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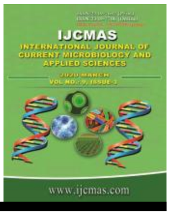

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Genetic Variability, Correlation and Path Analysis for Yield and its Attributes in Long Duration Pigeonpea [*Cajanus cajan*(L.)] Genotypes

T. Alaka[1], Ashutosh[1]*, A. Nishant Bhanu[1], M. N. Singh[1],
Sunil Kumar[1] and S. Swarnmala[2]

[1]*Department of Genetics and Plant Breeding, Institute of Agricultural Sciences,*
Banaras Hindu University, Varanasi-221005, India
[2]*Department of Botany, Institute of Science, Banaras Hindu University,*
Varanasi-221005, India

**Corresponding author*

ABSTRACT

The present investigation was carried out to obtain the information in relation to genetic variability, heritability, genetic advance, correlation and path coefficient for 12 characters involving 50 genotypes of Pigeonpea [*Cajanus cajan* (L.) Mill sp.].The highest GCV was recorded for secondary branches plant^{-1}(76.19) followed by yield plant^{-1}(45.46). Heritability in broad sense ranged from 52.0% (days to maturity) to 100% (secondary branches plant^{-1}). High genetic advance was observed for secondary branches (156.60), yield plant^{-1}(92.02), biological yield (87.61) and pods plant^{-1} (85.57) indicating the prevalence of additive gene action for inheritance of these traits. Correlation studies revealed that seed yield was positively and significantly correlated with biological yield plant^{-1}, pods plant^{-1} and plant height. Path coefficient analysis showcased the traits with direct and indirect effect analysis based on seed yield plant^{-1}, as a dependent variable, showed that significant for biological yield, pods plant^{-1}, plant height and secondary branches plant^{-1}. Both correlation and path analysis indicated that pods plant^{-1} and biological yield were the major indirect contributors to seed yield.

Keywords

Genetic variability, heritability, genetic advance, correlation and path coefficient

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Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.], (2n=2x=22) is the second most important pulses crop after chickpea in India and rank fifth in the world after soybean, groundnut, dry beans and pea. It is a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low-priced vegetarian foods. In fact, this crop has diversified uses such as food, feed, fodder and fuel wood. It is also helpful in checking the soil erosion and for maintaining the soil fertility. It is hardy, widely adapted and drought tolerant crop. Each and every part of the plant is valuable for the farmers. Globally, pigeonpea is cultivated in 27 million hectares area with an annual production of 18.5 million tonnes with mean productivity of 730 kg/ha (Anonymous, 2014). India is the leading producer of pigeonpea in the world accounting for 4.43 mha area and 4.25mt of production with average productivity of 960 kgha^{-1} (DAC&FW,2017-18). Major states to record the success have been Maharashtra (1.07 Mt), Madhya Pradesh (0. 84 Mt), Karnataka (0.77 Mt), Gujarat (0.34 Mt), Uttar Pradesh (0.33 Mt), Telangana (0.26 Mt) and Jharkhand (0.22 Mt).Pigeonpea seeds have 19–25% protein and are consumed as green peas, whole grain or split peas (Ajay *etal*. 2011).

The seed and pod husks make a quality feed, whereas dry branches and stems serve as domestic fuel. Fallen leaves from the plant provide vital nutrients to the soil and the plant also enriches soil through symbiotic nitrogen fixation (Varshney, 2010). Productivity of pigeonpea worldwide in comparison to cereals is very low and stagnant due to several biotic and abiotic stresses. This low productivity is attributed to its low harvest index because of limited man-made selections (Varshney *et al.,* 2010, Ajay *et al.,* 2011).

