

Original Research Article

Genetic Variability, Heritability and Genetic Advance Studies in Red Gram [*Cajanus cajan* (L.) Millspaugh]

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ABSTRACT

An investigation was carried out with 16 genotypes of pigeon pea for genetic variability studies. They were evaluated for twelve yield and yield attributing characters during kharif 2019. The analysis of variance revealed significant differences among the genotypes for all the characters studied except number of pods per cluster. Seed yield and number of seeds per pod had the high magnitude of genotypic coefficient of variation and phenotypic coefficients of variation which is an indicative of the genetic variability exists in the pigeonpea genotypes. The high magnitude of heritability was recorded for the seed yield and number of secondary branches per plant. Genetic advance as percentage of mean was recorded as high for the seed yield, number of seeds per pod and number of secondary branches per plant. High heritability coupled with high genetic advance was found for seed yield, number of seeds per pod and number of secondary branches per plant which indicated that the predominance of additive gene action in the expression of these characters which could be utilized through selection for the genetic improvement of these characters.

Keywords

Red gram, *Cajanus cajan*, Variability, Heritability, Genetic advance

Introduction

Pigeon pea (*Cajanus cajan* (L.) Millsp.) is one of the major grain legume (pulse) crops grown in about 50 countries in the tropics and subtropics. It is the second important pulse crop of India which has diversified uses as food, feed, fodder and fuel. It has been recognized as a valuable source of protein for the vegetarians in their daily diet (Vanisree *et al.*, 2013). The plants are drought resistant and can be grown in areas with less than 650 mm annual rainfall. Pigeon peas are food (dried peas, flour, or green vegetable peas) and forage/cover crop. It contains high levels of protein and important amino acids such as Methionine, Lysin and Tryptophan. If consumed in combination with cereals, it

makes well balanced human diet. Split pigeon pea (Tur Dal) is quite common in India. Being a legume crop, the pigeon pea enriches soil through symbiotic nitrogen fixation. It is useful in maintaining soil health through increasing microbial activities. It has also been reported that, pigeonpea root exudates dissolve phosphate-containing rocks (e.g. phosphate rocks) to make P available for crop use (Ae *et al.*, 1990).

The presence of genetic variability among traits is important for breeding and in selecting desirable types. Heritability of a trait is important in determining its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates

of heritability in order to plan an efficient breeding programme. The broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960). Genetic advance provides information on expected genetic gain resulting from selection of superior individuals. In this view, the present study was undertaken to investigate the genetic variability, heritability and genetic advance in pigeonpea genotypes.

Materials and Methods

The experimental material consists of sixteen genotypes of pigeonpea namely RPS 2008-4, RPS 2008-5, RP 192, RPS 2007-106-1, RP 98, RP 200, RPS 2014-4-2, RP 3, ICP 6994, RPS 2014-11-1, RPS 2007-10, RPS 2007-105-1, PPKCG-3, RPS 2007-109-1 along with two checks Rajeevlochan and Asha. The material was sown in Randomized Complete Block Design with three replications during kharif 2019 at research farm of IGKV Rajmohini Devi College of Agriculture and Research Station, Ambikapur, Chhattisgarh. All the recommended package of practices was followed to raise a healthy crop. Single plant per hill was maintained, border rows were planted to eliminate the border effect. Five plants were randomly selected and tagged in each genotype per replication for recording the observations for the characters: plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, Number of pod cluster per plant, Number of pods per cluster, pod length (cm), number of seeds per pod, 100 seed weight (g), and seed yield per plant (g). Days to 50% flowering, Days to maturity and seed yield (q/ha) was recorded on plot basis. Mean data was calculated and were subjected to statistical analysis to work out genotypic and phenotypic coefficient of variation,

heritability and genetic advance as per cent of mean. The coefficients of variation for different characters were estimated by formula as suggested by Burton and De Vane (1953). 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) and expected genetic advance was calculated by the formula given by Johnson *et al.*, (1955).

