypic standard deviation; δ^2p = phenotypic standard deviation; \bar{X} = population mean

Heritability in broad sense was calculated using the formula given by Singh and Chaudhary (1985) and the expected genetic gain was calculated using the procedure outlined by Johnson et al. (1955).

$$h^2b (\%) = [\delta^2g / \delta^2p] \times 100$$

where; h^2b = heritability in broad sense; δ^2g = genotypic variance; δ^2p = phenotypic variance;

$$\text{Genotypic variance, } \delta^2g = [MSG - MSE] / r$$

where; MSG = mean sum of square for genotype; MSE = mean sum of square for error; r = number of replicate; δ^2g = genotypic variance

RESULTS

Genotypic differences were highly significant ($p < 0.01$) for all the traits, indicating the considerable amount of variability (Table 1). The mean performance of the genotypes indicates that the genotype *Vom* had the maximum mean values for days to 50% flowering, plant height, number of leaves and number of branches. However, the genotype *Ashuku* recorded the maximum pod weight and seed yield (19.4 and 13.0 g, respectively). TGX1485-ID was the earliest to attain 50% flowering while *Vom* was the last to attain 50% flowering and was comparable with the genotype, *Lau*. In general, the genotype *Agbonkagoro* recorded the minimum mean values for most of the traits measured as revealed in Table 1. In the present study, the genotypes *Ashuku*, *Mangu* and *Akwanga* gave significantly higher seed yield

Table 1. Mean values of agronomic and yield traits in soybean.

Genotype	DF	PH (cm)	NL	NB	NP	PW (g)	SY (g)
AgbonKagoro	45.2	28.5	57.3	2.8	27.8	9.9	6.1
Akwanga	43.8	32.3	65.2	3.2	50.4	18.4	12.1
Andaha	47.4	28.5	67.9	3.2	38.2	13.5	8.5
Ashuku	44.8	36.3	76.5	3.5	57.5	19.4	13.0
Dadinkowa	46.0	31.5	71.9	3.1	32.2	13.0	8.6
Garkawa	44.3	34.0	73.2	3.3	40.5	13.8	9.2
Gwantu	44.8	33.8	70.9	3.8	41.3	14.2	9.3
Kafanchan	44.0	30.9	68.7	3.1	38.5	14.9	10.0
Kagoro	45.2	35.5	74.7	3.7	46.1	16.0	11.2
Langtang	46.7	32.0	89.5	3.6	43.6	17.7	11.8
Lau	51.0	34.8	81.8	3.7	54.7	17.6	11.6
Mangu	44.3	35.7	85.9	3.5	52.2	19.0	12.5
Mararaba	45.0	34.1	73.1	3.5	45.0	15.4	10.2
TGX1485-ID	42.3	30.8	78.3	3.7	40.3	14.8	9.6
TGX1448-2E	42.8	34.9	71.1	3.5	45.4	14.4	9.5
TGX1987-10F	44.0	33.0	69.2	3.0	37.0	15.7	10.1
TGX1835-10e	42.7	31.9	65.2	3.2	34.2	12.9	8.6
TGX1987-62F	47.3	37.1	72.8	2.9	43.7	14.6	9.7
Tiv Local	44.9	34.6	68.9	3.5	49.1	16.6	11.1
Vom	51.1	50.4	109.6	4.5	63.9	17.0	9.9
Grand mean	45.4	34.0	74.6	3.4	44.1	15.4	10.1
Range	42.3-51.1	28.5-50.4	57.3-109.6	2.8-45	27.8-63.9	9.9-19.0	6.1-12.5
LSD@5%	0.84	1.46	4.96	0.17	5.44	2.03	1.35
CV%	7.31	16.82	23.66	17.85	38.81	41.19	42.18

DF= days to 50% flowering, PH = plant height, NL = number of leaves, NB = number of branches, PW = pod weight, SY = seed yield.

Table 2. Analysis of variance for agronomic and yield traits.

