Elucidation of genetic variability for seed yield and its component traits along with association studies in pigeon pea *(Cajanus cajan L.)*

Abstract:The experimental material consisted of fifty-fivepigeonpea genotypes sown in Randomized Block Design (RBD) with three replications during *kharif*, 2020-2021 crop seasons at N. E. B. Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The component of genetic variance, correlation and path coefficient were estimated for seed yield and its component by using fifty-fivepigeonpea genotypes. The highest PCV (> 20%) were recorded for character*viz.*, number of secondary branches per plant (62.34%), number of primary branches per plant (37.65%), number of pods per plant (33.00 %) and seed yield/plant (31.84%) and lowest estimates (< 10%) of PCV were found for days to 50% flowering (9.45%) and days to maturity (5.74%). The high estimates of GCV (> 20%) were recorded for traits *viz.*, number of secondary branches (42.16%), number of pods per plant (32.65 %) and seed yield/plant (30.54%) and lowest estimates of GCV were (<10%) for days to 50% flowering (9.43%) and days to maturity (5.71%) number of seeds per pod (5.28 %) and 100- seed weight (9.51 %). The number of pods per plant (0.858) had high positive direct effects on the seed yield per plant along with positive and significant correlation (rp=0.77).

Keywords: Genetic variability, correlation , path, heritability and genetic advance.

Introduction: Pigeonpea [*Cajanus cajan* (L.) Millspaugh], commonly known as Arhar, tur and red gram. Pigeonpea is an often-cross-pollinated crop with 2n=2x=22 (diploid chromosome number) and a genome size of 833.07 Mb **(Varshney *et al.*, 2012)**. Pigeon pea ranked sixth globally after pea, broad bean, lentil, chickpea and common bean and cultivated over an area of 5.4 million hectares, producing 4.49 million tons annually **(Fatokimi and Tanimonure, 2021)**. It is the second-most significant pulse crop in India after chickpea, occupying 4.72 million hectares and producing 4.31 million tons annually with an average yield of 914 Kg/ha. It generates 15% of the nation's total output of pulses. Pigeonpea was grown on 3,000 hectares in Uttarakhand in 2020–21, producing 3.56 thousand tons overall with an average yield of 1185 Kg/ha **(Directorate of Economics and Statistics, 2021).**

The effectiveness of the breeding programme would largely rely on the level of genetic variability available for important economic traits. The genetic variability components like GCV, PCV along with heritability and genetic advance, correlation, and path coefficient are some of the useful parameters that breeders employ at different phases of the crop improvement programme.Heritability estimates are important, as it helps in determining the influence of the environment on the expression of genotype and the reliability of characters. Since the heritability estimate alone does not mean the amount of improvement anticipated from selection, the heritability estimate, along with thegenetic advance, is required to predict the particular impact from the selection of the most appropriate individuals (**Johnson*et al.*, 1955).**Since the expression of morphological characters is likely to be affected by environmental influences, therefore, the knowledge of existing genetic variability and heritability of economically important traits is of utmost significance, before executing any crop improvement programme. Similarly, it is essential to find out the genetic association between yield and its component characters, which will facilitate the selection of desirable genotype(s).

In addition to assessing the nature and magnitude of the correlation coefficient, path coefficient analysis, and genetic association between grain yield and its traits, it is crucial to identify traits contributing to yield through variability, correlation, and path coefficient analyses. Understanding the genetic variability and trait associations plays a significant role in selecting elite genotypes and exploiting heterosis breeding programs. While studies on genetic variability and correlation provide valuable insights, they alone may not precisely determine the relative importance of the direct and indirect influences of each component trait on grain yield. In such cases, path coefficient analysis becomes an essential technique for delineating the direct and indirect effects of independent variables on the dependent variable. Consequently, genetic variability, correlation, and path coefficient analyses serve as important tools for breeders aiming to enhance pigeonpea production and productivity. This study was conducted to evaluate genetic variability, heritability, and path coefficient analysis of yield and its component characters, providing essential information for pigeonpea improvement programs focused on enhancing grain yield.

