



Research Article

GENETIC ASSOCIATION STUDIES FOR YIELD AND YIELD RELATED TRAITS IN PIGEONPEA (*CAJANUS CAJAN*)

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Abstract: Twenty five Pigeonpea genotypes were evaluated in a randomized block design during Kharif 2017-2018. The objective of this research was to study correlation, direct and indirect effects among yield and other fifteen yield related traits aim for genetic improvement of Pigeonpea. Seed yield per plant had positive and highly significant correlation with biological yield (0.983), harvest index (0.788), number of seeds per pod (0.462), number of pod cluster per plant (0.311) and number of pods per plant (0.313). Thus, selection for higher yield on the basis of above characters would be consistent. Seed yield per plant exhibited positive but not significant correlation with days to flowering initiation (0.187), days to 50 % flowering (0.118), 100 seed weight (0.149), dal recovery (0.099) and rest all characters are negatively correlated with seed yield per plant. The characters viz., number of pod cluster per plant (1.655), biological yield (0.754), harvest index (0.288) showed high and positive direct effect on seed yield per plant and it was positive and moderate in case of number of primary branches (0.103). The direct effect of number of pods per plant (-1.625), number of secondary branches (-0.181), days to flower initiation (-0.074) seems to be high but in negative direction.

Keywords: Pigeonpea, trait, correlation, path analysis, harvest index, earliness, Seed yield

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Introduction

Pigeonpea also known as red gram [*Cajanus cajan* (L.) Millsp.], ($2n=2x=22$) is the world fifth highest growing crop and second in India after chickpea. It is growing in rainfed condition and provides food, fuel, wood and fodder. It is a major pulse growing crop of supportable agriculture grown tropical and sub-tropical parts of the world. Pigeonpea has better soil upgrading qualities such as release of soil-bound phosphorous, soil nutrients recycling, atmospheric nitrogen fixation, and addition of organic matter and other nutrients etc. It is mainly cultivated as a sole crop or as a mixed crop with cereals or legumes as well as with other short duration crops like cotton and groundnut. Pigeonpea is a hardy and drought tolerant crop assuring justifiable returns from marginal lands with short input, hence it is considered as very suitable crop for sustainable agriculture. Pigeonpea seeds having 20%-24% protein and rational amounts of essential amino acid making it an important source of dietary protein, mainly for vegetarian population. The seed and husks of pod make quality feed for animals, whereas stems and dry branches serve as domestic fuel. Fallen leaves from the plant provide vital nutrient to the next crop also enriches soil through symbiotic nitrogen fixation [1]. The trait for grain yield is controlled by complex gene action and hence traits attributing to yield must be considered and evaluated because the yield component may not necessarily be independent in nature. Hence, direct selection for yield may not be very effective. The selection practiced for one character may simultaneously bring change in the other traits. Thus, to bring change in any characters especially in seed yield proper understanding of interrelationship among yield and yield components characters is must. This may help in selection of traits with high expression and association with yield without affecting other traits. If association is positive, it significantly will accelerate the rate of desirable genes. While correlation in direct negative, will retard the genetic progress except for the traits like earliness.

Materials and methods

The details of experimental site, period of experiment, materials used, and

methods adopted for conduction of experiments and analysis of data during the course of investigation are described. The experiment was conducted at Research cum Instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during kharif 2017-18 under the AICRP on Pigeonpea, Department of Genetics & Plant Breeding. In Hybridization programme 5 parents namely Rajeevlochan, BSMR-571, BSMR-2, RPS-2007-10 and ASHA were crossed to each other in full diallel fashion to generate set of hybrids. A total of 20 hybrids were synthesized by hand emasculation and pollination. Sufficient numbers of hand pollinated seeds were produced during 2016-17 rainy season. In emasculation the bud most likely to shed pollen the next day were selected. These buds were approximately 60 percent's the size of a mature bud and were tightly closed. It is best to select two buds per inflorescence for emasculation and two to ten buds can be emasculated on branch and other buds are removed [2]. A fairly leveled and uniform plot was selected for experimentation. Field was prepared by cross ploughing by tractor after the harvest of previous crop. The weeds and crop residues were removed to get neat and clear field. Layout was done with the help of measuring tape, rope and sticks, etc. Sowing was done by hand dibbling in rows made with the help of kudali. 5 elite Pigeonpea genotypes and their Crossed in full diallel fashion were grown in Randomized Block Design (RBD) with two replications during kharif 2017-18. All the agronomical Package of practices recommended was adopted and fertilizer dose of 20N: 50P: 20K kg ha⁻¹ was applied. Sowing of genotypes was on 03/07/2017 keeping inter and intra row spacing of 60 and 20 cm, respectively. Each genotype was represented by 2 rows of 4 m length with border rows at either side of replication. Observations were recorded on single plant basis on five randomly selected competitive plants, separately from each replication. Whereas, observation on days to flower initiation, days to 50 percent flowering and days to maturity were recorded on plot basis. Protein analysis work was done in the Quality Laboratory, Department of Genetics & Plant Breeding, College of Agriculture, IGKV, Raipur, Chhattisgarh, 492012.