Parameter	Mean	CV (%)	MS	Error
DF	45.37	9.19	46.52**	17.38
PH	34.02	13.09	101.99**	19.82
NL	74.57	23.65	955.27**	310.94
NB	3.38	17.08	1.15**	0.33
NP	44.10	34.53	1159.911**	245.41
PW	15.43	36.77	154.26**	32.17
SY	10.11	38.46	70.12**	15.13

DF= days to 50% flowering, PH = plant height, NL = number of leaves, NB = number of branches, NP = number of pods, PW = pod weight, SY = seed yield, CV = Coefficient of variance, MS = mean square.

per plant compared to the grand mean (10.1g), therefore, may be utilized for the improvement of soybean yield.

The analysis of variance (ANOVA) showed that mean square due to genotypes were highly significant ($p < 0.01$) for all the traits under investigation (Table 2), indicating the enormous genotypic variability among the genotypes. This suggests that there is enough reasons for selection of traits from among the different sources of planting

materials for yield and yield component traits.

The level of varietal differences present in the soybean genotypes were estimated on the basis of genetic parameters viz., genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance coupled with different traits are presented in Table 3. A long range of differences was observed for all the traits. Phenotypic variance was greater than the genotypic

Table 3. Estimates of variability, heritability and genetic advance for the traits.

Trait	δ_p^2	δ_g^2	PCV	GCV	Hb ² (%)	GA	GA (%)
DF	51.21	48.81	15.92	15.55	95.31	14.06	31.28
PH	85.58	79.46	27.10	26.11	92.85	17.69	51.82
NL	527.72	392.50	27.93	24.09	74.38	13.90	16.90
NB	0.46	0.35	22.69	16.30	76.09	1.07	24.36
NP	323.38	249.27	32.67	28.68	77.08	28.55	51.86
PW	26.20	16.41	26.47	20.95	62.63	6.61	34.18
SY	11.60	6.59	27.07	20.41	56.81	3.99	31.72

DF= days to 50% flowering, PH = plant height, NL = number of leaves, NB = number of branches, NP = number of pods, PW = pod weight, SY = seed yield, δ_p^2 = phenotypic variance, δ_g^2 = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genetic coefficient of variance, Hb² = broad sense heritability, GA = genetic advance.

variance for the yield and yield component traits indicating the important effects of environment on these traits. The phenotypic variance and genotypic variance ranged from 0.46 and 0.35 for number of branches to 527.72 and 392.50 for number of leaves, respectively. Similarly, the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) showed that the values of PCV were higher than GCV for all the traits and this may be partly due to the interactive effect of the genotypes with the environment or other environmental factors influencing the expression of these traits (Table 3). PCV and GCV ranged from 15.92 and 15.55 for days to 50% flowering to 32.67 and 28.68 for number of pods, respectively. Moderate PCV (10-20) was recorded for days to 50% flowering whereas other traits showed high PCVs (> 20). The narrow difference observed between the PCV and GCV for days to 50% flowering indicated that this trait was less influenced by the environment. High magnitude of GCV observed in traits that include plant height, number of leaves and pod weight indicates the presence of wide variation for these characters to be allowed for further improvement by selection of the individual traits.

With GCV only, it is impossible to ascertain the extent of differences which is heritable. Thus, the knowledge of heritability of a character helps the plant breeder in predicting the genetic advance for any quantitative characters and aid in exercising necessary selection procedure. In this current study, the highest heritability values were recorded for days to 50% flowering, plant height, number of pods, number of branches and number of leaves. The availability of high heritable variation of these characters would be useful to plant breeder in the improvement of these traits. Heritability in broad sense estimates coupled with genetic advance will be more effective and reliable in predicting the response to selection (Johnson et al., 1955). Heritability in broad sense involves both the additive and non-additive gene effects. High heritability in broad sense together with high genetic advance for the following traits; number of pods per plant and plant height suggests that selection can be

effective for these traits based on phenotypic expression. High magnitude of broad sense heritability and low magnitude of genetic advance was observed for number of leaves which may be due to lack of genetic variability for that trait. In such a situation, advancement in this trait through usual selection may not be effective. However, recombination breeding and recurrent selection is advocated for improvement of such trait.

