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Study of heritability, genetic advance, and character association for yield contributing characters in pigeonpea [*Cajanus cajan* (L.) Huth]

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Abstract

The present study aimed to assess heritability, genetic advance, and character associations for yield in pigeonpea to identify superior genotypes for yield improvement. Eighteen genotypes comprising parents, F_1 , F_2 , backcross generations, and two checks were evaluated in a Randomized Block Design during *kharif* 2024-25 at Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. Analysis of variance revealed significant differences among genotypes for all traits, indicating substantial genetic variability. The highest seed yield per plant was recorded in BC₁ of PDKV Ashlesha $\times$ IPAE 20-05. High broad-sense heritability coupled with high genetic advance was observed particularly for number of branches per plant, number of pods per plant, pod length, 100-seed weight, and grain yield in specific crosses, suggesting the predominance of additive gene action. Genotypic correlations were generally higher than phenotypic correlations. Grain yield showed strong positive associations with plant height, branches per plant, pods per plant, pod length, seeds per pod, and 100-seed weight, indicating their importance as selection criteria in pigeonpea breeding programs.

Keywords: Pigeonpea, heritability, genetic advance, correlation

Introduction

Pigeonpea [*Cajanus cajan* (L.) Huth] is a multipurpose and protein-rich legume crop. It is an often cross-pollinated crop with diploid chromosome number of $2n = 22$. It is the second most important pulse crop after chickpea in India, commonly known as tur, red gram, arhar, Congo pea, no eye pea and tropical green pea. At present, pigeonpea is classified in family Leguminosae, sub-family Papilionaceae, genus *Cajanus*, and species *cajan*. Keeping in view the wide range of diversity in India, pigeonpea was considered to be of Indian origin (Vavilov, 1951) [24].

It is predominantly cultivated under rainfed conditions providing 40-60 kg N/ha to the subsequent crop and improves the soil fertility (Sarkar *et al.*, 2020) [20]. It is widely consumed in the form of *dhal* as an economical source of protein particularly in the vegetarian diet. The nutritional component of Pigeonpea makes it crucial for human nutrition. Pigeonpea is a dense source of nutrients with protein, carbohydrate, minerals and vitamins such as thiamine, riboflavin, niacin and B-complex. It contains high amount of lysine, leucine, aspartic acid, glutamic acid, arginine and provides essential amino acids when consumed with cereals (Talari *et al.*, 2018) [23].

Correlation helps in identifying the traits contributing to yield that are used to make significant genetic gain. Any crop improvement programme begins with identification of diversity among the plant genetic resources (Patel *et al.*, 2021) [16]. The selection of parents for varietal improvement programs depends on the knowledge of existing genetic variability in the crop. Hence, a research work was initiated with an objective to determine the heritability, genetic advance, principal components and association among the pigeonpea genotypes based on quantitative traits to select unique genotypes for different traits as it could be used in pigeonpea breeding programmes.

Materials and Methods

The experimental material consisted of eighteen genotypes, including sixteen genotypes along with two check varieties. The parental genotypes were crossed to obtain F_1 seeds of 3 crosses viz., PDKV Ashlesha $\times$ CORG-9701, PDKV Ashlesha $\times$ IPAE 20-05 and AKTE 12-04 $\times$ IPAE 20-05 during *kharif* 2022-2023. All F_1 s were grown during *kharif* 2023-2024 and selfed to get F_2 seeds as well as backcrossed with both parents to get BC_1 , and BC_2 , at the experimental field of Pulses Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. Four parents, three F_1 s, six backcrosses, three F_2 s (i.e. P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 generations each of cross) and two checks (total 18) were evaluated in Randomized Block Design (RBD) at the experimental field of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, during *kharif* season 2024-25. The experiment was laid out in a RBD with three replications. All 18 genotypes were planted with 90 cm distance between rows and 20 cm between plants. All recommended agronomic practices were adopted for proper crop growth. Observations were recorded on randomly selected five plants from each generation for recording the observations viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, length of pod bearing branch (cm), number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g) and grain yield per plant (g).

