



Research Article

A STUDY ON GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN PIGEON PEA [*Cajanus cajan* L. MILLSPAUGH]

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Abstract- Thirty varieties of pigeon pea were evaluated and a wide range of variation was found for almost all the traits under study. The phenotypic and genotypic variances, correlation and path coefficient, heritability and genetic advances were estimated for grain yield and yield traits in 30 pigeon pea genotypes. The highest GCV was recorded for number of secondary branches/plant followed by pods/plant. Heritability in broad sense ranged from 60.31 (seeds/pod) to 96.28 (days to 50% flowering). High genetic advance were observed for number of primary branches/plant indicating the prevalence of additive gene action for inheritance of these traits. Correlation and Path coefficient analysis (genotypic and phenotypic) revealed that pods/plant, 100 -seed weight, days to 50% flowering, primary branches and secondary branches had maximum direct effect resulted significantly positive correlation with grain yield/plant. These traits can be used to improve the grain yield of pigeon pea.

Keywords- Genetic variability, Correlation and Path coefficient, Pigeon pea.

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Introduction

Pigeon pea [*Cajanus cajan* L. Millsp.], ($2n=2x=22$) is the second most important pulses crop after chickpea in India and fifth rank in the world. It is major producer and consumer of pigeon pea in the world and presently occupies an area of about 27 million hectares with an annual total production of 18.5 million tonnes and mean productivity of 730 kg/hectare (Anonymous, 2014). As 'dal', pigeon pea is an important constituent of the Indian meal. It contains 20-21% protein [1] The per capita availability of protein in the country is 28 g/ day, while WHO recommended it should be 80 g/day, consequently most serious problem of the malnutrition existing among the poor people, where most of the people have vegetarian diet and avoid the animal protein [2]. It is needs fulfil its demand through pulses protein. Therefore, it is necessary to increase the production of pigeon pea, which could be done opting suitable, breeding methods. To overcome such situation, genetically stable genotypes having high yield potential are urgently needed. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genetic coefficient of variability (GCV), heritability estimates (H) and genetic advance (GA). Besides estimating the nature and magnitude of correlation coefficient, path coefficient analysis and genetic association between grain yield and yield traits, the traits that contributed to yield and are suitable to identified by variability, correlation and path coefficient analysis between grain yield and its attributes. The information on their genetic variability and traits association contributes with grain yield and among itself is of considerable importance in selection for elite genotype as well as exploitation of heterosis breeding programme. A study on genetic variability and correlation alone are not enough to give an exact figure of relative importance of direct and indirect influence of each of the component traits on grain yield. In such case, path coefficient analysis is an important technique for

partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable. It is therefore, genetic variability as well as correlation and path coefficient may be important tools for the breeder to enhancing the production and productivity of the pigeon pea. The present study was conducted to assess genetic variability, heritability and path coefficient analysis yield and its component characters to provide necessary information that could be useful in pigeonpea improvement programmes aimed at improving grain yield.

Materials and Methods

The experimental material comprised of thirty diverse genotypes of pigeon pea were sown in RBD with three replications, during Kharif, 2013-14 at Center of Excellence for Research on Pulses, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat. Spacing between genotypes and between the plants of same genotype was maintained 75 cm and 25 cm respectively. Each genotype was grown in single row of 4.0 m length. The observations were recorded on 5 randomly selected plants from the plot of each replication on days to flowering, days to maturity, plant height, primary branches, secondary branches, pods/plant, seeds/pod, pod length, 100 seed weight and seed yield per plant.

Genetic parameters of variability viz., phenotypic and genotypic variance and coefficient of variance, heritability, genetic advance, phenotypic and genotypic correlation coefficients were estimated using the formula suggested by [3]. All the data were analysed using Windows at version 8.6 from Department of Agricultural statistics, Sardarkrushinagar, Gujarat, India. Path co-efficient analysis was estimated according to the method proposed by [4].