To overcome such situation, genetically stable genotypes having high yield potential are required straightaway. 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 needs to be identified. The information on 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

Fifty germplasms of pigeonpea obtained from Pigeonpea Improvement Programme, Department of Genetics and Plant Breeding, I.Ag.Scs., Banaras Hindu University, Varanasi were undertaken for assessment of direct selection parameters (variability, heritability, and genetic advance) and indirect selection parameter (correlation and path coefficient analysis). This investigation was carried out at the Agriculture Research Farm of Institute of Agricultural Sciences, BHU, Varanasi (25°C18’N lat., 83°C03’ E long. and 129 m amsl.) during the *Kharif*,2016-17 in randomized block design (RBD) with two replications. Seeds of each genotype were sown in unit plot size of 4m long with a spacing of 30 x 10 cm. Standard agronomic package and practices were adopted for both replications. Observations were recorded on days to50% flowering (DF), days to maturity

(DM), plant height in cm (PH), number of primary branches (NPBR), number of secondary branches (NSBR), number of pods plant^{-1} (NPP), pod length in cm (PL), number of seeds pod^{-1} (NSPP), 100-seed weight in g (HSW), yield plant^{-1}in g (YPP), biological yielding (BY) and harvest index (HI). Days to 50% flowering, days to maturity, 100-seed weight, and harvest index were recorded on plot basis. Harvest index was determined as economic yield over total biomass

Ten plants were randomly selected for recording the data, the mean values over replications were subjected for analyzing the various parameters. 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 analyzed using Windostat version 8.6 from Indostat. Path co-efficient analysis was estimated according to the method proposed by Dewey and Lu (1959).

Results and Discussion

Variability Studies

The analysis of variance in 50 genotypes indicated highly significant genotypic differences for all the character studied indicating the presence of considerable amount of genetic variability in the present materials (Table 1). This indicated that there is enough scope for identifying genotypes with desirable character to improve yield, provided the material be subjected to sensible selection pressure. Genetic parameters of yield and their components are given in Table 2. In the present study, the highest genotypic variances were observed for secondary branches (76.19) followed by yield plant^{-1} (45.46), biological yield (42.74) and pods plant^{-1} (41.65), moderately significant for primary branches (22.85),harvest index (19.46), 100-seed weight(19.36), plant height(16.82), pod length (10.98) and seed pod^{-1}(9.61) respectively, while the lowest genotypic variance was found for days to 50% flowering(4.80) and days to maturity(0.54).

The highest phenotypic variances were found for secondary branches (76.36) followed by yield plant^{-1} (46.25), biological yield (42.94), podsplant^{-1} (41.76) and moderately significant for primary branches (22.95), harvest index (20.56) and 100-seed weight(20.08),plant height(16.94), pod length (13.74) and seed pod^{-1}(12.21) while lowest for days to 50% flowering(5.17) and days to maturity(0.75). In this study, the phenotypic variance was high as compared to genotypic variance for all the traits studied which was also observed earlier (Chetukur *et al.*, 2013; Kumara *et al.*, 2014; Vanisree and Sreedhar 2014)**.**

The highest genotypic and phenotypic coefficient of variances was found for secondary branches followed by yield plant^{-1} while lowest genotypic and phenotypic coefficient of variance was found for days to maturity. These results were in conformity with earlier reports of Mahamad *et al.*, (2006) for branches plant^{-1}; Saroj *et al.*, (2013) for secondary branches and pods plant^{-1}; Rekha *et al.*, (2013) forsecondary branches plant^{-1}, pods plant^{-1}, seed yield plant^{-1}, and primary branches plant^{-1}; Vanishree and Sreedhar (2014) for seed yield plant^{-1}, pods plant^{-1} and primary branches; Rao and Rao (2015) for pods plant^{-1}, seed yield and primary branches plant^{-1}; Ram *et al.*, (2016) for secondary branches plant^{-1} and pods plant^{-1}.The highest genotypic coefficient of variation observed for secondary branches, seed yield plant^{-1}, biological yield and pods plant^{-1} indicates the presence of exploitable genetic variability for these traits.

Highest heritability was observed for all the characters except for days to maturity, seed pod^{-1} and pod length. Greater heritability estimates for such traits as secondary branches, primary branches, plant height, biological yield, pods plant^{-1}, yield plant^{-1}, 100-seed weight, harvest index, pod length and seeds pod^{-1} indicate that these characters can be used as the genetic parameters for the improvement and selection of high yielding genotypes.

