

GENETIC ANALYSIS AND ASSOCIATION STUDIES FOR DEVISING AN EFFICIENT SELECTION IN PIGEONPEA

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ABSTRACT

A wide range of variation was observed in a diverse set of 178 pigeonpea germplasm lines for all the studied traits. The GCV and PCV estimates were the highest for seed yield/plot (35.48% and 36.12%) followed by pods/plant (31.57% and 32.58%). The little difference between PCV and GCV indicated their control largely by genetic factors. Seed yield/plot (96.46%), pods/plant (93.89%) and plant height (92.14%) recorded high heritability estimates. The high heritability coupled with high genetic advance recorded for seed yield/plot, pods/plant and primary & secondary branches/plant indicated the predominance of additive gene action controlling these traits and phenotypic selection would be effective. Skewness and kurtosis indicated the governance of primary branches and seed yield by complementary gene interaction with less number of dominant genes. Association studies identified primary & secondary branches/plant, pods/plant and seeds/pod as important yield components and due weightage should be given to these during selection for yield improvement.

Keywords: Correlation, Genetic variability, Kurtosis, Path analysis, Skewness

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], (2n=2x=22) is one of the leading and second most important pulse crop of India after chickpea being cultivated in arid and semi-arid regions of the world (Sharma *et al.*, 2020). Worldwide, India ranks first in pigeonpea cultivation with an area of 5.58 mha and production of 4.29 m tonnes (FAOSTAT, 2020). Eighty-three per cent contribution towards global pigeonpea production is by Asia, while Africa and Americas produce 14.2% and 2.2%, respectively. Being the important source of protein and minerals, this crop has great nutritional as well as economic value distinctively for poor people living in Asia, Africa, South America, Central America and the Caribbean region (Mula and Saxena, 2010). Pigeonpea seeds have 21-25% protein, supplementing energy rich cereals for a proportional diet (Kumar *et al.*, 2016).

Pigeonpea has remarkable contribution in flourishing the Indian agricultural economy but over the last few decades, its productivity has not shown significant increase and remained stagnant around 780 kg ha⁻¹ (Varshney *et al.*, 2012b). The major restrictions for attaining higher yields are lack of genetic variability, absence of an ideal plant type for different cropping systems, low yield potential, poor harvest index, susceptibility to biotic and abiotic stresses and high competition with weeds (Meena *et al.*, 2017). Variability is the fundamental requirement for efficient selection. Standard measures of variability such as range,

variance and standard error were commonly used to assess the variability and gene action. Analysis of Frequency distribution for the traits under study will help in assessing the desirable expression of a particular trait under selection. Breeding for high yield is the utmost requirement for any crop improvement programme. Crop yield is a complex character controlled by polygene's and influenced by environmental factors hence direct selection for yield *per se* would not be effective. Yield is composed of several component characters affecting the yield directly and indirectly. The traits which are highly heritable and show a strong correlation with yield are expected to increase the efficiency of selection. Therefore, it is essential to estimate relative amounts of genetic and non-genetic variability among different characters using various genetic variability parameters like genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability (H) and genetic advance (GA), skewness and kurtosis. Correlation and path coefficient analysis help to identify the real components of grain yield to be considered during selection. Thus, the present study was aimed at genetic analysis of different traits and association of yield and yield contributing characters in a diverse set of pigeonpea germplasm.

MATERIALS AND METHODS

The present study was conducted at Punjab Agricultural University, Ludhiana, India. The Punjab Agricultural University is situated between 30°56'N latitude and 75°52'E longitude at an elevation of 247 m above sea level. The material used for the study

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was comprised of a panel of 178 diverse pigeonpea germplasm lines which includes advanced breeding lines and indigenous collections. These lines were acquired from different institutes viz., Punjab Agricultural University, Ludhiana; CCS Haryana Agricultural University, Hisar; International Crop Research Institute for Semi-Arid Tropics, Patancheru; ICAR-National Bureau of Plant Genetic Resources, New Delhi; ICAR-Indian Agricultural Research Institute, New Delhi; ICAR-Indian Institute of Pulses Research, Kanpur; GB Pant University of Agriculture and Technology, Pantnagar and two released varieties (MN-1 and MN-5) from University of Minnesota, USA. The diverse panel was evaluated under field conditions during *kharif* seasons in 2018 and 2019. The genotypes were planted in a randomized complete block design with two replications in a single row plot of 4 m length with row spacing of 50 cm. The data were recorded on five randomly taken plants from each plot in each replication for plant height (PH), number of primary branches per plant (PB), number of secondary branches per plant (SB), number of pods per plant (PD), number of seeds per 10 pods (SP) and 100-seed weight (SW) at maturity. Observations for days to 50% flowering (DF), days to maturity (DM) and seed yield (YLD) were recorded on plot basis.

