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Research Article

Exploiting the natural variation and inter-relationship among medium maturity Pigeonpea [*Cajanus cajan*(L.) Millsp.] genotypes

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Abstract
The present investigation was conducted for character association and their causal effect of quantitatively inherited characters with 21 genotypes of pigeonpea. The genotypic and phenotypic coefficient of variation exhibited high for secondary branches per plant (21.07 and 21.94%, respectively), while low was found for days to maturity (3.71 and 3.82 %, respectively) and days to 50% flowering (4.82 and 5.25 %, respectively). Heritability coupled with genetic advance also observed high for secondary branches per plant (92.26 %). The seed yield showed highly significant and positive correlation with plant height (0.806 and 0.619) at both genotypic as well as phenotypic level, respectively. The path coefficient exhibited the highest positive direct effect of plant height (0.871) followed by primary branches per plant (0.423) and days to 50% flowering (0.171) on seed yield, at genotypic level. The highest positive direct effect on seed yield was exhibited by plant height (0.595) followed by primary branches per plant (0.235) and 100-seed weight (0.190), at phenotypic level. The genotypes *viz.,* BAUPP 1610, AKTM 1637, BDN 716, ICPL 15072, WRG 327 and GJP 1820 were found promising in terms of yield and its attributing traits.

Keywords: Pigeonpea, Genotypic and Phenotypic Coefficient of Variation, Heritability, Genetic Advance, Correlation and Path analysis

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] (2n=2x=22), is an important leguminous crop after chickpea in India. Pulses are the major source of protein (19-25%) and form an integral part of an Indian vegetarian diet (Saxena *et al.,* 2010). It enriches soil fertility through symbiotic nitrogen fixation (up to 235 kg/ha), thus serve as a source for sustainable agriculture (Peoples *et al.,* 1995). The term 'pigeonpea' was coined in Barbados, where its seeds were considered as an important pigeon feed. Globally, Pigeonpea is cultivated in ~6.99 m.ha. area with an annual production of ~5.96 m. t. and productivity is ~852 kg/ha (FAO, 2018). In India, Pigeonpea ranks 2nd in total pulse production after chickpea with an area, production and productivity *viz.,*4.43 m. ha., 4.25 m.t. and 960 kg /ha, respectively. Maharashtra contributes in the country is about 32% of the total production. Madhya Pradesh, Karnataka, Gujarat, Uttar Pradesh, Jharkhand and Telangana contributed about 15, 17, 10, 11, 6 and 7%, respectively (Anonymous, 2020-21 3rd advanced estimates, AICRPP Project Coordinator's Report Online Annual *Kharif* Pulses (Pigeonpea) Group Meet Report). Pigeonpea is an often-cross pollinated crop through entomophily. There are two major growth habit in pigeonpea, the determinate types (sequence of inflorescence developing in the direction of base) and its growth is terminated after flowering while indeterminate type (sequence of inflorescence developing

in both acropetally and basipetally) and its growth is not terminated and gives flowering throughout the life cycle of crops and they can tolerate major biotic and abiotic stresses due to their inherent capacity to regenerate. Pigeonpea crop suffers from major yield limiting factors *i.e.,* biotic and abiotic factors. The genotype used in the breeding programme with potentially higher yield, resistant to such stresses and genetically stable are necessary to use in breeding programme.

Genetic variability exists in the population and which is heritable, are important for making effective selection scheme in crop improvement programme. Seed yield (Polygenically inherited) is a complex character and highly influenced by the environmental fluctuation and it consists of various yield attributing components which affect the yield directly, while other factors indirectly. So, the selection of superior genotype directly for yield would not be much effective. Thus, breeding for high seed yield along with yield associated traits in existing germplasm is important. It is necessary to use genetically variable for making selection effective for the improvement of genotypes. Therefore, it is important to estimate genetic variability present in the population and character association for the yield contributing traits. Correlation coefficient do not gives an exact estimates of direct and indirect effect of yield. Path studies, gives an estimate of direct and indirect effect of independent variables on dependent variables. Hence, the character association and their causal relationship among the component traits with yield are important for the planning of suitable selection scheme.