Similar conclusions were also derived by Venkateswarlu (2001) for primary branches, secondary branches and yield plant^{-1}; Mahamad *et al.,* (2006) for plant height, branches plant^{-1}, pods plant^{-1}, 100-seed weight; Ram *et al.*, (2016) for seeds pod^{-1} and days to 50 % flowering; Rao and Rao (2015) for days to 50% flowering, seed yield plant^{-1}, pods plant^{-1}, test weight and plant height; Basavarajaiah *et al.*, (2000) for days to 50% flowering, yield plant^{-1} and 100-seed weight**.**
In the present study, moderate heritability was observed for days to maturity.

In contrary to high heritability for primary and secondary branches, Sarsamkar *et al.*, (2008) reported moderate to low heritability for these traits. Moderate heritability indicating that these traits are more influenced by environment and under the control of non-additive gene action. Therefore, selection of the plants should be based on secondary branches, primary branches, pods plant^{-1}, biological yield, plant height and yield plant^{-1} for effective selection.

Considerable estimates of high heritability coupled with high GCV estimates were observed for biological yield, number of primary and secondary branches, pods plant^{-1} and yield plant^{-1} further indicated the reliability of these traits for effective selection.

Heritability and genetic advance was high indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose. In the present study, high heritability with high genetic advance as percentage of mean were obtained for secondary branches, yield plant^{-1}, biological yield, pods plant^{-1}, primary branches, 100-seed weight, harvest indexand plant height. These results were in conformity with that of Rao and Rao (2015) for number of pods plant^{-1} and seed yieldplant^{-1} (Ali *et al.*, 2015) 100-seed weight, plant height, yield/plant and harvest index (Tiwari *et al.*, 2015) for number of pods plant^{-1} and 100 seed weight. In contrary to high heritability and low genetic advance for days to 50% flowering in the present study.

High heritability along with moderate or low genetic advance could be improved by inter mating superior genotypes of population developed from combination breeding. High heritability along with moderate or low genetic advance was observed for days to 50% flowering, pod length and seeds/pod in the present study. Kumar *et al.*, (2014) reported the same for days to 50%flowering and pod length. Moderate heritability coupled with low genetic advance as per cent of mean was observed for days to maturity in the current study.

From above discussion it was quite obvious that few important traits viz., number of primary branches and secondary branches, yieldplant^{-1}, biological yield, podsplant^{-1}, 100-seed weight, harvest index and plant height possessed high heritability and thus under the control of additive gene effect. On the other hand, low heritability coupled with low genotypic variation was observed for days to maturity. The results indicate that these traits were greatly influenced by the environment (Arshad *et al.*, 2002).

Correlation coefficient analysis

In plant breeding programme where the aim is for improving seed yield, it becomes necessary to gather the detailed information regarding the association of various components with seed yield and among themselves. Seed yield is a complex trait and is determined by the interactive effects of many component traits, which are in turn influenced by their genetic structures and the environment where the plant is grown. The estimation of correlation coefficient has been done at both phenotypic and genotypic level. The simple correlation is an important tool for this purpose as knowledge of correlation is essential when selection is to be made on several characters at a time through some simultaneous selection model (Singh, 1972). True association can only be known through genotypic correlation since phenotypic correlation includes the interaction between genotype and environment.

The magnitude of genotypic correlation was found slightly higher than phenotypic correlation for most of the traits studied. This indicated a greater role of genetic factors in determining these associations which reflected that the environment could not deviate the expression of phenotypic association(Table 3). The difference between genotypic and phenotypic correlation was found very less. So phenotypic correlation was considered as a parameter to get the interaction between different genotypes.

The analysis of variance indicated highly significant differences among all the genotypes for all the characters studied. The major advantages of phenotypic and genotypic correlation between yield and its contributing characters are basic and foremost important for effective selection. In the present investigation, biological yield (0.8943), podsplant^{-1} (0.7177), plant height (0.5933), number of secondary branches (0.5492), number of primary branches (0.4977), and harvest index (0.3201) showed positive and highly significant phenotypic correlation with yieldplant^{-1}. These results propound that any positive increase in such traits will improve the seed yield of pigeonpea. Similar results were also reported by Sarsamkar *et al.,* (2007) between podsplant^{-1} andBhadru, (2010) reported that number of pods, number of primary and secondary branches showed significantly positive correlation with seed yield at phenotypic levels. Significant and positive correlation of seed yieldplant^{-1} with plant height was reported by Singh *et al.,* (2008). Negative and non-significant correlation was observed between yield and pod length and that between yield and seeds/pod in the present study.

