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Component Analysis in Pigeonpea (*Cajanus cajan* L. Millsp)

Key words : Correlation, Heritability, Path Analysis, Pigeonpea, Variability

Pigeonpea is the second most important pulse crop after chickpea and is being grown throughout the country. It constitutes an important source of dietary protein in human vegetarian diet. Under rainfed situations, it provides more stable productivity over environments and seasons compared to cereals with which it is often intercropped. The pigeon pea plant which probably evolved under severe pressure for survival due to various biotic and abiotic stresses has developed several adaptability characteristic features like production of huge biomass and prolonged flowering (Okiror, 2002), endowed with these several unique characteristics, it finds an important place in the farming systems adapted by small holding farmers.

An understanding of the nature and magnitude of existing variability for important yield attributing characteristics is necessary for a successful breeding programme. Selection for yield *per se* generally remains unsuccessful in achieving desirable results because yield is dependent on various component characters. Therefore, knowledge of association and cause and effect relationship of yield component traits with yield would help in formulating effective selection schemes.

Experimental material for the present study had of ten parents and twenty four crosses evolved from L x T deign with six lines and four testers. The material was raised in a randomized block design with three replications at Agricultural Research Station, Tandur during *kharif* 2007. Each entry was sown in 5m long single row plot at 1m x0.2m spacing. Recommended package of practices were adopted to raise the crop. Observations on five randomly selected competitive plants were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pod clusters per plant, number of pods per plant, 100-seed weight and yield per plant. The genotypic correlations were worked out by the formula as suggested by Falconer (1964) and path analysis in accordance with Dewey and Lu (1959).

The results on mean performance of parents and crosses revealed substantial amount of variability for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pod clusters per plant, number of pods per plant, 100-seed weight and yield per plant (Table 1). The differences among the genotypes were highly significant for all the traits. Phenotypic and genotypic variability was low to moderate for all the characters studied. Genotypic coefficient of variability was highest for number of clusters per plant followed by number of primary branches per plant, 100- seed weight and days to 50% flowering. Similar finding was reported by Saxena and Kataria (1993). However, it was lowest for plant height, days to maturity and number of pods per plant.

The difference between genotypic and phenotypic coefficient of variability for days to 50% flowering, days to maturity, 100- seed weight and number of pod clusters per plant was low. The results were in agreement with the earlier reports of Natarajan *et al.,* (1990).

High heritability was registered by days to 50% flowering, days to maturity, number of primary branches per plant, number of clusters per plant and 100- seed weight. These results are in agreement with the earlier findings of Srinivas, (1996) and Aher *et al.,* (1998). Low heritability was recorded for plant height which was reported by Natarajan *et al.,* (1990). Moderate heritability estimates were obtained for number of pods per plant and seed yield per plant. Patil *et al.,* (1989) revealed similar results for these characters.

Genetic advance as per cent of mean was moderate for days to maturity, number of primary branches per plant, number of pod clusters per plant and 100-seed weight and it was low for days to maturity, plant height, number of pods per plant and seed yield per plant. Days to maturity and seed yield were registered low genetic advance as percent of mean.

Table 1. Estimates of mean, range, phenotypic and genotypic coefficients of variability, heritability and genetic advance for eight characters in pigeonpea

Character	Mean	Range		Genotypic coefficient of variation	Phenotypic coefficient of variation	Herita-bility %	Genetic advance	Genetic advance as% of mean
		Min.	Max.					
Days to 50 % flowering	106.53	76.67	126.67	10.41	10.56	97.00	22.54	21.16
Days to maturity	163.74	135.67	190.00	6.79	6.86	98.00	22.64	13.83
Plant height	177.37	142.23	198.87	4.71	9.16	26.00	8.83	4.98
No. of primary branches plant^{-1}	13.54	9.20	18.33	14.90	17.13	76.00	3.61	26.68
No. of clusters plant^{-1}	74.50	55.83	97.17	15.01	16.61	82.00	20.81	27.94
No. of Pods plant^{-1}	393.02	301.99	496.30	9.93	14.19	49.00	56.29	14.32
100 seed weight	11.41	8.41	13.54	11.88	12.59	89.00	2.63	23.08
Seed yield plant^{-1}	49.40	40.73	62.03	10.03	14.34	49.00	7.14	14.45

Table 2. Phenotypic and genotypic correlations for yield and its characters in pigeonpea

