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RESEARCH ARTICLE

Estimation of genetic variability, heritability and genetic advance for grain yield and yield components in soybean

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Abstract

The success of any crop improvement programme largely depends on the amount of variability present in the plant materials. The objective of this study was to estimate the genetic variability and heritability for grain yield and quality traits in soybean as selection criteria in breeding for higher grain yield. The experimental material for the study comprised of twenty soybean genotypes. The analysis of variance revealed significant variations among the genotypes. Estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation indicated that the values of PCV were higher than that of GCV. This portrayed the influence of environmental factors in the variation exhibited. High values of PCV and GCV were observed for number of pods, plant height, number of leaves and seed yield indicating presence of sufficient genetic variability for selection in these traits. High heritability coupled with high genetic advance observed for plant height and number of pods per plant suggests that selection could be effective for these traits.

Key words: Soybean, variability, heritability, trait, genetic advance

Introduction

Soybean (*Glycine max* L.) is one of the most important and most widely grown crops among the grain legumes. It has the highest protein content (38-42%) and edible oil (18-25%) therefore considered as one of the most important pulses and oil seed crops. Soybean occupies a pivotal place in Nigeria and sub-saharan African agriculture as a consequence of the increasing needs for protein from food and fodder. It also has the capacity for soil fertility improvement in the Guinea Savanna (Yusuf *et. al.,* 2006), since they are able to fix about 300kg N ha^{-1} of atmospheric nitrogen (Keyser and Li, 1992). Soybean residues (haulms) so obtained improve the soil condition, and on decay it supplies nutrients to subsequent crops.The improvement of genetic architecture of any crops depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable traits are heritable (Tiwari *et al*., 2011). Variability refers to the presence of differences among the individuals of plant population. Variation results due to differences either in genetic constitution of the individual 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 is also effective when there is significant amount of genetic variability among the individuals in the breeding materials. The selection of potential genotypes from the existing germplam, utilizing them in the hybridization programme and subsequently isolation of the superior segregants in the segregating population is the usual breeding strategy in highly self-pollinating crops like soybean.

Heritability estimates are considered in understanding the pattern of inheritance of quantitative trait such as seed yield. Estimate of heritability assist the breeder to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources (Patil *et. al.*, 2015). Broad sense heritability is estimated using the total genetic variance. As a rule, traits with greater heritability can be modified more easily by selection and breeding, than traits with lower heritability. Similarly, genetic advance is also a useful measure to predict gain in specified selection intensity. However, when it is considered along with heritability becomes more valuable to predict response to selection than the heritability estimate 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 is a complex trait and consists of components of quantitative nature, whose expression is determined by genetic and environmental factors as well as their interactions. Therefore, 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 of yield and yield related traits 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 Teaching and Research Farm, Department of Crop Science, University of Nigeria, Nsukka (Lat. $06^{o}52^{I}$ N, long. 07^{o} 24^{I} E and 447.26 masl). Nsukka is located in the Derived Savanna of South eastern Nigeria. The experiment was laid out in a Randomized Complex Block Design (RCBD) in three replications on a plot size of $4m^2$ and seeds sown at the spacing of 15cm between stands and 30cm between rows. Five plants were randomly selected from the two middle rows for data collection on days to 50% flowering, plant height, number of leaves per plant, number of pods per plant, number of branches per plant, pod weight (g) per plant and seed yield (g) per plant. 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). The phenotypic and genotypic coefficients of variation were computed as per the formula suggested by Burton and Devance (1953). Heritability in broad sense was calculated using the formula given by Singh and Claudhary (1985) and the expected genetic gain was calculated using the procedure given by Johnson *et. al.,* (1955).

Results and discussion

Genotypic differences were highly significant ($p<0.01$) for all the traits, indicating the considerable amount of variability (Table 1).

Table 1: Mean values of some agronomic yield traits in soybean

Genotype	DF	PH(cm)	NL	NB	NP	PW(g)	SY(g)
Agbon Kagoro	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

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

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 (19.4g and 13.0g, 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 *Agbon kagoro* 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 per plant than the grand mean (10.1g) hence, they could be utilized for the improvement of soybean yield. The analysis of variance revealed 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.