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Table-1 Genotypic (G), Phenotypic (P) and Environmental (E) correlation coefficients for seed yield and its components in Pigeonpea

SN	Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary Branches plant ⁻¹	Secondary Branches plant ⁻¹	No. of Pods plant ⁻¹	No. Pod clusters plant ⁻¹	Pod length(cm)	No. of Seeds pod ⁻¹	100 seed weight (g)	Biological yield	Protein (%)	Dal recovery (%)	Harvest Index(%)	Grain yield plant ⁻¹
1	Days to flower initiation	P	0.840**	0.428**	-0.267	-0.466**	-0.431**	0.223	0.196	-0.207	-0.045	0.446**	0.171	-0.057	-0.17	0.021	0.163
		G	0.990**	0.411**	-0.371**	-0.658**	-0.596**	0.239	0.224	-0.320*	-0.105	0.525**	0.208	-0.119	-0.207	0.12	0.187
		E	0.496**	0.464**	0.19	-0.018	0.068	0.212	0.123	-0.116	0.01	0.206	-0.003	0.182	-0.067	0.196	0.132
2	Days to 50% flowering	P		0.281*	-0.254	-0.365**	-0.345*	0.189	0.163	-0.128	-0.079	0.474**	0.094	-0.046	-0.049	0.105	0.088
		G		0.297*	-0.232*	-0.605**	-0.535**	0.164	0.17	-0.144	-0.234	0.519**	0.11	-0.173	-0.01	0.102	0.118
		E		0.268	0.093	0.279*	0.336*	0.360*	0.157	-0.133	0.086	0.337*	0.003	-0.04	-0.187	0.177	-0.156
3	Days to maturity	P			0.153	0.21	0.181	-0.091	-0.125	0.041	0.225	0.497**	-0.045	-0.202	0.043	0.064	-0.049
		G			220	0.282*	0.318*	-0.2	-0.227	0.273	0.186	0.566**	-0.054	-0.321*	-0.031	0.138	-0.046
		E			-0.015	0.095	-0.115	0.248	0.173	-0.137	0.264	0.527**	-0.245	0.088	0.225	-0.227	-0.163
4	Plant height (cm)	P				0.649**	0.653**	-0.163	-0.158	0.158*	-0.228	0.117	-0.329	-0.042	0.128	-0.155	-0.009*
		G				0.791**	0.723**	-0.199	-0.194	0.365**	-0.456**	0.119	-0.339*	-0.045	0.182	-0.186	-0.309*
		E				-0.042	0.135	0.239*	0.288*	-0.233	-0.155	0.096	-0.111	-0.013	-0.297*	0.354*	-0.088
5	Primary Branches plant ⁻¹	P					0.914**	-0.206	-0.213	0.237	-0.088	0.184	-0.328	-0.128	0.286	0.05	0.256
		G					1.031**	-0.24	-0.228	0.743**	-0.062	0.214	-0.381**	-0.15	0.421**	0.039	-0.310*
		E					0.518**	-0.066	-0.179	-0.312*	-0.135	0.062	-0.189	-0.042	-0.184	0.147	0.076
6	Secondary Branches plant ⁻¹	P						-0.215	-0.218	0.306*	-0.173	0.117	-0.481**	-0.048	0.235	-0.086	0.412
		G						-0.237	-0.231	0.784**	-0.096	0.133	-0.529**	-0.025	0.380**	-0.097	-0.464*
		E						-0.068	-0.135	-0.332	-0.366**	0.001	0.112	-0.193	-0.469**	0.003	0.12
7	No. of Pods plant ⁻¹	P							0.992	0.091	0.174	0.156	0.227	0.001	0.223	0.402	0.275
		G							1.000**	0.14	0.310*	0.191	0.239	0.028	0.232	0.419**	0.313*
		E							0.909**	0.052	0.007	0.247	0.183	0.26	0.175	0.176	0.487**
8	No. Pod clusters plant ⁻¹	P								0.095	0.177	0.158	0.226	0.008	0.227	0.398	0.276
		G								155	0.300*	-0.186	0.239	-0.043	0.254	0.418**	0.311*
		E								0.035	0.043	0.159	-0.197	-0.318*	0.056	0.133	-0.435**
9	Pod length(cm)	P								0.37	0.207	-0.264	-0.222	0.206	-0.07	-0.223	
		G								-0.128	-0.213	-0.459**	-0.344**	0.201	-0.088	-0.381**	
		E								0.121	-0.394	0.122	-0.123	0.292*	-0.111	-0.034	
10	No. of Seeds pod ⁻¹	P										-0.057	0.25	-0.146	0.034	0.173	0.229
		G										-0.084	0.434**	-0.435**	-0.046	0.397**	0.462**
		E										-0.043	-0.06	0.342*	0.17	-0.280*	-0.307*
11	100 seed weight (g)	P											0.019	-0.181	0.113	0.213	0.129
		G											0.123	-0.211	0.146	0.222	0.149
		E											0.017	0.119	-0.129	0.07	-0.237*
12	Biological yield	P												-0.291	0.027	0.614	0.971
		G												-0.311*	0.036	0.632**	0.983**
		E												0.194	-0.400**	-0.239	-0.247
13	Protein (%)	P													-0.252	0.437	-0.337
		G													-0.27	-0.474**	-0.367**
		E													-0.148	-0.012	0.111
14	Dal recovery (%)	P														0.289	0.093
		G														0.336*	0.099
		E														-0.084	0.067
15	Harvest Index(%)	P															0.755**
		G															0.778**
		E															0.165

