Journal of Food Legumes
36(1): 16-22, 2023
DOI: 10.59797/jfl.v36.i1.124

Research paper

Genetic variability and characters of association for yield and its components in pigeon pea [*Cajanus cajan* (L.) Millsp.]

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Handling Editor:
Dr. Debjyoti Sen Gupta, ICAR-Indian Institute of Pulses Research, Kanpur, India

***Received**: 7 August 2023*
***Accepted**: 3 September 2023*

ABSTRACT

Seventy-three pigeon pea genotypes along with three checks were evaluated to assess genetic variability parameters, correlation and path coefficients among the yield and yield component traits. Analysis of variance showed significant difference for all the characters under study except number of seeds per pod and pod length. The maximum PCV and GCV were observed for days to maturity and days to 50% flowering while the minimum for number of seeds per pods. Heritability in broad sense was high for days to 50% flowering followed by biological yield per plant and seed yield per plant whereas high genetic advance as per cent of mean was observed for days to 50% flowering followed by days to maturity. Characters namely days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, showed positive significant correlation with seed yield both at phenotypic and genotypic level. Harvest index, days to maturity, 100-seed weight, number of primary branches per plant and pod length highest exerted positive direct effect on seed yield per plant.

Key words: Genetic variability, Heritability, Genetic advance, Correlation coefficient, Path coefficient

INTRODUCTION

Pigeon pea [*Cajanus cajan* (L.) Millsp.] occupies second place after chickpea in pulses of India and has been rated the best as far as its biological value is concerned. It has been recommended for a balanced diet along with cereals, especially to fill the nutritional gap of proteins. In fact, this crop also possesses medicinal properties and has diversified uses such as food, feed, fodder and fuel wood. It acts as a check crop for soil erosion and improves soil fertility. It is hardy, widely adapted and drought tolerant crop. Pigeon pea is cultivated in about 14.66 m ha area with an annual production of 16.25 mt and a mean productivity of 789 kg/ha (FAOSTAT, 2019). India ranks first and accounts for 72% of area (10.57 m ha) grown to pigeon pea with an annual production of 11.22 mt followed by Myanmar (0.12 mt) and Malawi (0.08 mt) (FAOSTAT, 2019). In India, Maharashtra has the highest area- 1.22 m ha and production is 1.05 mt with highest ever productivity of 937 kg/ha followed by Madhya Pradesh, Karnataka, Gujarat and Uttar Pradesh. Uttar Pradesh has total area of 0.28 m ha, with annual production 0.303 mt which contributes 7.25% towards total national production (Source: Ministry of Agri. & FW, Govt. of India; 2018 3rd Advance Estimate). Pigeon pea seeds have 19–25% protein and are consumed as green peas, whole grain or split peas (Ajay *et al.*, 2012). Productivity of pigeon pea 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.*, 2012).

In order to make selections in segregating populations, knowledge about the genetics or inheritance of traits is very essential. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable selection parameters like genetic coefficient of variability (GCV), heritability estimates (h) and genetic advance (GA). Due to low heritability and the genotype × environment effect the improvement in polygenic traits rarely possible (Kumar *et al.*, 2021). So, estimating the nature and magnitude of character association, path coefficient analysis between seed yield and yield attributing traits are necessary to identified the yield contributing traits.

The information on genetic variability and character association contributes with grain yield and among itself is of considerable importance in selection for elite genotype as well as exploitation of heterosis in breeding programme. 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 one (yield). The information on genetic variability, correlation and path coefficient may be helpful to the breeder for planning suitable selection criteria for enhancing the genetic yield potential of the pigeon pea (Shukla *et al.*, 2022). The present study was conducted to assess genetic variability, heritability along with genetic advance, correlation coefficient analysis on yield and its component characters to provide necessary information that could be useful for selection in yield improvement programmes.