Results and Discussion

In the present investigation, all the traits exhibited highly significant difference among treatments, which indicated adequate genetic variability among the cultivars [Table-1]. It reveals that the section of superior cultivars for development of new varieties may be helpful. Relatively higher value of genotypic variance were found for pods/plant the genotypic coefficient of variation was the highest for secondary branches/plant followed by pods/plant and grain yield/plant, the lowest for days to maturity [Table-2]. The magnitude of the genotypic variance for all the yield components were however higher than the environmental variance. The low environmental influence observed compared to genetic factors suggests that the trait may be under genetic control rather than the environment, hence improvement can be achieved through selection similar findings were reported by [5-7]. The GCV of various characters varied from 5.08 to 61.81 it was found to be highest for secondary branches/plant (61.81), followed by pods/plant (38.34), grain yield/plant (34.27). Similar results were reported by [8] in pigeon pea. The minimum magnitudinal differences in GCV and PCV coupled with low ECV for all the traits studied implied that the traits are mostly governed by genetic factors with little role of environment in the phenotypic expression of these characters. Thus, selection of these traits on the basis of the phenotypic value may be effective. Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain. High values of heritability estimates were obtained in characters like days to 50% flowering (98.26), days to maturity (95.11), 100 seed weight (89.79), secondary branches/plant (89.18), grain yield/plant (87.53), pods/plant (83.69), plant height (81.28), Whereas moderate heritability were

recorded for pod length (79.13). While low heritability estimates were observed for seeds/pod. High heritability indicates the scope of genetic improvement of these characters through selection. Similar type of heritability was recorded by [8,9]. Whereas high heritability indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals. Heritability estimates along with the genetic gain are usually more useful [10]. The expected genetic advance is expressed as percent of mean ranged from 13.07 (days to maturity) to 154.10 (secondary branches/plant). It may be mentioned here that characters like days to 50% flowering, days to maturity, 100 seed weight, secondary branches/plant, grain yield/plant, pods/plant, plant height, pod length and seeds/pod were largely governed by additive gene and therefore to selection based on phenotypic performance is likely to yield beneficial results in improving these characters. High heritability accompanied with high genetic advance as percent of the mean in case of number of secondary branches/ plant, grain yield/plant, pods/plant, 100 seed weight, indicate that these are simply inherited traits and most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. However, days to maturity, pod length and seeds/pod had high heritability coupled with low genetic advance indicates non-additive gene effects. Genotypic correlations [Table-3] were higher in magnitude than the phenotypic correlation indicating strong inherent relationship among the characters except few, which could be due to modifying effects in the environment studied. Similar findings were reported by [12]. Genotypic correlation provides a measure of genotypic association among different traits and helps in identifying the traits in selection.

Table-1 Analysis of variance (ANOVA) for yield and yield related traits in 30 pigeonpea cultivars

Source of Variations	df	Days to 50% Flowering	Plant height (cm)	Primary Branches/Plant	Secondary Branches/Plant	Pods/Plant	Pod length (cm)	Seeds/ Pod	Days to Maturity	100 Seed Weight (gm)	Grain yield/ Plant
Replication	2	15.10	153.82**	0.02	2.01	961.16**	0.07	0.06	12.70	0.61	30.07
treatment	29	1367.22**	1978.18**	43.766**	60.19**	12637.48**	0.749**	0.175**	446.39**	14.67**	456.60**
Error	138	8.02	141.03	3.19	2.34	770.93	0.06	0.03	7.53	0.54	20.70

*, **: Significant at P=0.05 and P=0.01, level of probability, respectively,

Table-2 Estimation of genetic parameters for agronomic traits in pigeonpea cultivars

Parameters	Range	General Mean	Variance Genotypic	Variance Phenotypic	CV Genotypic (%)	CV Phenotypic (%)	Heritability (%)	Genetic Advance 1%	Genetic Advance 1% in %Mean
Days to 50% Flowering	62.67-164.33	123.66	453.07	461.09	17.21	17.36	98.26	55.70	45.05
Days to Maturity	146.33-249.33	238.31	146.29	153.82	5.08	5.20	95.11	31.14	13.07
Plant Height (cm)	56.63-232.17	174.10	612.39	753.41	14.21	15.77	81.28	58.90	33.83
Primary Branches/Plant	3.43-23.43	14.41	13.52	16.72	25.52	28.38	80.91	8.73	60.61
Secondary Branches/Plant	0.00-23.20	7.10	19.28	21.62	61.81	65.45	89.18	10.95	154.10
Pods/Plant	16.833-35.33	164.05	3955.52	4726.45	38.34	41.91	83.69	151.89	92.59
Pod Length (cm)	3.39-5.67	4.34	0.23	0.29	11.04	12.41	79.13	1.13	25.92
Seeds/ Pod	2.87-4.27	3.38	0.05	0.08	6.50	8.30	61.33	0.45	13.44
100 Seed Weight (gm)	7.00-18.37	10.69	4.71	5.25	20.31	21.44	89.79	5.43	50.82