Table-2 Direct and indirect effects of 10 quantitative characters on seed yield per plant in Pigeonpea

SN	Characters	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary Branches plant ⁻¹	Secondary Branches plant ⁻¹	No. of Pods plant ⁻¹	No. Pod clusters plant ⁻¹	Pod length(cm)	No. of Seeds pod ⁻¹	100 seed weight (g)	Biological yield	Protein (%)	Dal recovery (%)	Harvest Index (%)	correlationGrain yield plant ⁻¹
1	Days to flower initiation	-0.074	0.042	0.018	-0.019	-0.067	0.108	-0.388	0.037	-0.002	-0.008	0.157	0.001	0.013	0.012	0.034	0.187
2	Days to 50% flowering	-0.073	0.042	0.013	-0.016	-0.062	0.097	-0.266	0.281	0.001	-0.005	-0.008	0.008	0.001	0.001	0.028	0.118
3	Days to maturity	-0.03	0.012	0.045	0.011	0.029	-0.0576	0.324	-0.377	-0.003	0.005	-0.01	-0.0406	0.003	0.002	0.039	-0.046
4	Plant height (cm)	0.027	-0.0136	0.009	0.052	0.0814	-0.131	0.323	-0.32	-0.004	-0.011	-0.002	-0.255	0.001	-0.011	-0.053	-0.309*
5	Primary Branches plant ⁻¹	0.049	-0.0257	0.012	0.041	0.103	-0.187	0.389	-0.377	-0.009	-0.001	-0.003	-0.288	0.002	-0.026	0.0111	-0.310*
6	Secondary Branches plant ⁻¹	0.044	-0.022	0.014	0.037	0.106	-0.181	0.385	-0.382	-0.009	-0.002	-0.002	-0.398	0.001	-0.023	-0.027	-0.464*
7	No. of Pods plant ⁻¹	-0.017	0.006	0.008	-0.01	-0.024	0.042	-1.625	1.655	-0.002	0.008	0.003	0.18	-0.001	-0.014	0.112	0.313*
8	No. Pod clusters plant ⁻¹	-0.0164	0.0072	-0.01	-0.0099	-0.0234	0.0419	-1.6245	1.655	-0.0018	0.0075	0.0029	0.18	-0.0004	-0.0155	0.1187	0.311*
9	Pod length(cm)	0.02362	-0.0061	0.0122	0.0188	0.0764	-0.1422	-0.2291	0.2567	-0.0118	-0.0032	0.0034	-0.3463	0.0037	-0.0122	-0.025	-0.381**
10	No. of Seeds pod ⁻¹	0.0077	-0.0099	0.0083	-0.0235	-0.0063	0.0174	-0.5035	0.4965	0.0015	0.0252	0.0013	0.3271	0.0047	0.0028	0.1128	0.462**
11	100 seed weight (g)	-0.0387	0.022	0.0253	0.0061	0.0219	-0.0241	0.31	-0.3075	0.0025	-0.0021	-0.0159	0.0931	0.0022	-0.0089	0.0632	0.149
12	Biological yield	-0.0153	0.0046	-0.0024	-0.0174	-0.0392	0.0958	-0.3881	0.395	0.0054	0.0109	-19	0.7546	0.0034	-0.0022	0.1798	0.983**
13	Protein (%)	0.0087	-0.0073	-0.0143	-0.0023	-0.0153	0.0045	-0.0449	0.0712	0.004	-0.011	0.0034	-0.2349	-0.0108	0.0165	-0.1349	0.367**
14	Dal recovery (%)	0.0152	-0.0004	-0.0014	0.0093	0.0433	-0.0689	-0.37774	0.4204	-0.0023	-0.0011	-0.0023	0.0207	0.0029	-0.0611	0.0954	0.099
15	Harvest Index (%)	-0.0088	0.0043	0.0062	-0.0095	0.004	0.0176	-0.6812	0.6912	0.001	0.01	-0.0035	0.4772	0.0051	-0.0205	0.2844	0.778**