		Days to 50% flowering	Days to maturity	Plant height	No.of primary branches plant^{-1}	No.of clusters plant^{-1}	No. of pods plant^{-1}	100 seed weight	Seed yield plant^{-1}
Days to 50 % flowering	P	1.0000	0.8709**	0.5859**	0.6412**	0.5576**	0.4146*	0.4501**	0.3683*
	G	1.0000	0.8851**	1.1108**	0.7334**	0.6142**	0.6253**	0.4815**	0.5436**
Days to maturity	P		1.0000	0.5378**	0.5284**	0.5561**	0.4169*	0.3487*	0.3889*
	G		1.0000	1.0436**	0.6248**	0.6092**	0.6082**	0.3784*	0.5702**
Plant height	P			1.0000	0.4961**	0.4084*	0.3442*	0.2882	0.2890
	G			1.0000	1.0944**	0.7442**	1.1766**	0.6866**	0.9119**
No. of primary branches plant^{-1}	P				1.0000	0.6424**	0.5417**	0.5032**	0.5792**
	G				1.0000	0.8431**	0.8348**	0.6306**	0.9379**
No. of clusters plant^{-1}	P					1.0000	0.4228*	0.4073*	0.4895**
	G					1.0000	0.7740**	0.4791**	0.8366**
No. of pods plant^{-1}	P						1.0000	0.3520*	0.5405**
	G						1.0000	0.5251**	0.9891**
100 seed weight	P							1.0000	0.4734**
	G							1.0000	0.6944**
Seed yield plant^{-1}	P								1.0000
	G								1.0000

** Significant at 1 per cent level, * Significant at 5% level

Table 3: Genotypic and phenotypic estimates of direct and indirect effects between yield and its components in pigeonpea

		Days to 50% flowering	Days to maturity	Plant height	No.of primary branches plant^{-1}	No.of clusters plant^{-1}	No. of pods plant^{-1}	100 seed weight	Correlation with yield
Days to 50 % flowering	P	**[-0.3488]**	0.2351	-0.0152	0.2128	0.0688	0.111	0.1045	0.3683*
	G	**[-0.7710]**	0.2609	0.2805	0.331	0.1037	0.2325	0.1059	0.5436**
Days to maturity	P	-0.3037	**[0.2700]**	-0.014	0.1754	0.0686	0.1117	0.081	0.3889*
	G	-0.6824	**[0.2948]**	0.2635	0.282	0.1029	0.2261	0.0832	0.5702**
Plant height	P	-0.2043	0.1452	**[-0.0260]**	0.1646	0.0504	0.0922	0.0669	0.2890
	G	-0.8564	0.3076	**[0.2525]**	0.4939	0.1257	0.4375	0.151	0.9119**
No. of primary branches plant^{-1}	P	-0.2237	0.1427	-0.0129	**[0.3319]**	0.0793	0.1451	0.1169	0.5792**
	G	-0.5654	0.1842	0.2763	**[0.4513]**	0.1424	0.3104	0.1387	0.9379**
No. of clusters plant^{-1}	P	-0.1945	0.1502	-0.0106	0.2132	**[0.1234]**	0.1132	0.0946	0.4895**
	G	-0.4735	0.1796	0.1879	0.3805	**[0.1689]**	0.2878	0.1054	0.8366**
No. of pods plant^{-1}	P	-0.1446	0.1126	-0.0089	0.1798	0.0522	**[0.2678]**	0.0817	0.5405**
	G	-0.4821	0.1793	0.2971	0.3767	0.1307	**[0.3718]**	0.1155	0.9891**
100 seed weight	P	-0.157	0.0942	-0.0075	0.167	0.0502	0.0943	**[0.2322]**	0.4734**
	G	-0.3712	0.1115	0.1734	0.2846	0.0809	0.1952	**[0.2200]**	0.6944**

Values in parenthesis are direct effects
Genotypic residual effect = 0.3646
Phenotypic residual effect = 0.8792

* = Significant at 5 per cent level; ** = Significant at 1 per cent level

Correlations and path coefficients provide a realistic basis for allocation of weightage to each of the contributing characters in deciding upon a suitable selection criteria for genetic improvement of complex characters like yield. The nature and magnitude of genotypic correlation coefficients obtained among 8 characters in 24 crosses revealed that almost all characters exhibited significant positive correlation with yield (Table 2).

Correlation of yield with number of pods per plant was higher followed by number of primary branches per plant, plant height, number of clusters per plant, 100- seed weight, days to maturity and days to 50% flowering. These results are in agreement with the earlier findings of Lal *et al.,* (2002) and Chatopadhyaya and Dhiman (2005).

Path coefficient analysis (Table 3) revealed that number of primary branches per plant recorded the highest direct effect on seed yield followed by number of pods per plant, days to maturity and plant height. Days to 50% flowering recorded negative direct effect on seed yield. These results are in agreement with the earlier findings of Vannirajan (1997) and Lal *et al.* (2002).

Based on the studies of associations and path effects, it can be opined that, the traits *viz.,* primary branches per plant, pods per plant, 100-seed weight and clusters per plant can be considered as important for obtaining higher seed yield and therefore, selection may be initiated for the improvement of these component traits to achieve higher seed yield in redgram.

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