Original Research Article

Genetic Variability and Character Association for Yield and its Contributing Characters in Pigeonpea [*Cajanus cajan* (L.) Millsp.] in Central Plain Agro-Climatic Region of Uttar Pradesh (India)

Tarun Rathore[1*], A. K. Srivastava[2], C. Kushwaha[1] and B. Kumar[1]

[1]Department of Genetics and Plant Breeding,
[2]Department of Legume Section, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur 208002, India
Corresponding author

A B S T R A C T

Keywords

Genetic variability, Heritability, Genetic advance, Correlation and path coefficient

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 30 genotypes of Pigeonpea [*Cajanus cajan* (L.) Mill sp.]. The highest GCV was recorded for seed yieldplant[-1] (27.14) followed by Biological yield (25.70) and number of pods plant[-1] (23.36). Heritability in broad sense ranged from 58.00% (Number of seeds pod[-1]) to 99.54% (Biological yield). High genetic advance as percent of mean was observed for Seed yield plant[-1] (55.53), Biological yield (52.81), Number of pods plant[-1] (47.83) and Number of primary branches (43.56) 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, Number of Pods plant[-1], Days to Maturity, Number of primary and secondary branches. 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 plant height, primary and secondary branches plant[-1], pods plant[-1], biological yield. Both correlation and path analysis indicated that number of pods plant[-1] and biological yield were the major indirect contributors to seed yield.

Introduction

Pulses are the rich source of inexpensive plant-based proteins (20-25%), vitamins, minerals and dietary fibers, besides having low fat content, zero cholesterol and gluten and consequently have got significant place in the human meal where vegetarian diet is predominant (Anonymous, 2018). Pigeonpea [*Cajanus cajan* (L.) Millsp.], (2n = 2x = 22). Pigeonpea occupies second place after chickpea in India and has been rated the best as far as its biological value is concerned. It

has been recommended for a balanced diet with cereals, especially to fill the nutritional gap for proteins. In fact, this crop also possesses medicinal properties used as traditional medicine and has diversified uses such as food, feed, fodder and fuel wood. Also act as a check for soil erosion and maintain soil fertility. It is hard, widely adapted and drought tolerant crop.

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the sixth in global legume production and worldwide it is cultivated in about 6.9 million

ha area with an annual production of 5.9 million tonn and a mean productivity of 789 kg/ha (FAOSTAT 2018). India rank first and accounts for 72% of world area grown to pigeon pea or 5.58 million hectares area with an annual production of 4.29 million tonn *(FAO 2018 Official Data)* followed by Myanmar (0.12 mt) and Malawi (0.08 mt) *(FAOSTAT 2018), Source FAOSTAT 15.Dec. 2020)*.

In India, Maharashtra has the highest area 1.22 million ha., production 1.05 million tonn. followed by M.P, Karnataka, Gujrat, U.P. with highest ever Productivity level of 937 kg/ha. was achieved during 2017-2018. Uttar Pradesh has total Area 0.28 million ha., with annual production 0.303 million tonn of pigeonpea i.e. contribution of 7.25% towards total national production *(Source: Ministry of Agri. & FW, Govt. of India; 2018 3rd Advance Estimate)*.Pigeonpea seeds have 19–25% protein and are consumed as green peas, whole grain or split peas (Ajay *et al.,* 2012). 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.,* 2012).

At the end of this year 2019 Pandemic COVID- 19 falls all over the world and this pandemic is growing very fast in India.

For cope up of hunger during such pandemic conditions and to increase pulses production, one has to exploit maximum yield potential of crops.

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 selection parameters like genetic coefficient of variability (GCV), heritability estimates (H) and genetic advance (GA). Besides estimating the nature and magnitude of character association (correlation coefficient), path coefficient analysis between seed yield and yield attributing traits, the traits that contributed to yield needs to be identified.

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 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. 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 pigeonpea (Kesha Ram *et al.,* 2016).The present study was conducted to assess genetic variability, heritability along with Genetic advance, correlation coefficient and path coefficient analysis on yield and its component characters to provide necessary information that could be useful in pigeonpea improvement programmes aimed at improving seed yield.

