# Genetic diversity, variability and correlation studies in advanced genotypes of Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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## ABSTRACT

Field experiment was conducted at Agricultural Research Station, Raddewadgi, University of Agricultural Sciences, Raichur during *kharif* 2012-13 to study the genetic variability, genetic diversity and correlation on various morphological traits, yield and yield related components of Pigeonpea. The experiment was laid out with randomized complete block design involved nineteen advanced breeding lines of Pigeonpea with three replications. The range for plant height, 50 per cent flowering, number of pods per plant, number of grains per pod, 100 seed weight, seed yield per plant and seed yield per hectare were 124.80 to 164.40cm, 105.60 to 121.00 days, 137.40 to 194.80pods per plant, 3.30 to 4.00 grains per pod, 8.80 to 12.10 g, 34.90 to 54.90 g, 1469.00 to 2095.30kg/ha respectively. They were grouped in to nine 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 (39.03 per cent) followed by number of pods per plant (31.11 per cent) towards the divergence. All the nineteen genotypes 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 pods per plant, secondary branches, 100 seed weight, and days to 80 per cent maturity which reveals that selection based on these traits would ultimately improve the seed yield.

Keywords: variability, diversity, correlation, Pigeonpea, genetic advance

### **INTRODUCTION**

Pigeonpea (*Cajanus cajan* L.) is an leguminous crop grown in about 50 countries in tropics and subtropics. The major pigeonpea producing areas in the world are India, Eastern Africa, Central and South America, the Caribbean and West Indies, India with a total area of 36.3 lakh hectares and an average yield of 760.33 kg/ha produces nearly 92% of the world's entire pigeon pea crop, though the average seed yields are relatively low, the crop can yield 1600-2900 kg/ha under favourable management. It is mainly cultivated for its dry seeds and green vegetables in dry areas of the tropics and sub tropics. The bright colour of pigeon pea flowers were attracted by number of insects which affect cross fertilization with the average out crossing up to 20% (often cross pollinated crop).

Pigeon pea is highly proteinaceous and the seeds can be prepared into various meals and served as substitute for cow pea. It also provides fuel wood and fodder for the small scale farmer in subsistence agriculture in India. The success of recombination breeding depends on parental diversity to obtain progressive segregants. Yield is one of the complex characters controlled by several interacting genotypic and environmental factors. There are quite few yield components which are less complex, highly inherited and less influenced by the environmental changes. Determination of genetic diversity of any given crop species is necessary for improvement of the crop because it generates baseline data to guide selection of parental lines and design of breeding scheme. In the present study, the genetic variation among Pigeon pea genotypes was studied and diversity analysis for improvement of the crop yield based on the available breeding strategies for selection of parental lines. In plant breeding, correlation studies help us to know the association prevailing between highly heritable characters and give a better understanding of the contribution of each trait in the genetic makeup of the crop.

### MATERIALS AND METHODS

The field experiment was conducted during the *Kharif* season 2012 at Agriculture Research Station Raddewadgi, University of Agricultural Sciences, Raichur. 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  $17^{\circ}$  1' 0" N,  $76^{\circ}$  46' 0" E, 393m 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 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-LSDat 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 earlier.

#### **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 93-121 and 143-177.3 days respectively. Also, plant height primary, secondary branches are varied from 116.2-175.1 cm, 10.4-19.3 and 5.8-16.2 respectively. Moderately variation was observed pod bearing length, number of pods per plant and number of seeds per pod was varied from 22.2-52.9, 137.4-194.8 and 3.3-4.0 respectively. The greatest variation observed with respect to 100 seed weight and seed yield per plant and yield per hectare varied from 8.8-12.1 gm, 34.9-54.9 gm and 1469-2095.3 kg ha<sup>-1</sup> 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, Number of pods per plant, Number of seeds per pod, Days to 50% flowering,100 Seed weight (g), Yield per plant (g) and Yield kilogram per hectare were recorded high heritability (above 60.00%) and remaining traits show moderate heritability. Genetic advance as percent mean was high in Secondary branches, 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.

Table 1. Mean, range, minimum, maximum, standard deviation (SD) and coefficient of variability (CV %) of characters studied in Pigeonpea.