The results of correlation in present investigation revealed that grain yieldplant^{-1}, primary and secondary branchesplant^{-1}, podsplant^{-1}, biological yield, plant height and harvest index were the most important attributes and may contribute considerably towards higher grain yield. But grain yield is a quantitative trait which is influenced by its various components directly and indirectly via other traits, which creates a complex situation at the selection time.

Path coefficient analysis

In selection programme when inter-relationship of large number of variables with seed yield and among themselves is studied, the situation become very complex to understand the actual role of a variable for increasing yield. In such a situation, the information of correlation coefficient coupled with the information on path coefficient greatly helps in identification of suitable characters for giving due weightage during selection.

Table.1 Analysis of variance for 12 quantitative characters in long duration pigeonpea genotypes

Source of variation	**Mean Sum of Squares**											
	DF	**DM**	**PH**	**NPBR**	**NSBR**	**NPP**	**PL**	**NSPP**	**HSW**	**YPP**	**BY**	**HI**
Replication	0.1600	0.0025	0.0853	0.0013	0.0002	1.00	0.017	0.006	0.0012	0.024	0.03	1.2656
Treatment	72.80**	5.021**	1247.80**	17.76**	31.84 **	4495.08**	0.85**	0.26**	10.11**	153.86**	3893.62**	28.07*
Error	5.36	1.61	8.50	0.082	0.071	11.92	0.19	0.061	0.37	2.68	18.67	1.54

*=Significance at 5% and **=1%

Table.2 Genetic parameters for 12 quantitative characters in long duration pigeonpea genotypes

Character	**Mean**	**Range**	**PCV**	**GCV**	**H^2**	**GA%**
DF	120.62	106.50-146.00	5.17	4.80	86	9.18
DM	235.56	204.50-266.50	0.75	0.54	52	0.79
PH	147.99	94.16-194.74	16.94	16.82	99	34.41
NPBR	13.01	5.40-17.50	22.95	22.85	99	46.85
NSBR	5.23	0-15.03	76.36	76.19	100	156.60
NPP	113.68	16.50-199.50	41.76	41.65	99	85.57
PL	5.25	3.93-7.94	13.74	10.98	64	18.06
NSPP	3.27	2.52-4.91	12.21	9.61	62	15.57
HSW	11.40	6.04-18.01	20.08	19.36	93	38.45
YPP	19.13	4.47-46.17	46.25	45.46	97	92.02
BY	103	28.20-203.10	42.94	42.74	99	87.61
HI	18.72	10.93-28.39	20.56	19.46	90	37.95

*GCV-Genotypic coefficient of variation: PCV- Phenotypic coefficient of variation:H^2 -Heritability: GA%- Genetic advance as per cent of mean

Table.3 Genotypic and phenotypic correlation between 12 quantitative characters in long duration pigeonpea genotypes

Correlation		DM	BY	PH	NPBR	NSBR	NPP	PL	NSPP	HSW	HI	YPP
DF	**G**	0.0190	0.2826	0.3198	0.1049	0.1785	-0.0645	0.3875	-0.0205	0.2691	-0.4542	**0.0982**
	P	0.2312	0.2768*	0.3065*	0.1073	0.1732	-0.0515	0.1446	0.0581	0.1922	-0.4401**	**0.0928**
DM	**G**		0.2652	0.2976	0.3168	0.4067	0.2385	0.1896	-0.1996	-0.0681	0.0717	**0.3053**
	P		0.2113	0.2238	0.2376	0.3008*	0.1832	-0.1617	0.0520	-0.1485	-0.0205	**0.2158**
BY	**G**			0.7349	0.6075	0.6201	0.7274	0.0927	-0.0916	0.1571	-0.0952	**0.9055**
	P			0.7348**	0.6085**	0.6195**	0.7282**	0.0596	-0.0510	0.1474	-0.0946	**0.8943****
PH	**G**				0.5971	0.4489	0.5572	0.0651	0.0726	0.0384	-0.2211	**0.6002**
	P				0.5995**	0.4494**	0.5582**	0.0422	0.0667	0.0355	-0.2186	**0.5933****
NPBR	**G**					0.5461	0.6330	-0.3206	-0.2849	-0.2652	-0.1818	**0.5027**
	P					0.5467**	0.6334**	-0.2653	-0.2204	-0.2540	-0.1788	**0.4977****
NSBR	**G**						0.5843	-0.2213	-0.2996	-0.2254	-0.0424	**0.5558**
	P						0.5843**	-0.1831	-0.2232	-0.2210	-0.0458	**0.5492****
NPP	**G**							-0.3901	-0.3295	-0.3414	0.1792	**0.7258**
	P							-0.3162*	-0.2456	-0.3316*	0.1659	**0.7177****
PL	**G**								0.5297	0.7708	-0.4109	**-0.0695**
	P								0.3149*	0.6728**	-0.2263	**-0.0330**
NSPP	**G**									0.5257	-0.0160	**-0.0605**
	P									0.3383*	0.0014	**-0.0053**
HSW	**G**										-0.2776	**0.0448**
	P										-0.2038	**0.0554**
HSW	**G**											**0.3141**
	P											**0.3201***