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The experimental material consisted of fifty fivepigeonpea genotypes sown in Randomized Block Design (RBD) with three replications during *kharif*, 2020-2021 crop seasons at N. E. B. Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The observations were recorded for nine different morphological characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g) and seed yield/plant (g). The row to row distance of 60 cm and plant to plant distance of 20 cm was maintained. The recommended packages of agronomic practices relevant to the crop were followed throughout the crop period. The observations recorded for all the traits were subjected to the analysis of variance. The genotypic and phenotypic coefficient of variability were calculated by using the formula of Burton and De Vane (1953) , heritability and genetic advance by using formula of Burton and De Vane(1953) and the genetic advance as per cent of mean was evaluated as per the formula provided by Johnson *et al.* (1955). The correlation coefficients at phenotypic and genotypic levels were estimated from the analysis of variance and covariance as given by Searle (1961). Direct and indirect effects of various characters on seed yield were estimated with the help of path coefficient analysis as suggested by Wright (1921) and Dewey and Lu (1959).

Result and Discussion:

Study of ANOVA and genetic variability parameters

The analysis of variance (ANOVA) for the year 2020-2021 revealed that mean sum of squares for all the traits under study were highly significant indicating the considerable amount of genetic variability in the experimental material **Table 1**. The presence of sufficient genetic variability is an indication that selection would be effective to improve the traits. The significance of ANOVA for these traits was earlier also reported by Pandey *et al.* (2016) , Gaur *et al.* (2018) and Pal *et al.* (2018).

The results of variance analysis is presented in the**Table 1**,indicated that mean sum of squares (MSS) due to genotypes were highly significant for all studied characters except number of seeds/pods. These results indicated the preponderance of genetic variability in the studied experimental material and hence proved the suitability of experimental materials chosen for the present investigation. Significant differences for different characters among genotypes were also reported earlier by **Srivarsha*et al.*, (2017), Meena *et al.*, (2017), Pal *et al.*, (2018)** and **Gaur *et al.*, (2020).**

Table 1: Analysis of variance for nine different characters in fifty-fivepigeonpea genotypes

S.No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
	Degree of freedom	2	54	108
1.	**Days to 50% Flowering**	3.460**	181.923**	0.355
2.	**Days to Maturity**	7.460**	193.057**	0.559
3.	**Plant Height (cm)**	542.986	3152.242**	357.560
4.	**Number of Primary Branches / plant**	5.115	31.572**	18.695
5.	**Number of Secondary Branches/ plant**	137.618	177.356**	50.241
6.	**Number of Pods/ Plant**	60.187	25071.659**	176.058
7.	**Number of Seeds/ Pod**	0.224	0.646	0.520
8.	**100 - Seed Weight (g)**	0.004	1.850**	0.133
9.	**Seed yield/ Plant (g)**	33.049	1251.673**	35.283

* significance at 5 % and ** significance at 1 % level of probability

The GCV of various characters A critical analysis of **Table 1:** indicated that the Genotypic Coefficient of Variation (GCV) ranged from 5.28 (number of seeds per pods) to 42.16 (number of secondary branches), followed by number of pods per plant (32.65 %) and seed yield/plant (30.54%). PCV (Phenotypic Coefficients of Variation) estimates were higher than the corresponding GCV (Genotypic Coefficients of Variation) estimates for all the nine characters indicating the sufficient influence of environment on these characters. High estimate of PCV than the corresponding GCV estimates for different characters in pigeonpea were also reported earlier by **Rangare*et al.*, (2013), Sharma *et al.*, (2012), Lakhote*et al.*, (2015), Pandey *et al.*, (2015), Pal *et al.*, (2018) and Gaur *et al.*, (2020).** In the present study high estimates of both, the PCV and GCV were recorded for traits like number of secondary branches, number of pods per plant and seed yield/ plant which indicated that the sufficient genetic variability existed in the experimental genotypes for these traits and selection may be effective in bringing desirable improvements in these traits. These findings are in conformity with the earlier findings for these traits in pigeonpea by**Sharma *et al.*, (2012), Lakhote*et al.*, (2015), Pal *et al.*, (2018)** and **Gaur *et al.*, (2020).**

Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain**(Saroj, S. K. 2013).**

The ratio of genotypic variance to phenotypic variance or total variance is known as heritability in broad sense. It is generally expressed in percentage. The heritability is the heritable portion of phenotypic variance. It is a good index of transmission of characters from parents to their offspring **(Falconer, 1981).** The estimates of heritability help the plant breeder in selection of superior genotypes from diverse genetic populations.