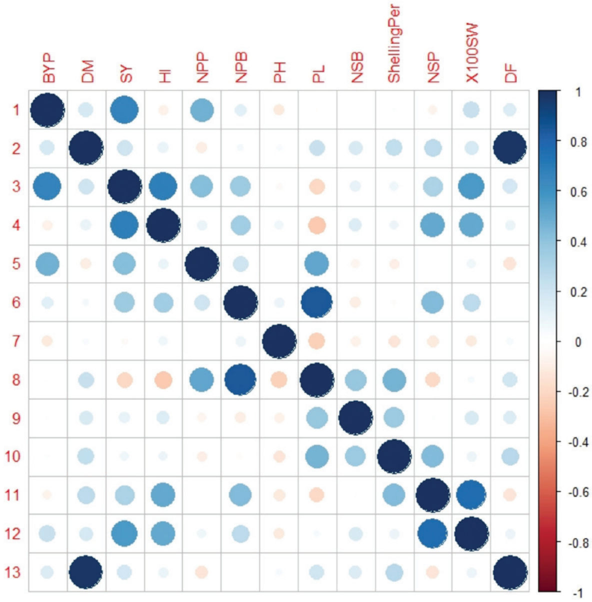

Fig. 1. Diagrammatic representation of phenotypic correlation between different yield and yield related traits in studied pigeon pea genotypes

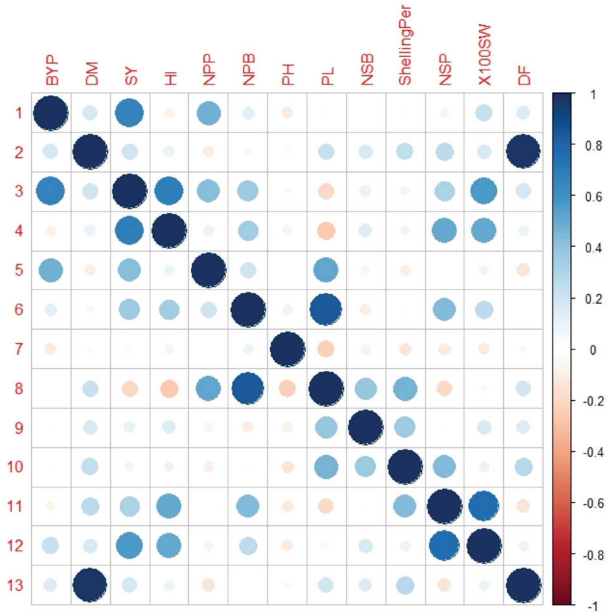

Fig. 2. Diagrammatic representation of genotypic correlation between different yield and yield related traits in studied pigeon pea genotypes

MATERIALS AND METHODS

The experimental material consisting of 73 genotypes/local land races varieties including three checks *viz.*, NDA-1, Bahar and Pant Arhar-291 which were procured from ICAR-Indian Institute of Pulses Research, Kanpur, India and local land races were collected from adjoining area of Banda. The trial was conducted at P.G. Research Block of College of Agriculture, Banda University of Agriculture and Technology, Banda, India in augmented block design under irrigated, normal soil conditions during *kharif* 2020-2021. The experimental site is located between latitudes 24°53′ and 25°55′ North and longitudes 80°07′ and 81°34′ East and at an altitude of 113 m above the mean sea level.

The data were recorded on 5 randomly selected plants from each strain per replication in respect of the characters and observations were recorded on days to 50% flowering (DF), days to maturity (DM), plant height (PH), number of primary branches (NPBR), number of secondary branches (NSBR), number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSPP), 100-seed weight (HSW), seed yield per plant (YPP), biological yielding (BY) and harvest index (HI). Days to 50% flowering, days to maturity, were recorded on plot basis by counting the days from the date of sowing. Harvest index was determined as seed yield over biological yield. The weight of 100 seeds determined as the seed weight.

