

**INTERNATIONAL JOURNAL OF ADVANCES IN  
PHARMACY, BIOLOGY AND CHEMISTRY****Research Article****Genetic diversity and variability studies of advanced  
breeding lines of Pigeonpea (*Cajanus cajana*. L)****Niranjana Kumara B\*, Dharmaraj P S, Vijaya B Wali.**

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**ABSTRACT**

An investigation was carried out in the experimental field located at Agricultural Research Station, Gulbarga, University of Agricultural Sciences, Raichur during *kharif* 2012-13 to study the genetic diversity, genetic variability and correlation on various morphological traits, yield and yield related components of Pigeonpea. The experiment was laid out with randomized complete block design involving nineteen advanced breeding lines of Pigeonpea with three replications. The range for days to 50 per cent flowering, days to 80 per cent pod maturity, plant height, number of pods per plant, 100 seed weight, seed yield per plant and seed yield per hectare was 109 to 119 days, 102 to 154 days, 116.8 to 188.2cm, 37.4 to 216.2 pods per plant, 8.17 to 11 g, 20.4 to 45.8 g, 314.78 to 1203.6 kg/ha respectively. Genotypes were grouped in to three clusters, based on various morphological traits, yield and yield related components, which indicated the presence of appreciable amount of genetic diversity. The seed yield per ha was the largest contributor (41.03 per cent) followed by number of pods per plant (34.11 per cent) and pod bearing length (27.52 per cent) towards the divergence. All the nineteen advanced breeding lines of Pigeonpea show moderate to high heritability and Genetic advance as per cent mean. At the phenotypic level, the correlation seed yield had shown the positive and significant association with the other component traits like number of primary branches per plant, secondary branches, and 100 seed weight which reveals that selection based on these traits would ultimately improve the seed yield.

**Key words:** Genetic advance, Heritability, Correlation, Pigeonpea, Seed**INTRODUCTION**

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], is one of the grain legume crop of rain-fed agriculture in the semi-arid tropics belongs to member of family *Fabaceae* and it is invariably cultivated as annual crop. Pigeonpea is an often cross pollinated (20-70%) crop with  $2n = 2x = 22$  diploid chromosome number. India is considered as the native of pigeonpea (Van der Maesen, 1980) because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country. Pigeonpea is a hardy, widely adapted, and drought tolerant crop. It has a wide range of maturity which helps in its adaption in a wide range of environments and cropping systems.

Information on the nature and magnitude of genetic diversity present in the genotypes is a pre-requisite. Parents to be selected on the basis of combining ability

and F1 heterosis for developing high yielding varieties through hybridization. Literature available on the nature and magnitude of genetic diversity in pigeonpea crop indicates that the studies in this kind are scanty and not properly documented. Therefore, an attempt in the present investigation was made to study the degree of genetic diversity, genetic variability and correlation in set of 19 genotypes collected in ARS Gulbarga.

**MATERIAL AND METHODS**

An investigation was carried out in the experimental field in Agricultural Research Station, Gulbarga, University of Agricultural Sciences, Raichur During *kharif* 2013. The experimental material consisted 19 breeding lines of pigeon pea including local checks for yield and other agronomic characters. The

genotypes are GRG-811, GPHR-08-11, GRG-2009, GRG-2010, GRG-2012, GRG-818, GRG-822, IPPF-C43, JKM-197, TARA, VIPUL, PKV-TARA, BSMR-853, GRG-109, GRG-107, GRG-825, MARUTI (Local Check), ASHA (LC), TS-3R (LC).

Total rainfall at the site between the months of June to December was 450mm in the year 2013. The soil type is Medium black. The latitude, longitude and mean sea level is 17° 19' N, 76° 54' E, 459 m respectively. This location is situated under North eastern dry zone of Karnataka. The experiment was laid with 6 rows of each genotypes having 5 metres of row length was maintained. The spacing adapted was 90 centimetres between rows to rows and 30 centimetres between plants to plants. Recommended package of practices were followed to attain a good crop stand. Five competitive plants were randomly selected for recording observations on each genotype. The following data were collected Days to 50% flowering, Days to 80% pod maturity, Plant height (cm), Number of primary branches per plant, Number of secondary branches per plant, Pod bearing length (cm), Number of pods per plant, Number of seeds per pod, Hundred seed weight (g), Seed yield per plant (g) and Seed yield per hectare (kg ha<sup>-1</sup>). All data collected were analyzed using IDOSTAT software version 9.1. Following Standard Analysis of Variance procedure, whenever difference between treatment means were significant, means were separated by F-LSD at P = 0.05. Those principal components with eigenvalues > 1.0 were selected. Correlation values between the original characters and the respective principal components were obtained by multiplying the square root of the eigen value for each component by the eigen vector of each of the characters evaluated. To select the relevant characters, those correlation values = 0.6 were considered as relevant for that principal component 4. The data were also subjected to K-means non-hierarchical clustering analysis. Phenotypic coefficient of variation (PCV), broad sense heritability and genotypic coefficient of variation (GCV) were computed following the procedures of Burton and De Vane, Expected genetic advance from selection was established using the formula by Allard, at 5% selection intensity. Phenotypic linear correlation coefficient was calculated for all possible comparisons using the formula suggested by Al-Jibouri *et al.* The data was analysed by using the SPSS software for correlation studies.