The high estimate of heritability (> 60%) were reported for days to 50 % flowering (99.42%), days to maturity (99.14 %), number of pods per plant (97.92%), seed yield per plant (91.99%) 100- seed weight (81.14 %) and plant height (72.26 %). and whereas, the heritability estimates were recorded to be low for the traits *viz.*, number of primary branches per plant (18.67%) and number of seeds/pod (7.46%). In the present study though, the high estimates of heritability in broad sense were obtained for the traits like days to 50 % flowering (99.42%), days to maturity (99.14 %), number of pods per plant (97.92%), seed yield per plant (91.99%) 100- seed weight (81.14 %) and plant height (72.26 %) indicating that these traits are least influenced by the environment. Similar results for the estimates of heritability were also reported earlier in pigeonpea by **Pal *et al.*, (2018), Bisht *et al.*, (2018)** and **Gaur *et al.*, (2020). High heritability indicates the scopeof genetic improvement of these characters through selection.Similar type of heritability was recorded by Patel and Patel(1998) and Linge *et al*. (2010).**

According to Johnson *et al.*,(1955) heritability estimates coupled with genetic advance as % of mean together provide a better judgment rather than heritability alone in predicating the resultant effect of selection. Table 2:High estimates of genetic advance as percent of mean (>20 %) were recorded for number of pods per plant (66.57 %), seed yield per plant (60.34 %), number of secondary branches per plant (58.75 %) and plant height (21.80 %), whereas low estimates of genetic advance as percent of mean (< 10 %) were obtained for number of seeds per pod (2.97 %). These results suggested that the traits like number of pods per plant, seed yield per plant, number of secondary branches per plant and plant height are governed by additive genes and the selection will be rewarding for improvement of these traits. **Sharma *et al.*, (2012), Lakhote*et al.*, (2015), Pal *et al.*, (2018)** and **Gaur *et al.*, (2020)**also reported similar results for different traits for the estimates of genetic advance. The traits like plant height, number of secondary branches, number of pods per plant and seed yield per plant exhibited high heritability coupled with high genetic advance indicating the for these characters, the high estimates of heritability were due to additive gene effects and the selection may be effective. The characters like days to flowering, days to maturity and 100- seed weight exhibited high heritability coupled with moderate / low estimates of genetic advance indicating that for these characters the high heritability is being exhibited due to favourable influence of environment rather than genotype and selection for these characters may not be rewarding.For rest of the traits viz., number of primary branches and number of seeds per pods the low estimates of heritability coupled with moderate/low estimates of genetic advance were obtained indicating that characters are highly influenced by the environment and selection would be totally ineffective. The results of heritability and genetic advance for different traits in the present study were in accordance with the earlier findings of **Shunyu*et al.*, (2013), Vanisree *et al.*, (2014)**, **Bhadru, (2011), Chethana *et al.*, (2015)** and **Hemavathy *et al.*, (2019).**

Table 2:Estimates of different genetic parameters for different characters in pigeonpea genotypes

	Characters	PCV	GCV	Heritability	Genetic advance	GA as (%) of mean
1.	**Days to 50% Flowering**	9.45	9.43	99.42	15.97	19.37
2.	**Days to Maturity**	5.74	5.71	99.14	16.42	11.72
3.	**Plant Height**	14.65	12.45	72.26	53.44	21.80
4.	**No. of Primary Branches**	37.65	16.27	18.67	1.84	14.48
5.	**No. of Secondary Branches**	62.34	42.16	45.75	9.07	58.75
6.	**No. of Pods/ Plant**	33.00	32.65	97.92	185.69	66.57
7.	**No. of Seeds/ Pod**	19.33	5.28	7.46	0.11	2.97
8.	**100 Seed Weight**	10.56	9.51	81.14	1.40	17.66
9.	**Seed yield/ Plant**	31.84	30.54	91.99	39.78	60.34

4.3.1. Character association studies

Correlation analysis is conducted in plant breeding experiments to estimate the association among two or more series of variables. The genotypic correlation coefficient (rg) estimates the magnitude of genotypic association among various characters, while phenotypic correlation (rp)measures both genotypic as well as environmental influences. As seed yield is a complex character thus correlation analysisis conducted to estimate mutual relationship between various plant characters based on which seed yield improvement can be done.It is well known facts that yield depend upon a number of component characters those are less complex and simply inherited. Usually these component characters are simply interlinked. Thus, selection pressure may be more easily exerted on those characters which are independent and are inter associated among themselves.