The recorded data were subjected to the analysis of genetic parameters of variability *viz*., phenotypic and genotypic variance and coefficient of variance by formula suggested by Johnson *et al*. (1955) and Burton (1952) heritability in broad sense by formula suggested by Allard (1960) genetic advance by Johnson *et al*. (1955). Phenotypic and genotypic correlation coefficients were estimated using the formula suggested by Robinson *et al*. (1951) and Path co-efficient analysis was estimated according to the method proposed by Dewey and Lu (1959). All the data were analyzed using XLSTAT (Indian Agricultural Statistics Research Institute ICAR- IASRI), R 4.1

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance was based on the mean value of 13 quantitative characters in 73 pigeon pea genotypes. The result revealed the highly significant differences among the genotypes in respect of all the characters under study (Table 1). These results indicate that there is significant inherent genetic variability among the genotypes which provide ample of 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). The highest genotypic coefficient of variance was observed for

Table 1. Analysis of variance of augmented block design for thirteen characters in pigeon pea genotypes

S. N.	Characters	Sources of variation					
		Blocks	Treatment	Genotype	Checks	Genotype vs Check	Error
d.f.		**(6)**	**(72)**	**(69)**	**(2)**	**(1)**	**(12)**
1.	**Days to 50% flowering**	34.19	1027.66*	816.64*	8511.04*	621.90*	21.04
2.	**Days to maturity**	94.15	4440.66*	3221.71*	48560.33*	309.36*	35.11
3.	**Plant height**	46.54*	170.20*	166.60*	133.16*	492.72*	14.22
4.	**Number of primary branches**	4.61*	6.11*	5.99*	6.41*	14.15*	1.50
5.	**Number of secondary branches**	15.76*	22.46*	19.31*	110.93*	62.87*	62.87
6.	**Number of pods per plant**	6964.17*	7523.04*	7110.45*	1627.72	47782.45*	898.83
7.	**Number of seeds per pod**	0.031*	0.013	0.012	0.047*	0.047	0.010
8.	**Pod length**	0.43*	0.19	0.17	0.95*	0.95	0.95
9.	**100-Seed weight**	1.49	3.04*	2.77*	13.24*	0.93	0.84
10.	**Biological yield per plant**	311.41*	1717.85*	1732.07*	544.16*	3084.24*	80.11
11..	**Harvest index**	2.73	22.63*	21.35*	62.49*	31.87*	3.77
12.	**Shelling**	69.52*	41.83*	32.94*	327.97*	83.02*	10.27
13.	**Seed yield per plant**	83.37	563.24*	538.48*	1693.13*	11.87	31.55

* indicates significant at 5% level of significance

Table 2. Range, general mean, GCV, PCV, heritability, genetic advance and genetic advance in per cent of mean for thirteen characters of pigeon pea germplasm

S. No.	Characters	Range		General mean	GCV (%)	PCV (%)	Heritability (b.s.) (%)	GA	GA as % of mean
		Min.	Max.						
1.	**Days to 50% flowering**	74.09	180.09	115.86	25.35	25.65	97.62	59.78	51.59
2.	**Days to maturity**	122.38	296.38	189.74	32.38	32.53	59.08	75.13	39.59
3.	**Plant height**	171.11	240.51	224.26	5.15	5.42	90.38	22.64	10.09
4.	**Number of primary branches**	16.22	29.82	24.67	8.06	9.46	72.49	3.48	14.13
5.	**Number of secondary branches**	48.88	74.28	64.30	5.97	6.95	73.71	6.79	10.56
6.	**Number of pods per plant**	526.90	953.47	763.60	9.86	10.62	56.33	94.10	12.32
7.	**Number of seeds per pod**	3.24	3.83	3.56	1.42	3.17	20.47	0.047	1.33
8.	**Pod length**	5.42	7.95	6.35	3.59	6.78	28.05	0.24	3.91
9.	**100-Seed weight**	5.64	12.52	9.88	13.87	16.72	68.88	2.34	23.72
10.	**Biological yield per plant**	241.94	516.05	381.09	9.83	10.10	94.60	75.06	19.69
11.	**Harvest index**	30.88	49.79	43.22	9.30	10.33	81.08	7.45	17.25
12.	**Shelling**	54.28	85.21	67.49	7.70	9.05	74.46	9.11	13.51
13.	**Seed yield per plant**	106.45	202.37	164.51	12.97	13.41	93.52	42.52	25.84