The data were subjected to analysis of variance as per the method suggested by Panse and Sukhatme (1967) [15]. Heritability (h^2) and genetic advance (GA) were analysed as per the methods given by Allard (1960) [1], Lush (1949) [9] and Johnson *et al.*, (1955) [7]. Correlation studies were analyzed as per method suggested by Falconer (1964) [6].

Results and Discussion

Analysis of variance revealed that mean squares due to treatments were highly significant for all the traits studied (Table 1). Here, treatments of the six generations i.e. P_1 , P_2 , F_1 , F_2 , BC_1 , and BC_2 of three crosses viz., PDKV Ashlesha $\times$ CORG 97-01, PDKV Ashlesha $\times$ IPAE 20-05, AKTE 12-04 $\times$ IPAE 20-05 including a check viz., Godawari and IPAE 15-06 significance of treatment differences indicated the presence of sufficient amount of variation for all the characters studied.

The mean performance of eighteen genotypes for yield and yield-related traits are presented in Table 2. The highest seed yield per plant was recorded in BC_1 generation of PDKV Ashlesha $\times$ IPAE 20-05 (45.50 g) followed by parent AKTE 12-04 (45.20 g). The high yield of the BC_1 generation of PDKV Ashlesha $\times$ IPAE 20-05 was attributed to a higher number of pods per plant. The BC_2 generation of PDKV Ashlesha $\times$ IPAE 20-05 and AKTE 12-04 $\times$ IPAE 20-05 was the earliest to flower (95 days). BC_2 generation of PDKV Ashlesha $\times$ CORG 97-01 and AKTE 12-04 $\times$ IPAE 20-05 took the shortest duration of time (141 days) for maturity. F_2 generation of PDKV Ashlesha $\times$ CORG 97-01 recorded as the tallest (215.47 cm). The highest number of branches was observed in parent AKTE 12-04 (23.03). The highest number of pods per plant was observed in parent PDKV Ashlesha (239.43). However, highest seeds per pod were observed in BC_2 generation of AKTE 12-04 $\times$ IPAE 20-05 (4.53) and pod length in F_1 generation of AKTE 12-04 $\times$ IPAE 20-05 (4.60).

The high magnitude of broad sense heritability was reported in PDKV Ashlesha $\times$ CORG 97-01 cross for number of branches per plant and 100 seed weight. In PDKV Ashlesha $\times$ IPAE 20-05 cross for the character number of branches per plant, length of pod bearing branch, number of pods per plant, pod length,

100 seed weight and grain yield per plant high broad sense heritability was noticed. In AKTE 12-04 $\times$ IPAE 20-05 cross for days to maturity, number of branches per plant, length of pod bearing branch, number of pods per plant, pod length, 100 seed weight and grain yield per plant high broad sense heritability was noticed. Chetukuri *et al.* (2013) [5], Saroj *et al.* (2013) [21] also reported high heritability for yield contributing characters. High narrow sense heritability was reported in PDKV Ashlesha $\times$ CORG 97-01 cross for days to maturity and grain yield per plant. In PDKV Ashlesha $\times$ IPAE 20-05 cross for the character days to 50% flowering and number of pods per plant high narrow sense heritability was noticed. In AKTE 12-04 $\times$ IPAE 20-05 cross for grain yield per plant high narrow sense heritability was noticed. These findings are supported by Sreelakshmi *et al.* (2011) [22], Bhadru (2011) [3], who reported similar narrow sense heritability.

