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Variability, Heritability and Genetic Advance for Quantitative Traits in Pigeonpea (*Cajanus cajan* (L.) Mill sp.)

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ABSTRACT

Study was carried out for genetic variability, heritability and genetic advance of sixteen characters in twenty eight genotypes including checks. Analysis of variance revealed significant difference among genotypes for all the sixteen characters studied. The magnitude of PCV and GCV was moderate to high for pods per plant, seed yield and primary branches per plant. High heritability was recorded for days to 50% flowering, seed yield per plant, number of pods per plant, test weight and plant height. High heritability combined with high genetic advance was recorded for number of pods per plant and seed yield per plant indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Key words: *Genetic variability, Heritability, Genetic advance, Quantitative traits, Pigeonpea*

INTRODUCTION

Pigeonpea is the second important pulse crop after chickpea in India. It plays an important role in subsistence agriculture because, it produces protein rich food with fewer inputs and can be grown in diverse cropping systems. The global production of pigeonpea is 4.32 Mt from an area of 5.32 Mha with a productivity of 813.2 kg/ha[5]. In India, pigeonpea is cultivated in 264.02 lakh ha with average productivity of 789 kg/ha[4]. To meet the protein needs of population, it is essential to increase the production of pulses. Success of crop improvement programme in pigeonpea depends upon the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. The seed yield of pigeonpea (*Cajanus cajan* (L.) Mill sp) is a complex and multiplicative character, which is highly influenced by environmental variations. Information on nature and magnitude of variability present in a population due to genetic and non genetic causes is an important prerequisite for systematic breeding programme.

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An attempt was made in the present investigation to assess the variability, heritability and genetic advance of some quantitative characters in a set of genotypes.

MATERIALS AND METHODS

Twenty eight pigeonpea genotypes were grown in 2 rows of 4m length in randomized complete block design (RBD) with three replications during *kharif* 2015-16. Row to row and plant to plant spacing were maintained at 75 and 50 cm, respectively. Observations were recorded for sixteen traits including days to 50% flowering, pollen fertility%, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, number of seeds plant^{-1},100-seed weight (g), seed yield plant^{-1}(g), biological yield plant^{-1},seed yield (kg ha^{-1}), harvest index(%), dal recovery% and seed protein content. The data were collected on five randomly selected competitive plants from each replication. The analysis of variance for yield and yield contributing characters was carried out as suggested by Panse and Sukhatme . The coefficient of variation was calculated as per Burton[3]. The genotypic and phenotypic coefficients of variation were calculated as per the formula suggested by Burton and De Vene[3] . Heritability in broad sense and genetic advance were calculated as per Johnson *et al*[8].

RESULTS AND DISCUSSION

The accomplishment of any breeding programme objective depends upon the extent of genetic variability in base population and it is essential to subject a population for selection for achieve improvement in a particular trait. In the present study the analysis of variation shown highly significant differences among the genotypes for all the characters studied *viz.*, days to 50% flowering, pollen fertility%, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, number of seeds plant^{-1}, 100-seed weight (g), seed yield plant^{-1}(g), biological yield plant^{-1}, seed yield (kg/ha), harvest index(%), dal recovery% and seed protein content, indicating the existence of considerable genetic variation in the experimental material. This variability can be utilized effectively to develop high yielding cultivars through hybridization followed by selection.

Perusal the components of variance revealed that the phenotypic coefficient of variation (PCV) were higher than Genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. Range, Mean, Coefficients of variations (CV%), Standard error (SE), Phenotypic Coefficients of Variations (PCV), Genotypic Coefficients of Variations (GCV), Heritability, Genetic Advance (GA) and Genetic Advance as percent of mean for sixteen characters presented in table 1. Magnitude of PCV and GCV was moderate to high for seed yield (kg/ha) (26.10&28.84), seed yield plant^{-1} (22.12&26.89), pods plant^{-1} (16.94&23.88), biological yield plant^{-1} (15.81&19.81), seeds plant^{-1} (13.89&16.96) and harvest index (12.95&18.56). These results were in conformity with that of Satish Kumar *et al*[10], Firoz mahamad *et al*[6] and Badru[1]. 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. In the present study, Heritability in broad sense was high in most of the characters *viz.*, days to 50%flowering (95.59%), pollen fertility% (87.86%), seed yield (kg/ha) (81.93%), seed yield plant^{-1} (67.66%), days to maturity (67.55%), number of seeds plant^{-1} (67.18%), Biological yield plant^{-1} (63.69%), plant height (62.12%) and 100-seed weight (61.54%). Medium to low heritability was recorded for dal recovery% (50.22%), number of pods plant^{-1} (50.33%), harvest index (48.66%), seed protein content (35.30%), number of secondary branches plant^{-1} (25.28%), number of seeds pod^{-1} (22.63%) and number of primary branches plant^{-1} (18.85%). Similar results were reported by Patel and

Patel[9]; Baskaran and Muthaiah[2] and Sreelakshmi *et al*[11], Jagan Mohan Rao and Thirumala Rao[7].

