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Devising selection criteria based on variability and association studies in segregating populations derived from an interspecific cross between *Cajanus scarabaeoides* × *C. cajan*

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ABSTRACT

Segregating populations (BC_1F_3 and $F_{3:4}$) from an interspecific cross (*C. scarabaeoides* × *C. cajan*) were evaluated for variability and association studies for yield and its component traits. In both the generations, high values of PCV and GCV were obtained for pods per plant, seed yield per plant and fruiting branches per plant. High estimates of heritability as well as genetic advance were observed for fruiting branches per plant followed by pods per plant and seed yield per plant. High heritability coupled with high genetic advance revealed the presence of less environmental influence and prevalence of additive gene action. Seed yield per plant had highly significant and positive association with pods per plant, fruiting branches and 100-seed weight. Path coefficient analysis revealed that pods per plant, fruiting branches and 100-seed weight contributing maximum towards seed yield per plant. The study revealed that fruiting branches and pods per plant could be used as selection criteria for improving yield.

Key words: Correlation, Genetic variability, Heritability, Interspecific hybridization, Pigeonpea.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is an important pulse crop in semi-arid tropical regions of the world and globally grown on 4.70 million ha area with a total production of 3.69 million tonnes in the world. India is the largest producer by contributing almost 80 per cent of the global area and production (Anonymous, 2018). Pigeonpea grains are a good source of protein (21%), carbohydrate, vitamins, lipids and certain minerals (Sodavadiya *et al*., 2009). Being an often cross pollinated, pigeonpea has moderate genetic variability but low yield potential due to multiplicative interactions of various yield attributing traits affected by environmental factors (Sharma *et al*., 2018). Exploitation of the genetic resources for improvement of pigeonpea is very limited and majority of diversity existing in the germplasm remained unexplored (Majumder and Singh, 2005). For overcoming these problems, introgression breeding is the most important strategy for creation of new genetic variability for yield and its component traits (Sharma and Upadhyaya, 2016; Sharma, 2017). Successful interspecific hybridization between cultivated pigeonpea and its wild relative *C. scarabaeoides* has been frequently reported (Pundir and Singh, 1986; Singh and Bajpai, 2005; Sandhu *et al*., 2009; Singh *et al*., 2018), but conclusive information related to extent of variability generated and association of yield contributing traits with yield is scanty in interspecific populations.

For conducting dynamic plant breeding programme, it is essential to study nature and magnitude of variability and heritability of various yield enhancing traits. The estimation of various parameters of genetic variability like phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) give an idea about the magnitude of genotypic and phenotypic variability present in a population.

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Further, it is advisable to split the overall variability into heritable and non-heritable components to give an idea about the effect of selection. Additionally, genetic advance analysis gives an idea regarding the genetic improvement of new population over original population of the selected plants. Association studies helps to understand the relationship between traits of economic importance that helps to devise selection criteria. Limited information is available on these aspects in the interspecific populations derived from cross of cultivated pigeonpea with wild species, *C. scarabaeoides*. Therefore, the present study was conducted to generate information on variability and association among yield and its component traits in the segregating generations of an interspecific cross involving cultivated pigeonpea and its wild relative for devising selection criteria for yield improvement.

MATERIALS AND METHODS

An inter-specific cross between wild species *C. scarabaeoides* (ICP 15683) and *C. cajan* (ICPL 20329) was

generated during *kharif* 2013. Successively, F_1 plants were selfed and backcrossed to produce F_2 (2014) and BC_1F_1 (2014) populations. These progenies were further selfed for two generations to get $F_{3:4}$ (2016) and BC_1F_3 (2016) progenies. Twenty progenies of selected promising plants from each $F_{3:4}$ and BC_1F_3 generations were raised along with parents in randomized complete block design with two replications during *kharif* 2017 in the experimental field area of Pulses Section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. Each progeny was accommodated in a single row plot of four meter length with row to row and plant to plant spacing of 50 and 25 cm, respectively. All the recommended cultural practices were followed to raise a healthy crop. Five desirable plants were selected on the basis of phenotypic superiority from each progeny to record the data on eight morphological traits *viz*; days to 50 per cent flowering, days to maturity, plant height (cm), number of fruiting branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant. Statistically analyses were employed for estimation of various genetic parameters *viz*; phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Burton and Devane, 1953; Johnson *et al*., 1955), heritability in broad sense (Allard, 1960), genetic advance (Miller *et al*., 1958), correlation coefficients (Al-Jibouri *et al*., 1958) and path coefficients analysis (Dewey and Lu, 1959).