The data were subjected to analysis of variance (ANOVA) as per randomized complete block design. Genetic parameters of variability viz., phenotypic and genotypic variance and coefficient of variance (Singh and Chaudhary, 1985), heritability (broad sense), genetic advance as percent of mean (Allard, 1960), phenotypic and genotypic correlation coefficients were estimated using R package of variability. The path coefficients were analyzed according to Dewey and Lu (1959) by using matrix method. Skewness, third degree statistics (K3), Kurtosis, fourth degree statistics (K4) and frequency distribution were estimated using Minitab17 for windows to discern the nature of gene action.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed highly

significant differences among the genotypes for all the traits studied which indicated the existence of sufficient variability and hence desirable improvement can be brought through selection. The phenotypic variance was subdivided into genotypic (heritable) and environmental (non-heritable) components. Relatively higher values of genotypic variance were observed for seed yield/plot followed by pods/plant (Table 2). In the total phenotypic variance, the magnitude of genotypic variance was higher than environmental variance for all the yield components indicating little effect of environment, hence improvement can be achieved easily through careful selection of traits. Similar results were also reported by Tsehaye *et al.*, 2020; Zerfu *et al.*, 2021.

The other genetic parameters such as genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, genetic advance as percent of mean, skewness and kurtosis were presented in Table 2. The GCV which shows extent of genetic variability for the traits studied varied from 3.23% to 35.48% and it was found to be maximum for seed yield/plot (35.48%) followed by pods/plant (31.57%), primary branches/plant (20.85%) and secondary branches/plant (20.71%). The values of PCV were ranged from 4.86% to 36.12% with maximum value of PCV observed for seed yield/plot (36.12%) followed by pods/plant (32.58%), primary branches/plant (24.06%) and secondary branches/plant (23.63%). It was observed that PCV was higher than the respective GCV for all the traits exhibiting the role of environment in total variance. The narrow range of difference between PCV and GCV for pods/plant (31.57% and 32.58%), seed yield/plot (35.48% and 36.12%) and days to maturity (4.52% and 4.86%) explained that these traits are governed largely by genetic factors with little role of environment. GCV indicates the extent of degree of genetic variation but the amount of heritable portion of the total variation can only be determined by the heritability and genetic advance estimates. Heritability in broad sense was estimated to be high for seed yield/plot (96.46%), pods/plant (93.89%), plant height (92.14%), days to 50 % flowering (88.69%), days to maturity (86.27%),

Table 1. Analysis of variance for yield attributing traits in pigeonpea

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Pods/plant	Seeds/10 pods	100 seed-weight (g)	Seed yield/plot (g)
Replication	1	837.40***	740.68***	344.43**	16.51**	27.81*	1671.2**	70.03**	13.06***	4502.1***
Treatments	177	138.44***	84.95***	866.82***	16.89***	32.51***	5924.2***	9.4*	1.05***	17209.5***
Residuals	177	8.30	6.26	35.47	2.4	4.27	186.7	6.72	0.21	310.0
S.E±m	-	2.04	1.77	4.21	1.09	1.46	9.66	1.83	0.32	12.45
CD at 5%	-	5.68	4.94	11.75	3.05	4.08	26.96	5.12	0.9	34.74
CV %	-	9.11	4.69	10.03	22.53	22.22	32.08	6.04	8.94	35.90