It was found that number of branches per plant, number of pods per plant and 100 seed weight in PDKV Ashlesha $\times$ CORG 97-01 cross exhibited high genetic advance as per cent of mean. In PDKV Ashlesha $\times$ IPAE 20-05 cross, number of branches per plant, length of pod bearing branch, number of pods per plant, pod length, 100 seed weight and grain yield per plant recorded high genetic advance as per cent of mean. Also in AKTE 12-04 $\times$ IPAE 20-05 cross, number of branches per plant, length of pod bearing branch, number of pods per plant, pod length, 100 seed weight and grain yield per plant recorded high genetic advance as per cent of mean. This supports earlier findings reported by Saroj *et al.* (2013) [21], Kumar *et al.* (2014) [8] and Chethana *et al.* (2015) [4] of high genetic advance as per cent of mean for yield component traits in pigeonpea.

High heritability combined with high genetic advance as a per cent of the mean was recorded for number of branches per plant in all three crosses. Number of pods per plant and grain yield per plant in PDKV Ashlesha $\times$ IPAE 20-05 cross. Number of pods per plant, pod length and grain yield per plant in AKTE 12-04 $\times$ IPAE 20-05 cross also recorded high heritability combined with high genetic advance as a per cent of the mean. This suggests the predominance of additive gene action and strong potential for effective genetic improvement through selection. These findings are in accordance with the results reported by Pandey *et al.* (2015) [14] and Mula *et al.* (2019) [11] for number of pods per plant.

In all ten characters the magnitude of genotypic correlation coefficient was higher than the corresponding phenotypic correlation coefficients (Table 4). Days to 50% flowering exhibited a strong and significant positive correlation with days to maturity and 100-seed weight at both genotypic and phenotypic levels. However, its association with grain yield per plant and most yield-contributing traits was positive but non-significant. Days to maturity showed a significant and positive association with 100-seed weight, plant height, number of pods per plant and grain yield per plant at both levels of correlation, with stronger relationships at the genotypic level. The relationship between days to maturity and number of seeds per pod was negative and non-significant. Plant height exhibited significant and positive correlations with grain yield per plant, number of branches per plant, number of pods per plant and 100-seed weight at both genotypic and phenotypic levels. Number of branches per plant emerged as an important yield-attributing trait, showing strong and significant positive correlations with grain yield, number of pods per plant, pod length and 100-seed weight under both correlation studies. Length of pod-bearing branch showed moderate but significant and positive association with pod length, number of branches

per plant and grain yield. Number of pods per plant exhibited one of the strongest positive correlations with grain yield per plant at both genotypic and phenotypic levels. Pod length also showed a highly significant positive association with grain yield, number of pods per plant, number of branches per plant and 100-seed weight. Number of seeds per pod exhibited positive correlations with grain yield. 100 seed weight maintained significant positive correlation with grain yield and major yield components. Similar relationship between days to 50%

flowering and days to maturity has been also reported by Bhadru (2010) [2], Rathore *et al.* (2020) [18], Sandeep *et al.* (2020) [19]. Whereas, Pandey *et al.*, (2016) [13] reported significant and positive correlation between number of pods per plant and grain yield per plant. Pal *et al.* (2018) [12] reported that number of seeds per pod has a positive significant relationship with seed yield per plant. It was also reported by Mittal *et al.* 2010 [10] and Patel and Acharya (2011) [17].

Table 1: Analysis of variance for yield and yield contributing characters in pigeonpea

Sources of variation	Degrees of freedom	Mean sum of square				
		Days to 50% flowering	Days to maturity	Plant height	Number of branches per plant	Length of pod bearing branch
Replications	2	15.38	2.96	21.67	2.77	13.67
Treatments	17	199**	100.62**	296.96**	36.63**	111.33**
Error	34	77.36	22.51	106.86	1.61	11.54
Sources of variation	Degrees of freedom	Mean sum of square				
		Number of pods per plant	Pod length	Number of seeds per pod	100 seed weight	Grain yield per plant
Replications	2	1264.14	0.07	0.40	1.08	8.28
Treatments	17	3211.30**	1.00**	0.49**	7.59**	92.27**
Error	34	426.34	0.11	0.17	0.32	25.24