MATERIALS AND METHODS
The present investigation was conducted during *Kharif,* 2019-20 at Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.). The experimental material consisted twenty-one diverse genotypes of pigeonpea obtained from the Indian Institute of Pulses Research, Kalyanpur, Kanpur (U.P.) (**Table 1**). The experiment was performed under the normal soil

and rainfed condition in Randomized Complete Block Design with three replications. Treatment was grown in 4 m long and 6 rows per plot with spacing 90 × 25 cm. The data was recorded for days to 50% flowering, primary branches per plant, secondary branches per plant, pods per plant, plant height (cm), days to maturity, 100 seed weight (g) and seed yield (kg/ha). The data was recorded for five randomly selected plants excluding border rows for eight quantitative characters. The analysis of variance was laid out based on the procedure given by Panse and Sukhatme (1954) and used software R software 4.1 (Agricole package) for analysis of data. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability in broad sense (h^2) was computed based on the following procedure by Burton and de Vane (1953). Genetic advance was estimated by the method outlined by Johnson *et al.* (1955). Characters association at genotypic and phenotypic levels was worked out based on the following method outlined by Al-Jibouri *et al*. (1958) and Path co-efficient analysis was worked out by the methods proposed by Dewey and Lu (1959).

RESULTS AND DISCUSSION
The average performance of the genotypes for eight quantitative traits is illustrated in **Table 2**. The estimate of genotypic and phenotypic coefficient of variation provides the extent of variability exists in the population. Heritability gives the amount of transmissible variance from parents to their offspring and helps in selection of elite genotype. Genetic advance is the measures of genetic gain under the selection; it refers to the improvement in the mean genotypic value of selected plants over the parental population. The Analysis of variance for 21 diverse genotype indicated highly significant differences for all the characters under the study and considerable amounts of genetic variability exists in the material (**Table 3**).

High values for GCV and PCV were recorded for secondary branches per plant (21.07 and 21.94 5, respectively). This suggested the possibilities for making further improvement

Table 1. Genotypes used during experimentation

S. No.	Genotypes	S. No.	Genotypes
1.	ICPL 87119	11.	PT 0904-1-1-2
2.	BDN 716	12.	AAUVT 13-20
3.	JKM 189	13.	ICPL 15072
4.	BAUPP 16-01	14.	ICPL 15062
5.	CRG 16-11	15.	GJP 1820
6.	WRG 327	16.	GJP 1801
7.	WRG 369	17.	IBTDRG 8
8.	SKNP 1614	18.	IBTDGR 10
9.	BDN 2013-5	19.	RPS 2007-106-1
10.	PT 10-36-1-2	20.	AKTM 1637
		21.	AKTM 1644

Table 2. Mean performance of genotypes for eight quantitative traits in pigeonpea

S.No.	Genotypes	Days to 50% flowering	Number of primary branches per plant	Number of secondary branches per plant	Number of pods per plant	Plant height (cm)	Days to maturity	100-Seed weight (g)	Seed yield (kg/ha)
1.	ICPL 87119	135.67	25.00	42.53	250.27	208.33	210.00	13.27	1559.67
2.	BDN 716	137.33	21.93	35.40	311.53	203.53	213.33	12.73	1202.00
3.	JKM 189	135.67	23.47	21.47	312.93	228.00	211.33	12.10	1475.33
4.	BAUPP 16-01	119.00	23.13	28.00	277.67	209.67	186.00	11.30	1650.00
5.	CRG 16-11	138.00	16.80	31.27	294.80	179.00	210.00	10.77	1164.67
6.	WRG 327	132.33	30.27	44.83	297.80	189.60	203.00	10.93	1190.67
7.	WRG 369	135.67	26.93	36.27	272.73	212.00	210.00	10.33	1431.00
8.	SKNP 1614	133.67	18.80	28.80	291.13	223.60	211.33	12.13	1250.67
9.	BDN 2013-5	136.67	19.53	19.47	153.73	207.67	212.67	11.43	1369.33
10.	PT 10-36-1-2	128.67	27.80	43.27	267.20	207.20	209.33	12.17	1370.67
11.	PT 0904-1-1-2	119.67	24.13	42.20	322.20	190.40	184.67	12.30	1329.67
12.	AAUVT 13-20	135.00	22.53	20.33	298.07	168.00	206.00	12.83	1180.00
13.	ICPL 15072	134.67	26.80	43.73	323.13	169.27	212.67	12.37	1107.33
14.	ICPL 15062	135.00	24.20	39.33	244.53	184.87	207.00	12.37	1166.33
15.	GJP 1820	138.67	24.00	36.07	274.13	199.13	204.00	12.83	1444.33
16.	GJP 1801	133.33	28.00	34.33	297.93	211.60	203.33	12.07	1348.00
17.	IBTDRG 8	138.00	27.07	36.53	239.93	188.47	212.33	12.80	1368.00
18.	IBTDGR 10	137.67	23.47	32.67	240.40	188.00	209.00	13.17	1242.67
19.	RPS 2007-106-1	131.67	24.80	40.80	242.87	201.47	210.00	12.53	1249.33
20.	AKTM 1637	116.00	26.00	34.23	264.07	198.00	213.33	14.33	1453.67
21.	AKTM 1644	121.67	26.67	37.67	279.33	199.20	211.33	13.20	1264.00
	Mean	132.10	24.35	34.72	274.11	198.43	207.17	12.28	1324.63
	Mininimum	116.00	16.80	19.47	153.73	168.00	184.67	10.33	1107.33
	Maximum	138.67	30.27	44.83	323.13	228.00	213.33	14.33	1650.00
	C.D.@5%	7.93	3.80	6.06	62.58	23.50	5.31	0.91	128.22
	C.V.(%)	3.64	9.45	10.57	13.83	7.18	1.55	4.48	5.87