**,*Significance at 1% & 5% probability level respectively

Table.4 Genotypic and phenotypic path coefficient analysis showing direct (diagonal) and indirect effect of eleven quantitative characters on yield per plant in long duration pigeonpea genotypes

Characters		**DF**	**DM**	**BY**	**PH**	**NPBR**	**NSBR**	**NPP**	**PL**	**NSPP**	**HSW**	**HI**	**YPP**
DF	**G**	**0.0668**	0.0034	0.3424	-0.0396	-0.0071	-0.0204	0.0085	-0.1041	-0.0033	-0.0071	-0.1412	**0.0983**
	P	**0.0006**	0.0049	0.2861	-0.0084	0.0035	-0.0039	0.0056	-0.0003	0.0024	-0.0099	-0.1866	**0.0940**
DM	**G**	0.0013	**0.1778**	0.3213	-0.0368	-0.0215	-0.0465	-0.0313	-0.0509	-0.0321	0.0018	0.0223	**0.3054****
	P	-0.0001	**0.0211**	0.2184	-0.0061	0.0078	-0.0067	-0.0201	0.0004	0.0021	0.0077	-0.0087	**0.2158***
BY	**G**	0.0189	0.0472	**1.2115**	-0.0910	-0.0412	-0.0709	-0.0956	-0.0249	-0.0147	-0.0042	-0.0296	**0.9055****
	P	-0.0002	0.0045	**1.0335**	-0.0201	0.0201	-0.0138	-0.0797	-0.0001	-0.0021	-0.0076	-0.0401	**0.8944****
PH	**G**	0.0214	0.0529	0.8904	**-0.1238**	-0.0405	-0.0513	-0.0732	-0.0175	0.0117	-0.0010	-0.0687	**0.6004****
	P	-0.0002	0.0047	0.7594	**-0.0274**	0.0198	-0.0100	-0.0611	-0.0001	0.0027	-0.0018	-0.0927	**0.5933****
NPBR	**G**	0.0070	0.0563	0.7359	-0.0739	**-0.0679**	-0.0625	-0.0832	0.0861	-0.0458	0.0070	-0.0565	**0.5025****
	P	-0.0001	0.0050	0.6289	-0.0164	**0.0330**	-0.0122	-0.0693	0.0006	-0.0091	0.0131	-0.0758	**0.4977****
NSBR	**G**	0.0119	0.0723	0.7512	-0.0556	-0.0371	**-0.1144**	-0.0768	0.0594	-0.0481	0.0060	-0.0132	**0.5556****
	P	-0.0001	0.0064	0.6403	-0.0123	0.0180	**-0.0223**	-0.0640	0.0004	-0.0092	0.0114	-0.0194	**0.5492****
NPP	**G**	-0.0043	0.0424	0.8813	-0.0690	-0.0430	-0.0668	**-0.1314**	0.1048	-0.0529	0.0090	0.0557	**0.7258****
	P	0.0000	0.0039	0.7526	-0.0153	0.0209	-0.0130	**-0.1095**	0.0007	-0.0101	0.0171	0.0703	**0.7176****
PL	**G**	0.0259	0.0337	0.1123	-0.0081	0.0218	0.0253	0.0512	**-0.2686**	0.0851	-0.0204	-0.1277	**-0.0695**
	P	-0.0001	-0.0034	0.0616	-0.0012	-0.0087	0.0041	0.0346	**-0.0022**	0.0129	-0.0347	-0.0959	**-0.0330**
NSPP	**G**	-0.0014	-0.0355	-0.1110	-0.0090	0.0193	0.0343	0.0433	-0.1423	**0.1607**	-0.0139	-0.0050	**-0.0605**
	P	0.0000	0.0011	-0.0527	-0.0018	-0.0073	0.0050	0.0269	-0.0007	**0.0411**	-0.0174	0.0006	**-0.0052**
HSW	**G**	0.0180	-0.0121	0.1903	-0.0047	0.0180	0.0258	0.0448	-0.2070	0.0845	**-0.0265**	-0.0863	**0.0448**
	P	-0.0001	-0.0031	0.1523	-0.0010	-0.0084	0.0049	0.0363	-0.0015	0.0139	**-0.0516**	-0.0864	**0.0553**
HI	**G**	-0.0303	0.0127	-0.1153	0.0274	0.0123	0.0049	-0.0235	0.1104	-0.0026	0.0074	**0.3108**	**0.3142****
	P	0.0003	-0.0004	-0.0977	0.0060	-0.0059	0.0010	-0.0182	0.0005	0.0001	0.0105	**0.4239**	**0.3201****