Materials and Methods

The experimental material consisting of 30 genotypes were obtained from the germplasm maintained by Pigeonpea Breeder at Legume Section of C.S.A., Department of Genetics and Plant Breeding, C.S.A University, Kanpur. The investigation was conducted at

Crop Experimental Research Farm, Chandra Shekhar Azad University of Agriculture and Technology, situated at NH 91, Vinayakpur, kalyanpur, Kanpur (26.4950^0 N lat., 80.2678^0 E long.) during Kharif season 2019-20 in a randomized block design (R.B.D.) with three replications. Each genotype was raised in a single row of 4m length with row to row distance 75 cm and plant to plant distance 25 cm respectively. Standard recommended agronomic practices were followed to raise good crop.

A number of 5 plants were selected at random 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 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), seed 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 seed yield over biological yield.

The investigation was undertaken for assessment of direct selection parameters (variability, heritability, and genetic advance) and indirect selection parameter (correlation and path coefficient analysis). Genetic parameters of variability viz., phenotypic and genotypic variance and coefficient of variance were estimated 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 SPAR 3.0 *(Indian Agricultural Statistics research institute* ICAR- IASRI).

Results and Discussion

Variability studies

The Analysis of variance was based on the mean value of 12 quantitative characters in 30 genotypes. The result of ANOVA revealed 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).

In the present study, the highest genotypic variances were observed for seed yield plant^{-1} (27.14) followed by biological yield (25.70), number of pods plant^{-1} (23.36) and number of primary branches (21.88), moderately significant for 100-seed weight (16.05), harvest index (12.92) and number of secondary branches (11.06) while the lowest genotypic variance was found for plant height (9.64) days to 50% flowering (9.57), number of seeds pod^{-1} (8.97), days to maturity (8.11) and pod length (7.78).

The highest phenotypic variances were observed for seed yield plant^{-1} (27.32) followed by biological yield (25.76), number of pods plant^{-1} (23.49) and number of primary branches (22.65), moderately significant for 100-seed weight (16.55), harvest index (13.03), number of secondary

branches (12.45) and number of seeds pod[-1] (11.78) while the lowest genotypic variance was found for pod length (9.95), plant height (9.83) days to 50% flowering (9.63) and days to maturity (8.16).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; Alaka *et al.,* 2020).

High phenotypic and genotypic coefficients of variation were recorded for seed yield plant[-1], biological yield, number of pods plant[-1] and number of primary branches. These results were in conformity with earlier reports of Bhadru *et al.,* (2010) for number of pods plant[-1], seed yield plant[-1]. Kumar *et al.,* (2014) for number of pods plant[-1], seed yield plant[-1]. Rajamani *et al.,* (2015) for number of primary branches, number of pods plant[-1], yield per plant. Ram *et al.,* (2016) observed high GCV for number of secondary branches and pods plant[-1].Mallesh *et al.,* (2017) for number of primary branches, pods plant[-1], seed yield. Thanga Hemavarthy *et al.,* (2018) observed highest GCV for number of secondary branches and pods per plant. Devi *et al.,* (2019) observed high estimate of GCV and PCV for number of pods plant[-1]. T. Alaka *et al.,* (2020) observed highest GCV for secondary branches plant[-1]followed by yield per plant. The highest genotypic coefficient of variation observed for, seed yield plant[-1], biological yield and pods plant[-1], number of primary branches indicates the presence of exploitable genetic variability for these traits. Therefore, there would be ample of opportunity of improvement through selection breeding programme.

Heritability and genetic advance

High heritability was observed for all the characters except for number of seeds pod, pod length, number of secondary branches

indicates that characters with high heritability can be used as the genetic parameters for the improvement and selection of high yielding genotypes. Similar conclusions were also derived by Vange and Moses (2009) observed high heritability for all the traits except seeds pod[-1]; Bhadru (2011) for days to 50% flowering and days to maturity. Rekha *et al.,* (2013) high heritability for all the traits except for protein content, days to 50% flowering and days to maturity. Thanga Hemavarthy *et al.,* (2018) for pod size and number of pods plant[-1]. PushpaValli *et al.,* (2018) for days to maturity, days to 50% flowering, number of pods per plant, 100-seed weight.