*= significance at 0.01, **= significance at .001 and ***= significance at .0001

Table 2. Estimation of genetic parameters for agronomic traits in pigeonpea

Parameter	Range	Mean	Phenotypic Variance	Genotypic variance	Environmental variance	GCV (%)	PCV (%)	Heritability (%)	GA as % of mean	Skewness	Kurtosis
Days to 50% flowering	69.50-112.00	91.33	73.37	65.07	8.30	8.83	9.38	88.69	17.14	0.13	0.04
Days to maturity	111.00-155.50	138.85	45.61	39.35	6.26	4.52	4.86	86.27	8.64	-1.33	3.05
Plant height (cm)	99.83-266.50	207.21	451.15	415.68	35.47	9.84	10.25	92.14	19.46	-1.20	4.28
Primary branches/plant	7.00-24.50	12.91	9.65	7.25	2.40	20.85	24.06	75.11	37.23	0.88	1.03
Secondary branches/plant	10.00-31.50	18.15	18.39	14.12	4.27	20.71	23.63	76.78	37.38	0.23	-0.49
Pods/plant	55.17-342.50	169.64	3055.43	2868.72	186.71	31.57	32.58	93.89	63.02	0.20	-0.68
Seeds/ 10 pods	17.90-44.17	35.82	8.06	1.34	6.72	3.23	7.92	16.62	2.71	-0.59	3.58
100-seed weight (g)	5.74-10.00	8.11	0.63	0.42	0.21	7.99	9.79	66.67	13.44	-0.61	0.14
Seed yield/ plot (g)	82.50-545.00	259.11	8759.74	8449.75	309.98	35.48	36.12	96.46	71.78	0.71	0.11

moderate for primary branches/plant (75.11%), secondary branches/plant (76.78%) and 100-seed weight (66.67) while seeds/pod recorded low estimates of heritability. High estimates of heritability indicated that improvement through selection for these traits would be rewarding. Similar results were also reported by Patel and Patel (1998), Linge *et al.* (2010) and Saroj *et al.* (2013). Heritability suggests the effectiveness of selection on the basis of phenotypic performance only; it does not indicate the genetic progress for selecting best individuals. Heritability estimates in association with the genetic advance were observed to be more useful for effective selection (Johnson *et al.* 1955). The high heritability accompanied with high genetic advance was recorded for seed yield/plot followed by pods/plant, primary and secondary branches/plant. It indicated that these traits are governed largely by additive gene action and selection based on phenotypic performance would be quite effective. However, days to 50% flowering and days to maturity had high heritability but low genetic advance indicating role of non-additive gene effects and direct selection would not be effective for the trait and for these traits, early generation intermating will be useful.

The nature of gene action and the number of genes controlling the traits is revealed through the study of distribution using skewness and kurtosis (Govintharaj *et al.*, 2018). Positive skewness is associated with complementary gene action while negative skewness is associated with duplicate (additive × additive)

gene interactions (Venkatesha *et al.*, 2016). Genes controlling the traits with skewed distribution tend to be dominant whether they are exerting increasing or decreasing effect on the trait. Kurtosis is less than zero or negative (Platykurtic) in the absence of gene interaction and greater than zero or positive (Leptokurtic) in the presence of gene interaction. The traits with leptokurtic and platykurtic distribution are said to be controlled by fewer and many genes, respectively. Days to 50% flowering, primary branches/plant, secondary branches/plant, pods/plant and seed yield/plot were found to be positively skewed indicating complementary gene action, whereas days to maturity, plant height, seeds/pod and 100-seed weight were negatively skewed suggesting duplicate gene action. Traits like days to 50% flowering, secondary branches/plant and pods/plant showed platykurtic distribution as the value of kurtosis was less than zero or negative. Whereas days to maturity, plant height, primary branches/plant, seeds/ 10 pods, 100-seed weight and seed yield/plot showed leptokurtic distribution as the value of kurtosis was greater than zero or positive indicated the presence of gene interaction and the trait was governed by a few number of genes. Overall, the traits like primary branches/plant and seed yield/plot showed complementary gene interaction with fewer number of segregating dominant genes. Findings of our study were in agreement with previous studies by Sumathi *et al.* (2018) and Mariyammal *et al.* (2019) on skewness and kurtosis distribution.

