

## Original Research Article

# Studies on Direct Selection Parameters for Quantitative Traits in Pigeonpea (*Cajanus cajan* L. Millsp.)

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## ABSTRACT

An experiment was conducted with twenty-seven genotypes of Pigeonpea for different quantitative traits to identify genotypes with desirable attributes for yield and its component traits. The results showed that there are highly significant differences for all the characters which indicate the presence of an ample amount of genetic variability. The GCV and PCV values were observed the highest for yield (kg per ha) followed by plant spread, number of pods per plant, and the number of branches per plant. The genotypes viz., IBTDRG-2, TRG 87, RPS 2008-5, and RVSA 15-8 were high grain yielders, while the genotypes RKPV310-09, GJP 1601 and BAUPP 15-22 were observed early maturing were identified based on the performance of different genotypes concerning different characters of economic importance such as grain yield per ha and days to maturity. High heritability coupled with high genetic advance as a percentage of mean was observed for traits like the number of branches per plant, seed yield kg per ha, number of pods per plant, and plant spread which indicates the presence of additive gene action. Such quantitative traits can be improved by simple selection procedure, and thus these traits need to be considered in a future breeding program.

### Keywords

Pigeonpea,  
Genetic variability,  
Selection  
parameter,  
Quantitative traits,  
Heritability

## Introduction

Pigeonpea is one of the most widely adopted, hardy, and drought-tolerant pulse crop. It was cultivated almost over more than 25 tropical and sub-tropical countries it was cultivated either as a sole crop or intermixed with cereals such Maize, Sorghum or Pearl millet, or other legumes like groundnut. It is also known popularly as 'Tur', 'Red Gram' or 'Arhar' belongs to the *Fabaceae* family. It is a diploid ( $2n=2x=22$ ) and often cross-pollinated crop (Saxena *et al.*, 2006). It is one of the richest sources of veg protein and a standard component of the daily diet. Besides

its protein richness, it is also a good source of carbohydrates, vitamins and minerals. Each 100g of the whole-grain sample contains around 16.93 to 26.92 g of proteins (Fatteparkar *et al.*, 2004). Pigeonpea is the fourth most crucial pulse crop in the world where as it is second most important next to chickpea in India. During 2019-20 it was cultivated over the area of 4.6 Mha with production of around 3.75 Mt having productivity of 751 kg/ha (Anonymous, Directorate of Economics and Statistics, 2020 a 3rd advance estimate).

The success of yield improvement largely depends upon the magnitude and nature of genetic variability present in the existing material. Assessment of genetic variability present in the population and the extent to which it is heritable are essential factors to have a significant selection in any breeding program. The scope for improvement in a crop is based upon the extent of genotypic and phenotypic variability existing in the population. The greater diversity in the material, the more the genetic potential and there are better chances of producing desired genotypes. For the detection of the amount of variability present in existing germplasm, the parameters like genotypic and phenotypic variances, also co-efficient of variation can be used effectively. Heritability estimates are essential, as it helps in determining the influence of environment on the expression of genotype and the reliability of characters. However, the gain from a selection for a particular character is the function of its heritability, selection pressure, and the variance existing in the base population. Hence, Burton and Dewane (1953) expressed genetic gain as the product of heritability, phenotypic standard deviation, and selection differential. Similarly, Johnson *et al.*, (1955b) explained utility regarding genetic advance as a more useful tool to predict the actual value of selection than heritability. In the present investigation, an attempt was made to estimate phenotypic and genotypic variance ( $V_p$  and  $V_g$ ), heritability ( $H^2$ ), and genetic advance (GA) for different quantitative traits to assess the magnitude of variance present in the population and which can help breeder in future for effective selection of desirable genotypes.

### **Materials and Methods**

Twenty-seven genotypes were during Kharif 2017-18 at Pulses Improvement Project, MPKV, Rahuri evaluated for different agro-

morphological characters in Randomized Block Design (RBD) with three replications. Each genotype consisted of four rows with the plant to plant distance of 25 cm while rows were spaced 90 cm apart. To raise a good crop, the recommended package of practice was followed throughout the cultivation season.

### **Quantitative traits recorded and sampling measurements**

Observations on nine metric traits were recorded on a single plant basis from five randomly selected competitive plants from each genotype in each replication separately. In contrast, observations on flowering and maturity were recorded on a plot basis. A total of nine characters was studied which are days to 50 % flowering, days to maturity, plant height (cm), plant spread (cm), number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g) and Seed yield (kg per ha).

### **Statistical analysis**

The analysis of variance for different characters was carried out using the mean data into different sources by following the method advocated by Panse and Sukhatme (1995); additional genotypic and phenotypic coefficients of variation were calculated as per Burton (1952).