The high genetic advance was recorded in characters *viz.*, seed yield (kg/ha) (46.48%), biological yield plant^{-1} (25.99%), number of pods plant^{-1}(24.76%) and seed yield plant^{-1}(g) (23.46%). However, low genetic advance was recorded in characters *viz.*, days to 50% flowering (11.52%), number of secondary branches plant^{-1} (9.92%), 100-seed weight (9.76%), plant height (8.74%), pollen fertility% (7.25%), number of primary branches plant^{-1}(6.62%), dal recovery% (5.23%), days to maturity (4.61%), seed protein content (3.23%) and number of seeds pod^{-1} (1.33%). According to Johnson *et al*[8], heritability estimates along with the genetic gain are usually more useful. High heritability coupled with high genetic advance as percent of mean was more for seed yield (kg/ha), yield plant^{-1}(g), biological yield plant^{-1} (g), number of pods plant^{-1} and seeds plant^{-1} indicating the role of additive gene in expressing these traits, suggesting better scope for improvement of these traits through direct selection. Jagan Mohan Rao and Thirumala Rao[7] also reported similar results in pigeonpea.

Table 1: Genetic parameters of variability in pigeonpea genotypes

Parameters	Mean	Range	CV%	SE	GCV (%)	PCV (%)	Broad sense heritability (%)	Genetic advance	Genetic advance as % of mean
Days to 50% flowering	104.93	97.67-119.67	1.23	0.74	5.72	5.85	95.59	12.09	11.52
Days to Maturity	151.99	147.67-167.67	1.89	1.66	2.72	3.31	67.55	7.01	4.61
Pollen fertility%	86.36	83-96.33	1.39	0.70	3.76	4.0	87.86	6.26	7.25
No.of primary branches plant^{-1}	21.94	16.67-27.67	15.38	1.95	7.41	17.05	18.85	1.45	6.62
No.of secondary branches plant^{-1}	56.60	41.0-71.0	16.54	5.41	9.58	19.05	25.28	5.62	9.92
Plant height	196.50	175.33-235.0	4.21	4.77	5.39	6.83	62.12	17.18	8.74
Pods plant^{-1}	575.13	362.33-858.0	16.84	55.90	16.94	23.88	50.33	142.39	24.76
Seeds pod^{-1}	3.57	3.42-3.70	2.51	0.05	1.39	2.85	22.63	0.05	1.33
Seeds plant^{-1}	2027.46	1437.80-3047.86	9.71	113.71	13.89	16.96	67.18	475.71	23.46
100-seed weight	9.80	8.81-11.17	4.77	0.27	6.04	7.69	61.54	0.96	9.76
Biological yield plant^{-1}	405.78	245.0-552.33	11.94	27.96	15.81	19.81	63.69	105.45	25.99
Seed yield(kg/ha)	2167.32	857.08-3312.30	12.26	153.39	26.10	28.84	81.93	1054.94	48.68
Harvest index	28.17	22.85-37.19	13.30	2.16	12.95	18.56	48.66	5.24	16.60
Dal Recovery %	66.80	62.17-71.17	3.57	1.38	3.59	5.06	50.22	3.49	5.23
Seed protein content	21.31	19.81-22.28	3.57	0.44	2.64	4.44	35.30	0.69	3.23
Yield plant^{-1}	141.35	60.0-194.95	15.29	12.48	22.12	26.89	67.66	52.99	37.49

CONCLUSION

Magnitude of phenotypic coefficients of variation in selected pigeonpea genotypes was higher than genotypic coefficients of variation, indicating that environmental factors are influencing studied characters. High genetic advance and medium to high heritability was recorded for seed yield (kg/ha), seed yield plant^{-1}, biological yield plaant^{-1}, number of pods plant^{-1} and number of seeds plant^{-1}, dal recovery%, harvest index, seed protein content, number of secondary branches plant^{-1}and number of primary branches plant^{-1} hence selections based on the traits could improve productivity in pigeonpea directly.

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