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GENETIC CORRELATION AND CHARACTER ASSOCIATION OF COMMON BEAN (*Phaseolus Vulgaris)* IN SUDAN SAVANNA OF NIGERIA

***Shaibu, A. S. and Ossai, A.**
Department of Agronomy, Bayero University, Kano

*correspondence author: asshuaibu.agr@buk.edu.ng

ABSTRACT

Variation is the foundation of crop breeding and its identification is the key to success or failure of any breeding programme. Knowledge about levels and pattern of genetic diversity can be an invaluable aid in crop breeding for diverse application as well as analysis of genetic variability in cultivars. This research was aimed at assessing the genetic correlation and character association of *Phaseolus vulgaris* (common bean) in Sudan Savanna of Nigeria. The materials used were five (5) accessions of *Phaseolus* bean which were laid in a Randomized Complete Block Design and replicated three times. The mean performance of the varieties was determined as well as correlation of the traits measured. The result obtained shows a highly significant genetic diversity among the *Phaseolus* cultivars studied in terms of morphological traits and agronomic performance. The correlation result also shows more of genetic effects than the environment. Hence, selection can be made on the accessions as ample genetic variation exist that could be utilized in the crop improvement.

Keywords*: Common bean; Correlation; Genetic diversity; Savanna;*

INTRODUCTION

Plant genetic resources are seeds and planting materials of traditional varieties and modern cultivars, crop wild relatives and other wild species useful as food, feed, fiber, clothing, shelter and energy. Local communities and researchers rely upon genetic resources to improve the quality and output of food production. When these resources are eroded, humankind loses potential means of adapting agriculture to new socio-economic and environmental conditions. The most significant of this erosion in the recent decades have resulted from the introduction of desirable plant varieties (Vellve, 1993; Clunies-Ross, 1995).

The genus *Phaseolus* has been reported to be of great economic importance in human and animal nutrition. Four species have been domesticated and these includes *Phaseolus vulgaris* (common bean), *Phaseolus lunatus* (lima bean), *Phaseolusacutifolious* (tepary bean), and*Phaseoluscoccineus* (runner bean), out of which *Phaseolusvulgaris* is the most cultivated and studied. *Phaseolusvulgaris* makes up half of the grain legumes consumed worldwide (Broughton *et al*., 2003) and is ranked the third most important grain legume worldwide superseded only by soya bean and groundnut (Stoilova and Berova, 2009). In Eastern and Southern African, it is the second most important source of protein and the fourth in tropical American (Petri *et al.*, 2015). It is also the third most important source of calories after maize and cassava (Wartmann *et al.*, 1998). It is considered one of the best non meat source of iron, providing 23-30% of daily recommended levels of iron from a single serving (Shimelis and Rakshit, 2005) and is also a good source of dietary fiber.

Common bean (*P.vulgaris*) grains represent the most important source of protein source especially for the low income people in Africa and the world at large (Gept *et al.*, 2008). Introduction of these crops in the Sudan Savanna can assist in providing protein source for the growing population. *P. vulgaris* has the ability to thrive well under drought as such will be favorable for the Sudan Savanna. Hence, there is need to assess the genetic variability of *P. vulgaris* species as genetic makeup can affect its symbiotic association with environment and subsequently the yield as well as the growth component.

The objectives of this study were therefore, to assess the performance of *P. vulgaris* in a Sudan Savanna ecology, determine the character association of *P. vulgaris* and assess the heritable variations of some agronomic traits in *P. vulgaris.*

MATERIALS AND METHODS

The experiment was conducted at the Teaching and Research Farm of Department of Agronomy, Faculty of Agriculture, Bayero University, Kano during the 2015 wet season. The materials used for the experiment were five (5) accessions of *P.vulgaris.* The accessions were laid out in a Randomized Complete Block Design (RCBD) with three replications and were planted in a row plot with each plot measuring 4m in length. The seeds were sown at intervals of 20 by 75cm intra and inter row spacing, respectively. The seeds were sown manually with a seed rate of 3 seeds per hole and later thinned to 2 stand/hole after 2weeks of planting.

Data were collected and recorded at different stages of the plant growth which includes; Days to emergence, chlorophyll content, leaf temperature, number of vines, canopy spread, days to flower, days to pod formation, number of pods, pod length, dry pod weight, seed per pod, grain yield and haulms weight. Data collected were analyzed using the PROC GLM statement. The analysis was done using SAS (2015). Replication was considered as a random effect and the accessions were considered as fixed effect.