While a broad sense heritability percentage in was calculated as per Burton and Devane (1953), Genetic advance (at 5 % selection intensity) was calculated by the formula given by Allard (1960) and prediction procedure for selection of desirable genotypes were adopted by criterion suggested by Johnson *et al.*, (1955a). All statistical analysis was carried with the help of INDOSTAT Statistical software.

## Results and Discussions

### Analysis of variance and mean performance

The mean values of different genotypes in respect of nine characters studied are presented in Table 2. From the analysis of variance (Table 1), it was cleared that sum of squares due to genotypes was highly significant for all characters which revealed the existence of considerable variability in the material. This variability can be utilized effectively to develop high yielding cultivars through hybridization followed by selection. From these results, it was cleared that there is scope to identify high yielding, dwarf and early Pigeonpea genotypes to improve different quantitative traits simultaneously with subject to judicious selection pressure. The performance of different desirable genotypes concerning different characters of economic importance is presented in Table 3. The genotypes viz., IBTDRG-2 (2630.16), TRG 87 (2617.34), RPS 2008-5 (2700), and RVSA 15-8 (2733.34) were high grain yielders, while the genotypes RKPV310-09 (168), GJP 1601(175) and BAUPP 15-22 (172.66) were early maturing. Similar results were reported by Chetukuri *et al.*, (2013), Visakho *et al.*, (2013), Pandey *et al.*, (2015), and Ram *et al.*, (2016).

### Genotypic and phenotypic coefficients of variation

In the present investigation GCV and PCV values for nine different characters are given in table 4. The highest GCV (20.9%) and PCV (21.78%) was found for yield kg/ha. Among the different yield attributing traits, plant spread had the highest magnitude of GCV (17.37%) and PCV (18.31%) followed by the number of pods per plant (16.57% and 18.7%). The moderate GCV and PCV were observed for the number of branches per plant (16.25% and 17.45%) followed by days

to 50% flowering (11.47% and 11.51%). The low GCV and PCV were observed for 100 seed weight (7.45% and 8.52%), the number of seeds per pods (5.6% and 7.47%), plant height (5.43% and 7.06%), and lowest for days to maturity (4.07% and 4.15%).

In the present investigation, there is a common trend for all characters where phenotypic variance was greater than the genotypic variances. The characters such as days to 50% flowering, days to maturity, plant height, plant spread, number of branches per plant, number of seeds per pod, and 100 seed weight showed greater phenotypic and genotypic variance was than the environmental variance which indicated there is very low to a negligible level of influence of environment on the expression of traits. Thus, it was cleared that selection for traits such as days to 50 per cent flowering, days to maturity, plant height, number of pods per plant, and grain yield per ha would be useful. Similar results were reported by Saroj *et al.*, (2015), Pandey *et al.*, (2015), Devi *et al.*, (2019), and Sahu and Ekka (2020).

A similar finding was also reported by Shunyu *et al.*, (2013) for days to 50 per cent flowering, days to maturity, the number of pods per plant and grain yield per plant. Also, Chethana *et al.*, (2015) for days to 50 per cent flowering, days to maturity, number pods per plant and grain yield per plant. At the same time, low estimates of genotypic and phenotypic variance were observed for the number of seeds per pod and 100 seed weight which coincides with earlier reports by Rangare *et al.*, (2013) for the number of seeds per pod and Chethana *et al.*, (2015) for number seeds per pod and 100 seed weight.

### Heritability and genetic advance

In the present investigation, high heritability estimates were reported for most of the

characters (Table 4). The highest heritability was recorded for the character days to 50% flowering (99.4%), days to flower initiation (96.0%), seed yield Kg/ha (92%) followed by plant height (cm) (90%) number of pods per plant (97.62%), number branches per plant (86.7%), number of pods per plant (78.5%) and 100 seed weight (76.3%). Moderate heritability was observed for plant height (59.1%) and the number of seeds per pod (56.1%). Only heritability estimates alone do not indicate the extent to which genetic improvement achieved through the selection of superior genotypes. Thus, heritability estimates coupled with genetic advance would be a reliable parameter to estimate genetic gain made through selection. Genetic advance as a percentage of the mean was calculated for useful comparison among genotypes.

Genetic advance as a percentage of mean was observed high for the number of yield kg per ha (41.28%), followed by plant spread (cm) (33.95%), number of branches per plant (31.15%), number of pods per plant (30.24%) and days to 50% flowering (23.58%). Genetic advance as a percentage of mean was

recorded as moderate for 100 seed weight (gm) (13.4%). The rest of the characters showed low genetic advance as a percentage of mean viz., for the number of seeds per pod (8.64%) followed by plant height (8.59%) and days to maturity (8.21%).

