

Estimation of Genetic Parameters and Character Association Studies for Yield and its Component Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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(Received: 01 March 2023; Revised: 14 April 2023; Accepted: 18 April 2023; Published: 20 May 2023)

(Published by Research Trend)

ABSTRACT: Present investigation comprised of 38 pigeonpea genotypes was conducted during *kharif*, 2022-23 crop season to estimate the genetic parameters, character association between yield and its component traits. High estimates of PCV and GCV were recorded for the characters like primary branches per plant, seed yield per plant, pods per plant, secondary branches per plant, plant height and 100-seed weight. High estimates of heritability associated with high genetic advance were obtained for the traits days to 50% flowering, plant height, pods per plant, pod length, seeds per pod, 100 seed weight and seed yield per plant representing that the heritability for these traits is most likely due to the additive gene effects. The trait number of pods per plant not only exhibited high positive direct effect but also positively and significantly correlated with seed yield per plant indicating that this component trait is governed by additive gene action and direct selection for this trait may cause desirable improvement in seed yield per plant.

Keywords: Pigeonpea, variability, heritability, genetic advance, correlation, path analysis.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], commonly known as Arhar, tur and red gram. Pigeonpea is an often cross-pollinated crop with $2n=2x=22$ (diploid chromosome number) and a genome size of 833.07 Mb (Varshney *et al.*, 2012). Pigeonpea ranked sixth globally after pea, broad bean, lentil, chickpea and common bean and cultivated over an area of 5.4 million hectares, producing 4.49 million tons annually (Fatokimi and Tanimonure 2021). It is the second-most significant pulse crop in India after chickpea, occupying 4.72 million hectares and producing 4.31 million tons annually with an average yield of 9.14 quintals/ha. It generates 15% of the nation's total output of pulses. Pigeonpea was grown on 3,000 hectares in Uttarakhand in 2020–21, producing 3.56 thousand tons overall with an average yield of 11.85 quintals/ha (Directorate of Economics and Statistics, 2021).

Seed yield is a very complex trait and dependent upon the several yield components like number of pods per plant, One hundred seed weight and number of seeds per pod, therefore, direct improvement in seed yield is not possible (Meena *et al.*, 2017; Pal *et al.*, 2018). Studies regarding various variability parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance provides the fair idea whether a particular trait can be improved upon by practicing selection or not. A

sound knowledge of character association between seed yield and its component traits and also among component traits is essential to formulate selection criterion to bring desired improvements in seed yield and yield components. Correlation studies provides an idea regarding the contribution of different traits towards seed yield and also reveals the type, nature and magnitude of character association between the seed yield and its component traits (Gaur *et al.*, 2020). Furthermore, the grain yield is influenced by its various components directly and/or indirectly through other traits that create a complex situation for plant breeders for making desirable selection. Therefore, path coefficient analysis developed by Wright (1921) could provide a more realistic picture of the relationship, as it partitions the correlation coefficients into direct and indirect effects of the variables. Dewey and Lu (1959) employed path analysis for the first time in plants to identify direct and indirect influences of the component traits on grain yield. Thus, character association and path analysis provide an information about the important yield contributing characters and a breeder can isolate superior yielding genotypes through selection by using the information provided by correlation and path analysis.

MATERIAL AND METHODS

The experimental material comprised of 38 elite pigeonpea genotypes developed at different research

institute in India and were evaluated in a randomized block design with three replications at Norman E. Borlaug Crop Research Centre (CRC) of G. B. Pant University of Agriculture and Technology, Pantnagar during *kharif* season of 2022 under normal sown conditions. Each genotype was raised in a six-row plot of four meter length. A row to row spacing of 60centimeters and plant to plant spacing of 20 cm was maintained. Recommended agronomic practices were adopted to raise a normal and healthy crop during the entire crop season. The observations on ten different metric traits *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). Data on five randomly selected competitive plants from each replication were recorded for all the traits under study except for days to 50% flowering and days to maturity, which were recorded on plot basis. The mean data was used for statistical analysis. The analysis of variance for randomized block design (RBD) was performed following Panse and Sukhatme (1985), genotypic and phenotype coefficients of variation (GCV and PCV) were calculated as per the formula suggested by Burton and De Vane (1953), heritability as per Allard (1960) and genetic advance as per Johnson *et al.* (1955). Correlation and path coefficients were worked out as per the method suggested by Al-Jibouri *et al.* (1958); Dewey and Lu (1959), respectively.