PCV= Phenotypic coefficient of variation (%), GCV= Genotypic coefficient of variation (%), h^2 (bs) = Broad sense heritability (%), GA= Genetic advance at 5%, GAM = Genetic advance as per cent of mean at 5% level.

days to maturity followed by days to 50% flowering, 100- seed weight and seed yield per plant whereas the number of pods per plant, biological yield per plant, harvest index, number of primary branches per plant, shelling percent, number of secondary branches per plant, plant height, pod length and number of seeds per pod showed low magnitude of GCV. The highest phenotypic coefficient of variance was observed for days to maturity followed by days to 50% flowering, 100-seed weight, seed yield per plant, number of pods per plant, harvest index and biological yield per plant. However, it was recorded low for number of primary branches per plant, shelling per cent, pod length, number of secondary branches per plant, plant height and number of seeds per pod. In this study, the phenotypic variance was high as compared to genotypic variance for all the traits studied which was also observed by Kumar *et al*. (2014), Alaka *et al*. (2020), Akshara *et al*. (2021) and Reddy *et al*. (2023).

Heritability and genetic advance

The high heritability in broad sense and high genetic advance was observed for days to 50% flowering, biological yield per plant, seed yield per plant, plant height, harvest index, shelling per cent, number of secondary branches, number of primary branches and 100-seed weight which indicating the prevalence of additive gene action for inheritance of these traits indicates that characters with high heritability can be used as the genetic parameters for the improvement and selection of high yielding genotypes. High heritability was observed for all

Table 3. Phenotypic correlation coefficients among different yield and yield component traits in pigeon pea germplasm

Characters	DF	DM	PH	NPB	NSB	NPP	NSP	PL	100-SW	BYP	HI	Shelling (%)	SY
DF	1	0.971*	0.039	0.006	0.135	-0.099	0.065	0.135	0.115	0.140	0.087	0.210	0.140
DM		1	0.027	0.040	0.133	-0.069	-0.069	0.107	0.155	0.161	0.107	0.201	0.203
PH			1	0.004	-0.134	-0.039	-0.098	-0.117	-0.134	-0.089	0.048	-0.166	-0.033
NPB				1	0.041	0.18	0.078	0.133	0.133	0.078	0.247*	0.078	0.260*
NSB					1	-0.105	-0.044	-0.047	0.121	-0.02	0.067	0.041	0.041
NPP						1	-0.052	0.256*	0.181	0.397**	0.165	0.002	0.432**
NSP							1	0.211	0.186	-0.202	0.216	0.204	0.167
PL								1	0.011	0.022	-0.074	0.224	-0.042
100-SW									1	0.209	0.372**	0.109	0.463**
BYP										1	-0.151	-0.032	0.607**
HI											1	0.169	0.691**
Shelling (%)												1	0.108
SY													1

*, Significant at 5%, **, Significant at 1% probability level; DF, days to 50% flowering; DM, days to maturity; PH, plant height; NPB, number of primary branches per plant; NSB, number of secondary branches per plant; NPP, number of pods per plant; NSP, number of seeds per pod; PL, pod length; SW, 100- Seed weight; BYP, biological yield per plant; HI, harvest index; SY, seed yield per plant

Table 4. Genotypic correlation coefficients among different yield and yield component traits in pigeon pea germplasm

