GENETIC VARIABILITY, HERITABILITY AND CORRELATION AMONG SOYBEAN [*Glycine max*. (L.) Merrill] VARIETIES

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ABSTRACT
The study was conducted at Teaching and Research Farm, Faculty of Agriculture, Bayero University, Kano (Lat 11^{0}59 `N, Long 8$^0$25 `E and 466m above sea level), during 2016 rainy season, to determine the variability, heritability and correlation among the soybean varieties. The treatments consist of eight soybean varieties, laid out in Randomized Complete Block Design (RCBD) and replicated four times; varieties were evaluated for fifteen characters to determine variability, estimate heritability and correlation. Analysis of variance revealed significant difference (P>0.01<0.05) with respect to four characters and highly significant (P≤0.01) four seven characters. The results indicated the presence of substantial variability among the varieties. GCV, PCV, ECV and heritability estimates ranges from 0.000039-169.18, 0.000066-187.55, 0.000053-122.28 and 0-100% respectively, the high Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV) and Environmental Coefficient of Variation (ECV) observed in this study indicated the existence of variability and selection can be done. Whereas high estimate of broad Sense heritability for the tested parameters indicated that these characters were highly heritable and selection can be imposed. Significant phenotypic correlation for GWha and FWha with FWP respectively revealed that, these characters were primarily influenced by their direct contribution to higher yield. It is therefore recommended for an effective selection of those characters could be adopted for cultivar improvement and hybridization program and more research is needed to validate the findings.
 Keywords: Genetic, Heritability , Soybean, Variability

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is a leguminous annual crop belonging to the family Fabaceae. It is an erect bushy plant with a well-defined main stem and branches, with numerous leaves. Soybean is grown primarily for the production of seed and has several uses in the food and industrial sectors (MoFA, 2011). It represents one of the major sources of edible vegetable oil and proteins for livestock feed. Soybean is important in Nigeria for several reasons. In Nigeria, soybean is consumed by humans, animals and it improves soil fertility. It is one of the few legume crops that have the greatest potential to contribute to employment and income generation in rural communities especially if its agro-industrial potentials are exploited. Among the grain legumes, soybean currently ranks third after groundnut and cowpea in terms of production and utilization (MoFA, 2011). According to FAO (2012), total world production at 2010 was 261.6 million metric tonnes. The three major world producing countries are U.S.A (90.6 million metric tonnes), Brazil (68.5 million metric tonnes) and Argentina (52.6 million metric tonnes). The total production in Africa was 1.5 million tonnes with West Africa producing 437,115 metric tonnes. Nigeria is the leading producer in West Africa with 393,860 metric tonnes (FAO, 2012).

According to the Ministry of Food and Agriculture (MoFA), 124,045 metric tonnes of soybean was produced in Ghana in 2010, with an additional import of 200 metric tonnes in that same year (MoFA, 2011). It is a leguminous vegetable of pea family that grows in tropical, subtropical and temperate climates, soybean was domesticated in 11th century BC around northeast of china. It is believed that it might be introduced to Africa in the 19th century by Chinese traders along the east coast of Africa (IITA, 2015). Information on genetic variability and relationships in crop plants are important for efficient selection of parental lines for new crosses and preservation of germ plasm by plant breeders (Tatineni *et al*., 1996). Traditionally, morphological traits have been used to distinguish crop varieties (Chowdhury *et al*., 2001). Genetic variation among traits is important for a crop improvement programme and in breeding or selecting desirable types. Information of variability patterns allows

breeders to comprehend the evolutionary associations among genotypes in a better way, to collect genotypes in a more organized manner, and to make plan to incorporate valuable material in their germ plasm (Bretting and Widrlechner, 1995). variation.

MATERIALS AND METHODS
Description of experimental site and experimental materials
The experiment was conducted at the Research and Teaching Farm, Department of Agronomy, Faculty of Agriculture, Bayero University, Kano (Lat $11^0 59`N$, Long $8^0 25`E$ and 466m above sea level) during 2016 rainy season. The materials used for the experiment were eight soybean varieties sourced from IITA selected based on their higher oil content as well as high yield. Brief descriptions of the varieties are presented in table 1.