RESULTS AND DISCUSSION

Yield is a complex trait as many component traits contribute towards it. Being a quantitative trait in nature it is affected by genotype (G) × environment (E) interactions. Hence to bring change in yield, deep understanding of extent of variability present in a population and also interrelationship among yield and yield attributing characters is necessary. The analysis of variance (ANOVA) carried out for BC_1F_3 and $F_{3:4}$ generations indicated significant genotypic variation for all the traits in both the generations (Table 1).

Genetic variability

Phenotypic coefficient of variation (PCV) estimates was higher than the respective genotypic coefficient of variance (GCV) for all the traits under study, indicating the influence of environment in the expression of these traits. Wide range of phenotypic variation was observed in BC_1F_3 and $F_{3:4}$ generations (Table 2). In BC_1F_3, the highest value of PCV was observed for pods per plant (33.63%) followed by seed yield per plant (33.12%) and fruiting branches per plant (30.72%). The highest value of GCV was observed for pods per plant (31.25%) followed by seed yield per plant (30.26%) and fruiting branches per plant (28.61%). The low GCV was observed for traits like 100-seed weight (8.37%), plant height (6.16%), days to 50 per cent flowering (5.52%), days to maturity (4.89%) and seeds per pod (3.98%) in BC_1F_3. While in $F_{3:4}$ generation, the highest value of PCV was observed for seed yield per plant (51.34%) followed by pods per plant

Table 1: Analysis of variance (ANOVA) for different traits in BC_1F_3 and $F_{3:4}$ generations of an interspecific cross in pigeonpea.

Source of variation	Generations	D.F.	Days to 50% flowering	Days to maturity	Plant height (cm)	Fruiting branches	Pods per Plant	Seeds per pod	100- seed weight (g)	Seed yield per plant
Replications	BC_1F_3	1	20.88	14.22	640.68	62.77	5945.99	0.22	0.59	3.38
(MSS)	$F_{3:4}$	1	1.22	1.02	139.62	132.58	247.11	0.06	0.08	113.85
Treatments	BC_1F_3	19	88.29**	118.42**	303.56**	97.92**	8629.21**	0.05**	0.77*	208.49**
(MSS)	$F_{3:4}$	19	268.79**	301.62**	633.58**	195.67**	25444.21**	0.13**	1.40**	802.87**
Error	BC_1F_3	19	12.92	15.75	60.22	6.94	631.79	0.02	0.28	18.76
(MSS)	$F_{3:4}$	19	18.13	24.77	142.45	19.83	2336.47	0.03	0.43	63.97
G.M.	BC_1F_3		111.04±1.81	146.42±2.06	178.99±2.19	23.57±1.55	202.33±15.35	3.07±0.04	5.91±0.20	32.18±2.56
± S.E.	$F_{3:4}$		112.87±2.65	149.31±2.76	165.97±3.08	28.01±2.17	263.25±25.57	2.96±0.06	5.42±0.23	40.55±5.27
CD 5%	BC_1F_3		7.48	8.26	16.14	5.48	52.28	0.08	1.10	9.01
	$F_{3:4}$		8.86	10.35	24.83	9.26	100.54	0.34	1.36	16.64
CV (%)	BC_1F_3		3.22	2.70	4.28	11.51	12.68	4.05	9.02	13.93
	$F_{3:4}$		3.80	3.36	7.04	16.54	19.02	5.43	11.74	21.40

D.F. = Degree of freedom, MSS = Mean sum of Square, G.M. = Generation mean, S.E. = Standard error, CD = Critical difference and CV = Coefficient of variation.
*Significant at 5% and **Significant at 1% level of significance.