Phenotypic and genotypic variance

These were calculated according to the formula given by Lush (1940) and Chaudhary and Prasad (1968).

Genotypic variance ($\delta^2 g$) = $\frac{GMS-EMS}{r}$

GMS = genotype mean sum of square,

EMS = error mean sum of square and

r = number of replication

The phenotypic variance ($\delta^2 p$), were estimated as the sum of genotypic variances ($\delta^2 g$) with the error variance ($\delta^2 e$), as given by the following formula,

$\delta^2 p = \delta^2 g + \delta^2 e$

Phenotypic and genotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were calculated by the formula suggested by Burton (1952).

Genotypic coefficient of variation (GCV) $= \frac{\delta g}{m} * 100$

Were δg= genotypic standard deviation and m= population mean

Phenotypic Coefficient of variance (PCV) $= \frac{\delta P}{m} * 100$

Where δp = Phenotypic standard deviation and m= population mean

GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (>20%) as indicated by Siva Subramanian and Menon (1973).

Heritability in broad sense

Heritability in broad sense (h^2) was calculated as a ratio of genotypic variance to the phenotypic variance (Hanson *et al.*, 1956).The heritability percentage was categorized as low (0-20%), moderate (30-60%) and high (>60%) as given by Robinson *et al.* (1949).

RESULTS

Significant differences were observed in days to emergence ($p<0.01$) and canopy spread (at $p<0.05$). Non-significant differences exist among the accessions on the following traits measured; chlorophyll content, leaf temperature, canopy temperature, number of vines and days to flowering (Table 1).The results on the reproductive stage showed in Table 2 reveals a non-significant difference only on number of seed per pod with all the accessions having virtually equal number of seeds on each pod. Highly significant differences exist among the accessions for days to pod formation, pod per plot, pod length, seed yield and haulms weight.

The mean performance of the different accessions is presented in Table 3. There were no significant differences between the accessions for chlorophyll content, leaf temperature, canopy temperature, numbers of vines and days to flowering. However, for canopy spread, the performance was different as the accessions shows significant differences in performance with accession 3having the highest (7.00) followed by accession 5 (6.60), accession 6 (6.47) accession 4 (6.40) and accession 1 having the lowest (6.00).

Table 4 reveals significant differences between the accessions for pod per plant, pod length, yield, haulms weight and dry pod weight. Accession 5 recorded the highest seed yield (9245.46 kgha^{-1}) followed by accession 4 (7516.59 kgha^{-1}) while accession 3 recorded the lowest seed yield (2079.98kgha^{-1}). For haulms weight accession 5 has the highest mean performance (14288.75kgha^{-1}) which was followed by accession 4 (10577.67kgha^{-1}), accession 1 (6681.04kgha^{-1}), accession 3 (2883.30kgha^{-1}) and the least was accession 6 (2797.75kgha^{-1}).

High genetic coefficient of variability (GCV) was observed for number of pods per plant (60.67%), dry pod weight (63.10%), pod length (22.50%), seed yield (50.06%), and haulms weight (62.32). A moderate GCV was observed for days to emergence (14.82%) and low GCV for chlorophyll content (4.67%), leaf temperature (2.15%) and canopy temperature (2.64%) (Table 5).The phenotypic coefficient of variability (PCV) was high for number of pods per plant (64.67%), pod length (23.47%), dry pod weight (86.52%), seed per plant (31.40%), seed yield weight (63.62%) and haulms weight (75.58%). Low PCV were observed for leaf temperature (7.77%), canopy temperature (8.99%), canopy spread (6.48%), days to flowering (4.40%) and days to podding (3.01%). The heritability estimate(Table 5) were high for most of the traits measured but low for chlorophyll content (0.18) leaf temperature (0.07) and canopy temperature (0.08).

The results of correlation between trait due to genotypic effect (Table 6) indicates that most of the traits shows significant correlation ($p<0.05$) with some positively correlated while others negatively correlated. However, a positive significant correlation exists between pod per plant and dry pod weight ($r = 0.98$), dry pod weight and seed yield ($r = 0.99$) and seed yield with haulms weight ($r = 0.98$). Also, a positive significant correlation ($p<0.05$) was observed between leaf temperature and pod per plot ($r = 0.82$) and number of pods per plant and haulms weight ($r = 0.95$).Negative correlation were observed between chlorophyll content and canopy spread ($r = -0.97$), leaf temperature and days to podding ($r = -0.94$) and canopy temperature and seed yield (-0.94).The result for the phenotypic correlation of the traits measured shows a non-significant correlation existing in all the traits except for number of pods per plant and seed weight (0.78), dry pod weight and seed weight ($r = 0.82$), dry pod weight and haulms weight ($r = 0.91$) pod per plant and haulms weight ($r = 0.83$) and seed yield with haulms weight.