Table 3. ANOVA for eight quantitatively inherited characters in pigeonpea

Characters	Mean Sum of Squares	
	Treatments	Error
Degree of freedom	20	40
Days to 50% flowering	144.57**	23.12
Number of primary branches per plant	31.86**	5.29
Number of secondary per branches plant	174.07**	13.47
Number of pods per plant	4417.36**	1438.36
Plant height	746.56**	2027.73
Days to maturity	187.99**	10.35
100-seed weight	2.65**	0.30
Seed yield	60897.56**	6037.59

** Significant at 1% probability level

in these characters. These findings are also reported by Hussain *et al.* (2021) for secondary branches per plant (28.14) and plant height (22.71), Alaka *et al.* (2020) for secondary branches per plant (76.49) followed by seed yield per plant (45.46)**,** Hemavathy *et al.* (2019) for secondary branches per plant (111.73) followed by pods per plant (40.73) and Singh *et al.* (2014) for plant height and number of branches per plant. Moderate values for GCV and PCV were reported for number of primary branches per plant (12.22 and 13.38%, respectively) followed by number of pods per plant (11.5 and 13.99 %, respectively) and seed yield (10.21 and 10.76 %, respectively) and this showed that environment has played significant role for the expression of these characters. The low GCV and PCV were observed for days to maturity (3.71 and 3.82%, respectively) and days to 50% flowering (4.82 and 5.25 %, respectively). This suggested that negligible influence of environment; hence phenotypic would be effective for these traits. These findings were in accordance with the result reported by Alaka *et al.* (2020) and Hemavathy *et al.* (2019) for days to 50% flowering and days to maturity. Very little differences of GCV and PCV were observed for days to maturity that means genetic factors played a greater role in the expression of these traits and ample scope for improvement. Heritability in broad sense was given in (**Table 4**). The heritability ranged from 67.44 per cent for pods per plant to 94.49 per cent for days to maturity. Very high heritability estimates was observed for days to maturity (94.49 %) and secondary branches per plant (92.26 %) followed by seed yield (90.09 %), 100-seed weight (88.55 %), days to 50% flowering (84.01 %), primary branches per plant (83.39%) and plant height (72.84%). These traits are controlled by additive type of gene action and can be used as a genetic parameter for the selection and improvement of the genotypes. Moderate estimate of heritability was found for pods per plant (67.44 %). This indicates that these traits are more influenced by environmental factors and governed by non-additive gene action. These results are in conformity with the results reported by Hussain *et al.* (2021) for days to 50%

flowering (97.20 %) followed by plant height (96.90 %) and days to maturity (96.70 %), Ranjani *et al.* (2021) for branches per plant (78.20 %) and pods per plant (80.51 %), Hemavathy *et al.* (2019) for secondary branches per plant, Singh *et al.* (2014), Alaka *et al.* (2020) for primary branches per plant, secondary branches per plant and yield per plant, Mahamad *et al.* (2006) for plant height, branches per plant, pods per plant, 100-seed weight and Saroj *et al.* (2013) for days to 50% flowering, yield per plant and 100-seed weight.