Table 1. Description of the Varieties Used for the Research

S/N	VARIETIES	SEEDCOAT COLOUR VARIATION	TEXTURE	SOURCE
1	TGx1987-10F	Pale-green and Yellow	Smooth	IITA
2	TGx1945-1F	Pale, Green, White and Yellow	Smooth	IITA
3	TGx1987-62E	Pale, Green and Yellow	Smooth	IITA
4	TGx1955-4F	White-brown punches, Yellow	Smooth	IITA
5	TGx1448-2E	Light brown and Yellow	Smooth	IITA
6	TGx1835-10E	Green, and Light Yellow	Smooth	IITA
7	TGx1485-1D	Pale-green and white	Smooth	IITA
8	TGx1740	white and light yellow	Smooth	IITA

Land Preparation and Experimental Design
The land used for the experiment was ploughed, harrowed and ridged. An area of $99m^2$ (12m by 8.25) was selected for this study. Eight plots of 2m length each were made and replicated four times. The treatments consisted of eight soybean varieties, laid out in Randomized Complete, Block Design (RCBD) and replicated four times, each plot row consist of 2m long with inter row spacing of 0.75m. Three seeds were planted per hill and later thinned to two plants at intra row spacing of 10m. Weeding was manually carried out using hoe at three and six weeks after sowing. The recommended fertilizer used was 40kg P/ha (single super phosphate per hectare) and 20kg K/ha (muriate of potash per hectare), all recommended agronomic practices were dully fallowed (IITA, 2015). Data were collected for: Number of Days to 50% flowering (NDF), Number of days to 95% at maturity (NDM), Plant height

(PH), Total dry matter (TDM), Total dry matter (kg) per hectare (TDMha), Number of pods per plot (NPP), Number of pods per hectare (NPha), Pod weight (g) per plot (PWP), Pod weight (g) per hectare (PWha), Grain weight (g) per plot (GWP), Grain weight (g) per hectare (GWha), Fodder weight per plot (FWP), Fodder weight (kg) per hectare (FWha), Chlorophyll content (CHL), Harvest index (HI),

Data Analysis
Data collected were subjected to analysis of variance (ANOVA) using SAS software version 9, (2002) and correlation was also determined. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and environmental coefficient of variation (ECV) were calculated according to (sivasubramanian and Menan, 1973) and heritability (H^2) was calculated according to (Johnson *et al.,* 1955).

$$h^2 = \sigma_g^2 / \sigma_{ph}^2 \times 100$$

$$\sigma_g^2 = \frac{M_g - M_e}{r} \quad \text{............................... (1)}$$

$$\sigma_{ph}^2 = \sigma_g^2 + \sigma_{gl}^2 + \sigma_e^2 \quad \text{........................... (2)}$$

$$\sigma_e^2 = \frac{M_e}{r} \quad \text{... (3)}$$

Where: σ_g^2 = Genotypic variance, σ_{ph}^2 = Phenotypic variance, σ_e^2 = environmental variance, r = Replications, M_g = Genotype mean square and M_e = Error mean square.

$$\text{Genotypic coefficient of variation (G.C.V \%)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (P.C.V \%)} = \frac{\sqrt{\sigma_{ph}^2}}{\bar{X}} \times 100$$

Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV) and Genetic Advance(GA) values were classified as low (<10%), moderate (10-20%) and high (>20%) as indicated by (Shukla *et al,* 2006) .

RESULTS
Mean square from ANOVA for yield and other Agronomic traits
Mean square from ANOVA is presented in (Table 2). The results indicated that significant difference (P<0.05) in respect to PH, HI, FWP and FWha. Whereas highly significant difference (P<0.01) for NDF, CHL, NDM, NPP, NPha, PWP and PWha.

GCV, PCV ECV and heritability (H^2) estimate.
Genetic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Environmental coefficient of variation (ECV), and heritability (H^2) estimate are presented in (table 3). The results indicated that GCV ranges from (0.000039-109.18), almost all the characters has the higher GCV with exception of NPha (0.000039), NDM (13.25), and NDF (16.44). PCV ranges from (0.000066-187.55), the results indicated higher PCV with the exception of NPha (0.000066), NDM (13.35) and NDF (17.11). Whereas ECV ranges from (0.000053-122.89) and almost all the characters tested has the higher ECV with the exception of NPha (0.000053), NDM (1.61), NDF (4.75) and PH (16.42). Broad sense heritability estimates ranges from (0-100%), only three parameters expressed moderate heritability TDM (38%), TDMP (38%) and NPha (36%) while the rest recorded highest heritability estimates.

Simple correlation coefficient
Simple Correlation Coefficient among fifteen soybean varieties is presented in (Table 4). The result indicated highly significant positive correlation for GWha with NPP (0.67), NPha (0.67), FWha (0.50), PWP (0.64), PWha (0.64) and GWP (1.00). Whereas negative correlation was recorded with NDF (-0.08) and NDM (-0.16). Significant and highly positive correlation for FWha with NPha (0.42) and PH (0.46) respectively were also observed.

