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Genetic variability studies in germplasm accession of pigeonpea (*Cajanus cajan* (L.) Millsp.)

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Abstract

Sixty genotypes of pigeonpea accession were evaluated for genetic variability, heritability and genetic advance. Observation were recorded on days to flower initiation, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, number of pods per plant, number of pod clusters per plant, number of pods per cluster, pod length, number of seeds per pod, 100 seed weight and seed yield per plant. Analysis of variance revealed that the mean sum of squares due to genotypes were highly significant for all the characters indicating existence of sufficient variability among the genotypes. Among the different yield attributing traits, number of pods per cluster had the highest magnitude of GCV and PCV. The high magnitude of GCV and PCV was observed for number of pods per cluster followed by secondary branches per plant number of pod clusters per plant, number of pods per plant, seed yield per plant which is an indicative of the genetic variability exists in the pigeonpea germplasm accessions. High heritability coupled with high genetic advance as percentage of mean was found for number of pods per cluster, secondary branches per plant, number of pod clusters per plant, number of pods per plant, seed yield per plant, which indicated that the predominance of additive gene action in the expression of these characters

Keywords: Pigeonpea, genetic variability, heritability, germplasm, genetic advance

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the fourth most important pulse crop in the world and second most important pulse crop of India after chickpea. Pigeonpea is a drought tolerant crop and one of the most important legumes grown in the tropics and sub tropics. It belongs to the family 'Fabaceae' and is also known as 'Arhar' or 'Tur', generally used in preparing dal which is rich in protein, carbohydrate, vitamins, lipids and minerals and eaten by majority of Indian vegetarian population. It is a diploid ($2n=22$) and often cross pollinated (20-70%) crop (Saxena, 2006) [14]. Pigeonpea cultivated throughout tropical, sub-tropical and in the warm temperate regions. On the basis of wide range of diversity present in India, pigeonpea is considered to be of Indian origin (Vavilov, 1951) [18]. Pigeonpea is cultivated both as food crop (dried peas, flour, or green vegetable peas) and also as forage/cover crop. Pigeonpea is a rich source of protein, carbohydrates, vitamins and certain minerals. Protein content in commonly grown pigeonpea cultivars ranges between 16.93 g to 26.92 g per 100 g whole grain samples (Fattepurkar *et al.*, 2004) [5]. Plant breeders are constantly using various biometrical techniques to have a greater understanding of nature of gene action for various quantitative traits to plan an effective breeding programme for the improvement of seed yield and protein content. In a breeding programme, genetic improvement primarily depends upon the amount of genetic variability present in the population. The existing variability can be used to further enhance the yield level of the cultivars following the appropriate breeding strategies. Heritability of a genetic trait is very important in determining the response to selection because it implies the extent of transmissibility of that trait into the next generations. Estimation of genetic variability does not give a clear indication of the possible improvement that can be achieved through selection and it should be used in conjunction with heritability and genetic advance. Therefore, the present study was conducted to assess the genetic variability parameters in germplasm of pigeonpea for yield contributing traits.

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Materials and Methods

The present experiment was conducted at, RMD CARS, Research and Instructional Farm, Ambikapur during *Kharif* 2016-17. This is located at latitude of 20° 8' N, longitude of 83° 15' E and altitude of 613.07 m MSL (mean sea level). The place of investigation is a sub-humid region. The experimental materials for the present study consisted of 60 genotypes of pigeonpea. The experiment was laid out in Randomized Complete Block Design (RBD) with three replications. The every genotype was sown in double row of 4.0 m length with row to row and plant to plant spacing of 60 cm and 20 cm, respectively. Sowing was done on July 09, 2016. Recommended dose of fertilizer *i.e.* NPK 20:50:20 kg per ha was applied in the rows before sowing. Recommended package of practices were adopted to raise a normal crop. The data obtained from the individual plant observations from randomized block design experiment were analyzed statistically as per the procedure given by Cochran and Cox (1957) [3]. The coefficients of variation for different characters were estimated by formula as suggested by Burton and De Vane (1953) [2]. Heritability in broad sense (h^2_{bs}) defined as the proportion of the genotypic variance to the total variance (phenotypic) was calculated as per the formula suggested by Burton and De Vane (1953) [2] and expected genetic advance was calculated by the formula given by Johnson *et al.* (1955) [7].