The expected genetic advance as percentage of mean is presented in (**Table 4**). High estimates were found for secondary branches per plant (41.69 %) followed by primary branches per plant (22.99 %), while moderate level was found for seed yield (19.96 %) followed by pods per plant (19.45 %), 100-seed weight (13.96 %) and plant height (11.93 %). This indicates that these traits are controlled by additive type of gene action and selection will be effective for the improvement of such traits. Low estimate was found for remaining characters. These are governed by non-additive type of gene action and heterosis may be useful. Heritability along with genetic advance as percentage of mean was found high for secondary branches per plantand primary branches per plant. Improvement in these characters through direct selection is permissible. Thus, selection would be effective with characters having high heritability along with high expected genetic advance as percentage of mean. This is in conformity with Hussain *et al.* (2021) for secondary branches per plant(48.60 %), Ram *et al.* (2016) for secondary branches per plant, Singh (1999) for pods per plant, seed yield per plant, branches per plant and biological yield per plant, Baskaran and Muthiah (2006) for clusters per plant, plant height, branches per plant, pods per plant and seed yield per plant. High heritability along with moderate or low genetic advance was observed for seed yield and 100-seed weight, these characters also exhibited high heritability accompanied with high genetic advance.

Table 4. Genetic parameters for eight quantitative traits in pigeonpea

Traits	Mean	Range	GCV (%)	PCV (%)	h² (%)	GAM
Days to 50% flowering	132.1	116.00-138.67	4.82	5.25	84.01	9.09
Number of primary branches per plant	24.35	16.80-30.27	12.22	13.38	83.39	22.99
Number of secondary branches per plantper branches plant	34.2	19.47-44.83	21.07	21.94	92.26	41.69
Number of pods per plant	274.11	153.73-323.13	11.50	13.99	67.44	19.45
Plant height (cm)	198.43	168.00-228.00	6.79	7.95	72.84	11.93
Days to maturity	207.17	184.67-213.33	3.71	3.82	94.49	7.44
100-seed weight (g)	12.28	10.33-14.33	7.20	7.65	88.55	13.96
Seed yield (kg/ha)	1324.63	1107.33-1650.00	10.21	10.76	90.09	19.96

GCV= Genotypic coefficient of variation; PCV= Phenotypic coefficient of variation; h²=Heritability; GAM= Genetic advance as % of mean

The genotypic and phenotypic correlation analysis for the eight characters is given in **Table 5**. The seed yield showed highly significant and positive correlation with plant height, at genotypic level. If any positive increase in such traits will improve seed yields in pigeonpea. Positively significant correlation of seed yield per plant with plant height was also observed by Singh *et al.* (2008). The seed yield showed highly significant and positive correlation with plant height (0.806 and 0.619), while exhibited significant and negative correlation with days to 50% flowering (-0.382 and -0.328) and days to maturity (-352 and -0.314) at both genotypic and phenotypic level. These results also reported by Parveen *et al.* (2011) for pods per plant with seed yield. The 100-seed weight showed significant and positive correlation with days to maturity (0.271 and 0.241), while exhibited significant and negative correlation of 100-seed weight with days to 50% flowering (-0.265 and -0.240) at both genotypic and phenotypic level.

The days to maturity showed that significant and positive correlation at both genotypic and phenotypic level with days to 50% flowering (0.554 and 0.497); significant and positive correlation of secondary branches per plant with primary branches per plant (0.677 and 0.621). The positive correlation has also been reported by these workers *i.e.* Tharageshwari and Hemavathy, (2020); Kingshlin and Subbraman, (1999) and Singh *et al.* (1999). Baldaniya *et al.* (2018) for characters i.e. days to 50 % flowering, days to maturity, plant height, branches per plant, pods per plant, pod length, seeds per pod and 100-seed weight at both genotypic and phenotypic level. In this study correlation revealed that seed yield per plant and plant height are most important component traits for higher yield.

The genotypic and phenotypic correlation coefficient was further partitioned into direct and indirect effects using path coefficient analyses were illustrated in **Table 6**. The highest positive direct effect on seed yield as exhibited by plant height (0.871) followed by primary branches per plant (0.423) and 100-seed weight (0.362), while the highest negative direct effect on seed yield was exhibited by days to maturity (-0.649) at genotypic level. Therefore, direct selection for these characters would be very effective for the improvement of seed yield. At phenotypic level, the path coefficient showed the highest positive direct effect on seed yield by plant height (0.596) followed by primary branches per plant (0.235), 100-seed weight (0.190), while the highest negative direct effect on seed yield was exhibited by days to maturity (-0.438), pods per plant (-0.260), secondary branches per plant (-0.239) and days to 50% flowering (-0.028) and these characters exhibited substantial negative direct effect on seed yield at phenotypic level. These findings are in conformity with the result reported by Ravika and Solanki (2017) for primary branches per plant and exhibited the highest genotypic magnitude on seed yield followed by days to 50% flowering and plant height and Ranjani *et al*. (2018) for pods per plant, plant height, and days to maturity, branches per plant and days to 50% flowering.