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

Heritability in broad sense is effective as a selection parameter when it is coupled with genetic advance. High heritability coupled with high genetic advance ensures 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 number of primary and secondary branches, number of podsplant[-1], 100-seedweight, seed yieldplant[-1], biological yield and harvest index. These results were in conformity with that of Galian *et al.,* (2015) for plant height, number of primary and secondary branches, number of podsplant[-1], 100 seed weight and seed yieldplant[-1]; Mallesh *et al.,* (2017)for number of pods plant[-1], seed yield plant[-1]; Devi *et al.,* (2019)

for number of primary branches, secondary branches plant^{-1}and number of pods plant^{-1}. T. Alaka *et al.,* (2020) observed high heritability in broad sense and high genetic advance for secondary branches, yield plant, biological yield and pods plant^{-1}indicating the prevalence of additive gene action for inheritance of these traits.

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 as percent of mean for days to 50% flowering, days to maturity, plant height, pod length in the present study. Bhadru (2011) observed for days to 50% flowering and days to maturity. Rekha *et al.,* (2013) for days 50% flowering and days to maturity (Alaka *et al.,* 2020) High heritability along with moderate or low genetic advance was observed for days to 50% flowering, pod length and seeds per pod.

Moderate heritability coupled with moderate or low genetic advance as percent of mean was observed for number of seeds per pod in the current study (Table 2). Kumar *et al.,* (2014) observed same for seeds per pod.

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 not 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 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 estimation of correlation coefficient has been done at both phenotypic and genotypic level but 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 (Table 3).

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 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 ANOVA 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 (0.875), days to maturity (0.333), plant height (0.381), number of primary branches (0.243), number of secondary branches (0.209), number of podsplant^{-1}(0.409) and harvest index (0.313) showed positive and significant phenotypic correlation with seed yieldplant^{-1}. These results set forth that significant increase in these traits will improve the seed yield (Fig. 1 and 2).

Table.1 Analysis of variance for 12 quantitative characters in 30 genotypes of pigeonpea

Source of variation	DF	DM	PH	NPBR	NSBR	NPP	PL	NSPP	HSW	YPP	BY	HI
Replication	3.33	0.03	14.29	0.38	5.86	12.88	0.18	0.51	1.51	0.19	2.64	0.00
Treatment	413.71**	1102.73**	785.91**	22.10**	22.18**	3731.84**	0.57**	0.31**	8.86**	109.92**	2983.77**	16.76**
Error	1.83	4.37	10.22	0.51	1.82	14.43	0.10	0.06	0.18	0.50	4.58	0.09

*, ** *significant at 5% and 1% level, respectively.*

Table.2 Genetic parameters for 12 quantitative characters in 30 pigeonpea genotypes

Character	Mean	Range (Min - Max.)	PCV	GCV	h^2_b	GA %
DF	122.47	86.67 - 145.00	9.63	9.57	98.69	19.58
DM	235.83	168.33 - 265.00	8.16	8.11	98.82	16.61
PH	166.73	122.07 - 195.73	9.83	9.64	96.20	19.49
NPBR	12.26	7.47 - 17.07	22.65	21.88	93.35	43.56
NSBR	23.56	18.47 - 29.47	12.45	11.06	78.84	20.22
NPP	150.72	79.67 - 201.33	23.49	23.36	98.85	47.83
PL	5.07	4.13 - 6.13	9.95	7.78	61.05	12.52
NSPP	3.20	2.60 - 3.80	11.78	8.97	58.00	14.08
HSW	10.60	8.07 - 14.37	16.55	16.05	94.03	32.07
YPP	22.25	12.80 - 42.70	27.32	27.14	98.66	55.53
BY	122.63	75.87 - 203.90	25.76	25.70	99.54	52.81
HI	18.24	14.30 - 23.32	13.03	12.92	98.44	26.42