Characters	DF	DM	PH	NPB	NSB	NPP	NSP	PL	100-SW	BYP	HI	Shelling (%)	SY
DF	1	0.977**	0.043	-0.001	0.151	-0.137	-0.137	0.191	0.085	0.155	0.097	0.273*	0.183
DM		1	0.038	0.051	0.161	-0.102	0.266*	0.224	0.171	0.178	0.099	0.245*	0.204
PH			1	0.089	-0.085	0.000	-0.118	-0.238	-0.113	-0.113	0.073	-0.133	-0.037
NPB				1	-0.107	0.206	0.430**	0.842**	0.261*	0.126	0.340**	-0.027	0.355**
NSB					1	-0.069	0.016	0.386**	0.162	-0.013	0.148	0.360**	0.105
NPP						1	0.003	0.510**	0.075	0.471**	0.094	-0.091	0.423**
NSP							1	-0.197	0.767**	-0.077	0.509**	0.439**	0.317**
PL								1	0.049	-0.01	-0.261	0.464**	-0.205
100-SW									1	0.229*	0.508**	0.086	0.562**
BYP										1	-0.085	0.019	0.669**
HI											1	0.081	0.680**
Shelling (%)												1	0.07
SY													1

*, Significant at 5%; **, Significant at 1% Probability level; DF, days to 50% flowering; DM, days to maturity; PH, plant height; NPB, number of primary branches per plant; NSB, number of secondary branches per plant; NPP, number of pods per plant; NSP, number of seeds per pod; PL, pod length; SW, 100- Seed weight; BYP, biological yield per plant; HI, harvest index; SY, seed yield per plant

the characters except for number of seeds pod, pod length, number of seeds pod (Alaka *et al.*, 2020). Similar conclusions were also derived by Vange and Moses (2009) who observed high heritability for all the traits except seeds per pod; Bhadru (2011) for days to 50% flowering and days to maturity; Rekha *et al*. (2013) for all studies traits except number of seed per pod and pod length; Valli *et al*. (2018) for days to maturity, days to 50% flowering, number of pods per plant and 100-seed weight. Considerable estimates of high heritability coupled with high GCV estimates were observed for number of primary branches, number of pods per plant, seed yield per plant and biological yield further indicated the reliability of these traits for effective selection. From above discussion it was quite obvious that traits that possess high heritability coupled with high genetic advance are under the control of additive gene effect and are less influenced by the environment and those traits that possess moderate or low heritability were greatly influenced by the environment.

Correlation coefficient analysis

In plant breeding programme, seed yield improvement is the major criteria, as seed yield is a

Table 5. Phenotypic path coefficient analysis for direct and indirect effects of different characters on seed yield per plant in pigeon pea germplasm

Characters	DF	DM	PH	NPB	NSB	NPP	NSP	PL	100-SW	BYP	HI	Shelling (%)
DF		-0.0475	-0.0042	0.0048	-0.0003	-0.0019	-0.003	-0.0066	-0.0102	-0.0031	-0.0056	-0.0489
DM	0.0081		0.0054	-0.0035	0.0020	0.0013	0.0054	0.0067	0.0102	0.0051	0.0078	0.0493
PH	0.0005	-0.0001		0.0002	0.0000	-0.0061	0.0007	0.0008	0.0010	0.0006	0.0008	-0.0002
NPB	0.0001	0.0000	0.0005		0.0022	0.0000	0.0002	0.0000	0.0001	0.0001	0.0005	0.0000
NSB	0.0000	0.0001	0.0001	-0.0001		-0.0001	0.0000	0.0014	0.0003	0.0000	0.0001	0.0001
NPP	0.0050	-0.0008	0.0021	0.0128	0.0023		0.0032	-0.0013	0.0000	-0.0006	0.0023	-0.0012
NSP	0.0000	-0.0005	-0.0011	0.0002	-0.0003	0.0004		0.0002	-0.0011	-0.0055	-0.0010	-0.0003
PL	0.0000	-0.0004	0.0003	-0.0010	-0.0005	0.0004	-0.0041		-0.0009	-0.0008	0.0000	-0.0002
100-SW	0.0030	0.0022	0.0053	0.0026	0.0034	-0.0019	0.0001	0.0017		0.0026	0.0144	0.0016
BYP	0.7160	0.1154	-0.1079	0.2845	0.0560	-0.0640	0.0157	-0.0146	-0.0229		0.1499	0.1003
HI	-0.1193	0.0847	0.7915	0.1309	0.1957	0.0382	-0.0582	0.0532	0.1338	0.1710		0.0688
Shelling%	0.0001	-0.0007	-0.0006	0.0000	-0.0002	0.0006	-0.0008	-0.0008	-0.0036	-0.0007	-0.0004	
SY	0.1400	0.2030	-0.0330	0.2600	0.0410	0.4320	0.1670	-0.0420	0.4630	0.6070	0.6910	0.1080
Direct effect	**-0.0068**	**0.0508**	**-0.0002**	**0.0004**	**0.0000**	**-0.0005**	**-0.0011**	**0.0001**	**0.0015**	**-0.0011**	**0.294**	**-0.0007**

