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Studies on genetic variability and character association in Pigeonpea (*Cajanus cajan* (L.) Mill sp.)

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Abstract

Forty eight Pigeonpea (*Cajanus cajan* (L.) Mill sp) genotypes were evaluated for yield and yield component characters indicated the existence of considerable genetic variation in the present investigation. 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. The magnitude of PCV and GCV was moderate to high for seed yield per plant and number of pods per plant. Heritability in broad sense was higher in most of the characters viz., test weight, days to maturity, days to 50 per cent of flowering, seed yield per plant, number of pods per plant and number of branches per plant. High heritability coupled with high genetic advance as percent of mean was observed for seed yield per plant, number of pods per plant and test weight. indicating the role of additive gene in expressing these traits. Seed yield was significant positive association with number of pods per plant, number of branches per plant and test weight and these are major yield contributing traits to be given selection pressure for improving yield.

Keywords: Variability, heritability, genetic advance, correlation, Pigeon pea

Introduction

Pigeon pea (*Cajanus Cajana*. (L.) Millsp.) is one of the major food legume crops of both tropics and subtropics. Pigeon pea belonging to the *Cajaninae* sub-tribe of the economically important leguminous tribe Phaseoleae. Based on the natural genetic variability in local germplasm and the presence of numerous wild relatives, Van der Maesen (1990) [18] concluded that India is probably primary centre of origin. Pigeon pea is an important pulse crop that performs well in semi-arid tropics where moisture availability is unreliable or inadequate (Reddy *et al.*, 1993) [12]. Productivity of pulses worldwide in comparison to cereals is very low. This low productivity is attributed to its low harvest index and limited man-made selections (Ganapathy *et al.*, 2012) [6]. Progress in breeding programme depends on amount of variability created during hybridization. Success of any plant breeding programme will depend on variability existing in the populations. Hence study of genetic variability, heritability and genetic advance becomes important for effective selection and utilization of genotypes in breeding programme. Yield is a complex character and depends on number of component characters which are quantitatively inherited. The knowledge on nature of association of the yield and its attributes enable a plant breeder to plan an effective breeding programme. Correlation can provide a better insight into the relationship between different pairs of characters. The present study was conducted to know the genetic variability, heritability and genetic advance, extent of character association between yield and its components of pigeon pea.

Materials and Methods

The present study was undertaken with forty-eight genotypes of Pigeon pea. These genotypes were sown in randomized complete block design (RBD) with three replications at Professor Jayashankar Telangana State Agricultural University, Regional Agricultural Research Station, Warangal during *Kharif*, 2014-15 (Set- I). Each genotype was raised in 4m length with spacing of 120 X 20 cm. Recommended agronomic practices were followed to raise a good crop.

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Observations were recorded on days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, Number of pods per plant, test weight (g), seed yield per plant (g). The mean values were used for analysis of variance. The coefficient of variation was calculated as per Burton (1952)^[5]. Heritability in broad sense and genetic advance were calculated as per Johnson *et al.*, (1955)^[8]. The correlation coefficients were carried out following the methods of Al-Jibouri *et al.*, (1958)^[1].

Results and Discussion

The analysis of variation revealed highly significant differences among the genotypes for all the characters studied *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, test weight (g) and seed yield per plant (g) indicating the existence of considerable genetic variation in the experimental material. 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 (Table 1). The phenotypic coefficient of variation (PCV) in general was higher than genotypic coefficient of variation (GCV) for all the traits studied indicating the influence of the environment on manifestation of these characters. The genotypic coefficient of variation for various characters varied from 6.50 to 37.59 per cent. High genotypic coefficient of variation was observed for seed yield per plant, number of pods per plant. While, moderate GCV was observed for number of branches per plant and test weight. Low GCV values are observed for days to 50% flowering, Plant height and days to maturity. The phenotypic coefficient of variation for various characters varied from 6.67 to 39.26 per cent. High phenotypic coefficient of variation was observed seed yield per plant and number of pods per plant and number of branches per plant. While, moderate PCV was observed for test weight, Low PCV values are observed for Plant height, days to 50% flowering and days to maturity. Similar results for high PCV and GCV were reported by Dahat *et al.* (1997) for primary branches per plant, secondary branches per plant, number of pods per plant, seed yield per plant and plant height; Basavarajaiah *et al.*, (1999)^[3] for 100-seed weight; Saroj *et al.*, (2013)^[13], JM Rao and T Rao (2015)^[7] Pushpavalli *et al.*, (2018)^[10], Satyanarayana *et al.*, (2018)^[14], Anuradha and Patro (2019)^[2] reported for seed yield per plant.