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

Table.3 Genotypic & Phenotypic correlation coefficient among 12 quantitative traits in 30 Pigeonpea genotypes

Characters		DF	DM	PH	NPBR	NSBR	NPP	PL	NSPP	HSW	YPP	BY	HI
DF	r_g	1.000	0.912**	-0.086	0.208*	0.256*	-0.136	0.335**	0.194	0.285**	0.186	0.279**	-0.173
	r_p	1.000	0.898**	-0.083	0.202	0.227*	-0.134	0.265*	0.151	0.271**	0.183	0.277**	-0.173
DM	r_g		1.000	-0.106	0.163	0.177	-0.118	0.152	0.036	0.236*	0.336**	0.330**	0.051
	r_p		1.000	-0.105	0.161	0.161	-0.116	0.115	0.019	0.225*	0.333**	0.328**	0.053
PH (cm)	r_g			1.000	-0.155	0.115	0.702**	0.195	-0.203	-0.020	0.393**	0.586**	-0.408**
	r_p			1.000	-0.154	0.085	0.683**	0.151	-0.130	-0.033	0.381**	0.574	-0.401**
NPBR	r_g				1.000	0.674**	0.031	0.092	0.037	0.550**	0.250*	0.296**	-0.041
	r_p				1.000	0.677**	0.029	0.105	0.073	0.523**	0.243*	0.286**	-0.035
NSBR	r_g					1.000	0.311**	0.161	-0.093	0.529**	0.229*	0.421**	-0.315**
	r_p					1.000	0.269*	0.144	0.017	0.466**	0.209*	0.375**	-0.270*
NPP	r_g						1.000	0.009	-0.212*	-0.150	0.412**	0.517**	-0.197
	r_p						1.000	0.009	-0.160	-0.149	0.409**	0.513**	-0.192
PL (cm)	r_g							1.000	0.214*	0.517**	0.143	0.341**	-0.355**
	r_p							1.000	0.357**	0.405**	0.115	0.266*	-0.268*
NSPP	r_g								1.000	0.088	-0.224*	-0.272**	0.012
	r_p								1.000	0.052	-0.165	-0.205	0.016
HSW (gm)	r_g									1.000	0.089	0.290**	-0.352**
	r_p									1.000	0.087	0.281**	-0.336**
YPP (gm)	r_g										1.000	0.876**	0.304**
	r_p										1.000	0.875**	0.313**
BY (g)	r_g											1.000	-0.174
	r_p											1.000	-0.166
HI (%)	r_g												1.000
	r_p												1.000

*significant at 5% level of significance, **significant at 1% level of significance.
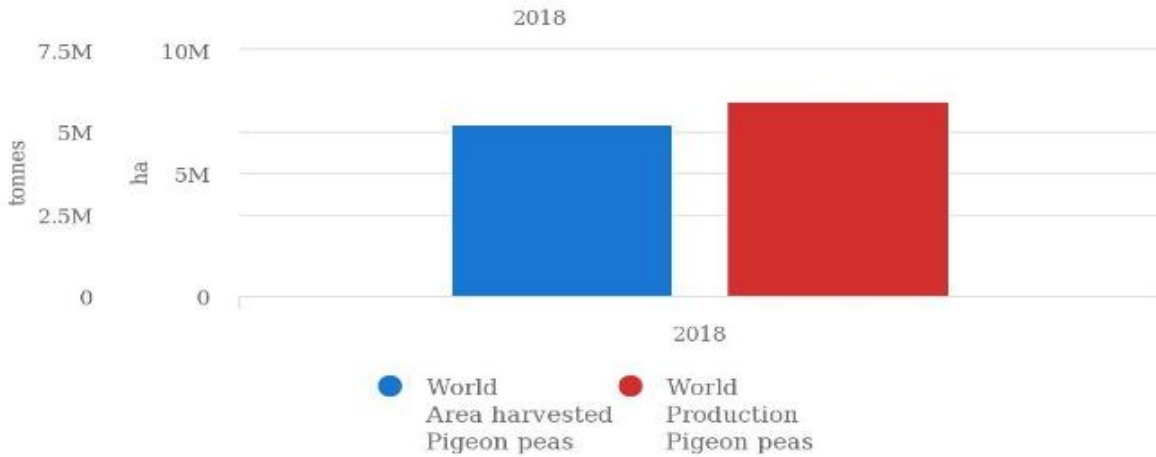
Table.4 Genotypic & Phenotypic path coefficient analysis showing direct (Bold) and indirect effect of 12 quantitative traits on seed yield