## RESULTS AND DISCUSSION

The average performances of the nineteen pigeon pea genotypes are shown in the Table 1. The characters of genotypes varied significantly for all the traits

studied. Days to 50% flowering, Days to 80% pod maturity varied between 109-119 and 102-154 days respectively. Also, plant height primary, secondary branches are varied from 116.8-188.2 cm, 7-28 and 6-18 respectively. Moderately variation was observed with respect to 100 seed weight and seed yield per plant and number of seeds per pod varied from 8.8-12.1 and 3.8-4.0 respectively. The greatest variation observed with respect to seed yield per hectare, number of pods per plant and pod bearing length varied from 1469-2095.3 kg ha<sup>-1</sup> 37.4-216.2 and 7.6-44.6 respectively.

The genetic, phenotypic and heritability variances are shown in table 2. Generally the phenotypic variance was higher than genotypic variance. Considerable Genetic variability was observed among the advanced genotypes, Pod bearing length, Days to 50 per cent flowering, Days to 80 per cent pod maturity, Yield per plant (g) and Yield kilogram per hectare were recorded high heritability (above 65.00%) and remaining traits show moderate heritability. Genetic advance as percent mean was high in Pod bearing length, Number of pods per plant, Yield per plant (g) and Yield kilogram per hectare and remaining traits show Low to Moderate Genetic advance as percent mean.

The phenotypic correlations between all the pairs of characters studied are presented in Table 3. The correlation coefficients for some of the characters revealed the presence of strong positive association between dry grain yield (kg ha<sup>-1</sup>); Dry grain yield showed significant positive association with number of pods per plant, number of primary branches and pod bearing length.

Also, dry grain yield positively correlated with number of secondary branches and number of seeds per pod. The results also revealed that negative correlation with the days to 50 per cent flowering and day's maturity.

The variation observed from the traits studied showed adequate variability in the germplasm. The greatest variation was observed in number of pods per plant phenotypic coefficient of variability and genotypic coefficient of variability. The minimum pods per plant were 37.4 with the maximum value of 216.2 pods per plant. Seeds per pod and dry grain yield also varied significantly among the genotypes. Since knowledge of the existing genetic variation of the various yield contributing characters are essential for developing high yielding genotypes<sup>1</sup>, the observed variation in this work will enhance the genetic improvement of the crop for any of the characters evaluated. The high value of genotypic and phenotypic variation suggest that there is good scope for yield improvement through selection for

Pods/plant, seeds/pod and yield/plant. These findings are in agreement with other reports<sup>2</sup>.

Generally the phenotypic variance was higher than genotypic variance. The environmental variance was, however, low. This indicates that environmental influences were low compared to genetic factors in the variability observed indicating that the traits have broad genetic base hence improvement can be achieved through selection. The phenotypic coefficient of variability and genotypic coefficient of variability were relatively high. Genetic variability was observed among the advanced genotypes, Pod bearing length, Days to 50 per cent flowering, Days to 80 per cent pod maturity, Yield per plant (g) and Yield kilogram per hectare and remaining traits show moderate heritability. High heritability coupled with high genetic advance indicates the predominance of additive gene effect<sup>3,4</sup>.

The above discussion clearly shows wide variation from one cluster to another in respect of cluster means for eleven characters, which indicated that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in Pigeonpea<sup>5</sup>.

The correlation coefficients for some of the characters revealed the presence of strong positive association between dry grain yield; Dry grain yield showed significant positive association with number of primary branches. Also, dry grain yield had positive correlation with number of pods per plant and plant height. Significant positive correlation between number of pods per plant and yield<sup>6</sup>. The highest and positive direct influence of pods/plant on yield indicated that it is an important yield component. These results are also corroborated with the pods/plant was an important trait in yield component in pigeon pea.