As traits such as seed yield kg per ha, days to 50 per cent flowering, plant spread, number of branches per plant, and number of pods per plant showed high heritability coupled with a high genetic advance which indicates there is the predominant role of additive gene action. Hence, these traits can be improved through selection. While, remaining traits such as seeds per pod, plant height, days to maturity and 100 seed weight showed high to moderate heritability estimates coupled with moderate to low genetic advance which indicates the presence of non-additive gene action in their expression high heritability coupled with moderate genetic advance was found in the number of 100 seed weight (gm). Similar findings were reported by Chetukuri *et al.*, (2013), Kothimbire *et al.*, (2016), Mallesh *et al.*, (2017), Verma *et al.*, (2018), and Sahu and Ekka, (2020).

**Table.1** Analysis of variance for 9 quantitative characters in Pigeonpea

Sr. No.	Characters	Mean Sum of Square		
		Replications (2)	Genotypes (26)	Error (52)
1	Days to 50% flowering	16.07**	579.37**	1.08
2	Days to maturity	5.64	163.5**	2.26
3	Plant height (cm)	3.21	825.98**	155.02
4	Plant Spread (cm)	112.42	1098.72**	39.32
5	No. of Branches/plant	0.17	36.15**	1.76
6	No. of pod/plant	641.14	3135.63**	262.69
7	No. of seeds/pod	0.06	0.17**	0.03
8	100 seed wt (gm)	0.48	2.2**	0.2
9	Yield kg/ha	28318.12	630124.32**	17736.9

\*\* Significant at 1% probability

\* Significant at 5% probability

**Table.2** Mean performance of 27 genotypes evaluated for 9 quantitative traits

Sr. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. branches /plant	No. pods/plant	No. seeds / pod	100 seed wt. (gm)	Yield (kg/ha)
		1	2	3	4	5	6	7	8	9
1	BDN 2	123.33*	183.33*	257.53	116.77	18.48	186.67	3.83	10.80	2180.32
2	ICPL 87119	135.00*	185.67*	267.20	136.70*	25.33*	249.67*	3.68	11.70*	2725.94*
3	JKM 189	117.67	178.33	285.00	126.17*	21.93	227.67*	3.83	11.50	2364.02
4	CRG 2015-007	122.67	172.67	305.40*	122.73*	17.33	190.33	3.81	11.50	2148.15
5	PT 0723-1-2-3	122.33	177.00*	278.20	99.27	21.33	197.93	4.01	10.60	2082.23
6	LRG 208	136.33*	187.00*	289.33	107.77	18.97	199.33	3.80	8.10	2057.08
7	IBTDRG-3	135.00*	190.33*	269.73	91.60	18.87	161.67	4.03	10.60	1766.16
8	RKPV 310-09	101.33	168.00	263.93	106.25	17.33	194.00	3.84	10.40	2455.02*
9	RKPV 455-02	129.67*	178.67	253.53	97.08	15.67	174.67	3.99	10.63	2075.64
10	BDN 2014-2	129.67*	187.00*	261.67	90.30	22.27	208.00	3.64	11.00	2317.99
11	IBTDRG-2	96.00	172.33	291.73	109.85	21.93	200.33	3.73	10.10	2630.16*
12	BAUPP 15-22	93.33	172.67	278.67	104.97	21.83	167.67	4.01	11.10	2015.87
13	GJP 1601	120.33	175.00	274.33	127.52*	19.33	170.00	3.99	12.10*	2250.26
14	WRG 303	124.67*	184.00*	295.00	79.10	21.60	163.00	3.76	11.80*	1676.19
15	NPMK 15-02	127.00*	183.00*	251.13	80.68	17.37	149.33	3.95	11.10	1803.76
16	VRG 08-004	123.00*	179.00	301.40*	83.85	20.33	188.33	3.76	9.10	1822.75
17	TRG 87	135.33*	191.67*	254.87	128.43*	29.40*	232.33*	3.88	11.77*	2617.34*
18	WRG 311	97.33	169.67	266.30	83.22	17.60	139.67	3.95	11.73*	1296.12
19	GJP 1606	128.00*	172.33	280.27	105.98	20.27	159.67	3.83	11.63	1994.71
20	RPS 2008-5	145.67*	186.67*	299.93*	108.33	24.90*	223.00*	3.84	10.86	2700.00*
21	BAUPP 15-22	107.33	173.00	250.4	93.17	20.27	150.67	3.65	10.83	2111.11
22	IBTDRG-1	136.33*	196.67*	276.87	79.17	14.67	110.67	2.87	11.63	737.05
23	RVSA 15-8	113.33	179.67	293.40	139.12*	25.00*	221.33*	4.31*	11.40	2733.33*