Characters		DF	DM	PH	NPBR	NSBR	NPP	PL	NSPP	HSW	BY	HI	YPP
DF	G	**0.0755**	-0.0600	-0.0035	0.0016	-0.0107	0.0004	-0.0166	0.0072	0.0023	0.2731	-0.0828	0.1860
	P	**0.0384**	-0.0266	-0.0034	0.0029	-0.0068	0.0008	-0.0085	0.0052	-0.0022	0.2653	-0.0823	0.1830
DM	G	0.0689	**-0.0658**	-0.0043	0.0012	-0.0074	0.0004	-0.0076	0.0013	0.0019	0.3227	0.0245	0.336**
	P	0.0345	**-0.0296**	-0.0043	0.0023	-0.0048	0.0007	-0.0037	0.0006	-0.0018	0.3141	0.0252	0.333**
PH (cm)	G	-0.0065	0.0070	**0.0406**	-0.0012	-0.0048	-0.0022	-0.0097	-0.0075	-0.0002	0.5724	-0.1952	0.393**
	P	-0.0032	0.0031	**0.0404**	-0.0022	-0.0026	-0.0040	-0.0048	-0.0045	0.0003	0.5496	-0.1908	0.381**
NPBR	G	0.0157	-0.0107	-0.0063	**0.0075**	-0.0281	-0.0001	-0.0045	0.0014	0.0045	0.2897	-0.0195	0.250*
	P	0.0077	-0.0048	-0.0062	**0.0143**	-0.0202	-0.0002	-0.0033	0.0025	-0.0042	0.2743	-0.0165	0.243*
NSBR	G	0.0193	-0.0116	0.0047	0.0050	**-0.0417**	-0.0010	-0.0080	-0.0034	0.0043	0.4118	-0.1508	0.229*
	P	0.0087	-0.0048	0.0035	0.0097	**-0.0299**	-0.0016	-0.0046	0.0006	-0.0038	0.3597	-0.1284	0.209*
NPP	G	-0.0103	0.0077	0.0285	0.0002	-0.0130	**-0.0031**	-0.0004	-0.0078	-0.0012	0.5055	-0.0941	0.412**
	P	-0.0052	0.0034	0.0276	0.0004	-0.0080	**-0.0058**	-0.0003	-0.0055	0.0012	0.4919	-0.0913	0.409**
PL (cm)	G	0.0253	-0.0100	0.0079	0.0007	-0.0067	0.0000	**-0.0496**	0.0079	0.0042	0.3333	-0.1699	0.1430
	P	0.0102	-0.0034	0.0061	0.0015	-0.0043	-0.0001	**-0.0319**	0.0122	-0.0033	0.2551	-0.1275	0.1150
NSPP	G	0.0147	-0.0023	-0.0083	0.0003	0.0039	0.0007	-0.0106	**0.0368**	0.0007	-0.2658	0.0058	-0.224*
	P	0.0058	-0.0006	-0.0053	0.0010	-0.0005	0.0009	-0.0114	**0.0342**	-0.0004	-0.1965	0.0075	-0.1650
HSW (gm)	G	0.0215	-0.0155	-0.0008	0.0041	-0.0221	0.0005	-0.0256	0.0032	**0.0082**	0.2836	-0.1685	0.0890
	P	0.0104	-0.0067	-0.0013	0.0075	-0.0139	0.0009	-0.0129	0.0018	**-0.0081**	0.2693	-0.1599	0.0870
BY (g)	G	0.0211	-0.0217	0.0238	0.0022	-0.0176	-0.0016	-0.0169	-0.0100	0.0024	**0.9774**	-0.0832	0.876**
	P	0.0106	-0.0097	0.0232	0.0041	-0.0112	-0.0030	-0.0085	-0.0070	-0.0023	**0.9581**	-0.0791	0.875**
HI (%)	G	-0.0131	-0.0034	-0.0166	-0.0003	0.0131	0.0006	0.0176	0.0005	-0.0029	-0.1699	**0.4786**	0.304**
	P	-0.0066	-0.0016	-0.0162	-0.0005	0.0081	0.0011	0.0085	0.0005	0.0027	-0.1592	0.4762	0.313**