DISCUSSION

The highly significant variations for all the traits indicate that both the genotypes and the environmental factors had enormous effects on the agronomic and yield traits. This observation is in agreement with the findings of Adugna and Labuschgne (2003) who also observed highly significant variation in both agronomic and yield traits in cowpea. Similarly, Jandong et al. (2019) observed highly significant variation in most parameters among the soybean genotypes signifying the existence variability. The range of phenotypic variability was high for all the traits, indicating the different sources of the genotypes. A wide range of variability for different traits has also been reported by Narayanankutty et al. (2005). The highly significant mean squares due to genotypes signified the presence of variability within the genetic materials used for the research. The estimates of PCV and GCV showed that the values of PCV were higher than that of the GVC. This portrayed the importance of environment in the variation exhibited and confirms the results reported by Nath and Alam (2002). The closer difference between the PCV and GCV for days to 50% flowering expressed the little influence of environmental factors for that trait. This finding is in agreement with the report of Karnwal and Singh (2009). The low magnitude of PCV and GCV for days to 50% flowering is in agreement with the finding of Bangaret al. (2003) and Baraskaret al. (2014). High values of PCV and GCV for number of pods per plant observed in this present study is in conformity with the result of Gohil et al. (2007) which

is supported by Baraskar et al. (2014). Similarly, Olayiwola and Soremi (2014) reported high estimates of PCV and GCV for number of pod per plant in cowpea.

The high values of phenotypic and genotypic coefficients of variation obtained for plant height in the present study is in conformity with the findings of previous researchers like Karnwal and Singh (2009) and Neelima et al. (2018). The highest heritability values were observed for days to 50% flowering (95.3%), plant height (92.9%), mean number of pods (77.1%), mean number of branches (76.1%) and mean number of leaves (74.4%). This finding validate the results of Baraskar et al. (2014) who reported high heritability estimates for plant height, days to 50% flowering, number of branches per plant and number of pods per plant in soybean. Similarly, Patel et al. (2016) also reported high heritability for plant height, number of branches per plant and number of pods per plant in cowpea. Some researchers also reported high magnitude of heritability for yield and its components in soybean (Bangar et al., 2003; Malik et al., 2006; Neelima et al., 2018). This indicates that selection based on phenotypic levels would be useful for the improvement of the traits by repeated mass selection or hybridization between selected genotypes, showing varying degree of variation for such traits. It should be noted that broad sense heritability only cannot be a true reflection of genetic gain that is expected from selection because it involves both the additive and non-additive aspects of the variability (Singh et al., 2013).

The importance of estimate of genetic advance in percentage is to ascertain the real development made by isolating outstanding genotypes for a given trait (Allard, 1960). In the study being reported, it was discovered that genetic advance as a percentage of the mean (GAM) for number of pods per plant was of relatively low heritability (77.1%) when compared with plant height (92.9%). Similarly, seed yield per plant had relatively low heritability (56.8%) comparable to GAM. This suggest that plant height and days to 50% flowering had greater non-additive variance and environmental influence compared with number of pods per plant and seed yield per plant per plant respectively (Pradeepkumar et al., 2001). According to Johnson et al. (1955), high heritability estimates in conjunction with high genetic advance is indicative of additive gene action and selection based on these parameters would be more effective and reliable.

Conclusion

In the present investigation, the analysis of variance revealed the enormity of phenotypic variability that exists among the genotypes. On the basis of mean seed yield performance, the genotypes *Ashuku*, *Mangu* and *Akwanga* exhibited high seed yield per plant. Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicated that the values of

PCV were greater than those of GCV, revealing the significant effect of environmental factors. Estimates of heritability were shown to be high for days to 50% flowering plant height, mean number of pods, mean number of branches and mean number of leaves. However, high magnitude of genetic advance was observed for number of pods per plant and plant height whereas pods weight per plant exhibited moderate genetic advance. High heritability estimates coupled with high genetic advance expressed as percentage of mean were observed for plant height and number of pods per plant, could be ascribed to the predominance of additive gene effects and high selective index and thus, possibilities of effective selection for improvement of these traits.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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