DISCUSSION

The highly significant difference in mean squares implied that there is discernable evidence of inherent genetic variability among the *Phaseolus* accessions with respect to days to podding, pod per plot pod length, dry pod weight per hectare. The result of the variance components in this study showed that the genotypic variance was higher than the phenotypic variance in all the traits studied. The magnitude of the genotypic variance for all the yield components were however higher than the environmental variance. This result is in accordance with the report of these authors (Damarany, 1994; Umaharan *et al*., 1997; Ubi *et al*., 2001; Omoigui *et al*., 2006) on *Phaseolus*.

The low environmental influence observed compared to genetic factors suggests that the traits may be under genetic control rather than the environment, hence improvement can be achieved through selection (Vange and Egbe, 2009; Oyiga and Uguru, 2011). The minimum magnitudinal differences in GCV and PCV coupled with high heritability for all the traits studied implied that the traits are mostly governed by genetic factors with little role of environment in the phenotypic expression of these characters. Thus, selection of these traits on the basis of the phenotypic value may be effective. Nausherwan *et al*. (2008) reported that polygenic variation may be phenotypic, genotypic or environmental and the relative values of these three types of coefficients give an idea about the magnitude of the variability.

Also, a replicating effect of results at vegetative stage was seen at reproductive stage which implies that differences and similarities observed at these stages does not alter or changed till maturity which means that selection can be made at any growth stage of the plant as variability at any stage from vegetative to maturity is due to a constant effect.The findings reveals uneven contribution PCV, GCV and heritability on the characters measured by rating as low (0-10%), moderate as (10-20%), and high as (>20) for GCV and PCV indicated by Siva Subramanian and Menon (1973) and low (0-20%), moderate (30-60%) and high (>60%) for heritability as given by Robinson *et al*. (1949). The uneven contributions implies that for breeding purposes adequate selection can be made for different characters and an hybrid with high cumulative improved character can be developed. The significant correlations observed due to genotype more than the environment is a confirmation that the association between traits that exist among the accessions is more of genotypic than the environment which also agrees with the work of Becerra *et al*. (2010) and these variations which help in plant breeding allows for an increase in yield without much influence from the environment.

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Table 1: Mean squares of some vegetative traits of *Phaseolus vulgaris*

Sources	DF	Days to emergence	Chlorophyll content	Leaf temperature (^{0}C)	No of vines	Canopy spread (cm)	Days to Flowering
Replication	2	0.07	188.59	4.32	0.20	0.11	1.07
Accession	4	2.00**	38.17	2.42	0.43	0.39*	1.93
Error	8	0.15	22.80	3.22	0.53	0.07	5.87

*, ** = significant at 5% and 1% level of probability, respectively. DF = degree of freedom

Table 2: Mean squares of some reproductive trait of *Phaseolus vulgaris*

Sources	DF	Days to podding	Pod per plant	Pod length (cm)	Dry pod kgha^{-1}	Seed/ Pod	Yield kgha^{-1}	Haulms weight kgha^{-1}
Replication	2	4.27	2.97	0.10	94203888	0.60	10119676.1	25367004.5
Accession	4	15.23**	39.60**	5.21**	314356916*	0.40	29955455.3**	74730089.4**
Error	8	1.18	1.55	0.19	71323029	0.60	5098980.2	10132473.1

*, ** = significant at 5% and 1% level of probability, respectively. DF = degree of freedom

Table 3: Mean Performance for Some Vegetative Traits of *Phaseolus vulgaris*

Accession	Days to emergence	Chlorophyll content	Leaf temperature	No of vines	Canopy spread (cm)	Days to flowering	Days to Podding
Accession 1	5.00	47.33	23.67	4.67	6.00	60.33	81.00
Accession 3	4.33	46.37	23.27	4.67	7.00	61.33	81.33
Accession 4	6.00	45.23	23.43	4.33	6.40	60.60	82.00
Accession 5	5.00	49.03	25.47	5.33	6.60	60.67	76.33
Accession 6	6.33	54.33	24.33	5.00	6.47	62.00	80.67
SE±	0.22	2.76	1.04	0.42	0.16	0.49	0.63
Level of significance	**	NS	NS	NS	*	NS	**

*, ** = significant at 5% and 1% level of probability, respectively. NS = Non significant