(44.47%) and fruiting branches per plant (37.05%). The highest value of GCV was observed for seed yield per plant (47.40%) followed by pods per plant (40.83%) and fruiting branches per plant (33.47%) in $F_{3:4}$ generation. It was interesting to note that extent of variability was reduced in BC_1F_3 as compared to $F_{3:4}$ generation, which was probably due to reduction of wild genome as a result of one backcross. Generation of abundant variability for these traits is generally expected in the inter-specific crosses in pigeonpea as earlier reported by Bohra *et al*. (2015). Presence of variability for different traits was also reported by Bhadru (2010), Sharma *et al*. (2012), Rangare *et al*. (2013), Singh *et al*. (2014), Ram *et al*. (2016), Mallesh *et al*. (2017), Reddy and Jayamani (2019) and Watsal (2019) in cultivated pigeonpea. Above results suggested that due to higher values of PCV and GCV for pods per plant, fruiting branches per plant and seed yield per plant in both the generations, the selection will be more effective for these traits in subsequent generations for improving yield.

Heritability and genetic advance

Perusal of Table 2 indicated high estimates of heritability for fruiting branches per plant (86.76%), pods per plant (86.35%) and seed yield per plant (83.48%), whereas moderate heritability was recorded for days to maturity (76.52%), days to 50 per cent flowering (74.46%) and plant height (66.89%) in BC_1F_3 generation. The highest heritability in $F_{3:4}$ was recorded for days to 50 per cent flowering (87.36%) followed by seed yield per plant (85.24%), days to maturity (84.82%), pods per plant (83.17%) and number of fruiting branches per plant (81.59%). Whereas, for plant height (63.27%), seeds per pod (62.50%) and 100-seed weight (53.00%), moderate heritability was recorded. Similar findings were reported by Sharma *et al*. (2012), Rangare *et al*. (2013), Nagy *et al*. (2013), Reddy and Jayamani (2019) in cultivated pigeonpea and by Bohra *et al*. (2015) in interspecific crosses in pigeonpea.

The highest genetic advance was recorded in BC_1F_3 generation (Table 2) for pods per plant (59.82%) followed by seed yield per plant (56.96%), while the lowest genetic advance was recorded for seeds per pod (5.37%). However, in $F_{3:4}$ generation, the highest estimate of genetic advance was recorded for seed yield per plant (90.11%) followed by pods per plant (76.70%), while seeds per pod recorded the lowest genetic advance (12.30%). Present results were in confirmation with results obtained by Patel *et al*. (2011), Prasad *et al*. (2013), Rao *et al*. (2013), Shunyu *et al*. (2013), Meena *et al*. (2017) and Watsal (2019) who also obtained high genetic advance for pods per plant and seed yield per plant in cultivated pigeonpea.

In both the generations, high heritability coupled with high genetic advance for fruiting branches per plant and pods per plant revealed that these two traits are important yield components and selection should be focused on these for yield improvement. These results revealed the presence of low environmental influence and prevalence of additive gene action in the expression of these traits. Moderate or low heritability estimates coupled with low genetic advance were recorded for seeds per pod and 100-seed weight indicating that these traits were governed by non-additive gene action and highly influenced by environment so direct selection would not be effective for improving yield.

Association studies (correlation and path analysis)

Correlation analysis clearly revealed that the phenotypic and genotypic correlations have similar trend in direction but the magnitude of genotypic correlations was higher than the phenotypic correlations. Low phenotypic correlation could be the result of masking and modifying effect of the environment on the association of traits. Correlation coefficients among all the traits in BC_1F_3 generation presented in Table 3. Seed yield per plant had significantly high and positive correlation with pods per plant (0.92) followed by fruiting branches per plant (0.85), 100-seed weight (0.52) and seeds per pod (0.32). Sinha and Singh (2005), Baskaran and Muthiah (2007), Prasad *et al*. (2013), Pandey *et al*. (2016), Pushpavalli *et al*. (2017) and Baldaniya *et al*. (2018) also found significant and positive correlations between seed yield per plant and number of pods per plant. In $F_{3:4}$ generation, results also showed highly significant and positive correlation of seed yield per plant with pods per plant (0.88) followed by fruiting branches per plant (0.85) and seeds per pod (0.41). Similar, results were reported by Singh *et al*. (2018) in BC_1F_2 and $F_{2:3}$ generations of the same

Table 2: Parameters of genetic variability for different traits in BC_1F_3 and $F_{3:4}$ generations of an interspecific cross in pigeonpea.