RESULTS AND DISCUSSION

The mean square due to genotypes is highly significant for all the traits studied, indicating the presence of sufficient amount of genetic variability in the experimental material used. The data pertaining to genetic variability for all traits are given in Table 1.

The estimates of variability indicated that phenotypic coefficients of variation (PCV) were slightly higher than corresponding genotypic coefficients of variation (GCV) for all the traits, indicating the minimum effect of environment on the expression of characters studied. It is evident from the Table 1, the high estimates of PCV and GCV (>20%) were recorded for the characters like primary branches per plant (33.90%, 22.40%), seed yield per plant (33.57%, 32.31%), pods per plant (29.66%, 27.32%), secondary branches per plant (27.99%, 20.15%), plant height (25.84%, 24.55%) and 100-seed weight (20.44%, 20.25%). For pod length (17.32%, 16.35%), number of seeds per pod (14.85%, 13.02%) and days to 50% flowering (13.29%, 13.20%), the estimates of PCV and GCV were moderate (10-20%), while the low values of PCV and GCV (<10%) were recorded for days to maturity (7.16%, 7.09%).

Similar to the present findings, the high values of PCV and GCV for different traits in pigeonpea were earlier obtained by Sarsamkar *et al.* (2008); Bhadru (2010); Rekha *et al.* (2013); Ram *et al.* (2016); Kumar *et al.* (2018), Ranjani *et al.* (2018); Vanniarajan *et al.* (2021); Ranjani *et al.* (2021).

The estimates of broad sense heritability were high for the traits days to 50% flowering (98.70%), 100-seed weight (98.20%), days to maturity (98.00%), seed yield per plant (92.70%), plant height (90.20%), pod length (89.10%), pods per plant (84.80%), seeds per pod (76.90%). Moderate heritability was observed for secondary branches per plant (51.80%) and primary branches per plant (43.60%). Though the estimates of heritability are high for most of the traits studied, the selection for improvement of these traits may not be very beneficial, as the estimates of broad sense heritability are based on total genetic variance which include both fixable (additive) as well as non-fixable (dominance and epistatic) variances (Bohra *et al.*, 2015; Pal *et al.*, 2018; Verma *et al.*, 2018; Gaur *et al.*, 2020). It is further evident from the Table 1 that the estimates of genetic advance as percent mean were high (>20%) for the traits *viz.* seed yield per plant (64.08%), pods per plant (51.83%), plant height (48.04%), 100-seed weight (41.34%), pod length (31.78%), primary branches per plant (30.47%), secondary branches per plant (29.89%), days to 50% flowering (27.01%) and seeds per pod (23.51%). High values of heritability alone did not assure that the selection may bring the desirable change in the character and therefore, heritability associated with genetic advance as percent mean gives better idea regarding the effectiveness of selection (Verma *et al.*, 2018; Gaur *et al.*, 2020). In the present investigation, high estimates of heritability associated with high genetic advance were obtained for the traits days to 50% flowering, plant height, pods per plant, pod length, seeds per pod, 100-seed weight and seed yield per plant indicating that the heritability for these traits is most likely due to the additive gene action and the selection may be effective. These results are in conformity with those of Rekha *et al.* (2013); Meena *et al.* (2017); Kumar *et al.* (2018); Verma *et al.* (2018); Hemavathy *et al.* (2019); Vanniarajan *et al.* (2021); Mourya *et al.* (2022).

In present investigation, values of genotypic correlation coefficients were higher than those of their respective phenotypic correlation coefficients in most of the cases (Table 2), indicating the presence of strong association between the traits genetically. In some cases, however, the phenotypic correlation was slightly higher than their genotypic counterpart, which implied that the non-genetic causes (environmental factors) increased the value of phenotypic correlation. Similar findings were also reported by Satyanarayana *et al.* (2018); Verma *et al.* (2018) in pigeon pea. A critical insight of Table 2 revealed that seed yield per plant exhibited positive and significant correlation with plant height (cm), primary branches per plant, secondary branches per plant, pods per plant, pod length (cm) and 100-seed weight (g) at both genotypic as well as phenotypic level. The present finding indicated that an improvement in these component traits may bring desirable improvements in the seed yield per plant. Present results indicated that the character 100-seed weight also exhibited positive and significant correlation with all the characters except pods per plant and seeds per pod (Table 2). The character pods per plant exhibited positive and

significant correlation with pod length, 100-seed weight and seed yield per plant. The present finding of correlation between different traits were in perfect conformity of the earlier findings of Saroj *et al.* (2013); Birhan *et al.* (2013), Verma *et al.* (2018); Devi *et al.* (2019) in pigeonpea.

