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GENETIC VARIABILITY, CORRELATION AND HERITABILITY STUDIES FOR YIELD AND YIELD COMPONENTS IN SOME SOYBEAN (*GLYCINE MAX L.*) GENOTYPES IN LAKE GARIO, YOLA

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ABSTRACT

A study was carried out during the 2010/2011 cropping season to determine genetic variability, correlation and heritability of yield and yield components in five soybean genotypes at Lake Gerio, Yola. Significant differences among the genotypes for characters viz., plant height, days to 50% flowering, 50% maturity, number of branches/plant, number of nodes/plant, pods/plant, dry matter, pod length, seeds/pod, 100-seed weight and grain yield were recorded. Means of agronomic characters varied considerably. High heritability for yield-related and some morphological characters were observed. Correlation coefficient of yield was significant and positive with branches per plant, pods per plant, dry matter, pod length, seeds per plant and seed weight. Increase in these traits will ultimately increase the grain yield. High heritability was recorded in days to maturity, flowering and pod length indicating the additive type of gene effect. High genetic advance as well as positive associations of the characters obtained can be explored in the selection of soybean for high yield improvement.

Keywords: Genetic variability, correlation coefficient, Heritability, yield components, soybean.

INTRODUCTION

Soybean (*Glycine max* L.) is a legume that grows in tropical, sub tropical and temperate climates. It belongs to the family leguminosae, is a papilionoid legume that has a fairly wide range of climatic conditions for adaptation. The crop is mostly cultivated on rainfed lands (Fageria *at al.*, 1997). Soyabean is an important source of high quality, inexpensive protein and oil. It has the highest protein content of (40-42%) of all other food crops and is second only to groundnut in terms of oil content (18 to 22% comprising 85% unsaturated fatty acids and is free from cholesterol) among food legumes, so it is highly desirable in human diet (Antalina *et al.*, 1999). Examination of genetic variance is important to plant breeders in general and particularly in a new introduced crop like soyabean, which is not grown commercially in Yola. However, genetic variability for many characters is limited (Sabu *et al.*, 2009). Correlation analysis is a handy technique, which provides information about the degree of relationship between important plant trait and is also a good index to predict the yield response in the change of a particular character. However, many workers have expressed apprehension about total reliance on yield components analysis (Arshad *et al.*, 2006). If the overall performance of a genotype vary due to changes in the environment, and if the heritability for the characters is higher, then selection process become easier and thus response to selection will be greater (Larik *et al.*, 2000; Soomoro *et al.*, 2008). Genetic improvement of crops for quantitative characters require reliable estimates of genetic diversity, heritability and genetic advance (Chand *et al.*, 2008). An understanding of the relations among various characters with seed yield is essential so as to find appropriate selection criteria. Quite often, characters are correlated and selection for one character may lead to either positive or negative response in the other characters. This response can be predicted if the correlation and heritability of the characters are known (Morakinyo, 1996). This research work aims to study the genetic variability, correlation and extent of inheritance among five soyabeen genotypes.

MATERIALS AND METHODS

The experiment was conducted during the rainy seasons of 2010/2011 at Lake Gerio, Yola. The farm site is located within Latitude 9^0 14’ North and Longitude 12^0 38’ east at an altitude of 200m above sea level within the Sudan Savanna ecological zone of Nigeria, the soil type is clay loam (Adebayo, 1999). The experiment was laid out in a randomized complete block design with three replications. Five soybean genotypes- Ex Gerio, Barkinladi, TGx1945-1F, TGx1740-2E and TGx1935-3F were used. Seeds were sown at the spacing of 60cm and 10cm within row, and seedlings were thinned, two weeks after emergence to one/hole. Normal cultural practices were adopted. Ten plants from the two middle rows were randomly sampled for data recording for the parameters studied. Data were collected on plant height 6WAP, days to 50% flowering, 50% maturity, number of branches/plant 6WAP, number of nodes/plant 6WAP, pods/plant, dry matter, pod length, seeds/pod, 100-seed weight and grain yield and were statistically analyzed using SAS software 2002 version. LSD test at 5% degree level was used to compare mean difference among genotypes. Heritability estimates were obtained using the formula given by Allard (1999) as the ratio of the genotypic variance (∂^2g) to the phenotypic variance (∂^2ph), Pearson correlation coefficient was used to determine relationship of plant characters. Genetic parameters such as were computed according to Singh and Chaudhary (1979) while genetic advance was calculated as described by Johnson *et al*. (1955)

Results and Discussion

The mean squares of various traits (Table 1) indicated that there were significant differences among the genotypes observed in plant height, 50% flowering, 50% maturity, dry matter, pod length, seeds/pod, 100-seed weight, and grain yield. Similarly, replicates revealed significant effect for all character which indicated that there were wide differences among the genotypes investigated. The results in this study corroborate those of Omoigui *et al* (2005) and Zafar *et al* (2008) that there existed a wide range of genotypic variability in the characters studied for cowpea.