Traits	PCV (%)		GCV (%)		h^2 (%)		GA		GA as % of mean	
	BC_1F_3	$F_{3:4}$	BC_1F_3	$F_{3:4}$	BC_1F_3	$F_{3:4}$	BC_1F_3	$F_{3:4}$	BC_1F_3	$F_{3:4}$
Days to 50% flowering	6.40	10.61	5.52	9.91	74.46	87.36	10.91	21.54	9.82	19.08
Days to maturity	5.59	8.55	4.89	7.87	76.52	84.82	12.91	22.31	8.81	14.94
Plant height (cm)	7.53	11.86	6.16	9.44	66.89	63.27	18.58	25.67	10.38	15.46
Fruiting branches	30.72	37.05	28.61	33.47	86.76	81.59	12.93	17.44	54.89	62.28
Pods per plant	33.63	44.77	31.25	40.83	86.35	83.17	121.03	201.93	59.82	76.70
Seeds per pod	6.09	9.55	3.98	7.55	42.85	62.50	0.16	0.36	5.37	12.30
100-seed weight (g)	12.26	17.64	8.37	12.84	46.66	53.00	0.69	1.04	11.78	19.26
Seed yield per plant (g)	33.12	51.34	30.26	47.40	83.48	85.24	18.33	36.54	56.96	90.11

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2= Heritability in broad sense, GA = Genetic advance.

Table 3: Correlation coefficients among all possible combinations of traits in BC_1F_3 and $F_{3:4}$ generation.

Traits	Generations	Days to maturity	Plant height (cm)	Fruiting branches	Pods per plant	Seeds per pod	100-seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	BC_1F_3	0.97**	0.29*	-0.30*	-0.42**	-0.22	-0.39**	-0.46**
	$F_{3:4}$	0.98**	0.21	0.25	0.16	0.07	0.01	0.17
Days to maturity	BC_1F_3		0.27	-0.26	-0.39**	-0.30*	-0.42**	-0.45**
	$F_{3:4}$		0.16	0.24	0.14	0.02	-0.15	0.15
Plant height (cm)	BC_1F_3			-0.21	-0.18	0.38**	0.18	-0.14
	$F_{3:4}$			0.21	0.24	0.62**	0.24	0.26
Fruiting branches	BC_1F_3				0.96**	0.01	0.10	0.85**
	$F_{3:4}$				0.95**	0.17	-0.08	0.85**
Pods perPlant	BC_1F_3					0.13	0.27	0.92**
	$F_{3:4}$					0.22	-0.07	0.88**
Seeds perPod	BC_1F_3						0.57**	0.32*
	$F_{3:4}$						0.41**	0.41**
100-seed weight (g)	BC_1F_3							0.52**
	$F_{3:4}$							0.25

Critical value of r at 5% = 0.29 and at 1% = 0.38. *Significant at 5% and **Significant at 1% level of significance.

Table 4: Direct and indirect effects of various traits on seed yield per plant in BC_1F_3 and $F_{3:4}$ generations of an interspecific cross in pigeonpea.

Traits	Generations	Days to 50% flowering	Days to maturity	Plant height (cm)	Fruiting branches	Pods per plant	Seeds per pod	100-seed weight (g)	Correlation with Seed yield (g)
Days to 50%	BC_1F_3	**0.078**	-0.063	-0.024	-0.106	-0.202	-0.023	-0.126	-0.46**
flowering	$F_{3:4}$	**-0.147**	0.173	-0.032	0.021	0.133	0.014	0.003	0.17
Days to maturity	BC_1F_3	0.076	**-0.065**	-0.022	-0.090	-0.188	-0.030	-0.136	-0.45**
	$F_{3:4}$	-0.146	**0.175**	-0.025	0.021	0.120	0.004	-0.004	0.15
Plant height (cm)	BC_1F_3	0.023	-0.018	**-0.082**	-0.075	-0.087	0.039	0.059	-0.14
	$F_{3:4}$	-0.032	0.029	**-0.150**	0.019	0.204	0.121	0.070	0.26
Fruiting branches	BC_1F_3	-0.024	0.017	0.018	**0.344**	0.463	0.001	0.034	0.85**
	$F_{3:4}$	-0.037	0.043	-0.033	**0.086**	0.783	0.034	-0.024	0.85**
Pods per plant	BC_1F_3	-0.033	0.025	0.014	0.331	**0.482**	0.013	0.086	0.92**
	$F_{3:4}$	-0.024	0.025	-0.037	0.082	**0.818**	0.044	-0.022	0.88**
Seeds per pod	BC_1F_3	-0.018	0.019	-0.031	0.005	0.063	**0.101**	0.182	0.32*
	$F_{3:4}$	-0.011	0.003	-0.093	0.015	0.186	**0.195**	0.044	0.41**
100-seed weight (g)	BC_1F_3	-0.031	0.027	-0.015	0.037	0.131	0.058	**0.318**	0.52**
	$F_{3:4}$	-0.001	-0.002	-0.037	-0.007	-0.063	0.080	**0.285**	0.25