Significant and positive phenotypic association between grain yield and other yield variables are quite desirable in plant breeding, because it facilitates the selection process. The results also revealed the presence of significant negative relationship between dry grain yield and days to 50% flowering and days to maturity. Praveen Pandey et al., reported significant negative correlation of days to 50% with yield in green gram<sup>8</sup>. Days to maturity had significant negative correlation with pod length, dry pod weight and significant positive correlation with number of branches.

#### Cluster analysis

A dendrogram was obtained by INDOSTAT using a total of 11 qualitative traits. Nineteen genotypes irrespective of their source were grouped in a single large cluster (fig.1). 'GRG-2012' was the most diverse genotype among the tested genotypes; further other genotypes also were genetically diverse for the component traits and could be useful genetic resources. Genetic drift and selection in different environments have caused genetic diversity than the geographical distance as suggested by earlier studies in cluster bean (9, 10).

#### CONCLUSION

This investigation suggested hybridization programme between the genotypes of distinct group to obtain superior genotypes from the segregating generation to overcome the yield constraints in *khariif* Pigeonpea. The variability among the genotypes also will help to select the parents for hybridization. The selection combined yield related traits will reduce the more breeding work therefore suggested that yield correlated traits selection with respective genotypes.

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**Table: 1 Mean, Range, Minimum, Maximum, Standard deviation (SD) and Coefficient of variability (C V %) of characters studied in Pigeonpea.**

Characters	Mean	Minimum	Maximum	Range	SD	C V %
Days to 50 per cent flowering	111.44	109	119	17	4.70	0.72
Days to 80 per cent maturity	130.13	102	154	52	19.70	0.68
Plant height (cm)	164.61	116.8	188.2	72.1	15.24	7.05
Primary branches plant <sup>-1</sup>	14.23	7	28	21	3.83	20.25
Secondary branches plant <sup>-1</sup>	1.60	6	18	12	2.33	14.24
Pod bearing length (cm)	17.86	7.60	44.60	37	7.92	18.66
Pods plant <sup>-1</sup>	117.80	37.4	216.2	178.8	35.56	20.91
Grains pod <sup>-1</sup>	3.96	3.8	4	0.2	0.069	1.57
100 seeds weight (g)	9.64	8.17	11	2.83	0.80	12.26
Seed yield per plant (g)	33.96	20.4	45.8	25.4	6.70	8.26
Yield (kg ha <sup>-1</sup> )	727.35	314.78	1203.6	888.80	234.66	7.8

**Table 2: Genetic parameters for pigeon pea at Agricultural research station (Gulbarga)**

	PHT	PB	SB	PBL	NPPP	NSP P	DFP	D 80%M	100S W	YLDP P	KG/HA
Vg	58.82	6.91	2.30	52.4 3	615.22	0.00	22.17	401.54	0.40	41.14	52349.8 3
Vp	106.4 7	15.2 1	5.03	63.5 4	1222.1 0	0.01	22.82	402.32	1.80	49.02	55643.9 1
GCV	4.96	18.4 7	13.0 7	40.5 3	21.06	0.86	4.23	15.40	6.58	18.88	31.46
PCV	6.67	27.4 1	19.3 3	44.6 2	29.68	1.79	4.29	15.41	13.92	20.61	32.43
h <sup>2</sup> (Broad Sense)	0.55	0.45	0.46	0.83	0.50	0.23	0.97	1.00	0.22	0.84	0.94
Genetic Advancement 5%	11.74	3.65	2.11	13.5 5	36.25	0.03	9.56	41.24	0.62	12.11	457.17
Gen. Adv as % of Mean 5%	7.60	25.6 3	18.2 1	75.8 3	30.77	0.86	8.58	31.69	6.41	35.64	62.85
General Mean	154.6 1	14.2 3	11.6 0	17.8 7	117.81	3.96	111.4 5	130.13	9.65	33.97	727.35

PHT (cm) : Plant height,

PB : Primary branches,

SB: Secondary branches,

PBL (cm) : Pod bearing length,

NPPP : Number of pods per plant,

NSPP: Number of seeds per pod,

DFP : Days to 50% flowering,

D 80% M : Days to 80 per cent pod maturity,

100 SW : 100 Seed weight (g),

YPP: Yield per plant (g),

YLD (kg ha<sup>-1</sup>) : Yield kilogram per hectare,**Table: 3. Phenotypic correlation coefficients among 11 different quantitative traits in 19 genotypes of pigeonpea (*Cajanus cajan*)**