Character association

The information regarding inter relationship of different traits with yield is essential before commencing any breeding programme for crop improvement. It aids in selection programme for selecting the individuals based on correlated and assist the breeder for conducting effective selection. In the present study, the genotypic correlation coefficients were found to be higher in magnitude than the phenotypic correlation coefficients for all the traits studied (Table 3). It indicated that genotypic effects were more important than environmental factors (Falconer, 1981). Similar results were reported by Pandey and Singh (2002). Seed yield/plot had shown highly significant positive correlation with pods/plant, primary branches/plant, secondary branches/plant and seeds/pod. It indicated that these traits can be considered for direct selection towards high grain yield. Primary branches/plant, secondary branches/plant and pods/plant were found to be associated significantly and positively with each other. Days to 50% flowering was found to be positively correlated with days to maturity. These results were in conformity with that reported by Mahajan *et al.* (2007), Bhadru (2010), Bal *et al.* (2018) and Rao *et al.* (2019). Plant height showed significant positive correlation with days to 50% flowering and days to maturity. Plant height had also shown significant positive correlation with primary branches/plant and secondary branches/plant.

Pods/plant had shown significant positive correlation with seeds/pod. On the other hand, seeds/pod had shown significant negative correlation with 100-seed weight but phenotypic correlation was negligible. Rao *et al.* (2019) had also reported significant negative correlation between seeds/pod and test weight. However, Chetukuri *et al.* (2013) reported significant negative correlation between these two traits. Investigation on correlation studies from the present study has revealed that the traits like pods/plant, seeds/pod, primary branches/plant and secondary branches/plant were important attributes contributing towards higher grain yield in pigeonpea. The direct selection for these component traits would be effective in achieving the high grain yield.

Knowledge based on the correlation analysis alone may not be always true because two traits might be correlated via another common trait. It describes association in statistical terms and does not provide clear picture about the cause and effect relationship. In order to get a clear picture of interrelationship among different traits at genotypic level, direct and indirect effects of various traits on seed yield were estimated using path analysis. It divides the correlation coefficient into direct and indirect effects and would provide the actual information on contribution of traits. The genotypic and phenotypic correlation coefficients of different traits partitioned into direct as well as

Table 3. Phenotypic (P) and Genotypic (G) correlation coefficient among various traits in pigeonpea

Trait		Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Pods/plant	Seeds/10 pods	100-seed weight (g)	Seed yield/ plot (g)
Days to 50% flowering	G	0.744	0.173	-0.112	-0.116	0.077	0.203	-0.066	-0.086
	P	0.739**	0.160**	-0.071	-0.088	0.072	0.095	-0.049	-0.074
Days to maturity	G		0.232	-0.108	-0.109	0.014	0.376	0.024	-0.094
	P		0.209**	-0.074	-0.094	0.017	0.126*	0.027	-0.084
Plant height (cm)	G			0.154	0.159	0.100	0.021	0.082	0.136
	P			0.127 *	0.137**	0.092	-0.002	0.063	0.127*
Primary branches/plant	G				0.869	0.765	0.104	0.150*	0.851
	P				0.816**	0.713**	0.074	0.129*	0.785**
Secondary branches/plant	G					0.793	0.120	0.146	0.828
	P					0.735**	0.136*	0.122 *	0.774**
Pods/plant	G						0.526	0.137	0.879
	P						0.192**	0.113*	0.866**
Seeds/pod	G							-0.264	0.403
	P							-0.046	0.172**
100 seed weight (g)	G								0.112
	P								0.092

* = Significance at 0.05 and ** = Significance at 0.01

*, **: Significance at P = 0.05 and 0.01, level of probability, respectively, Residual effect R = 0.172 (Phenotypic path), R = 0.118 (Genotypic path)