Path coefficient analysis revealed that the maximum contribution towards the seed yield per plant was exhibited by the trait pods per plant (0.7653) (Table 3). It is further evident that the trait pods per plant not only had high direct effect but also positively and significantly correlated with seed yield per plant. It

indicated the true relationship between seed yield per plant and pods per plant. Direct selection for this trait will be rewarding for yield improvement. Present findings regarding the contribution of different component traits towards the seed yield per plant were well supported by the earlier finding obtained by Vijayalakshmi *et al.* (2013); Hemavathy *et al.* (2019) ; Vanniarajan *et al.* (2021) in pigeonpea. The overall picture of path analysis revealed that for improving yield in pigeonpea, selection advantage should be given to number of pods per plant as this recorded high positive direct effect on seed yield per plant.

Table 1: Phenotypic range, coefficient of range, phenotypic and genotypic coefficients of variation, heritability and genetic advance as percent mean for various characters in pigeonpea.

Sr. No.	Characters	Phenotypic range	Coefficient of range (%)	Mean \pm S.E.	Phenotypic coefficients of variation (%)	Genotypic coefficients of variation (%)	Heritability in broad sense (%)	G. A. expressed as per cent of mean (%)
1.	Days to 50% flowering	54.00-113.33	35.45	97.14 \pm 0.84	13.29	13.20	98.70	27.01
2.	Days to maturity	120.66-171.66	17.44	151.79 \pm 0.89	7.16	7.09	98.00	14.45
3.	Plant height (cm)	65.66-335.14	67.15	259.77 \pm 12.10	25.84	24.55	90.20	48.04
4.	No. of primary branches per plant	1.96-7.65	59.20	5.37 \pm 0.79	33.90	22.40	43.60	30.47
5.	No. of secondary branches per plant	3.26-10.88	53.89	7.51 \pm 0.84	27.99	20.15	51.80	29.89
6.	No. of pods per plant	80.52-308.50	58.60	188.69 \pm 12.58	29.66	27.32	84.80	51.83
7.	Pod length (cm)	1.88-6.24	53.69	5.26 \pm 0.17	17.32	16.35	89.10	31.78
8.	No. of seeds per pod	2.66-6.33	40.82	4.32 \pm 0.18	14.85	13.02	76.90	23.51
9.	One hundred seed weight (g)	2.96-9.92	54.03	7.96 \pm 0.13	20.44	20.25	98.20	41.34
10.	Seed yield per plant (g)	30.22-93.95	51.32	52.00 \pm 2.73	33.57	32.31	92.70	64.08

Table 2: Estimates of genotypic (r_g) and phenotypic (r_p) correlation coefficients among 10 characters in pigeonpea.

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of Primary branches per plant	No. of secondary branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	One hundred seed weight (g)
Seed yield per plant (g)	r_g	0.2139	0.1498	0.4179**	0.4503**	0.5168**	0.7825**	0.4065*	0.1042	0.3259*
	r_p	0.2015	0.1457	0.4202**	0.4241**	0.5086**	0.7882**	0.3713*	0.0756	0.3183*
Days to 50% flowering	r_g		0.8977**	0.8173**	0.6631**	0.6392**	-0.0567	0.7934**	-0.2890	0.7589**
	r_p		0.8888**	0.7772**	0.4424**	0.4555**	-0.0564	0.7405**	-0.2451	0.7490**
Days to maturity	r_g			0.7753**	0.5960**	0.4617**	-0.1161	0.7230**	-0.2224	0.7199**
	r_p			0.7343**	0.4072*	0.3342*	-0.1066	0.6694**	-0.2032	0.7155**
Plant height (cm)	r_g				0.7608**	0.6813**	0.0969	0.8259**	-0.1231	0.8194**
	r_p				0.6185**	0.5841**	0.1407	0.7216**	-0.1146	0.7742**
No. of Primary branches per plant	r_g					0.8235**	0.1036	0.7992**	-0.1051	0.6535**
	r_p					0.7724**	0.2570	0.4713**	-0.0076	0.4462**
No. of secondary branches per plant	r_g						0.2033	0.6713**	-0.1624	0.6621**
	r_p						0.3601*	0.4465**	-0.1090	0.4812**
No. of pods per plant	r_g							0.0862	-0.1152	-0.0513
	r_p							0.0837	-0.0936	-0.0464
Pod length (cm)	r_g								0.1176	0.7917**
	r_p								0.1465	0.7302**
No. of seeds per pod	r_g									0.0437
	r_p									0.0286

*Significant at 5% and **Significant at 1% levels, respectively.