Residual effect = 0.00684; Direct effects on main diagonal (bold figures), *Significant at 5%, ** significant at 1%

Results and Discussion

The correlation co-efficient and path analysis for grain yield per plant and its contributing characters for 25 genotypes at phenotypic and genotypic and environment levels are presented in Table 1 and Table 2 respectively. Breeder always goes for the selection of superior genotypes on the basis of phenotypic expression. But due to quantitative characters, genotypes are influenced by environment, thereby affecting the phenotypic expression finding breeder difficult for selecting an appropriate character which affecting yield. *i.e.*, why the genotypic correlations were, in general, higher in magnitude than the corresponding correlations at phenotypic level. Genotypic correlation will provide the genotypic association between different yield attributing traits and helpful for the plant breeders to correctly identify the appropriate traits. Correlation positive value shows that the changes of one with other variables are in the same direction, *i.e.*, high value of one variable are associated with high values of another variable and vice-versa. When correlation is negative the two variables movements are not in same directions, *i.e.*, high values of one variable are associated with low values of other. Seed yield per plant had positive and highly significant correlation with biological yield (0.983), harvest index (0.788), number of seeds per pod (0.462), number of pod cluster per plant (0.311) and number of pods per plant (0.313). Thus, selection for greater yield on the basis of above characters would be profitable. These characters have also been identified as strong associate of yield by scientist [3-6]. However, seed yield exhibited positive but not significant correlation with days to flowering initiation (0.187), days to 50 % flowering (0.118), 100 seed weight (0.149), dal recovery (0.099). Scientist [7] also reported positive association of 50% flowering with grain yield. Similar results were reported by scientist [8-12]. Studies indicated highly significant positive association of number of pods per plant both at phenotypic and genotypic level with seed yield per plant. Scientist [8, 12-14] noted the positive and significant association of grain yield per plant with number of pods per plant. But non-significant negative correlation noticed with days to maturity (-0.046). Biological yield per plant showed significant positive correlation with harvest index (0.632), number of seeds per pod (0.434) and positive non-significant with 100 seed weight (0.123), days to 50% flowering (0.110), days to flowering initiation (0.208) indicating that improvement in biological yield, if selection imparted may boost the per se performance of these characters. Similar finding was also reported by [15]. Correlation does not provide exact picture of the direct and indirect causes of such association, which can be clearly understand through path analysis. Direct selection of any character is only useful when its direct effect is near to same magnitude as that of total effect and when its indirect effect is responsible for bringing total effect indirect selection is practiced. Path coefficient analysis as resulted shows the partitioning of correlation coefficients into direct and indirect effects and gives a more accurate relationship of the characters and helps in identifying the effective contributing traits. In the present investigation, path analysis was carried out using genotypic correlation of component traits on seed yield per plant. At genotypic level the analysis had residual effect of PR = 0.00684. The characters viz., number of pod cluster per plant (1.655), biological yield (0.754), harvest index (0.288) showed high and positive direct effect on seed yield per plant and it was positive and moderate in case of number of primary branches (0.103). The direct effect of number of pods per plant (-1.625), number of secondary branches (-0.181), days to flower initiation (-0.074) seems to be high but in negative direction. This clearly specifies that character seed yield can be improved by deliver to selection for all these traits. 100-seed weight (-0.0108) and Pod length (-0.0118) had low and negative direct effect on seed yield per plant. This indicated that this trait is not so important trait for seed yield improvement programme. Hence based on path analysis, number of pod cluster per plant, biological yield, harvest index, number of pods per plant, number of secondary branches, days to flower initiation should be given importance in seed yield improvement programme. Hence, direct selection for these traits could be practiced for developing high yielding and bold seeded Pigeonpea genotypes. Harvest index exhibited high order positive indirect effects on seed yield per plant via number of pod cluster per plant (0.6912) and biological yield (0.4772). Similarly, biological yield per plant exerted substantial positive indirect effects on seed yield per plant via number of seeds per pod (0.3271), number of pod per plant (0.180), number of pod cluster per plant (0.180),

100 seed weight (0.0931). Similar findings were also reported by scientist [4-6, 16-19]. This research shows plant height had positive direct effect on seed yield per plant. [16] reported plant height had direct effect on grain yield per plant. Scientist [20] reported days to flowering had negative direct effect on seed yield which is accordance as in the present investigation.