Residual effect = 0.055 (BC_1F_3) and 0.084 ($F_{3:4}$) *Significant at 5% and **Significant at 1% level of significance.
Bold figure indicated direct effect.

cross for fruiting branches and pods per plant which indicated that correlations of traits remained consistent in different generations. An overall observation of correlation coefficient analysis revealed that fruiting branches per plant and pods per plant showed positive correlation with seed yield per plant. Hence, direct selection for these traits will be quite effective to improve yield in pigeonpea. It was interesting to note that days to 50% flowering showed significant negative correlation with fruiting branches, pods per plant, 100-seed weight and seed yield per plant in BC_1F_3 population, while in $F_{3:4}$ generation, these correlation were very low or non-significant. Similarly, days to maturity showed significant negative correlation with seed yield per plant in BC_1F_3 generation, while in $F_{3:4}$ these correlations were very low or non-significant. This indicated that selection for high yield should be focused on early flowering and early maturity plants in segregating progenies where one backcross has been performed while in $F_{3:4}$, selection for both early and late maturity can be done without sacrificing yield.

Correlation simply indicates the types of relationship among the characters but does not provide information on extent of relationship (direct or indirect effect). Path coefficient analysis was carried out to understand the extent of relationship by taking seed yield per plant as dependent

variables and rest of the traits as independent variables. At phenotypic level in BC_1F_3 generation (Table 4), the highest direct effect on seed yield per plant was exerted by pods per plant (0.482) followed by fruiting branches per plant (0.344) and 100-seed weight (0.318). Whereas, the plant height (-0.082) and days to maturity (-0.065) showed negative direct effect on the seed yield per plant. Indirect positive effects on seed yield per plant were revealed by number of fruiting branches per plant (0.463), 100-seed weight (0.131) and seeds per pod (0.063) via pods per plant. In $F_{3:4}$ generation, pods per plant (0.818) exhibited the highest direct effect on seed yield per plant followed by 100-seed weight (0.285) and seeds per pod (0.195), While fruiting branches per plant (0.783), plant height (0.204), seeds per pod (0.186), days to 50 per cent flowering (0.131) and days to maturity (0.120) exerted indirect positive effect on grain yield per plant via pods per plant. Similar findings were reported by Thanki and Sawargaonkar (2010), Devi *et al*. (2012), Chaithanya *et al*. (2014), Vijayalakshmi *et al*. (2013), Chandana *et al*. (2014), Kothimbire *et al*. (2016), Ram *et al*. (2016), Kumar (2017) and Ranjani *et al*. (2018) in pigeonpea. Hence, in both generations direct selection for the pods per plant and fruiting branches per plant could be effective in developing high yielding genotypes in pigeonpea.

CONCLUSION

Results of variability, heritability, genetic advance, correlation and path analysis revealed that pods per plant and fruiting branches per plant are the main yield components and selection for these traits should be practiced for the improvement of grain yield in interspecific populations in pigeonpea.

REFERENCES

Al-Jibouri, H.A., Millar, P.A. and Robinson, H.F. (1958). Genotypic and environment variance and covariances in an upland cotton cross of interspecific origin. Agronomy Journal. 50: 633-636.

Allard, R.W. (1960). Principles of Plant Breeding. John Wiley and Sons, Inc, New York, London. pp. 485.

Anonymous, (2018). Project Coordinator's Report. ICAR-Indian Institute of Pulses Research, Kanpur. pp. 3.

Baldaniya, J.D., Kale, B.H., Mungra, K.S., Patel, H.N., Lad, M.D. and Chauhan, D.A. (2018). Genetic variability, correlation and path analysis for morphological and quality traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. International Journal of Chemical Studies. 6: 2584-2587.