Table 3: Phenotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in pigeonpea.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of Primary branches per plant	No. of secondary branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	One hundred seed weight (g)	Phenotypic correlation with seed yield per plant
Days to 50% flowering	-0.0222	-0.0197	-	-0.0098	-0.0101	0.0012	-	0.0054	-0.0166	0.2015
Days to Maturity	-0.0140	-0.0157	-	-0.0064	-0.0053	0.0017	-	0.0032	-0.0112	0.1457
Plant height (cm)	0.0913	0.0863	0.1175	0.0727	0.0686	0.0165	0.0848	-0.0135	0.0909	0.4202**
Primary branches per plant	0.0002	0.0002	0.0003	0.0005	0.0004	0.0001	0.0002	0.0000	0.0002	0.4241**
Secondary branches per plant	0.0330	0.0242	0.0423	0.0559	0.0724	0.0261	0.0323	-0.0079	0.0348	0.5086**
No. of pods per plant	-0.0432	-0.0816	0.1076	0.1967	0.2756	0.7653	0.0641	-0.0176	-0.0355	0.7882**
Pod length (cm)	0.0181	0.0164	0.0176	0.0115	0.0109	0.0020	0.0245	0.0036	0.0179	0.3713*
No. of seeds per pod	-0.0367	-0.0304	-	-0.0011	-0.0163	-	0.0219	0.1497	0.0043	0.0756
One hundred seed weight (g)	0.1748	0.1661	0.1807	0.1042	0.1123	-	0.1705	0.0067	0.2334	0.3183*

Diagonal bold values represent direct contribution of traits on seed yield per plant

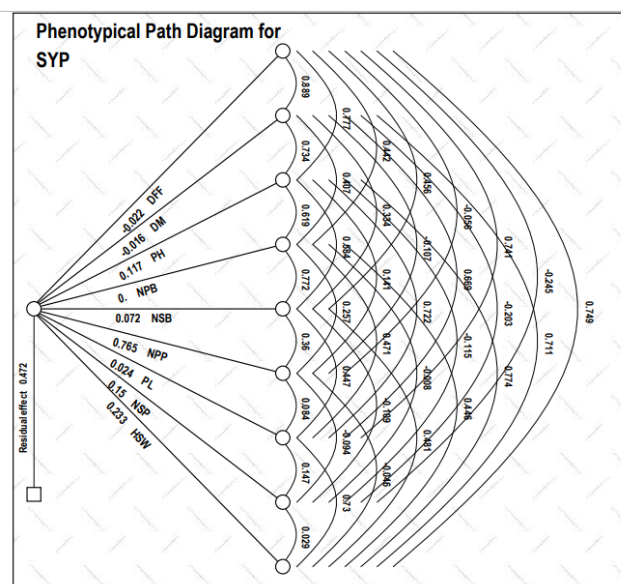


Fig. 1. Diagrammatic representation of phenotypic path analysis among the ten traits in pigeonpea.

CONCLUSIONS

On the basis of present findings, it can be concluded that the trait like pods per plant not only exhibited high estimates of heritability and genetic advance as percent mean, but it also contributed maximum towards the dependent variable seed yield per plant besides showing high positive correlation with seed yield per plant. This indicated that this component trait is governed by additive gene action and direct selection for this component trait may result in desirable improvement in seed yield per plant.

Acknowledgement. I extend my sincere thanks to Prof. (Dr.) S. K. Verma (Advisor) and to my advisory committee members for giving me proper guidance throughout the course of study. I also sincerely thank Directorate of Research, GBPUA&T, Pantnagar, for supporting the research financially by awarding me Fellowship.

Conflict of Interest. None.

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How to cite this article: S.G.P. Karthikeya Reddy, S.K. Verma, R.K. Panwar, Anju Arora, Arvind Chauhan and Shubham Kumawat (2023). Estimation of Genetic Parameters and Character Association Studies for Yield and its Component Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Biological Forum – An International Journal*, 15(5): 1066-1070.