The days to 50% flowering had significant and strongly positive association with grain yield/ plant, primary branch/ plant, pods/plant, days to maturity, 100 seed weight and plant height in both genotypic and phenotypic level. It indicated that these characters are useful for taking them as the basis of selection for high grain yield. Similar trend was reported by [1,2,8] in pigeon pea. Thus, providing that these attributes were more influencing the yield in pigeon pea and they can serve as important traits for improvement of grain yield/plant. The character grain yield/plant was found to be significantly and positively correlated with plant height, primary branches/ plant, pods/plant while, 100 seed weight had strong interrelationship with pods/plant. Similarly, primary branches/ plant had significant and positive association with plant height and pods/plant. These results were in agreement with those reported by [13]. The results of correlation in present investigation revealed that grain yield/plant, primary branches/ plant, pods/plant, 100 seed weight and plant height were the most important attributes and may contribute considerably towards higher grain yield. But grain yield is a complex

trait which is influenced by its various components directly and indirectly via other traits, which creates a complex situation at the selection time. The path coefficient analysis [Table-4] provides a more realistic evidence of the interrelationship, as it considers direct and indirect effects of the variables by partitioning the correlation coefficients. The genotypic as well as phenotypic correlation coefficients between grain yield and different traits were subjected to path coefficient analysis separately partitions into direct as well as indirect effects via various yield contributing characters are summarized in [Table-3]. Coefficient analysis showed that pod/plant had maximum direct effect (1.011 and 0.950) followed by 100 seed weight (0.493 and 0.433), seeds/ pod (0.092 and 0.082) and days to maturity (0.012 and 0.007) on grain yield /plant. [13-15] reported positive direct effect on grain yield with days to maturity, pods/plant, pod length, seeds/pod and 100 seed weight. Days to 50% flowering (-0.087 and -0.054), plant height (0.078 and -0.058), primary branches/plant (-0.031 and -0.007) and secondary branches/plant (-0.011 and 0.001) showed negative direct effect on grain yield in both genotypic

and phenotypic level. Except secondary branches/plant, in this case genotypic had showed negative direct effect but phenotypic had positive and direct effects on the grain yield. it is evident that the highly significant and positive correlation of pods/plant had found with grain yield due to their maximum direct and indirect

effect via seeds/pod and seeds/pod respectively. 100 grain wt showed medium positive direct effect and their genotypic correlation with grain yield was significant. Therefore, these traits would be suitable selection criteria for improvement of seed yield in pigeon pea.

Table-3 Phenotypic (P) and Genotypic (G) correlation coefficient among agronomic characters in pigeonpea

Character		Plant Height (cm)	Primary Branches/ Plant	Secondary Branches/ Plant	Pods/ Plant	Pod length (cm)	Seeds/ Pod	Days to Maturity	100 Seed Weight (gm)	grain yield/plant
Days to 50% Flowering	G	0.345**	0.496**	0.231	0.432**	0.147	0.103	0.417**	0.337**	0.486**
	P	0.298 *	0.438 **	0.211	0.401 **	0.131	0.074	0.415 **	0.320 **	0.458 **
Plant Height (cm)	G		0.285*	0.050	0.373**	-0.035	0.109	0.050	0.077	0.308**
	P		0.262 *	0.054	0.295 *	0.008	0.074	0.044	0.038	0.228
Primary Branches/ Plant	G			0.528**	0.454**	-0.144	-0.170	0.408**	0.136	0.412**
	P			0.440 **	0.377 **	-0.083	-0.069	0.345 **	0.116	0.357 **
Secondary Branches/ Plant	G				0.396**	0.040	0.021	0.175	-0.015	0.346**
	P				0.3326 **	0.045	0.034	0.144	-0.005	0.3023 *
Pods/ Plant	G					-0.258*	-0.160	0.153	-0.096	0.865**
	P					-0.199	-0.134	0.134	-0.082	0.858 **
Pod Length cm	G						0.633**	0.289*	0.513**	0.052
	P						0.516 **	0.241 *	0.446 **	0.066
Seeds/ Pod	G							0.208	0.326**	0.084
	P							0.141	0.275 *	0.080
Days to Maturity	G								0.145	0.204
	P								0.133	0.182
100 Seed Weight gm	G									0.391**
	P									0.370 **

*, **: Significant at P=0.05 and P=0.01, level of probability, respectively,

Table-4 Phenotypic (P) and Genotypic (G) path coefficient analysis showing direct and indirect effects of different characters in pigeonpea