Table 2: Analysis of variance for agronomic and yield traits

Parameter	Mean	CV (%)	Mean square	Error
Days to 50% flowering	45.37	9.19	46.52^{**}	17.38
Plant height	34.02	13.09	101.99^{**}	19.82
Number of leaves	74.57	23.65	955.27^{**}	310.94
Number of branches	3.38	17.08	1.15^{**}	0.33
Number of pods	44.10	34.53	1159.91^{**}	245.41
Pod weight (g)	15.43	36.77	154.26^{**}	32.17
Seed yield (g)	10.11	38.46	70.12^{**}	15.13

This suggests that there is ample scope for selection of traits from these diverse sources for yield and its component traits. The significant variation for these seven traits observed in the base population could be utilized simple breeding methods. The range of phenotypic variability was high for all the traits. A wide range of variability for various traits has been reported by previous researcher in soybean (Narayanankutty *et.al.,* 2005). The highly significant mean squares due to genotypes signified the presence of variability in the genetic materials used for the study. The extent of variability present in soybean genotypes was measured in terms of genetic parameters *viz.*, genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance along with different traits are presented in Table 3.

Table 3: Estimation of variability, heritability and genetic advance for the traits

Traits	δ^2_p	δ^2_g	PCV	GCV	Hb^2(%)	GA	GA(%)
Days to 50% flowering	51.21	48.81	15.92	15.55	95.31	14.06	31.28
Plant height	85.58	79.46	27.10	26.11	92.85	17.69	51.82
Number of leaves	527.72	392.50	27.93	24.09	74.38	13.90	16.90
Number of branches	0.46	0.35	22.69	16.30	76.09	1.07	24.36
Number of pods	323.38	249.27	32.67	28.68	77.08	28.55	51.86
Pod weight (g)	26.20	16.41	26.47	20.95	62.63	6.61	34.18
Seed yield (g)	11.60	6.59	27.07	20.41	56.81	3.99	31.72

Where, δ^2_p = phenotypic variance, δ^2_p = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variance, Hb^2 = broad sense heritability, GA = genetic advance.

A wide range of variance was observed for all the traits. Phenotypic variance was higher than the genotypic variance for the yield and its contributing traits indicating the influence of environmental factors 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 partly due to interaction 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 observed for days to 50% flowering whereas the remaining 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 for traits such as number of pods, plant weight and number of leaves indicate the presence of wide variation for these characters to be allowed for further improvement by selection of the individual traits.

With GCV alone, it is impossible to determine the extent of variation 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 the present 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 estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et. al.*, 1955). Heritability in broad sense includes both additive and non-additive gene effect. High broad heritability accompanied by high genetic advance for 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, improvement in this trait through simple selection may not be effective. However, recombination breeding and recurrent selection is advocated for improvement of such trait. 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 Bangar *et. al.*, (2003) and Baraskar *et. 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 this study is in agreement with those reported by 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%), number of pods per plant (77.1%), number of branches per plant (76.1%) and number of leaves per plant (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. However, broad sense heritability alone does not always give a full indication of genetic gain that can be made through selection since it includes both additive and non additive components of the variation (Singh *et. al.*, 2013). It is necessary to estimate the genetic advance as a percentage of the mean to determine the actual progress by selecting the best performance genotypes for a given trait (Allard, 1960). When the genetic advance as a percentage of the mean (GAM) was estimated, it was discovered that though number of pods per plant had a relatively low heritability (77.1%) when compared with plant height (92.9%), they had almost the same GAM. Similarly, seed yield per plant had relatively low heritability (56.8%) comparable 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.

Hence in conclusion the present investigation, the analysis of variance revealed the enormous 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 higher than that of GCV, revealing the influence of environmental factors. Estimates of heritability were observed to be high for days to 50% flowering plant height, number of pods per plant, number of branches per plant and number of leaves per plant. However, high magnitude of genetic advance were 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, which may be attributed to the preponderance of additive gene action and high selective value and thus, selection pressure could profitably be applied on these traits for their rationale improvement.

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