Table no. 3indicated that in general both phenotypic (rp) and genotypic (rg) correlation coefficients possesssimilar sign. The magnitude of genotypic correlation coefficients wasfound to be more as compared to the magnitude of corresponding phenotypic correlation coefficients. The high magnitude of genotypic correlation coefficients than the corresponding phenotypic correlation coefficients clearly indicates that there is strong association between these two traits genetically, however the genotypic values were lessened by the significant interaction of environment. Similar trend of genotypic and phenotypic correlation coefficients in sign and magnitude were also reported earlier in pigeonpea by **Bisht *et al.*, 2018 and Gaur *et al.*, (2020).**In generalSeed yield/plant exhibited positive and significant phenotypic association with all other studied characters. Positive and significant association of these characters with seed yield/plant was also reported by several workers (**Bisht *et al.* (2018)** and **Gaur *et al.*, (2020**).The character days to 50% flowering showed significant and positive correlation with days to maturity (rp=0.75 and rg= 0.76), plant height (rp=0.37 and rg= 0.44), number of pods per plant (rp=0.66 and rg= 0.66), number of seeds per pod (rp=0.28 and rg= 1.00) and hundred seed weight (rp=0.43 and rg= 0.49) at both genotypic and phenotypic level. Plant height exhibited significant and positive correlation with number of pods per plant, number of seeds per pod and hundred seed weight at both genotypic and phenotypic level. Number of pods plant exhibited significant and positive association with number of seeds per pods and hundred seed weight. Similar kind of results between these traits in pigeonpea were also reported earlier by **Rangare*et al.*, (2013), Sharma *et al.*, (2012), Pal *et al.*, (2018)** and **Gaur *et al.*, (2020).**

Table 3: Phenotypic (r_p) and genotypic (r_g) correlation coefficients among various characters in Pigeonpea

Characters		**DF**	**DM**	**PH**	**NPB**	**NSB**	**NPP**	**NSP**	**HSW**	**SYP**
DF	rp	1.00	0.75**	0.37*	-0.03	-0.12	0.66**	0.28**	0.43**	0.46**
	rg	1.00	0.76**	0.44*	0.01	-0.19	0.66**	1.00**	0.49**	0.49**
DM	rp		1.00	0.17*	-0.02	-0.14	0.38**	0.24**	0.32**	0.36**
	rg		1.00	0.21	-0.04	-0.20	0.38*	0.91**	0.35*	0.38*
PH	rp			1.00	0.17*	-0.09	0.47**	0.18*	0.29**	0.30*

	rg			1.00	0.01	-0.06	0.55**	0.80**	0.38*	0.56**
NPB	rp				1.00	0.45**	0.21**	0.05	0.16*	0.26**
	rg				1.00	1.00**	0.51 **	1.00**	0.39**	0.25
NSB	rp					1.00	0.16*	0.18*	0.06	0.16*
	rg					1.00	0.25	0.52**	0.10	0.32
NPP	rp						1.00	0.31**	0.49**	0.77**
	rg						1.00	1.00**	0.56**	0.81**
NSP	rp							1.00	0.26**	0.28**
	rg							1.00	0.72**	0.99**
HSW	rp								1.00	0.44**
	rg								1.00	0.51**
SYP	rp									1.00
	rg									1.00

*** refers to significance at 5 % and ** refers to significance at 1 %**

Where, DF= days to 50 % flowering; DM= days to maturity; PH= plant height; NPB= number of primary branch; NSB= number of secondary branch; NPP= number of pods per plant; NSP= number of seeds per pod; HSW= 100-seed weight; SYP= seed yield per plant

4.3.2.Path Coefficient Studies

Path coefficient analysis is used to partition observed correlation coefficient into a series of direct and indirect effects of yield components on yield. The term path coefficient was first time used by **Wright, (1921)** and its use was elaborated by **Dewey and Lu, (1959).** Path coefficient analysis quantifies the direct effect of independent variable and its indirect effect through other variables on dependent variable. In the present study, path coefficient analysis was carried out by taking seed yield/plant as dependent and all other traits as independent variable. The results of path coefficient analysis are presented in Table no.4.