It is concluded that the estimates of genetic variability, character association and path co-efficient analysis indicated a scope for crop improvement through selection. The residual factors were found moderate at genotypic and phenotypic level (0.2076 and 0.6045). Emphasis should be given for traits *viz*., primary branches per plant, secondary branches per plant, plant height, 100-seed weight, and pods per plant for the selection of genotype with high yield potential and such genotype may be useful

Table 5. Estimates of genotypic and phenotypic correlation for eight quantitative characters in pigeonpea

Traits		Days to 50% flowering	Number of primary branches/ plant	Number of secondary branches /plant	Number of pods/ plant	Plant height	Days to maturity	100-Seed weight	Seed yield
Days to 50% flowering	G	**1.000**	-0.213	-0.150	-0.159	-0.096	0.554**	-0.265*	-0.382**
	P	**1.000**	-0.239	-0.156	-0.169	-0.090	0.497**	-0.240	-0.328*
Number of primary branches /plant	G		**1.000**	0.677**	0.131	-0.214	-0.089	0.111	0.102
	P		**1.000**	0.621**	0.149	-0.049	-0.059	0.136	0.106
Number of secondary branches /plant	G			**1.000**	0.196	0.292*	-0.089	0.111	-0.186
Number of pods/ plant	G				**1.000**	-0.259*	-0.352**	-0.127	-0.322**
	P				**1.000**	-0.120	-0.279	-0.053	-0.214
Plant height	G					**1.000**	0.034	-0.202	0.806**
	P					**1.000**	0.033	-0.131	0.619**
Days to maturity	G						**1.000**	0.271*	-0.352**
	P						**1.000**	0.241	-0.314*
100-Seed weight	G							**1.000**	0.018
	P							**1.000**	0.038

*Significant at 5% probability level, ** Significant at 1% probability level
G and P: Genotypic and Phenotypic Correlation coefficient, respectively

Table 6. Direct and indirect effects for different characters on seed yield at both genotypic and phenotypic level

Traits		Days to 50% flowering	Number of primary branches/ plant	Number of secondary branches /plant	Number of pods/ plant	Plant height	Days to maturity	100-Seed weight	Correlation coefficient for seed yield
Days to 50% flowering	G	**0.171**	-0.036	-0.026	-0.027	-0.016	0.095	-0.045	-0.382**
	P	**-0.028**	0.007	0.004	0.005	0.003	-0.014	0.007	-0.328*
Number of primary branches /plant	G	-0.090	**0.423**	0.287	0.055	-0.090	-0.038	0.047	0.102
	P	-0.056	**0.235**	0.146	0.035	-0.011	-0.014	0.032	0.106
Number of secondary branches /plant	G	0.036	-0.162	**-0.239**	-0.047	0.070	0.021	-0.027	-0.186
	P	0.030	-0.120	**-0.193**	-0.043	0.043	0.016	-0.020	-0.175
Number of pods/ plant	G	0.041	-0.034	-0.051	**-0.260**	0.068	0.092	0.033	-0.322**
	P	0.043	-0.038	-0.056	**-0.252**	0.030	0.070	0.013	-0.214
Plant height	G	-0.084	-0.186	-0.254	-0.226	**0.871**	0.029	-0.176	0.806**
	P	-0.054	-0.029	-0.131	-0.072	**0.595**	0.020	-0.078	0.619**
Days to maturity	G	-0.360	0.058	0.058	0.229	-0.022	**-0.649**	-0.176	-0.352**
	P	-0.217	0.026	0.035	0.122	-0.015	**-0.438**	-0.105	-0.314*
100-Seed weight	G	-0.096	0.040	0.040	-0.046	-0.073	0.098	**0.362**	0.018
	P	-0.046	0.026	0.020	-0.010	-0.025	0.046	**0.190**	0.038

G and P: Genotypic and Phenotypic Path Coefficient, respectively
Residual effect = P-0.6045 and G-0.2076 ; Direct Effect on Main Diagonal (Bold Figure)

in the crop improvement programme for yield component traits. Correlation results revealed that grain yield and plant height are important traits for higher yield. Path coefficient results indicated that 100-seed weight, plant height, pods per plant, secondary branches per plant, primary branches per plant and days to 50% flowering are the traits that to improve seed yield through direct selection. Consequently, the genotypes *viz.,* BAUPP 1610, AKTM 1637, BDN 716, ICPL 15072, WRG 327 and GJP 1820 were found promising and best performers in terms of yield and their contributing characters at field condition in Chitrakoot region.

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