* Significance at 5%, ** Significance at 1% level of significance

Table 2: Mean performance of various generations of three crosses in pigeonpea

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Length of pod bearing branch (cm)	Number of pods per plant	Pod Length (cm)	Number of seeds per pod	100 seed weight (g)	Grain yield per plant (g)
Cross I										
PDKV Ashlesha x CORG 9701										
P ₁	119.00	155.00	191.77	14.60	47.87	190.73	4.20	4.17**	10.83	31.37
P ₂	108.00	154.00	210.97	12.53	45.47	143.23	3.60	3.80	9.57	28.00
F ₁	104.00	149.00	198.60	22.03**	56.13	228.30	4.70**	4.37**	12.03**	41.20
F ₂	110.00	152.00	215.47**	19.17	52.80	206.63	4.30	3.43	11.27	35.40
BC ₁	114.00	160.00	212.67**	15.57	47.70	206.20	4.10	4.37**	12.07**	31.70
BC ₂	96.00**	141.00**	195.30	15.67	46.77	174.07	3.70	3.93	8.20	27.23
Cross II										
PDKV Ashlesha x IPAE 20-05										
P ₁	119.00	155.00	191.77	14.60	47.87	190.73	4.20	4.17**	10.83	31.37
P ₂	99.00	149.00	211.87	18.13	49.87	207.63	4.40**	3.37	8.30	33.27
F ₁	97.00	149.00	194.50	21.00**	65.90**	237.20**	5.20**	3.47	11.63	36.03
F ₂	104.00	153.00	211.20	17.57	58.27**	203.83	4.30	3.20	11.10	34.47
BC ₁	106.00	155.00	214.07**	22.20**	54.03	252.00**	5.00**	3.77	12.23**	45.50**
BC ₂	95.00**	143.00**	207.47	16.10	50.27	180.40	4.00	4.53**	9.27	28.80
Cross III										
AKTE 12-04 x IPAE 20-05										
P ₁	118.00	157.00	214.80**	23.03**	53.33	239.43**	4.90**	3.40	12.65**	45.20**
P ₂	99.00	149.00	211.87	18.13	49.87	207.63	4.40**	3.37	8.30	33.27
F ₁	104.00	147.00**	192.17	18.70**	66.07**	209.50	5.40**	3.80	10.00	34.50
F ₂	99.00	149.00	210.30	16.37	59.47**	201.90	4.60**	3.77	8.43	31.30
BC ₁	109.00	158.00	214.23**	18.10	48.80	198.70	4.20	3.87	8.47	31.47
BC ₂	95.00**	141.00**	192.6	12.63	53.23	144.70	3.50	3.33	8.00	28.77
Checks										
Godawari	119.00	156.00	195.07	16.20	48.10	201.57	3.80	3.43	10.73	33.63
IPAE 15-06	111.00	152.00	188.30	13.00	51.00	140.17	3.70	3.37	9.00	27.17
SE(m) ±	5.08	2.74	5.97	0.71	1.79	10.87	0.19	0.23	0.32	3.00
CD at 5%	14.59	7.87	17.15	2.10	5.15	34.26	0.55	0.65	0.93	8.34
CV (%)	8.30	3.14	5.07	7.69	6.43	10.32	8.26	10.61	5.71	16.90

* Significance at 5%, ** Significance at 1% level of significance

Table 3: Estimates of heritability and genetic advance in three crosses of pigeonpea for seed yield and other traits