Baskaran, K. and Muthiah, A.R. (2007). Associations between yield and yield attributes in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 30: 64-66.

Bhadru, D. (2010). Studies on genetic parameters and interrelationships among yield and yield contributing traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 33: 23-27.

Bohra, A., Bajpai, G.C. and Verma, S.K. (2015). Yield factor analysis in F_4 and F_5 progenies derived from interspecific hybridization between cultivated and wild pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 38: 303-307.

Burton, G.W. and Devane, E.H. (1953). Estimating heritability in tall Fescue (*Festuca arundinaceia*) from replicated clonal material. Agronomy Journal. 45: 478-481.

Chaithanya, B.K., Prasanthi, L., Reddy, K.H. and Reddy, B.V. (2014). Association and path analysis in F_2 populations of pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 37: 561-567.

Chandana, K.C., Prasanthi, L., Sekhar, M.R. and Reddy, B.B. (2014). Studies on correlation and path analysis for yield and its attributes in *rabi* redgram. Indian Journal of Agricultural Research. 48: 47-51.

Devi, S.R., Prasanthi, L., Reddy, K. and Reddy, B.V. (2012). Studies on interrelationships of yield and its attributes and path analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 35: 207-213.

Dewey, D.R. and Lu, K.H.A. (1959). Correlation and path coefficient analysis of component in crested wheat grass seed production. Agronomy Journal. 5: 515-518.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. Agronomy Journal. 47: 314-318.

Kothimbire, S.S., Arbad, S.K. and Choulwar, S.B. (2016). Characters association and path analysis for seed yield and its components in pigeonpea *Cajanus cajan* (L.). Indian Journal of Genetics. 8: 1556-1559.

Kumar, A. (2017). Genetic analysis for seed yield and its components in *rabi* pigeonpea [*Cajanus cajan* (L.) Millsp.] Ph. D. Dissertation. Indira Gandhi Krishi Vishwavidhyalaya, Raipur, Chhattisgarh, India.

Majumder, N.D. and Singh, F. (2005). Pigeonpea improvement in India, in Souvenir 4th International Food Legume Research Conference, 18-22 October, 2005, New Delhi. pp. 53-66.

Mallesh, P., Nanda, H.C., Durgaraju, C., Sameer Kumar, C.V., Nidhi, M. and Lee, J. (2017). Variability, heritability and genetic advance for quantitative traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. International Journal of Pure and Applied Bioscience. 5: 25-28.

Meena, S.S., Verma, S.K., Choudhary, R., Panwar, R.K. and Singh, J.P. (2017). Genetic variability and inter-relationship among yield contributing characters in advance lines of pigeonpea [*Cajanus cajan* (L.) Millsp.] grown at different altitudes. Chemical Science Review and Letters. 6: 1120-1128.

Miller, P.A., Williams, J.E., Robinson, H.F. and Comstock, R.E. (1958). Estimates of variance and co-variance in upland cotton and their implications in selection. Agronomy Journal. 50: 126-131.

Nagy, K., Sharma, R.N., Nandah, C. and Kanwar, S.S. (2013). Genetic variability and association studies among yield attributes in pigeonpea [*Cajanus cajan* (L.) Millsp.] accessions of bastar. The Ecoscan. 4: 267-271.

Pandey, P., Kumar, R. and Pandey, V.R. (2016). Genetic association studies for yield and yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 39: 189-193.

Patel, J.B., Acharya, S., Joshi, V.C. and Vaghela, K.O. (2011). Genetic variability and character association study in Indo African derivatives of pigeonpea. Annals of Arid Zone. 50: 167-169.

Prasad, Y., Kumar, K. and Mishra, S.B. (2013). Studies on genetic parameters and inter-relationships among yield and yield contributing traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. The Bioscan. 8: 207-211.

Pundir, R.P.S. and Singh, R.B. (1986). Inheritance pattern for pod length and ovule number in wide crosses among *Cajanus* and *Atylosia* species. Euphytica. 35: 649-652.

Pushpavalli, S.N.C.V.L., Sudhakar, C., Rani, C.S., Rajeswari, R.R. and Rani, C.J. (2017). Genetic divergence, correlation and path coefficient analysis for the yield components of pigeonpea genotypes. Legumes Research. 40: 439-443.