Conclusion

It is to be stated that, on the basis of correlation and path analysis studied, grain yield per plant could be improved through simultaneous selection of trait. Considering correlation study traits like; biological yield, harvest index, number of seeds per pod, number of pod cluster per plant and number of pods per plant emerged as most important associates of seed yield.

Application of research: Path analysis identified pod cluster per plant, biological yield, harvest index showed high and positive direct effect on seed yield per plant and it was positive and moderate in case of number of primary branches are noticed as most important direct yield contributing traits. It is desirable to give more weightage to these characters in selection programme for seed yield. Better selection strategy aimed at developing high yielding varieties in Pigeonpea.

Research Category: Genetics and Plant Breeding

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Study area / Sample Collection: Protein analysis work was done in the Quality Laboratory, Department of Genetics & Plant Breeding, College of Agriculture, IGKV, Raipur, Chhattisgarh, 492012

Cultivar / Variety name: *Cajanus cajan* (L.) Millsp

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

References

- [1] Varshney R.K. (2010) *Mol breed.*, 26(3), 393-408.
- [2] Sharma D., Green J.M. (1980) *Pigeon pea*. In WR. Fehr and H.H. Hadley (eds). *Hybridization of Crop plant*, Madison, ASA, 471-481.
- [3] Kanade P.B., Harer P.N. and Kshirsagar A.N. (2010) *J. Maharashtra Agric. Univ.* 35,494-496.
- [4] Sodavadia P.R., Pithia M.S., Savaliya J.J., Oansuriya A.G. and Korat V.P. (2009) *Legume Res.* 32, 131-134.
- [5] Mittal V.P., Paramjit Singh and Brar K.S. (2010) *Madras Agric. J.* 97, 319-320.
- [6] Devi S.R., Prasanthi L., Reddy K.H.P. and Reddy B.V.B. (2012) *Legume Res.* 35, 207-213.
- [7] Aher R.P., Thombre B.B. and Dahat D.V. (1998) *Legume Res.*, 21(1), 41-44.
- [8] Mahendran (2011) *Morphological and Biochemical Characterization of Short Duration Pigeonpea (Cajanus cajan (L.) Millsp) Genotypes*. Ph.D. Thesis. Tamil Nadu Agricultural University, Madurai.

- [9] Saroj S.K., Singh M.N., Kumar R., Singh T., Singh M.K. (2013) *The Bioscan*, 8(3),941–4.
- [10] Katiyar P.K., Dua R.P. Singh I.P. Singh B.B., Singh F. (2004) *Legume Res.*, 27 (3), 164-170.
- [11] Kesha Ram, Saxena Kanak, M. Shrimali Tushar and Bisnoi Geeta (2016) *International Journal of Agriculture Sciences*, 8(51), 2287-2289.
- [12] Gowda M.B., Shambulingappa K.G., Shathala J. and Prakash J.C. (1996) *Mysore J. Agric. Sci.*, 30, 64-68.
- [13] Paul P.R., Singh R.M. and Raina R. (1996) *Legume Res.*, 33 (3), 196-200.
- [14] Praveen Pandey, Rajesh Kumar and Vankat Raman Pandey (2015) *Legume Research*, 39 (2), 189-193.
- [15] Sreelakshmi C., Sameer Kumar C.V., Shivani D. (2010) *Electron J Plant Breed* 1(6), 1488-1491.
- [16] Nag Y.K. and Sharma R.N. (2012) *Electronic J. Plant Breeding*, (2), 818-824.
- [17] Yerimani A.S., Mehetre S. and Kharde M.N. (2013) *Molecular Plant Breeding*, p. 136-140.
- [18] Jaggal L.G., Talikoti M.M. and Jakkeral S.A. (2012) *Legume Res.*, 9(2), 64- 67.
- [19] Sreelakshmi C., Shivani D. and Kumar C.V.S. (2011) *Electronic J. Plant Breeding*, 2(3), 413-416.
- [20] Rao P.J.M., Malathi S., Reddy D.V.V. and Upender M. (2013) *Intl. J. of Scientific and Res. Publications*, 3(8), 2250-3153.