

GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR YIELD ATTRIBUTES IN PIGEONPEA

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ABSTRACT

The phenotypic and genotypic variances, correlation and path coefficient, heritability and genetic advances were estimated for grain yield and yield traits in 70 pigeonpea genotypes. The highest GCV was recorded for number of secondary branches/plant (61.81) followed by pods/plant (38.34). Heritability in broad sense ranged from 61.33 (seeds/pod) to 98.26 (days to 50% flowering). High genetic advance were observed for number of primary branches/plant (60.61), number of secondary branches/plant (154.10), 100-seed weight (50.82), grain yield/plant (84.65), pods/plant (92.59), plant height (33.83) and days to 50% flowering (45.05) indicating the prevalence of additive gene action for inheritance of these traits. Correlation and Path coefficient analysis (genotypic and phenotypic) revealed that pods/plant (0.858**), 100-seed weight (0.370**), days to 50% flowering (0.458**), primary branches (0.357**) and secondary branches (0.302**) had maximum direct effect resulted significantly positive correlation with grain yield/plant. These traits can be used to improve the grain yield of pigeonpea.

INTRODUCTION

Pigeonpea [*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 pigeonpea in the world and presently occupies an area of about 4.6 million hectares with an annual total production of 3.4 million tonnes and mean productivity of 780 kg/hectare. The area under pigeonpea in India is around 4.04 million hectare with a production of approximately 2.65 million tonnes. (Anonymous, 2012). As 'dal', pigeonpea is an important constituent of the Indian meal. It contains 20-21% protein (Sodavadiya *et al.*, 2009).

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 (Prasad *et al.*, 2013). It is needs fulfil its demand through pulses protein. Therefore, it is necessary to increase the production of pigeonpea, 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 pigeonpea. 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 seventy diverse genotypes of pigeonpea were sown in CRBD with three replications, during *Kharif*, 2008-09 at Agricultural Research Farm, Banaras Hindu University, Varanasi (25°18'N lat.,

83°C03' E long. and 129 m amsl.). 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 10 randomly selected plants from the plot of each replication on days to flowering, plant height, primary branch, secondary branch, pods/plant, pod length, seeds/pod, days to maturity, 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 Singh and Chaudhury (1979). All the data were analysed using Windostat version 8.6 from Indostat service Hyderabad, India. Path co-efficient analysis was estimated according to the method proposed by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The results of variance analysis is presented in the table no. 1, as see all the traits exhibited highly significant difference among treatments which indicated adequate genetic variability among the cultivars. It reveals that the selection 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 3). 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 Vange and Egbe (2009), Oyiga and Uguru (2011) and Mahiboobsa *et al.*, (2012).

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 Linge *et al.*, (2010) in pigeonpea. 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 Patel and Patel (1998) and Linge *et al.* (2010).

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. According to Johnson *et al.*, (1955), heritability estimates along with the genetic gain are usually more useful. 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 4) 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 Pandey and Singh (2002). Genotypic correlation provides a measure of genotypic association among different traits and helps in identifying the traits in selection.

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 Sodavadiya *et al.* (2009) and Linge *et al.* (2010) and Prasad *et al.* (2013) in pigeonpea. Thus, providing that these attributes were more influencing the yield in pigeonpea 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

Table 1: Analysis of variance (ANOVA) for yield and yield related traits in 70 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	100Seed Weight (gm)	Grain yield/ Plant
Replicate	2	15.10	153.82**	0.02	2.01	961.16**	0.07	0.06	12.70	0.61	30.07
Treatments	69	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

* = Singificance at 0.05 and ** = 0.01

Table 2: List of 15 selected superior cultivars of pigeonpea on the basis of yield and yield related traits

Cultivars	Grain yield/ Plant	Days to 50 % Flowering	Days to Maturity	Plant Height (cm)	Primary Branches/ Plant	Secondary Branches/ Plant	Pods/ Plant	Pod Length (cm)	Seeds/ Pod	100 Seed Weight (gm)
MAL 13	69.50	134.67	235.67	183.03	15.90	4.00	259.63	4.54	3.53	13.41
AMAR	64.50	126.33	234.33	182.17	14.90	10.27	330.33	4.13	3.17	11.36
AZAD	58.38	125.00	237.67	164.60	12.10	7.67	254.00	4.37	3.40	12.25
ICP 13626	57.68	143.00	235.33	166.10	11.50	10.00	287.67	4.50	3.73	9.81
DA 11	55.91	137.00	249.33	213.83	15.27	5.40	276.00	4.43	3.23	10.93
ICP 9149	51.61	122.00	249.33	158.37	17.67	16.47	268.87	4.64	3.30	10.17
BAHAR	51.35	114.67	237.00	165.00	14.17	10.20	200.43	4.26	3.50	12.89
BSMR 853	50.56	136.33	243.00	176.07	14.57	9.90	158.63	4.71	3.33	16.80
KPBR 80-2-1	50.27	132.33	244.33	166.83	14.00	6.23	235.17	4.50	3.40	11.41
ICPR 3760	49.55	116.00	234.33	164.50	19.93	18.27	210.17	4.35	3.43	12.08
MAL 6	49.38	144.00	238.67	198.23	22.00	5.00	223.00	4.32	3.27	11.70
MAL 3	48.94	153.67	236.33	217.50	17.67	3.33	281.13	3.44	3.20	9.67
WF 10-1	46.88	120.67	243.33	159.17	20.03	4.90	155.83	3.70	3.27	16.12
ICPR 4105	45.62	125.00	237.00	191.67	15.00	4.17	210.77	4.39	3.43	10.75
MAL 24	44.36	114.00	239.67	162.13	14.67	10.55	208.40	4.27	3.23	11.18