Ram, K., Saxena, K., Tushar, S.M. and Geeta, B. (2016). A study on genetic variability, correlation and path analysis in pigeon pea [*Cajanus cajan* (L.) Millspaugh]. International Journal of Agriculture Sciences. 8: 2287-2289.

Rangare, N.R., Reddy, G.E. and Kumar, S.R. (2013). Study of heritability, genetic advance and variability for yield contributing characters in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Trends in Biosciences. 6: 660-662.

Ranjani, M.S., Vanniarajan, C., Sameer Kumar, C.V., Saxena, R.K., Sudhagar, R. and Hingane, A.J. (2018). Genetic variability and association studies for yield and its attributes in super-early pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes. Electronic Journal of Plant Breeding. 9: 682-691.

Rao, P.J.M., Upender, M. and Bhaskar, A.V. (2013). Variability and genetic diversity studies in redgram [*Cajanus cajan* (L.) Millsp]. International Journal of Applied Biology and Pharmaceutical Technology. 4: 48-51.

Reddy, S.D. and Jayamani, P. (2019). Genetic diversity in land races of pigeonpea [*Cajanus cajan* (L.) Millsp.]. Electronic Journal of Plant Breeding. 10: 667-672.

Sandhu, J.S., Gupta, S.K. and Khanna, V. (2009). Introgression of yield and component traits through wide hybridization in pigeonpea. Crop Improvement. 36: 50-54.

Sharma, P., Singh, I., Sirari, A., Singh, S. and Khosla, G. (2018). Genetic divergence studies through microsatellite markers in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 43(3): 312-319. (https://doi.org/10.18805/LR-4022).

Sharma, R., Gangwar, R.K. and Yadav, V. (2012). A study on genetic variability and correlation in pigeonpea [*Cajanus cajan* (L.) Millsp.]. International Journal of Science and Research. 3: 826-828.

Sharma, S. (2017). Pre-breeding using wild species for genetic enhancement of grain legumes at ICRISAT. Crop Science. 57: 1132-1144.

Sharma, S. and Upadhyaya, H.D. (2016). Pre-breeding to expand primary genepool through introgression of genes from wild *Cajanus* species for pigeonpea improvement. Legume Perspectives. 11: 17-20.

Shunyu, V., Chaturvedi, H.P., Changkija, S. and Singh, J. (2013). Genetic variability in pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes of Nagaland. Indian Research Journal of Genetics and Biotechnology. 5: 165-171.

Singh, G., Singh, I., Singh, S., Gupta, M. and Sharma, P. (2018). Evaluation of BC_1F_2 and F_3 populations derived through wide hybridization for yield and component traits in pigeonpea. Agricultural Research Journal. 55: 633-638.

Singh, J. and Bajpai, G.E. (2005). Analysis of gene effects for yield and yield attributing traits in interspecific crosses of pigeonpea [*Cajanus cajan* (L.) Millsp.]. Indian Journal of Genetics. 65: 133-134.

Singh, R.M., Singh, M.N. and Kumar, M. (2014). Genetic variability and diversity in pigeonpea [*Cajanus cajan* (L.) Millsp.] under rainfed conditions. Journal of Food Legumes. 27: 13-16.

Sinha, S.K. and Singh, M.K. (2005). Genetic variability and character association analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.] in northern hill zone of Chhattisgarh. Crop Science. 16: 143.

Sodavadiya, P. R., Pithia, M.S., Savaliya, J.J., Pansuriya A.G., and Korat, V.K. (2009). Studies on characters association and path analysis for seed yield and its components in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legumes Research. 32: 203-205.

Thanki, H.P. and Sawargaonkar, S.L. (2010). Path coefficient analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Electronic Journal of Plant Breeding. 1: 936-939.

Vijayalakshmi, P., Anuradha, C., Pavankumar, D., Sreelaxmi, A. and Anuradha, G. (2013). Path coefficient and correlation response for yield attributes in pigeon pea [*Cajanas cajan* (L.) Millsp.]. Legumes Research. 36: 23-29.

Watsal, K. (2019). Genetic variability and character association in *rabi* pigeonpea (*Cajanus cajan* L.). Ph. D. Dissertation. Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India.