The amount of heritable portion due to high degree of genetic variation can only be determined with the help of heritability estimates and genetic gain. High heritability estimates indicated that the characters are least influenced by the environmental factors and have capacity of the characters for transmission to subsequent generation. High heritability estimates were observed for test weight, days to maturity, days to 50 per cent of flowering, seed yield per plant, number of pods per plant and number of branches per plant. While, moderate heritability estimates were observed for Plant height. Similar results were reported by Patel and Patel (1998)^[9]; Baskaran and Muthaiah, (2006)^[4]; Sreelakshmi *et al.*, (2010)^[15]; JM Rao and T Rao (2015)^[7] and T. Rao *et al.*, (2016)^[17]. The success of genetic advance under selection

depends on the magnitude of genetic variability present in base population and heritability of the character under consideration. The genetic advance is usually expressed as percentage of mean. High genetic advance as per cent of mean were observed for seed yield per plant, number of pods per plant followed by test weight, number of branches per plant, days to 50% flowering. While, moderate genetic advance as percent of mean was observed for days to maturity and plant height. According to Johnson *et al.* (1955)^[8], heritability along with genetic advance is mostly useful and more reliable in predicting the resultant effects of selection. Selection can only be achieved when high heritability is accompanied with high genetic advance (Burton, 1952)^[5]. In the present study, high estimates of heritability coupled with high genetic advance as per cent of mean were observed for the characters *viz.*, seed yield per plant, number of pods per plant and test weight, Suggesting better scope for these traits for direct selection.

In the present investigation the genotypic and phenotypic correlations are on par with each other suggesting the less influence of environment. Hence, in this paper the genotypic correlations only discussed (Table 2). Seed yield was significant positive association with number of pods per plant, number of branches per plant and test weight. Non significant positive association of seed yield noticed with plant height. However, significant negative association with days to 50% flowering and days to maturity. These results are in accordance with the reports of Viridi *et al.*, (2004); Rahman *et al.*, (1999)^[11]; Sreelakshmi *et al.* (2011)^[16] and T. Rao *et al.* (2016)^[17].

Inter correlation among yield components revealed days to 50% flowering has significant positive association with days to maturity, significant negative association with number of pods per plant, Number of branches per plant and test weight. Non significant negative association with plant height. Days to maturity has significant negative association with number of pods per plant, number of branches per plant and test weight. Non significant negative association with plant height. plant height has significant positive association with number of branches per plant, non significant positive association with number of pods per plant and non significant negative association with test weight. Number of branches per plant has significant positive association with test weight and number of pods per plant. Number of pods per plant has significant positive association with test weight.

Based on the present study, it can be concluded that high degree of variability was observed for all the characters studied since variation is the basic step in crop improvement. The values of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters indicating the influence of environment. High heritability accompanied with high genetic advance as per cent of mean was observed in seed yield per plant, number of pods per plant and test weight indicates that most likely heritable and will be helpful to develop high yielding varieties. Association studies revealed that number of pods per plant, number of branches per plant and test weight were the major yield contributing traits through which high yielding genotypes of Pigeon pea may be selected.

Table 1: Estimates of variability, heritability and genetic advance in Pigeon pea

Character	Mean	Range	GCV (%)	PCV (%)	Heritability in Broad sense (H ²)	Genetic advance	GA as percent of mean
Days to 50% flowering	122.4	92-136	8.68	9.04	92.3	26.98	22.03
Days to maturity	166.9	136-180	6.50	6.67	95.1	27.96	16.75

Plant height	174.1	138-200	6.59	9.92	44.2	20.15	11.56
Number of branches per plant	13.5	7-19	16.21	21.60	56.3	4.34	32.12
Number of pods per plant	222.7	102-439	36.36	38.28	90.2	203.17	91.19
Test weight(g)	8.06	5.8-10.6	14.59	14.66	99.0	3.09	38.34
Seed yield per plant(g)	46.0	18-88	37.59	13.26	91.6	43.68	94.91

Table 2: Genotypic correlation coefficients between different traits in Pigeon pea

Traits	DF	DM	PH	NB	NP	TW	Seed Yield per plant
Days to 50% flowering	1.0000	0.9989**	-0.0662	-0.2501*	-0.3980 **	-0.1748*	-0.4539**
Days to maturity		1.0000	-0.0688	-0.2469**	-0.3811**	-0.1684*	-0.4310**
Plant height			1.0000	0.2219**	0.0298	-0.0297	0.0712
Number of branches per plant				1.0000	0.7735**	0.2475**	0.7607**
Number of pods per plant					1.0000	0.3045**	0.9096**
Test weight(g)						1.0000	0.2290**

*, ** Significant at P=0.05 and P = 0.01 level respectively

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