Results and Discussion

Genotypic and Phenotypic coefficients of variation are simple measures of variability these measures are commonly used for

the assessment of variability. 49 The relative values of these types of coefficients gives an idea about the magnitude of variability present in a genetic population. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed. Analysis of variance revealed that the mean sum of squares due to genotypes were highly significant for all the characters indicating existence of sufficient variability among the genotypes (Table 1). The phenotypic coefficients of variation were marginally higher than the corresponding genotypic coefficient of variation indicated the influence of environment in the expression of the character under study (Table 2). Among the different yield attributing traits, number of pods per cluster had the highest magnitude of GCV (64.56%) and PCV (91.74%). The high magnitude of GCV (43.92%) and PCV (49.55%) was also observed for secondary branches per plant followed by number of pod clusters per plant (23.01 and 25.65%), number of pods per plant (20.51 and 22.33%), seed yield per plant (20.04 and 22.51%) which is an indicative of the genetic variability exists in the pigeonpea germplasm accessions. The moderate GCV and PCV were observed for 100 seed weight (15.85% and 17.41%), pod length (12.15% and 13.41%) and the GCV (11.33%) was observed for number of primary branches per plant. Similar findings were also reported earlier by Saxena and Kataria (1993) [13], Patel and Patel (1998) [11], Pansuriya *et al.* (1998) [10], Singh (1999) [15], Mahamad *et al.* (2006) [8], Venge and Egbe Moses (2009) [16], Bhadru (2010) [1], and Gendley *et al.* (2015) [6].

Table 1: Analysis of variance for seed yield and its components in pigeonpea

Source of Variation	Df	Days to flower initiation	Days to 50% flowering	Days to maturity	No. of primary branches/plant	No. of secondary branches/plant	Plant height (cm)	No. of pods/plant	No. of pod cluster/plant	No. of pods/cluster	Pod length (cm)	No. of seeds/pod	100 seed weight (g)	Seed yield/plant (g)
Replication	2	2.71	5.48	10.31	33.60	8.03	938.33	239.55	73.71	0.08	0.09	0.009	1.56	12.18
Treatment	59	145.96**	141.96**	242.07**	10.49**	31.62**	832.22**	3440.08**	292.85**	0.27**	1.29**	0.28**	9.03**	222.64**
Error	118	3.91	3.24	3.88	4.59	2.63	421.25	201.38	22.30	0.05	0.08	0.46	0.65	17.88

*Significant at 5% probability level** Significant at 1% probability level

Table 2: Genetic parameters of variation for seed yield and its components in pigeonpea

Characters	Mean	Range		GCV%	PCV%	h^2_{bs} (bs)	Genetic Advance	GA as % of mean
		Max	Min					
Days to flower initiation	115.83	69.33	125.00	5.94	6.18	92.4	13.62	11.75
Days to 50% flowering	126.68	82.00	137.33	5.38	5.55	93.8	13.59	10.72
Days to maturity	197.70	148.33	209.00	4.51	4.62	95.5	17.96	9.08
No. of primary branches/plant	12.61	8.60	17.40	11.33	20.31	31.1	1.64	13.00
No. of secondary branches/plant	7.08	1.73	16.13	43.92	49.55	78.6	5.68	80.22
Plant height (cm)	205.11	163.00	257.53	5.69	11.52	24.4	11.89	5.79
No. of pods/plant	160.25	85.67	227.87	20.51	22.33	84.3	62.17	38.79
No. of pod clusters/plant	41.34	21.33	68.13	23.01	25.65	80.5	17.58	42.52
No. of pods/cluster	3.73	3.07	4.40	64.56	91.74	49.5	4.05	108.57
Pod length (cm)	5.25	3.97	7.60	12.15	13.41	82.2	1.19	22.66
No. of seeds/pod	4.42	3.80	5.07	6.34	8.03	62.4	0.46	10.40
100 seed weight (g)	10.66	7.13	15.43	15.85	17.41	82.9	3.17	29.73
Seed yield/plant (g)	41.20	16.47	66.07	20.04	22.51	79.3	15.14	36.74

Heritability governs the resemblance between parents and their progeny whereas; the genetic advance provides the knowledge about expected gain for a particular character after selection. However, the knowledge of heritability alone does not help in formulating concrete breeding programme, genetic advance along with heritability helps to ascertain the possible genetic control for any particular trait. The highest heritability was recorded for the character days to maturity (95.5%), days to 50% flowering (93.8%), flower initiation (92.5%), number

of pods per plant (84.3%), 100 seed weight (82.9%), pod length (82.2%), number of pod clusters per plant (80.5%), seed yield per plant (79.3%) and number of secondary branches per plant (78.6). The moderate heritability was observed only for number of seeds per pods (62.4%). High heritability coupled with high genetic advance as percentage of mean was found for number of pods per cluster, secondary branches per plant, number of pod clusters per plant, number of pods per plant, seed yield per plant, which indicated that

the predominance of additive gene action in the expression of these characters which could be utilized through selection for improvement of these characters. High heritability coupled with high genetic advance for secondary branches per plant, number of pods per plant, seed yield per plant was reported by Deshmukh *et al.* (2000)^[4] and Satish Kumar *et al.* (2006)^[12]. Similar results also reported by Mahamad *et al.* (2006)^[8] Bhadru (2010)^[1], Nag and Sharma (2012)^[9], Vanisree *et al.* (2013)^[17], and Gendley *et al.* (2015)^[6].

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