Table 4: Mean Performance for some Reproductive Traits of *Phaseolus vulgaris*

Variety	Pod per plant	Pod Length (cm)	Drypod weight(kgha^{-1})	Seed per pod	Yield (kgha^{-1})	Haulms weight (kgha^{-1})
Accession 1	8.00	8.00	12643.21	2.67	7175.48	6681.04
Accession 3	2.67	2.67	5073.28	2.00	2079.98	2883.30
Accession 4	6.00	6.00	17926.49	2.67	7516.59	10577.67
Accession 5	10.00	10.07	29930.81	2.67	9245.46	14288.75
Accession 6	2.00	2.00	5699.94	3.00	2733.31	2797.75
SE±	0.25	0.78	4875.89	0.45	1303.71	1837.80
Level of significance	**	**	*	NS	**	**

*, ** = significant at 5% and 1% level of probability, respectively. NS = Non significant

Table 5: Estimates of genetic parameters for some traits of *Phaseolus vulgaris*

Characters	VE	VG	VP	GCV	PCV	GCV (%)	PCV (%)	h^2
Days to emergence		0.62	0.77	0.15	0.17	14.82	16.52	0.80
CHLOROPHYLL CONTENT	22.8	5.12	27.92	0.05	0.11	4.67	10.90	0.18
Leaf temperature	3.22	0.27	3.49	0.02	0.08	2.15	7.77	0.07
Number of vines	0.53	0.03	0.56	0.04	0.16	3.80	15.63	0.06
Canopy spread	0.07	0.11	0.18	0.05	0.06	5.03	6.48	0.60
Days to flowering	5.87	1.31	7.18	0.02	0.04	1.88	4.40	0.18
Days to podding	1.18	4.68	5.86	0.03	0.03	2.70	3.01	0.80
Pod per plant	1.15	12.68	14.23	0.61	0.64	60.67	64.67	0.89
Pod length (cm)	0.19	1.67	1.86	0.22	0.23	22.50	23.47	0.90
Seed/plant	0.6	0.07	0.67	0.10	0.31	9.93	31.40	0.1
Seed yield (kgha^{-1})	5098980.2	8285491.7	13384471.9	0.50	0.64	50.06	63.62	0.61
Haulms weight (kgha^{-1})	10132473.1	21532538.77	31665011.82	0.62	0.76	62.32	75.58	0.68

VE = Environmental variation, VG = Genetic variation,VP = Phenotypic variance, GCV = Genetic coefficient of variability, PCV = Phenotypic coefficient of variability, h^2 = Heritability

Table 6: Genotypic (below diagonal) and phenotypic (above diagonal) correlation among some Traits of *Phaseolus vulgaris*

	DTE	CC	LT	DTF	DTP	PPP	PL	DPW	SP	SW	HW
DTE	1	0.23	-0.02	0.04	0.14	-0.24	0.47	0.01	0.37	0.06	0.03
CC	0.35	1	0.01	0.49	-0.14	-0.22	-0.37	-0.27	0.27	-0.29	-0.15
LT	0.23	0.06	1	-0.13	-0.31	0.35	-0.10	0.51	0.01	0.32	0.39
DTF	-0.26	0.09	0.85*	1	-0.18	-0.52	-0.44	-0.38	0.37	-0.47	-0.47
DTP	0.06	-1.71	-0.94*	0.13	1	-0.60	0.23	-0.57	-0.16	-0.43	-0.29
PPP	0.16	-0.5	0.82*	-0.89*	-0.72	1	0.21	0.82**	0.06	0.78**	0.79**
PL	-0.67	-0.46	-0.53	-0.01	0.41	0.19	1	0.32	0.15	0.44	0.41
DPW	0.01	-0.29	0.78	-0.85*	-0.91	0.98**	0.33	1	0.24	0.83**	0.91**
SP	0.14	0.03	0.66	-0.82*	-0.11	0.25	0.29	0.02	1	0.33	0.32
SW	0.01	-0.45	0.61	-0.17	-0.59	0.07	0.52	0.99**	0.06	1	0.88**
HW	-0.08	-0.05	0.77	-0.95*	-0.73	0.95**	0.51	0.05	-0.14	0.98**	1

*, ** = significant at 5% and 1% level of probability, respectively.

KEY: DTE: days to emergence
LT: Leaf Temperature
DTF: Days to Flowering
PPP: Pod per Plant
DPW: Dry Pod Weight
CC: Chlorophyll content
SW: Seed Weight
HW: Haulms Weight
DTP: Days to Podding
PL: Pod Length
SP: Seed per Pod