*, ** significant at 5% and 1% level, respectively. Residual effect (genotypic) = 0.0139; Residual effect (Phenotypic) = 0.0150
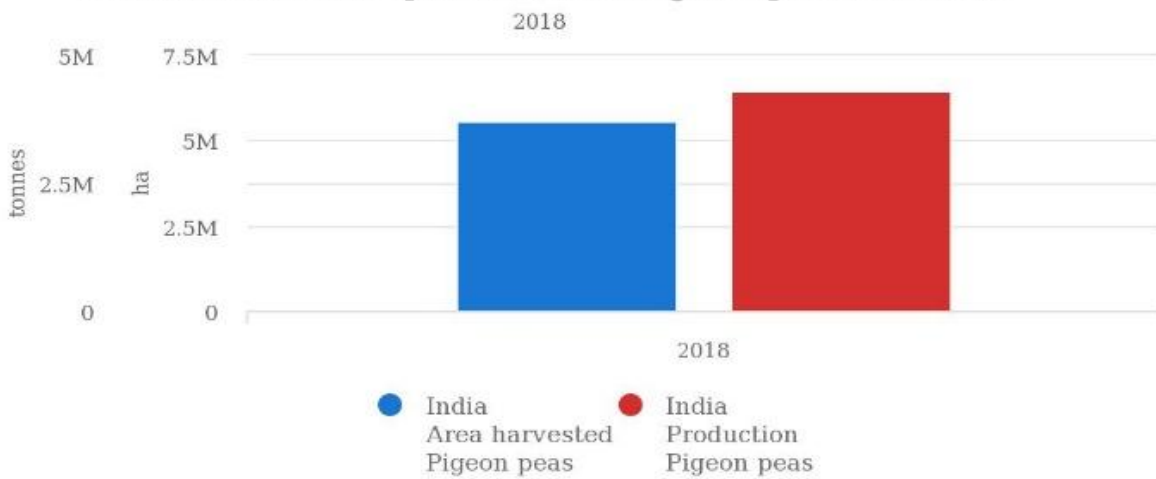
Fig.1

Production/Yield quantities of Pigeon peas in World + (Total)

Source: FAOSTAT (Dec 15, 2020)

Fig.2

Production/Yield quantities of Pigeon peas in India

Source: FAOSTAT (Dec 15, 2020)

These results were in conformity with that of Yerimani *et al.,* (2013) for day to maturity, number of pods per plant; Chandana *et al.,* (2014) for days to flowering, days to maturity, number of primary and secondary branches, podsplant[-1], plant height and harvest index with seed yieldplant[-1]; Ram *et al.,* (2016) observed that the seed yieldplant[-1] had significant and positive association with days to 50% flowering, pods plant[-1], 100-seed weight, number of primary and secondary branches. Jasti Srivarsha *et al.,* (2018)for days to flowering, plant height, days to maturity with seed yield plant[-1]Similar results were also reported by Pushpa Valli *et al.,* (2018) and Alaka *et al.,* (2020) observed positively and significantly correlated with biological yield, pods per plant and plant height. Negative and non-significant phenotypic correlation was observed between

seed yieldplant[-1] and number of seeds per pod in the present study.