A critical preview of Table no. 3 revealed that the number of pods per plant (0.858) had high positive direct effects on the seed yield per plant along with positive and significant correlation (rp=0.77). Since the magnitude of phenotypic correlation coefficient between number of pods / plant is almost equal to the direct effect of this trait on seed yield, it revealed the true relationship between these two traits and direct selection for improvement in number of pods / plant will certainly result in the enhanced seed yield. Similar results for high direct effect of pods / plant on seed yield / plant were also reported earlier by **Gaur *et al.*, (2020).**Days to maturity also exhibited high positive direct effect on seed yield (0.236) along with positive and significant association (rp=0.36). Rest of the traits exhibited very low direct effect on seed yield and were also non-significantly associated with seed yield. The low magnitude of direct effect of different traits were also reported earlier by **Rangare*et al.*, (2013), Sharma *et al.*, (2012), Lakhote*et al.*, (2015), Pandey *et al.*, (2015), Pal *et al.*, (2018).**

Table 4 : Path coefficient analysis showing direct and indirect effect of various characters on seed yield at phenotypic level

Characters	Correlation with SYP	Direct effect	Indirect effect via							
			DF	DM	PH	NPB	NSB	NPP	NSP	HSW
DF	0.46**	-0.291	-	0.178	-0.029	-0.001	0.006	0.567	0.010	.028
DM	0.36**	0.236	-0.220	-	-0.014	-0.002	0.006	0.329	0.008	0.021
PH	0.30*	-0.079	-0.109	0.042	-	0.004	-0.079	0.404	0.006	0.019
NPB	0.26**	0.111	0.001	-0.005	-0.013	-	-0.022	0.186	0.002	0.010
NSB	0.16*	-0.049	0.036	-0.033	0.007	0.050	-	0.142	0.006	0.003
NPP	0.77**	0.858	-0.192	0.090	-0.037	0.024	-0.008	-	0.011	0.032
NSP	0.28**	0.036	-0.082	0.058	-0.014	0.006	-0.008	0.272	-	0.017
HSW	0.44**	0.065	-0.127	0.076	-0.023	0.017	-0.002	0.426	0.009	-

Table 5: List of 20 selected superior cultivars of pigeonpea on the basis of yield and yield related traits.

Genotypes	DF	DM	NPB	NSB	PH	NPP	NSP	HSW	SYP
PA 426	80	135	23	32	260	393.3	4.7	8.25	101.6
PUSA 2015-1	95	149	8.7	8.3	280	395	4	8.84	97.3
PA 421	82	137	19	37	222.5	390	3.7	7.66	96
PA 455	92	146	12	18.3	270	406.7	4.7	8.07	95

AL 2046	92	146	11.7	3.3	295	391.7	3	8.37	95
AL 1932	92	147	11.3	6.3	285	330.3	4	8.05	93.3
PA 443	81	135	12.3	11.7	257.5	385	4	9.17	91.7
PA 444	92	147	14.3	14	177.5	384.3	4	8.23	91.7
AL 1758	92	144	9.3	3.7	270	400.7	4.3	7.83	91.7
PA 477	84	135	10.3	14	270	379.3	4	7.89	87.3
PA 493	95	150	11.7	4	270	369.3	3.7	8.84	85
PA 449	92	146	17.3	40.3	237.5	313.3	4.3	8.72	84.7
GAUT 98023	82	147	13.1	15	247.1	258.3	4	7.76	81.9
PA 441	90	148	9.3	13	245	303.3	4.7	8.49	81.7
PA 429	81	134	15	21.7	295	385	4	8.14	81.2
PUSA 992	80	125	15.3	16	250.3	293.3	4	8.15	81
PA 374	81	135	23	33.7	275	376.7	4.3	8.96	80.2
PA 440	81	135	15.7	13	252.5	346.7	4	8.68	80
ICPL 93081	80	147	14	19	252	266.7	4	8.31	78.73
PUSA 2002-1	75	147	12	11	179	260	3	7.44	78.53
PA 426	80	135	23	32	260	393.3	4.7	8.25	101.6

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