Characters	Mean	Minimum	Maximum	Range	SD	CV %
Davia to 50 non cont flowering	110.22	02	121	28.00	6.24	2.12
Days to 50 per cent nowering	110.55	93	121	28.00	0.24	2.15
Days to 80 per cent maturity	162.44	143	177.3	34.30	10.16	8.42
Plant height (cm)	154.61	116.2	175.1	58.90	13.39	4.46
Primary branches plant <sup>-1</sup>	12.92	10.4	19.3	8.90	2.11	16.67
Secondary branches plant <sup>-1</sup>	10.79	5.8	16.2	10.40	2.65	11.51
Pod bearing length (cm)	35.68	22.2	52.9	30.70	7.75	17.85
Pods plant <sup>-1</sup>	163.78	137.4	194.8	57.40	15.53	19.65
Grains pod <sup>-1</sup>	3.75	3.3	4.0	0.70	0.19	5.80
100 seeds weight (g)	10.36	8.8	12.1	3.30	1.00	2.52
Seed yield per plant (g)	48.3	34.9	54.9	20.00	5.52	22.9
Yield (kgha <sup>-1</sup> )	1841.9	1469	2095.3	626.30	156.81	10.95

Table 2. Genetic parameters for pigeon pea at Agricultural Research Station (Raddewadgi).

Parameters	PHT	PB	SB	PBL	NPPP	NSPP	DFF	D 80%M	100SW	YLDPP	KG/HA
Vg	145.75	3.03	4.37	46.51	754.68	0.04	37.06	103.42	0.90	92.16	42439.46
Vp	246.06	7.67	8.65	87.10	931.71	0.06	42.59	246.24	0.97	112.39	51755.44
GCV	8.49	13.47	16.03	19.11	16.77	5.33	5.52	6.26	9.15	19.84	11.18
PCV	11.04	21.43	22.55	26.15	18.64	6.53	5.92	9.66	9.50	21.91	12.35
h2(Broad Sense)	0.59	0.40	0.51	0.53	0.81	0.66	0.87	0.42	0.93	0.82	0.82
GA 5%	19.07	2.28	3.09	10.19	50.93	0.33	11.70	13.58	1.89	22.60	384.29
GA as % of Mean 5%	13.41	17.66	23.70	28.55	31.09	8.88	10.60	8.36	18.21	46.70	20.86
General Mean	142.13	12.92	13.04	35.68	163.78	3.75	110.33	162.44	10.36	48.39	1841.98

GA - Genetic Advancement, 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, DFF: 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.

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 and number of primary branches. 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 phenotypic coefficient of variability and genotypic plant. The minimum pods per plant were 42 with the maximum value of 668 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 [1], 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 [2].

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	X10	X11
X1	1.000	0.659**	0.164	0.292	0.179	-0.389	0.241	-0.044	0.034	0.319
X2		1.000	0.096	0.253	0.372	-0.569	0.113	-0.180	0.136	0.064
X3			1.000	0.732**	0.098	0.127	0.003	0.237	-0.213	0.334
X4				1.000	0.352	-0.401	-0.193	-0.066	-0.076	0.425
X5					1.000	-0.611	0.010	0.024	0.334	-0.104
X6						1.000	0.231	0.294	0.000	0.005
X7							1.000	0.547*	0.183	-0.104
X8								1.000	0.036	-0.296
X9									0.290	0.202
X10									1.000	0.037
X11										1.000

\* - Significant at 5 per cent, \*\* - Significant at 1 per cent, X1: Plant height, X7: Days to 50 percent flowering, X2: Primary Branches, X8: Days to 80% pod maturity, X3: Secondary branches, X4: Pod bearing length, X9: 100 Seed weight, X5: Number of pods per plant, X10: Yield per plant, X6: Number of seeds per pod.

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, Number of pods per plant, Number of seeds per pod, Days to 50% flowering,100 Seed weight (g), Yield per plant (g) and Yield kilogram per hectare were recorded high heritability (above 60.00%) and remaining traits show moderate heritability. High heritability coupled with high genetic advance indicates the predominance of additive gene effect (Table 4) [3,4]. 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 [5]. 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 has been observed [6,7]. 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.

Table 4. Percent contribution of characters towards genetic diversity.

Characters	Contribution %
Yield (kgha <sup>-1</sup> )	39.03
Pods plant <sup>-1</sup>	31.11
Days to 80 per cent maturity	20.82
Plant height (cm)	6.21
Pod bearing length (cm)	2.8
100 seeds weight (g)	0
Days to 50 % flowering	0



Figure 1. Clustering by toucher method.

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. It has also been reported significant negative correlation of days to 50% with yield in greengram [8]. Days to maturity had significant negative correlation with pod length, dry pod weight and significant positive correlation with number of branches.

A dendrogram was obtained by INDOSTAT using a total of 12 qualitative traits. Nineteen genotypes irrespective of their source were grouped in a single large cluster (Figure 1). 'GRG-109' was the most diverse genotype among the tested genotypes; further 'GRG-209' and 'GRG-822' 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.

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