Residual factor = 0.00487; DF, days to 50% flowering; DM, days to maturity; PH, plant height; NPB, number of primary branches per plant; NSB, number of secondary branches per plant; NPP, number of pods per plant; NSP, number of seeds per pod; PL, pod length; SW, 100-Seed weight; BYP, biological yield per plant; HI, harvest index; SY, seed yield per plant

Table 6. Genotypic path coefficients analysis for direct and indirect effects of different characters on seed yield per plant in pigeon pea germplasm

Characters	DF	DM	PH	NPB	NSB	NPP	NSP	PL	100-SW	BYP	HI	Shelling (%)
DF		-0.0300	-0.0029	0.0041	0.0000	-0.0013	-0.0058	-0.0046	-0.0083	-0.0076	-0.0026	-0.0307
DM	0.0050		0.0027	-0.0028	0.0014	0.0010	0.0062	0.0045	0.0068	0.0074	0.0048	0.0274
PH	0.0004	-0.0001		0.0000	-0.0003	-0.0043	0.0010	0.0003	0.0005	0.0005	0.0004	-0.0001
NPB	-0.0006	-0.0002	-0.0018		-0.0052	-0.0004	-0.0044	0.0005	0.0001	-0.0022	-0.0013	0.00001
NSB	0.0000	0.0006	0.0006	-0.0002		-0.0003	0.0015	0.0040	0.0014	0.0000	0.0006	0.0006
NPP	0.0018	-0.0004	0.0003	0.0039	0.0008		0.0020	-0.0002	-0.0003	0.0000	0.0003	-0.0005
NSP	-0.0007	0.0024	0.0046	0.0000	0.0039	-0.001		0.0001	0.0040	0.0092	0.0070	0.0023
PL	-0.0001	0.0024	-0.0028	0.0055	0.0091	-0.0025	0.0108		0.0050	-0.0130	0.0005	0.0020
100-SW	0.0029	0.0022	0.0065	0.0009	0.0034	-0.0014	0.0006	0.0021		0.0099	0.0129	0.0011
BYP	0.7275	0.1295	-0.0615	0.3423	0.0916	-0.0824	-0.0074	-0.0095	0.0135		0.1667	0.1129
HI	-0.0622	0.0725	0.7360	0.0689	0.2503	0.0539	-0.1919	0.1087	0.0599	0.3749		0.0715
Shelling %	-0.0002	-0.0035	-0.0011	0.0013	0.0003	0.0019	-0.0066	-0.0051	-0.0142	-0.0062	-0.0012	
SY	0.1830	0.2040	-0.0370	0.3550	0.1050	0.4230	0.3170	-0.2050	0.5620	0.6690	0.6800	0.0700
Direct effect	**-0.0047**	**0.0281**	**-0.0003**	**-0.0010**	**-0.0004**	**0.0000**	**-0.0110**	**0.0042**	**0.0011**	**-0.0557**	**0.3736**	**-0.0039**