Table 1. Mean squares of 5 soybean genotypes for eleven characters grown at Lake Gario in -2010/2011

	PH	D50%F	D50%M	NBP	NNP	NPP	DM	PL	SP	100SW	GY
Genotype	13.64*	7.78**	38.9**	27.10	24.67	16.77	85.77*	0.41*	0.12*	60.19*	402.06*
Replicate	19.76*	0.87*	0.80*	149.07*	123.8*	84.87*	301.07*	0.23*	0.15*	30.11*	272.44*
Error	13.17	0.87	0.55	34.15	30.97	33.87	73.82	0.01	0.05	10.91	89.13
CV(%)	14.96	2.08	0.83	35.49	37.10	50.46	35.02	7.85	8.73	90.24	31.37*

* Significant at 0.05 probability level

Key: PH= plant height, D50%= days to 50% flowering, D50%M= days to 50% maturity, NBP= number of branches per plant, NNP= number of nodes per plant, NPP= number of pods per plant, DM= dry matter, PL= pod length, SP= seeds per pod, 100Sw= 100 seeds weight GY= grain yield.

Table 2. Reveals that plant height had a close range of 22.13-27.01 cm, days to 50% flowering range from 42.60- 48.40 while dry matter ranges from 18.39-34.78. For number of branches per plant, a range of 12.99-20.33 was obtained. The result in this study is at variance with those of Malik *et al*. (2006) who reported a range of 4-11. This may however be due to the type of varieties used and the environmental factors. Number of nodes per plant and number of nodes per branch followed the same trend of variability. Nodes/plant ranged from 12.45-19.25. The indeterminate soybean genotypes have been observed to produce more nodes per plant while the determinate genotypes produce fewer nodes per plant (Whigham, 1983).

Table 2. Mean, Ranges and LSD for eleven agronomic characters of five soyabean genotypes grown at Lake Gario, Yola in -2010/2011.

Genotype	PH	D50% F	D50%M	NB/P	NN/P	NP/P	DM	PL	S/P	100SW	G Y
Ex Gerio	23.12	42.60	84.67	13.61	16.22	15.00	25.81	4.46	2.40	14.33	30.22
Barkinladi	21.13	44.50	87.39	18.30	19.25	9.35	23.10	4.50	2.54	17.09	30.993
TGx1945-1F	25.60	45.40	93.77	20.30	12.40	11.29	18.90	3.14	2.30	13.34	20.94
TGx1740-2F	24.39	43.60	89.12	17.24	15.05	13.78	34.70	3.70	2.31	13.30	47.78
TGx1935-3F	27.01	48.40	92.05	12.90	12.08	9.23	20.14	4.45	2.80	16.79	18.82
Mean	24.25	44.90	89.40	16.47	15.00	11.53	24.53	4.05	2.47	14.97	29.75
Range	22.13-27.01	42.6-48.4	87.3-94.23	12.9-20.3	12.4-19.2	9.23-15.0	18.9-34.7	3.7-4.5	2.4-2.8	13.3-16.7	18.8-47.9
LSD	6.03	1.75	1.40	11.0	10.48	10.96	16.18	0.60	0.41	2.61	17.76

The phenological characteristics in respect of days to 50% flowering and 50% maturity showed low range of variations. For days to 50% flowering, a range of 42.6.0-48.40 days was obtained among the genotypes while a range of 87.30-94.23 days was obtained for maturity in the soyabean genotypes. Results in this study for days to flowering is in agreement with those of earlier findings (Malik *et al.*, 2006) and (Ghatge and Kadu, 1993; Malik *et al.*, 2006) for days to maturity. The results in this study agrees with those of Arshad *et al.* (2006) but disagreed with the finding of Malik *et al*. (2006) who had reported profuse number of pods production per plant. However, the low number of pods/plant and pods/branch observed may be due to the magnitude of stress during pod development such as flowering and fruit dropping and genetic background of the genotypes used in this study. 100Seed weight character showed significant variability among the genotypes with a range of 13.30-16.79g. The results are similar to those of Maestri *et al*. (1998) and Arshad *et al*. (2006) who reported ranges of 13.9-20 g and 14.67-25.67 g for 100-seed weight respectively. The partitioning of variance components showed low, moderate and high heritability estimates in the broad sense for the characters (Table 3). High heritability estimates for 50% flowering, 50% maturity, pod length, seeds/pod, seed weight and grain yield (89.9, 98.6, 83.14, 71.46, 76.40 and 82.13%) respectively were obtained. High heritability had been previously reported for these characters (Malik *et al.,* 2006). Moderate heritability effects of 50.8, 53.7, 46.3, 44.2 and 40.5% were observed for plant height, dry matter yield, nodes/branch, nodes/plants and branches/plant. The high heritability estimates together with high genetic advance for days to flowering and seed weight indicate the role of additive gene action which could be explored through selection for improvement in these character.