Seed yield is a quantitative character which is influenced by its contributing characters that create a complex situation at the time of selection. In the present investigation the correlation studies result reveled that biological yield, days to maturity, plant height, number of primary and secondary branches, number of podsplant[-1] and harvest index were the most important attributing characters considerable towards higher seed yield.

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. This will give due weightage during selection and help in identification of suitable characters.

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). In order to understand these effects, genotypic correlation coefficient of different characters with seed yield was partitioned 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 plant[-1] was recorded by biological yield (0.9774 and 0.9581) and harvest index(0.4786 and 0.4762) followed by plant height (0.0406 and 0.0404), number of seeds pod[-1](0.0368 and 0.0342), days to 50% flowering (0.0755 and 0.0384) and number of primary branches (0.0075 and

0.0143). These results clearly gave an indication that the selection based on these characters would directly improve the seed yield in pigeonpea. These results were in conformity with that of Nethravathi and Patil (2014) observed positive direct effect on seed yield/plant by harvest index; Thanga Hemavathy *et al.,* (2018) observed that days to 50% flowering exerted high positive direct effect on seed yield. Alaka *et al.,* (2020) showed highest positive direct effect for biological yield followed by harvest index, days to maturity, seedspod[-1] and days to 50% flowering on grain yield plant[-1].

Days to maturity (-0.0658 and -0.0296), No. of secondary branches (-0.0417 and -0.0299), No. of pods plant[-1](-0.0031 and -0.0058), pod length (-0.0496 and -0.0319) showed negative direct effect on grain yield in both genotypic and phenotypic level. Except, 100-seed weight in this case genotypic had showed positive direct effect but phenotypic had negative direct effect on the grain yield.

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 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. Alaka *et al.,* (2020) 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 seed yield through selection. Emphasis should be given on the traits *viz.,* plant height, number of primary and secondary branches, pods plant[-1], 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. Considering the above relationships, an ideal plant type in pigeonpea would have a greater number of primary and secondary branches of Optimum height with good pod bearing for harnessing higher yield.

References

Thanga Hemavathy, A., M. Priyadarshini, J. R. Kannan Bapu (2018) Genetic variability, correlation and path coefficient in pigeonpea [*Cajanus cajan (L.)* Millsp.] core collection. Indian Journal of Agricultural Research 10.18805/ IJARe.A-5123.

Ajay, B.C., Ganesh, B.N. and Ganapathy, K.N. 2012. Genetic analysis of yield and quantitative traits in pigeonpea *(Cajanus cajan L.* Millsp.). Euphytica, 186 (3): 705–714.

Anonymous. (2018). Ministry of Agri. & FW, Govt. of India; 2018 3rd Advance Estimate).

Anonymous. (2018). FAO Statistical Database. FAO, Rome, Italy. Retrieved from http://faostat3.fao.org

Bhadru, D. (2010). Correlation and path analysis for yield and its attributing traits in white coated pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legume Research Vol. 33 No. 3 196-200.

Bhadru, D. (2011). Genetic studies in pigeonpea [*Cajanus cajan* (L.) Mill sp.]. Electronic Journal of Plant Breeding, 2(1), 132-134.

Chandana, K. C., Prasanthi, L., Reddi Sekhar, M. and Bhaskara Reddy, B.V. (2014). Studies on Correlation and Path Analysis for Yield and its Attributes in Rabi Red Gram. Indian Journal Agricultural Research, 48(1), 47 -51.

Chetukuri, A., Vijayalakshmi, P., Bhargavi, V., Kumar, P.D., Sreelaxmi, A. and Siddiq, E.A. 2013. Correlation, Variability and Heritability in Pigeon Pea. Advances in Bioresearch, 4(2): 129- 134.

Dewey, D. R. and Lu, K.H. (1959). A correlation path coefficient analysis of components of crested wheat grass. Agronomy Journal, 51(1): 515-518.