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	1.00	-0.262	-0.181	0.044	0.157	0.119	0.038	0.376	0.371	0.163	0.211
X2		1.00	0.221	-0.210	0.030	0.000	-0.240	-0.288	0.041	-0.076	-0.079
X3			1.00	0.339	0.278	0.317	0.038	-0.423	-0.176	0.117	0.362
X4				1.00	0.541*	0.524*	-0.371	-0.598*	-0.173	-0.473	0.354
X5					1.00	0.029	-0.243	-0.452	-0.167	-0.182	0.826**
X6						1.00	-0.044	-0.237	0.249	-0.285	0.086
X7							1.00	0.554*	0.240	0.314	-0.003
X8								1.00	0.336	0.425	-0.236
X9									1.00	0.065	0.018
X10										1.00	0.144
X11											1.00

\* - Significant at 5 per cent \*\* - Significant at 1 per cent

X1=====Plant height

X2=====Primary Branches

X3=====Secondary branches

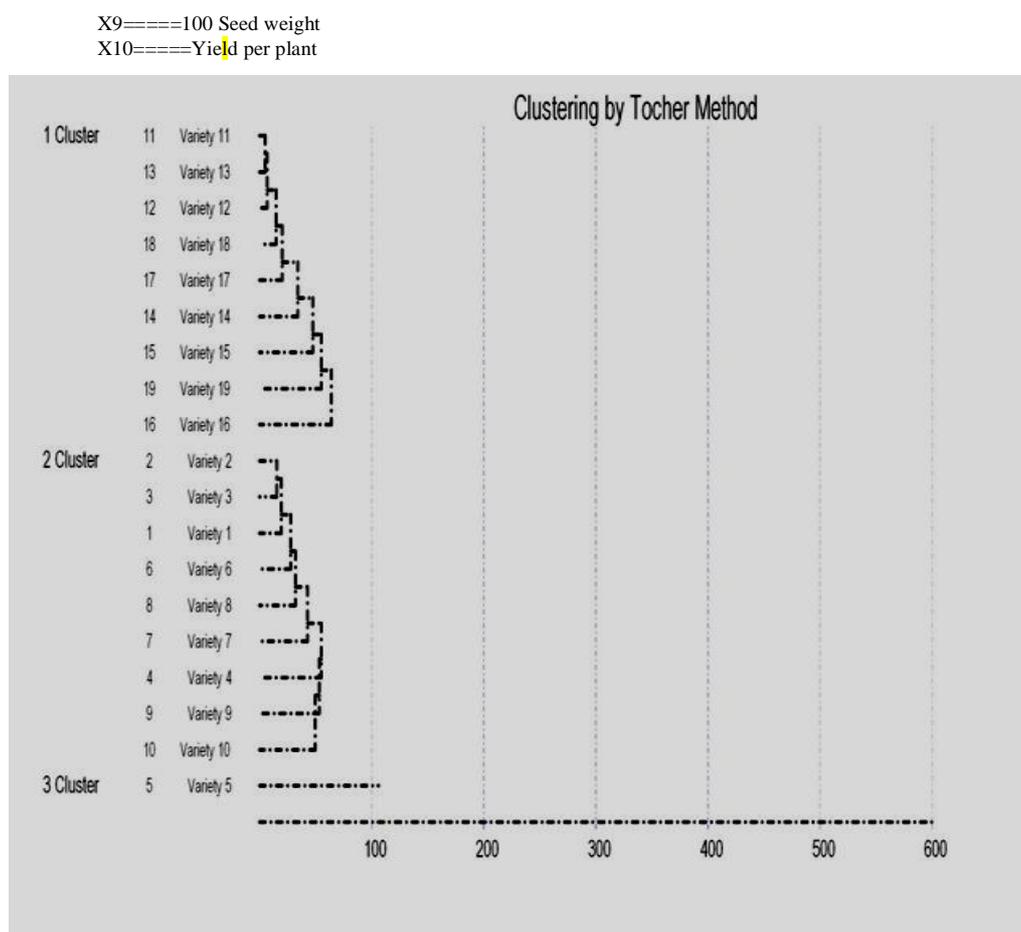
X4=====Pod bearing length

X5=====No. of pods per plant

X6=====No. of seeds per pod

X7=====Days to 50 percent flowering

X8=====Days to 80% pod maturity



**Fig1: Clustering by toucher method.**

**Table 4. Per cent contribution of characters towards genetic diversity.**

Sl.No.	Characters	Contribution %
1	Yield ( $\text{kg ha}^{-1}$ )	38.03
2	Pods $\text{plant}^{-1}$	14.11
3	Days to 80 per cent maturity	15.82
4	Plant height (cm)	4.21
5	Pod bearing length (cm)	22.8
6	100 seeds weight (g)	0
7	Days to 50 % flowering	5.03

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