Character		Days to 50% Flowering	Plant Height (cm)	Primary Branches/ Plant	Secondary Branches/ Plant	Pods/ Plant	Pod length (cm)	Days to Maturity	100 Seed Weight (gm)	Correlation with grain yield/plant
Days to 50% Flowering	G	-0.087	-0.027	-0.015	-0.003	0.436	0.436	0.005	0.166	0.486
	P	-0.054	-0.017	-0.003	0.000	0.381	0.381	0.003	0.139	0.458 **
Plant Height (cm)	G	-0.030	-0.078	-0.009	-0.001	0.377	0.377	0.001	0.038	0.308
	P	-0.016	-0.058	-0.002	0.000	0.280	0.280	0.000	0.016	0.228
Primary Branches/ Plant	G	-0.043	-0.022	-0.031	-0.006	0.459	0.459	0.005	0.067	0.412
	P	-0.024	-0.015	-0.007	0.001	0.358	0.358	0.002	0.050	0.357 **
Secondary Branches/ Plant	G	-0.020	-0.004	-0.016	-0.011	0.400	0.400	0.002	-0.007	0.346
	P	-0.011	-0.003	-0.003	0.001	0.316	0.316	0.001	-0.002	0.302 **
Pods/ Plant	G	-0.038	-0.029	-0.014	-0.004	1.011	1.011	0.002	-0.047	0.865
	P	-0.022	-0.017	-0.003	0.000	0.950	0.950	0.001	-0.035	0.858 **
Pod length	G	-0.013	0.003	0.004	0.000	-0.261	0.003	0.058	0.004	0.253
	P	-0.007	0.000	0.001	0.000	-0.189	0.025	0.042	0.002	0.193
Seeds/ Pod	G	-0.009	-0.008	0.005	0.000	-0.162	-0.261	0.003	0.161	0.084
	P	-0.004	-0.004	0.000	0.000	-0.127	-0.189	0.001	0.119	0.080
Days to Maturity	G	-0.036	-0.004	-0.013	-0.002	0.155	-0.162	0.012	0.072	0.204
	P	-0.022	-0.003	-0.002	0.000	0.128	-0.127	0.007	0.058	0.182
100 Seed Weight (gm)	G	-0.029	-0.006	-0.004	0.000	-0.097	0.155	0.002	0.493	0.391
	P	-0.017	-0.002	-0.001	0.000	-0.078	0.128	0.001	0.433	0.370 **

*, **: Significant at P=0.05 and P=0.01, level of probability, respectively

Conflict of Interest: None declared

References

- [1] Sodavadiya M.S., Pithia J.J., Savaliya A.G. and Korat V.K. (2009) *Legume Research*, 32(3), 203-205.
- [2] Prasad Y., Kumar K. and Mishra S.B. (2013) *The bioscan*, 8(1), 207-211.
- [3] Singh R.K. and Chaudhury B.D. (1979) *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, Ludhiana, New Delhi, India.
- [4] Dewey J.R. and Lu K.H. (1959) *Agron. J.*, 51, 515-518.
- [5] Vange T. and Egbe M.O. (2009) *World J.Agric. Sci.*, 5(6), 714-719.
- [6] Oyiga B.C. and Uguru, M.I. (2011) *Inter. J. Plant Breed.*, 5(1), 58-63.
- [7] Mahiboobsa M., Dharmaraj P.S., Muniswamy S., Yamanura., Sony T., Avinalappa H., Patil R. and Bankar C. (2012) *Karnataka J. Agric. Sci.*, 25(4), 525-526.
- [8] Linge S.S., Kalpande H.V., Sawargaonkar S.L., Hudge B.V. and Thanki H.P. (2010) *Electronic j. plant breed.*, 1(4), 929-935.
- [9] Patel K.N. and Patel D.R. (1998) *Studies on genetic variability in pigeonpea. International chickpea and pigeonpea Newsletter*, 5, 28-30.
- [10] H.W., Robinson H.F. and Comstock R.E. (1955) *Agron. J.*, 47(10), 77-183.
- [11] Pandey N. and Singh N.B. (2002) *Madras Agric. J.*, 88, 640-643.
- [12] Sidhu P.S., Verma M.M., Cheema H.S. and Sra S.S. (1985) *Indian J. Agric. Sci.*, 55, 232-235
- [13] Dahiya S.K. and Singh S. (1994) *GAU Res. J.*, 20, 160-163.
- [14] Salunke J.S., Aher R.P., Sinde G.C. and Kute N.S. (1995) *Legume Research*, 18, 162-166.
- [15] Paul P.R., Singh R.M., Nandan R. and Raina R. (1996) *Madras Agric. J.*, 83, 34-37.
- [16] Thanki H.P. and Sawargaonkar S.L. (2010) *Electronic J., Plant Breed.*, 1(4), 936-939.