Galian, J. L., Nidhi Mohan, Kumar, C. V. S., Mallesh, P. (2015). Genetic Variability Studies in Pigeonpea [*Cajanus cajan* (L.) Millsp.]. Journal of Research Acharya N. G. Ranga Agricultural University, 43 (3&4), 1-7.

Jasti Srivarsha, J.E. Jahagirdar, D.K. Patil, A.J. Hingane, C.V. Sameer Kumar (2018) Correlation Studies for Grain Yield and Yield Contributing Characters in Short Duration Genotypes of Pigeonpea [*Cajanus cajan* (L.) Millsp.]. Bulletin of Environment, Pharmacology and Life Sciences ISSN 2277-1808.

Kumar, S., Singh, S. S., Elanchezhian, R. and Shivani. (2014). Studies on genetic variability and inter-relationship among yield contributing characters in pigeonpea grown under rainfed lowland of eastern region of India. Journal of Food Legumes, 27. (2)104-107.

Nethravathi, K. H., Patil, B. R. (2014). Character association and path coefficient analysis for yield and its components in pigeonpea. Karnataka Journal Agricultural Science, 27 (2), 225.

Oinam Priyadarshini Devi, Malini Barthakur Sharma, Kigwe Seyie and Chubatemsu Ozukum (2019) performance of pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes under mid altitude condition of Nagaland. International Journal of Recent

Scientific Research Vol. 10, Issue, 06(C), pp. 32886-32888, Jun, 2019.

P. Mallesh, H. C. Nanda, Durga Raju, C. V. Sameer Kumar, Nidhi Mohan, (2017) Variability, Heritability and Genetic Advance for Quantitative Traits in Pigeonpea [*Cajanus cajan* (L.) Mill sp.] International. Journal of Pure and Applied Bioscience. 5 (5): 25-28 (2017).

PushpaValli SNCVL, K.N. Yamini (2018) Genetic variability and correlation in pigeonpea genotypes. Electronic Journal of Plant Breeding, 9 (1): 343-349 (Mar 2018) ISSN 0975-928X.

Ram, Kesha, Saxena, Kanak, Shrimali T. M. and Bishnoi Geeta. (2016). A Study on Genetic Variability, Correlation and Path Analysis in Pigeon Pea [*Cajanus cajan* (L.) Mill Spaugh]. International Journal of Agriculture Sciences, 8 (51) 2287-2289.

Rajamani, S., Sreekanth, M. and Rao, Y. K. (2015). Evaluation of Pigeonpea Genotypes for Their Genetic Variability, Heritability and Genetic Advance. Journal of Research Acharya NG Ranga Agricultural University, 43 (3&4), 93-95.

Rekha, R., Prasanthi, L., Reddi, M. S. and Priya, M. S. (2013). Variability, character association and path analysis for yield and yield attributes in pigeonpea. Electronic Journal of Plant Breeding, 4 (4) 1331-1335.

T. Alaka, Ashutosh, A. Nishant Bhanu, M. N. Singh, Sunil Kumar and S. Swarnmala (2020) Genetic Variability, Correlation and Path Analysis for Yield and its Attributes in Long Duration Pigeonpea [*Cajanus cajan* (L.) Millsp.] Genotypes. International Journal of Current Microbiology and Applied Sciences ISSN: 2319-7706 Volume 9 Number 3.

Vange, T. and Moses, E. O. (2009). Studies on Genetic Characteristics of Pigeon Pea Germplasm at Otobi, Benue State of Nigeria. World Journal of Agricultural Sciences, 5: (6) 714-719.

Varshney R.K, Penmetsa R.V, Dutta S. and Kulwal, P.L. 2010. Pigeonpea Genomics Initiative (PGI): An international effort to improve crop productivity of pigeonpea [*Cajanus cajan* (L.) Millsp.]. Molecular Breeding,26: 393-408.

Yerimani, A.S., Subhash Mehetre and Kharde, M.N. (2013). Association analysis for yield and its component traits in F3 and F4, populations pigeonpea [*Cajanus cajan* (L.) Millsp.]. Molecular Plant Breeding 189-195.