Genetic parameter	Characters														
	Days to 50% flowering			Days to maturity			Plant height			Number of branches per plant			Length of pod bearing branch		
Cross	I	II	III	I	II	III	I	II	III	I	II	III	I	II	III
Heritability In b.s. (%)	39.01	25.59	35.47	58.94	46.67	62.57	35.22	25.03	48.39	86.91	84.60	92.39	53.10	79.57	81.83
Heritability In n.s. (%)	10.49	74.15	21.35	79.67	26.60	15.44	49.61	26.81	16.18	23.26	31.49	34.26	46.09	51.83	45.18
Genetic advance	8.54	6.48	8.09	9.33	5.84	9.75	9.71	6.98	13.11	6.46	4.72	7.91	5.94	12.03	13.09
Genetic advance as % of mean	7.87	6.26	7.79	6.14	3.87	6.50	4.76	3.40	6.36	41.58	26.49	46.14	12.41	22.84	24.84
Genetic parameter	Characters														
	Number of pods per plant			Pod length			Number of seeds per pod			100 seed weight			Grain yield per plant		
Cross	I	II	III	I	II	III	I	II	III	I	II	III	I	II	III
Heritability In b.s. (%)	53.95	78.67	88.27	58.10	69.31	83.57	39.74	40.15	17.32	79.92	79.92	92.39	9.34	85.83	74.68
Heritability In n.s. (%)	14.87	58.83	9.32	38.01	41.21	47.02	23.92	62.25	8.67	14.18	8.87	14.66	75.54	56.92	62.86
Genetic advance	39.35	58.00	84.52	0.60	0.99	1.36	0.39	0.54	0.13	2.45	2.50	3.45	1.57	12.01	13.88
Genetic advance as % of mean	21.15	28.17	45.23	15.19	22.55	31.36	9.59	14.60	3.65	23.35	23.98	37.27	5.07	35.55	43.56

Table 4: Estimate of genotypic and phenotypic correlation coefficient

GCV ↓ → PCV	Days to 50% flowering	Days to maturity	Plant height	Number of branches per plant	Length of pod bearing branch	Number of pods per plant	Pod length	Number of seeds per pod	100 seed weight	Grain yield per plant
Days to 50% flowering	1	0.864**	0.153	0.177	0.167	0.202	0.278*	0.119	0.921**	0.232
Days to maturity	0.818**	1	0.610**	0.267	0.004	0.356**	0.344*	-0.018	0.796**	0.379**
Plant height	0.027	0.273*	1	0.507**	0.187	0.500**	0.397**	0.076	0.558**	0.552**
Number of branches per plant	0.115	0.231	0.317*	1	0.660**	0.876**	0.941**	0.238	0.435**	0.960**
Length of pod bearing branch	0.010	0.028	-0.093	0.280*	1	0.317*	0.601**	0.004	0.281*	0.424**
Number of pods per plant	0.165	0.248	0.310*	0.768**	0.093	1	0.977**	0.433**	0.461**	0.980**
Pod length	0.219	0.195	0.212	0.742**	0.287*	0.840**	1	0.400**	0.461**	0.981**
Number of seeds per pod	-0.138	-0.089	0.119	0.182	-0.164	0.238	0.229	1	0.052	0.296*
100 seed weight	0.493**	0.539**	0.358**	0.403**	0.185	0.425**	0.352**	0.016	1	0.525**
Grain yield per plant	0.154	0.222	0.314*	0.740**	0.095	0.913**	0.847**	0.219	0.435**	1

* Significance at 5%, ** Significance at 1% level of significance

Conclusion

The high broad sense heritability indicated that the characters were less influenced by environment and direct selection for these traits in respective cross would be effective for further genetic improvement. Narrow sense heritability estimates appeared moderate to low in most of the cases, it showed that there was a preponderance of non-additive gene action and heterosis breeding may be useful.

The result showed that there was no consistency observed in magnitude of genetic parameters in any cross combination. However, for number of branches per plant in all crosses, high magnitude of heritability coupled with high genetic advance as per cent of mean, indicates that the heritability was due to additive gene effects and which could be helpful for improvement of these traits by simple selection. Low heritability coupled with low genetic advance as per cent of mean indicated the great influence of environmental effects and selection would be ineffective for these traits in respective cross.

Correlation analysis revealed strong and positive genotypic and phenotypic correlations of seed yield with plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod and 100-seed weight. Genotypic correlations were generally higher than their respective phenotypic counterparts, suggesting strong genetic associations among traits, while phenotypic correlations were somewhat reduced due to environmental effects.

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