Table 4. Phenotypic (P) and Genotypic (G) path coefficient analysis in pigeonpea

Trait		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Pods/plant	Seeds/10 pods	100- seed weight (g)	Correlation with yield/plant
Days to 50% flowering	G	0.082	-0.165	0.006	-0.054	-0.029	0.008	0.073	-0.006	-0.086
	P	-0.099	-0.004	0.007	-0.018	-0.008	0.045	0.029	0.001	-0.074
Days to maturity	G	0.061	-0.221	0.007	-0.052	-0.027	0.001	0.135	0.002	-0.094
	P	-0.074	-0.005	0.009	-0.019	-0.009	0.011	0.004	-0.001	-0.084
Plant height (cm)	G	0.014	-0.051	0.032	0.075	0.040	0.010	0.008	0.008	0.136
	P	-0.016	-0.001	0.044	0.032	0.013	0.057	-0.000	-0.002	0.127*
Primary branches/plant	G	-0.009	0.024	0.005	0.485	0.218	0.077	0.038	0.014	0.851**
	P	0.007	0.000	0.006	0.255	0.079	0.440	0.002	-0.004	0.785**
Secondary branches/plant	G	-0.009	0.024	0.005	0.421	0.251	0.080	0.043	0.013	0.828**
	P	0.009	0.000	0.006	0.208	0.097	0.454	0.004	-0.003	0.774**
Pods/plant	G	0.006	-0.003	0.003	0.371	0.199	0.101	0.189	0.013	0.879**
	P	-0.007	0.000	0.004	0.182	0.071	0.618	0.006	-0.003	0.866**
Seeds/pod	G	0.017	-0.083	0.001	0.051	0.030	0.053	0.360	-0.024	0.403**
	P	-0.009	-0.000	-0.000	0.019	0.013	0.119	0.030	0.001	0.172**
100-seed weight (g)	G	-0.005	-0.000	0.003	0.073	0.037	0.014	-0.095	0.092	0.112
	P	0.004	-0.001	0.003	0.033	0.012	0.070	-0.001	-0.028	0.092

indirect effects using path analysis are summarized in Table 4. Primary branches/plant (0.485 and 0.255) had maximum positive direct effect on seed yield/plot followed by seeds/pod (0.455 and 0.030) and secondary branches/plant (0.251 and 0.097). The direct effects of primary branches/plant were mainly due to indirect effects via secondary branches/plant (0.421 and 0.208) and pods/plant (0.371 and 0.182). Days to maturity (-0.221 and -0.005) had negative direct effect on seed yield. The highly significant positive correlation of primary branches/plant with seed yield was due to its direct effect and indirect effects via secondary branches/plant, pods/plant and seeds/pod. Kumar *et al.* (2014), Vanisree and Sreedhar (2014) reported similar

results. The correlation analysis revealed that these are the major yield contributing traits and can be taken as selection criteria for achieving higher yield. Based on evaluation, few promising genotypes compared to check varieties were identified for different traits. These were ICPL920, PADT16, AL2091, AL2204, AL2025, MN5, H0535 for early flowering and early maturity; PADT 16, AL 2204, AL 2091, IC245350 for short stature; H0512, H0535, H005, IC3977, AL997, IC245176, AL 1856 for profuse podding and seed yield.

The present study revealed the sufficient variability for the traits studied in the pigeonpea germplasm used. Based on various genetic parameters, it can be concluded that direct selection for primary branches/

Table 5. List of promising genotypes for important yield component traits of pigeonpea

Trait	Genotypes
Days to 50% flowering	ICPL920 (71.5), PADT 16 (72.3), AL2091 (74.3), AL2204 (76.0), AL2025 (74.3), MN5 (70.3), H0535 (77.8), AL882(79.0)
Days to maturity	ICPL920 (119.5), PADT 16 (124.3), AL2091 (123.5), AL2204 (122.5), AL2025 (129.5), MN5 (129.8), H0535 (132.0), AL882(133.3)
Pods/plant	H0512 (329.0), H0535(327.3), H005 (286.5), IC3977 (272.8), AL997 (243.8), IC245176 (256.8), AL1856 (245.0), AL882 (161.0)
Seed yield/ plot (g)	H0512 (513.8), H0535(496.3), H005 (522.5), IC3977 (427.5), AL997 (478.8), IC245176 (417.5), AL1856 (375.0), AL882 (360.0)
Plant height (cm)	AL2204 (102.5), AL2091 (132.8), PADT16 (137.5), IC245350 (175.8), AL882 (181.8)

plant, pods/plant and seeds/pod contribute directly towards seed yield. Primary branches/plant and pods/plant showed high heritability coupled with high genetic advance as percent of mean therefore controlled by the additive gene action and major proportion of the variation is heritable. Under such situations, focus should be on high number of primary branches/plant and more number of pods/plant as it will help in selecting superior genotypes for attaining higher yield. The promising genotypes identified for different traits should be used as parents in breeding programme for developing high yielding pigeonpea varieties.

Authors' contribution

Conceptualization of research work and designing of the experiments (IS, SS); Execution of field / lab experiments and data collection (HK, SS); Analysis of data and interpretation (HK, DB); Preparation and finalization of manuscript (HK, IS, SS).

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