**,* Significance at 1% & 5% probability level respectively, Residual Effect=0.054

The Path coefficient analysis was done for yield and yield attributes to estimate the direct and indirect effects of various characters on seed yield (Dewey and Lu, 1959). Path coefficient analysis considers direct as well as indirect effects of the variables by partitioning the correlation coefficients.

In order to understand these effects, genotypic correlation coefficient of different characters with seed yield was portioned into their direct and indirect effects (Table 4). This facilitates the selection of genotypes on the basis of those traits which will eventually contribute more towards seeds yield.

Path coefficient analysis in the present study revealed that the highest positive direct effect on seed yield was recorded by biological yield followed by pods plant^{-1}, plant height, number of secondary branches and harvest index and days to maturity. These results clearly gave an indication that the selection based on these characters would directly improve the seed yield in pigeonpea.

Coefficient analysis showed that biological yield had maximum direct effect (1.2115 and 1.0335) followed by harvest index (0.3108 and 0.4239), days to maturity (0.1778 and 0.0211), seedspod^{-1} (0.1607 and 0.0411) and days to 50% flowering (0.0668 and 0.0006) on grain yield plant^{-1}. 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 and seeds/pod.

Plant height (-0.1238 and -0.0274), primary branches/plant (-0.0679and -0.0330) secondary branches/plant (-0.1144 and 0.0223) pods/plant (-0.1314 and -0.1095) and pod length (-0.2686 and -0.0022) showed negative direct effect on grain yield in both genotypic and phenotypic level. Except primary branches/plant, in this case genotypic had showed negative direct effect but phenotypic had positive and direct effects on the grain yield.

An important consideration in formulating the path diagram is that all the important causal factors affecting the seed yield are included. The complex nature of yield as a character reduce the feasibility of inclusion of all the related factors, under such circumstances provision is made for residual effect which explains the effect of those factors that are not considered in the study.

In the present study, the residual effect on seed yield per plant was very low indicating that most of the contributing characters were included in the path analysis. Lal *et al.*, (2000) also reported low residual effect.

The results suggest that the estimation of genetic variability, heritability, correlation and path analysis indicated a scope for improvement of grain yield through selection.Emphasis should be given on the traits *viz.*,plant height, numberof primary and secondary branches, pods/plant, biological yield and harvest index for selecting high yielding genotypes and such genotypes could be utilized in hybridization program for improvement in yield and its component traits in pigeonpea genotypes, especially the landraces.

Additionally, path coefficient results explicitly indicate that the biological yield, plant height, number of primary and secondary branches, podsplant^{-1}, and harvest index which indirectly contributed substantially towards seed yield, should be indices for selection in pigeon pea.

Interestingly, the correlation and path coefficients results are in agreement confirming the importance of these traits during selection.

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