Table 3: Estimation of genetic parameters for agronomic traits in pigeonpea cultivars

Parameters	Range	General Mean	Variance Genotypic	Phenotypic	CV Genotypic (%)	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	16.83-335.33	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
Grain yield/ Plant	9.57-68.32	35.17	145.30	166.00	34.27	36.63	87.53	29.77	84.65

Table 4: 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 **

* = Singificance at 0.05 and ** = 0.01

reported by Sidhu, *et al.* (1985), Bhongale and Raut (1987), Dhedhi *et al.* (1997) 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 5) 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 4). 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. Dahiya and Singh (1994), Salunke *et al.* (1995), Paul *et al.* (1996), Thanki *et al.* (2010) and Bhadru (2011) 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

Table 5: Phenotypic (P) and Genotypic (G) path coefficient analysis showing direct (bold) 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)	Seeds/ Pod	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	0.000	0.010	0.005	0.166	0.486
	P	-0.054	-0.017	-0.003	0.000	0.381	0.003	0.006	0.003	0.139	0.458 **
Plant Height (cm)	G	-0.030	-0.078	-0.009	-0.001	0.377	0.000	0.010	0.001	0.038	0.308
	P	-0.016	-0.058	-0.002	0.000	0.280	0.000	0.006	0.000	0.016	0.228
Primary Branches/ Plant	G	-0.043	-0.022	-0.031	-0.006	0.459	0.000	-0.016	0.005	0.067	0.412
	P	-0.024	-0.015	-0.007	0.001	0.358	-0.002	-0.006	0.002	0.050	0.357 **
Secondary Branches/ Plant	G	-0.020	-0.004	-0.016	-0.011	0.400	0.000	0.002	0.002	-0.007	0.346
	P	-0.011	-0.003	-0.003	0.001	0.316	0.001	0.003	0.001	-0.002	0.302 **
Pods/ Plant	G	-0.038	-0.029	-0.014	-0.004	1.011	-0.001	-0.015	0.002	-0.047	0.865
	P	-0.022	-0.017	-0.003	0.000	0.950	-0.005	-0.011	0.001	-0.035	0.858 **
Pod Length (cm)	G	-0.013	0.003	0.004	0.000	-0.261	0.003	0.058	0.004	0.253	0.052
	P	-0.007	0.000	0.001	0.000	-0.189	0.025	0.042	0.002	0.193	0.066
Seeds/ Pod	G	-0.009	-0.008	0.005	0.000	-0.162	0.002	0.092	0.003	0.161	0.084
	P	-0.004	-0.004	0.000	0.000	-0.127	0.013	0.082	0.001	0.119	0.080
Days to Maturity	G	-0.036	-0.004	-0.013	-0.002	0.155	0.001	0.019	0.012	0.072	0.204
	P	-0.022	-0.003	-0.002	0.000	0.128	0.006	0.012	0.007	0.058	0.182
100 Seed Weight (gm)	G	-0.029	-0.006	-0.004	0.000	-0.097	0.002	0.030	0.002	0.493	0.391
	P	-0.017	-0.002	-0.001	0.000	-0.078	0.011	0.023	0.001	0.433	0.370 **

*, **: Significant at P=0.05 and P=0.01, level of probability, respectively, Residual effect R = 0.235 (Phenotypic path), Residual effect R = 0.077 (Genotypic path)

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. 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.

From the present investigations here concluded that the estimation of genetic variability, correlation and path analysis, are more useful to identification of superior cultivars for yield and yield traits (Table 2). The cultivars MAL 13, AMAR, AZAD, ICP 13626 and DA 11 on the basis of *per se* performance were found high yielder in all 70 cultivars. These cultivars may be used to breeding program for development of high yielding varieties.

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