24	IPA 17B-11	113.00	178.67	283.67	132.02*	24.63*	220.33*	3.81	11.03	2469.84*
25	RVSA 15-9	102.33	174.00	250.33	107.50	17.33	158.00	3.65	10.80	2195.54
26	SKNP 1416	129.67*	189.00*	275.93	131.27*	24.13*	211.00	3.72	10.37	2569.33*
27	IPA 17B-10	120.33	178.33	282.13	131.72*	24.60*	186.67	3.97	11.07	2593.79*
	<b>GM</b>	120.96	180.14	275.48	108.17	20.84	186.74	3.82	10.94	2162.58
	<b>S.E.</b>	0.6	0.86	7.18	3.62	0.76	9.36	0.11	0.26	76.89
	<b>CD at5%</b>	1.71	2.46	20.39	10.27	2.18	26.55	0.31	0.74	218.2
	<b>C.V.</b>	0.86	0.83	4.52	5.8	6.37	8.68	4.94	4.15	6.15

\*Statistically significant (at par)

**Table.3** Most desirable genotypes identified for high mean performance for 9 traits

Sr. No.	Characters	Genotypes
1	Days to 50% flowering	RPS 2008-5, TRG-87, BDN-2, VRG-08-004, WRG-303,
2	Days to maturity	RKPV 310-09, GJP 1601, BAUP15-22, BDN-2, ICPL 87119
3	Plant height (cm)	RPS 2008-5, CRG-2015-007, VRG-08-004,
4	Plant Spread (cm)	ICPL 87119, CRG 2015-007, GJP 1601, TRG 87, RVSA 15-8
5	No. of Branches/plant	ICPL 87119 , TRG 87, RPS 2008-5, RVSA 15-8 , IPA 17B-11
6	No. of pod/plant	ICPL 87119, TRG 87, RPS 2008-5, RVSA 15-8, IPA 17B-11
7	No. of seeds/pod	RVSA 15-8
8	100 seed wt (gm)	GJP 1601, WRG 303, TRG 87, WRG-311
9	Yield kg/ha	RKVP 310-09, IBTDRG-2, TRG 8, RPS 2008-5, RVSA 15-8

**Table.4** Genetic variability parameters for nine different traits in 27 genotypes

Sr. No	Characters	Range		General Mean	$\sigma^2_g$	$\sigma^2_p$	$\sigma^2_e$	GCV (%)	PCV (%)	ECV (%)	Heritability % (b.s.)	Genetic Advance	GA as a % of mean
		Min	Max										
1	Days to 50% flowering	93.34	145.67	120.96	192.76	193.85	1.08	11.48	11.51	0.86	99.4	28.52	23.58
2	Days to maturity	168	196.66	180.13	53.74	56	2.26	4.1	4.15	0.834	96.0	14.79	8.21
3	Plant height (cm)	250.47	305.4	275.48	223.65	378.68	155.02	5.43	7.06	4.52	59.1	23.68	8.6
4	Plant Spread (cm)	79.17	139.12	108.17	353.13	392.46	39.32	17.37	18.31	5.8	90.0	36.72	33.95
5	No. of Branches/plant	14.66	25.33	20.84	11.46	13.23	1.76	16.25	17.45	6.37	86.7	6.49	31.15
6	No. of pod/plant	110.67	249.66	186.74	957.65	1220.34	262.7	16.57	18.71	8.68	78.5	56.47	30.24
7	No. of seeds/pod	2.87	4.3	3.82	0.046	0.08	0.04	5.6	7.47	4.95	56.1	0.33	8.64
8	100 seed wt (gm)	8.1	12.1	10.94	0.66	0.87	0.21	7.45	8.52	4.15	76.3	1.46	13.4
9	Yield kg/ha	737.05	2733.34	2162.58	204129.2	221866	17736.8	20.9	21.78	6.16	92.0	892.74	41.28

In conclusion, from the analysis of variance, it was cleared that there is existence of the considerable amount of variability in the existing material as the mean sum of squares due to genotypes were highly significant for all the characters under investigation. Based on high mean performance for yield and component traits genotypes such as IBTDRG-2, TRG 87, RPS 2008-5, and RVSA 15-8, RKPV310-09, GJP 1601, and BAUPP 15-22 can be utilized as donor parents in hybridization program to develop high yielding and early maturing varieties. The quantitative traits such as yield kg per ha, plant spread, number pods per plant, and the number of branches per plant showed the highest value for GCV and PCV which shows there is considerable scope for yield improvement in existing genotypes. As the high heritability estimates coupled with high genetic advance as a percentage of mean was observed for traits like the number of branches per plant, seed yield kg per ha, number of pods per plant and plant spread. So, these traits suggesting the presence of additive gene action, and it could be improved through selection. While rest of traits such as seeds per pod, plant height, days to maturity and 100 seed weight showed relatively high to moderate heritability with moderate to low genetic advance which revealed the role of non-additive genetic action in their expression and these traits can be exploited through heterosis breeding.

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