DISCUSSION
Mean square from ANOVA revealed significant (P≤0.05) and highly significant difference (P≤0.01) among the characters measured indicating the presence of substantial variability among the varieties and this is similar to the findings of (IITA 2010) and Similar results were also reported (Rao *et al.*,1976.,1998; Maestri *et al.*, 1998., and Danshiel.,1993) in soybean. The result also indicated that almost all the parameter tested had GCV, PCV, and ECV above (20%) with the exception of NPha (0-10% low), NDM and NDF (10-20% medium) as categorized by (Suvasubrahamanian and Menan, 1973). This revealed the existence of substantial variability and selection can be imposed for further improvements. Similar results were reported by Yavad *et al.*, (2000) and Malik *et al.*, (2007) whereas low and moderate GCV, PCV and ECV revealed low variability.

Majority of the parameters evaluated had higher broad sense heritability (≥60%) with the exception of TDMha, TDMP and NPha (30-60% moderate) as categorized by (Robinson *et al.* (1955). The high estimate of broad sense heritability revealed that the characters could be effectively used for cultivar development and hybridization program Heritable variation is useful for permanent genetic improvement (Singh, 2000). The most important function of heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Dabholkar, 1992; Falconer and Mackay, 1996). Similar findings were also reported (Mohd Rafii *et al.*, 1994 and Ramitake, 2010). Whereas the low and moderate heritability estimate obtained for TDMha, TDMP and NPha indicated that, little progress could be achieved if selection is based on these characters. High heritability estimates for some of the characters indicate less influence of the environment, and so there is a good scope for the improvement of these traits through direct selection (Kumar *et al.,* 2012).

Highly significant positive correlation for GWha with NPP, NPha, FWha, PWP, PWha and GWP revealed that, grain yield per hectares was primarily affected by NPP, NPha, FWha, PWP, PWha and GWP. This indicated that these characters contribute directly to grain yield. Significant correlation recorded for FWha with NPha and PH indicated that, FWha has strong link with PH and NPha. Whereas negative GWha recorded for NDF and NDM indicated that, grain yield per hectare is inversely related to days to 50% flowering and days to 90% maturity. Similar results were reported (Malik *et al.*, 2006 and Rajkumar *et al.,* 2010) but in contrast to the findings of Sharma *et al.,* (1983) who reported that, days to maturity and flowering contributed significantly to grain yield.

CONCLUSION
Conclusively, highly significant mean squares observed in this study indicated the presence of substantial variability among the varieties, the result also indicated that, all the parameters tested had high GCV, PCV and ECV with the exception of NPha, NDM and NDF indicating the existence of variability, therefore, selection can be effectively done. High estimate of broad sense heritability for the parameter tested indicated that, these parameters were highly heritable and therefore selection for these parameters would be effective for cultivar development and hybridization program. Whereas significant positive correlation for GWha and FWha indicated that, GWha and FWha were strongly influenced by parameters tested. However negative correlation recorded for GWh, NDF and NDM, revealed that grain yield per hectare was negatively associated with number of days to 50% flowering and days to 95% maturity. It is therefore recommended that, more research are needed to validates the findings and almost all the characters were highly heritable and therefore selections for these characters would be very effective for cultivar development and hybridization program.

Table 2: Mean square from ANOVA for yield and other agronomic traits

SOV	DF	NDF	PH	CHL	NDM	NPP	NPha	TDMP	TDMha
Variety	7	70.00**	203.50*	323.70**	198.80**	336151.40**	1.50**	0.30	14328869.00
Rep	3	16.3	62.9	183.4	32.3**	18216.0	809597685185	0.1	3049768.5
Error	21								
Total	31								

Key: SOV: Source Of Variation,NDF: Number of Days to 50% flowering, PH: Plan height, CHL: Chlorophyll content, NDM: Number of days to 95% at maturity, NPP: No of pods per plot, NPha: No of pods per hectare,
TDMP: Total dry matter(kg) per   plot , TDMha: Total dry matter (kg) per hectare, HI: Harvest index, FWP: Fodder weight (kg) per plot, FWha: Fodder weight (kg) per hectare, PWP: Pod weight (g) per plot,

SOV	DF	HI	FWP	FWha	PWP	PWha	GWP	GWha
Variety	7	394.50*	0.40*	15586587.30*	120474.00**	5354399.00**	20398.20	906587.30
Rep	3	144.6*	0.0	1653333.3	11734.1	521516.2	2612.5	116111.1
Error	21							
Total	31							

 PWha: Pod weight (kg) per hectare, GWP: Grain weight   (g) per plot, GWha: Grain weight (kg) per hectare
Key: SOV: Source Of Variation, NDF: Number of Days to 50% flowering, PH: Plan height, CHL: Chlorophyll content, NDM: Number of days to 95% at maturity, NPP: No of pods per plot, NPha: No of pods per hectare,
TDMP: Total dry matter(kg) per plot , TDMha: Total dry matter (kg) per hectare, HI: Harvest index, FWP: Fodder weight (kg) per plot, FWha: Fodder weight (kg) per hectare,
PWP: Pod weight (g) per plot, PWha: Pod weight (kg) per hectare, GWP: Grain weight (g) per plot, GWha: Grain weight (kg) per hectare

Table 3: GCV, PCV, ECV and Broad Sense Heritability Estimates.