Table 3. Genotypic, phenotypic and heritability of eleven characters

	PH	D50%F	D50%M	NBP	NNP	NPP	DM	PL	SP	100SW	GY
Vg	13.64	7.78	38.9	27.10	24.67	16.77	85.77	0.41	0.12	6.19	402.06
Vp	26.81	8.65	39.45	61.25	55.64	50.64	159.59	0.51	0.17	8.10	491.19
GCV	15.23	6.21	6.97	31.60	33.11	35.51	37.75	15.81	14.02	16.12	67.40
PCV	21.35	6.55	7.02	47.51	49.72	61.71	51.50	24.69	16.69	19.01	74.49
H^2 (%)	50.8	89.94	98.61	44.24	44.34	33.12	53.74	80.39	70.59	76.42	81.85
GA	5.43	6.06	12.76	7.13	6.81	4.86	13.99	1.18	0.6	4.49	37.37

Key: PH= plant height, D50%= days to 50% flowering, D50%M= days to 50% maturity, NBP= number of branches per plant, NNP= number of nodes per plant, NPP= number of pods per plant, DM= dry matter, PL= pod length, SP= seeds per pod, 1000Sw= 1000 seeds weight GY= grain yield Vg = genetic variance, Vp= phenotypic variance, GCV= genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H^2 = heritability(broad sense), GA= genetic advance.

The estimates of genotypes and phenotypic coefficients of variation (GCV and PCV) as percent of character means (Table 3) revealed wide variability. Generally, PCV is higher than GCV, except for days to flowering and maturity that showed close variation. GCV values ranged from 6.97 (maturity) to 67.40 (grain yield) while PCV ranged from 6.55 (flowering) to 74.49 (grain yield). This suggests that environmental factors affected the characters. The interrelationship among quantitative characters studied is shown in Table 4. Generally, significant positive relations existed between most of the characters. Grain yield positively associated with number of branches/plants, pod/plant, dry matter, pods length, seeds/pod and seed weight with (r= 0.752*, 0.69*, 0.49*, 0.53*. 0.97* and 0.82*). The positive significant correlation observed in this study agreed with the finding of Oz *et al.* (2009). This suggests that selection based on these characters are good potentials for improvement.

Significant positive associations were found for plant height with days to flowering (r=0.823*). There was positive significant correlations of plant height and days to flowering with maturity (r-0.98* and 0.63*) respectively. Pod length significantly associated with all characters except for plant height and dry matter. Seeds/pod correlated with plant height 0.63*, days to flowering 0.78* dry matter 0.56*and pod length 0.581* while 100- seed weight correlated with flowering 0.61* days to maturity 0.67* and seeds/pod 0.93. The results agreed with the finding of Idahosa *et al*. (2010) who found that seeds/pod associated with flowering and 100-seed weight in cowpea.

Table 4. Correlation coefficients (r) for Eleven agronomic characters in five soybeans genotypes

Character	PH	D50%F	D50%M	NBP	NNP	NPP	DM	PL	SP	100SW	GY
PH	1.00										
D50%F	0.82*	1.00									
D50%M	0.98*	0.63*	1.00								
NBP	0.21	0.17	0.63*	1.00							
NNP	0.39	0,71*	0,60*	0,00	1.00						
NPP	0.28	0.18	0.60	0.00	0.00	1.00					
DM	0.12	035	0.25	0.5*	0.25	0.37	1.00				
PL	0.26	0.24*	0.98*	0.93*	0.90*	0.9*	0.49	1.00			
SP	0,63*	0.78*	0.35	0.31	0.21	0.21	0.56*	0.58*	1.00		
1000SW	0.12	0.61*	0.67*	0.37	0.35	0.40	0.39	0.05	0.93*	1.00	
GY	0.252	0.244	0.235	0.752*	0,403	0.691*	0.49*	0.53*	0.97*	0.82*	1.00

* Significant at 5% probability level

KEY: PH= plant height, D50%= days to 50% flowering, D50%M= days to 50% maturity, NBP= number of branches per plant, NNP= number of nodes per plant, NPP= number of pods per plant, DM= dry matter, PL= pod length, SP= seeds per pod, 100Sw= 100 seeds weight GY= grain yield.

Conclusion

The results from this research have shown that enough variability and genetic heritability exist in the studied traits among the tested soybean genotypes. High mean values for yield and its components taits, high genotypic coefficients of variation, high heritability and genetic advance coupled with high genotypic and phenotypic positive significant association among yield and yield contributing traits warrants effective selection for further improvement. This study identified genotypes TGx1740-2F and Barkinladi for further genetic studies based on the highest seed weights and high number of seeds per plant.

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