Residual factor = 0.00487; DF, days to 50% flowering; DM, days to maturity; PH, plant height; NPB, number of primary branches per plant; NSB, number of secondary branches per plant; NPP, number of pods per plant; NSP, number of seeds per pod; PL, pod length; SW, 100-Seed weight; BYP, biological yield per plant; HI, harvest index; SY, seed yield per plant complex trait and it is determined by various other contributing traits. Therefore, it becomes necessary to know the detailed information regarding the association of various contributing traits with seed yield and among themselves. The magnitude of genotypic correlation was found slightly higher than phenotypic correlation for most of the traits studied (Table 3 & 4). This indicates that genetic factors play a greater role in determining these associations which reflected that the environment could not deviate the expression of phenotypic association. The less difference was found between genotypic and phenotypic correlation so that the phenotypic correlation was considered as a parameter to get the interaction between different genotypes. In the present investigation, days to maturity, harvest index, pod length, biological yield per plant and 100-seed weight per plant showed positive and significant phenotypic correlation with seed yield per plant. These results showed that significant increase in these traits will improve the seed yield (Fig. 1 & 2). Similarly, the significant and positive correlation of seed yield with number of branches per plant, 100-seed weight, days to maturity, number of pods per plant and days to 50 per cent were reported by Vanniarajan *et al*. (2021) and Reddy *et al*. (2023). The major advantages of phenotypic and genotypic correlation between yield and its contributing characters are basic and foremost important for effective selection.

Path coefficient analysis

To understand the actual role of a contributing trait for increasing yield it is necessary to understand the information of correlation coefficient coupled with the information on path coefficient. In order to understand these effects, genotypic correlation coefficient of different characters with seed yield was partitioned into their direct and indirect effects (Table 5 & 6). Phenotypic path coefficient analysis revealed highest positive direct effect on seed yield per plant exerted by harvest index), followed by days to maturity while other characters such as 100-seed weight, number of primary branches, pod length, number of secondary branches were contributing considerably. Days to 50% flowering, number of seeds per pod, biological yield per plant, shelling per cent, number of pods per plant and plant height showed negative direct effect on seed yield per plant. These results clearly indicated that the selection based on these characters would directly improve the seed yield. These results were in conformity with that of Borah *et al.* (2020), Alaka *et al.* (2020) showed highest positive direct effect for biological yield followed by harvest index, days to maturity, seeds per pod and days to 50% flowering on grain yield per plant.

Days to maturity exhibited positive indirect effect via biological yield per plant, harvest index, 100-seed weight, number of secondary branches per plant, number of primary branches per plant for seed yield and days to 50% flowering while the number of pods per plant, shelling per cent, number of seeds per pod, pod length and plant height displayed negative indirect effect on seed yield per plant. Genotypic path coefficient analysis revealed highest positive direct effect on seed yield per plant exerted by harvest index, followed by days to maturity while other traits contributing considerably were pod length and 100-seed weight. Similar results for these characters were also reported by Chisa *et al*. (2021), Pankaj *et al.* (2023) and Ramasamy *et al*. (2021). An important consideration in formulating the path tables is that all the important causal factors affecting the seed yield are included. The complex nature of yield as a character reduces 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. Alaka *et al.* (2020) also reported low residual effect.

CONCLUSION

There is significant genetic variability among the genotypes which provide ample scope for identifying genotypes with desirable characters to improve yield. The results suggested that the estimation of genetic variability, heritability, correlation and path analysis indicated a scope for improvement of seed yield through selection. Emphasis should be given on the traits *viz*., plant height, number of primary and secondary branches, pods per 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 pigeon pea genotypes. Considering the above relationships, an ideal plant type in pigeon pea would have a greater number of primary and secondary branches of optimum height with high pod bearing for harnessing higher yield.

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