CRTS	EV	GV	PV	GCV	PCV	ECV	H^2(%)
NDF	5.83	70.00	75.83	16.44	17.11	4.75	92
PH	80.28	203.53	283.81	26.14	30.87	16.42	72
CHL	65.73	323.72	389.45	72.90	79.96	32.85	83
NDM	2.92	198.79	201.71	13.25	13.35	1.61	99
NPP	59991.76	336151.42	396143.18	124.13	134.74	52.44	85
Npha	2.67	1.49	4.16	0.000039	0.000066	0.000053	36
TDMP	0.52	0.32	0.84	95.89	155.34	122.22	38
TDMha	23293154.80	14328869.00	37622023.80	96.39	156.19	122.89	38
HI	110.28	394.47	504.75	87.07	98.49	46.03	78
FWP	0.13	0.35	0.48	159.89	187.25	97.45	73
Fwha	5816216.90	15586587.30	21402804.20	160.05	187.55	97.77	73
PWP	17371.62	120473.99	137845.61	68.71	73.49	26.09	87
Pwha	772071.76	5354399.80	6126471.56	169.18	180.97	64.24	87
GWP	9141.07	20398.21	29539.28	118.39	142.48	79.26	69
GWha	406269.84	906587.3	1312857.14	118.40	142.48	79.26	69

Key: CRTS: Characters, EV: Environmental variation, GV: Genetic variation, PV: Phenotypic variation, GCV: Genotypic coefficient
Variation, PCV: Phenotypic coefficient variation, ECV: Environmental coefficient variation, H^2: Heritability, NDF: Number of Days
To 50% flowering, PH: Plant height, CHL: Chlorophyll content, NDM: Number of days to 95% at maturity, NPP: No of pods per plot, NPha: No of pods per hectare, TDMP: Total dry matter (kg) per plot, TDMha: Total dry matter (kg) per hectare, HI: Harvest index, FWP: Fodder weight (kg) per plot, FWha: Fodder weight (kg) per hectare, PWP: Pod weight (g) per plot, PWha: Pod weight (kg) per Hectare, GWP: Grain weight (g) per plot, GWha: Grain weight (kg) per hectare

Table 4: Simple correlations coefficient among fifteen soybean varieties

	NDF	PH	CHL	NDM	NPP	NPha	TDMP	TDMha	HI	FWP	FWha	PWP	PWha	GWP	GWha
NDF	1														
PH	0.10	1													
CHL	-0.05	0.53**	1												
NDM	0.74**	0.30	0.19	1											
NPP	-0.15	0.30	0.28	-0.10	1										
NPha	-0.15	0.30	0.29	-0.10	1.00**	1									
TDMP	0.22	-0.09	-0.04	0.18	0.10	0.10	1								
TDMha	0.22	-0.09	-0.04	0.18	0.10	0.10	1.00**	1							
HI	0.13	-0.11	-0.33	-0.11	-0.14	-0.14	0.40*	0.40*	1						
FWP	0.10	0.46**	0.32	0.31	0.42*	0.42*	-0.02	-0.02	-0.18	1					
FWha	0.10	0.46**	0.32	0.31	0.42*	0.42*	-0.02	-0.02	-0.18	1.00**	1				
PWP	-0.08	0.45**	0.47**	0.14	0.89**	0.89**	0.03	0.03	-0.28	0.62**	0.62**	1			
PWha	-0.08	0.45**	0.47**	0.14	0.89**	0.89**	0.03	0.03	-0.28	0.62**	0.62**	1.00**	1		
GWP_	-0.08	0.21	0.18	-0.16	0.67	0.67	0.10	0.10	-0.03	0.50**	0.50**	0.64**	0.64**	1	
GWha_	-0.08	0.21	0.18	-0.16	0.67**	0.67**	0.10	0.10	-0.03	0.50*	0.50**	0.64**	0.64**	1.00**	1

Key: NDF: Number of Days to 50% flowering, PH: Plant height, CHL: Chlorophyll content, NDM: Number of days to 95% at maturity, NPP: No of pods per plot, NPha: No
Of pods per hectare, TDMP: Total dry matter (kg) per plot, TDMha: Total dry matter (kg) per hectare, HI: Harvest index, FWP: Fodder weight (kg) per plot, FWha: Fodder
  Weight (kg) per hectare, PWP: Pod weight (g) per plot, PWha: Pod weight (kg) per hectare, GWP: Grain weight (g) per plot, GWha: Grain weight (kg) per hectare

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