Results and Discussions

The analysis of variance revealed significant differences among the genotypes for all the characters except number of pods per cluster (Table 1). Significant mean squares due to seed yield and attributing characters revealed existence of considerable variability in the material studied for the improvement of various traits. The relative values of genotypic and phenotypic coefficients of variation 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. 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, seed yield and number of seeds per pod had the high magnitude of genotypic coefficient of variation and phenotypic coefficients of variation which is an indicative of the genetic variability exists in the pigeonpea genotypes. The moderate magnitude of genotypic coefficient of variation and phenotypic coefficients of variation was observed for number of primary branches per plant, number of secondary branches per plant,

number of pods per plant and 100 seed weight while number of pod cluster per plant recorded moderate magnitude of genotypic coefficient of variation and high magnitude of phenotypic coefficients of variation.

The low genotypic coefficient of variation and phenotypic coefficients of variation were observed for days to 50% flowering, days to maturity, plant height, number of pods per cluster and pod length. Similar findings were also reported earlier by Singh *et al.*, (1990), Saxena and Kataria (1993), Patel and Patel (1998), Pansuriya *et al.*, (1998), Basavarajaiah *et al.*, (2000), Mahamad *et al.*, (2006), Venge and Egbe Moses (2009) and Bhadru (2010).

The high magnitude of heritability was recorded for the seed yield and number of secondary branches per plant. The moderate heritability was observed for 100 seed weight, seed yield, days to maturity, days to 50% flowering, number of seeds per pod and number of secondary branches per plant. Genetic advance as percentage of mean was recorded as high for the seed yield, number of seeds per pod and number of secondary branches per plant. Genetic advance as percentage of mean was recorded as moderate for 100 seed weight, number of pods per plant, number of pod cluster per plant and number of primary branches per plant. It was low for days to 50% flowering, days to maturity, plant height, pod length and number of pods per cluster.

Table.1 Analysis of variance for seed yield and its components in red gram

S.No.	Source of variation	Mean sum of square			
		Replication	Genotype	Error	
	Characters freedom	Degree of	2	15	30
1.	Days to 50% flowering		2.33	131.23**	1.08
2.	Plant height (cm)		172.88	417.79**	230.34
3.	Number of primary branches per plant		3.10	4.45**	0.85
4.	Number of secondary branches per plant		3.42	8.21**	0.71
5.	Number of pods per plant		158.08	926.27**	191.90
6.	Number of pod cluster per plant		182.41	88.84*	49.23
7.	Number of pods per cluster		0.04	0.12	0.11
8.	Pod length (cm)		0.06	0.18**	0.05
9.	Number of seeds per pod		0.01	1.66 **	0.07
10.	Days to maturity		0.25	312.73**	0.38
11.	100 seed weight (g)		0.04	4.39**	0.07
12.	Seed yield (q/ha)		6.19	35.64**	3.67

** Significant at 1% level of probability, * Significant at 1% level of probability

Table.2 Genetic parameters of variation for seed yield and its components in red gram

S. No.	Characters	Mean	Range		σ^2_g	σ^2_p	GCV (%)	PCV (%)	h^2 (bs) (%)	GA as % of mean
			Min	Max						
1.	Days to 50% flowering	136.95	130	166	43.38	44.47	4.81	4.87	97.55	9.58
2.	Plant height (cm)	238.74	203.4	266.8	62.49	292.82	3.31	7.17	21.34	3.12
3.	Number of primary branches per plant	8.48	6.2	12.2	1.20	2.05	12.91	16.92	58.24	20.52
4.	Number of secondary branches per plant	9.02	5.6	12.4	2.49	3.21	17.52	19.87	77.75	31.87
5.	Number of pods per plant	137.39	99	206	244.79	436.69	11.38	15.21	56.06	17.32
6.	Number of pod cluster per plant	30.28	13.6	43.6	13.20	62.44	12.00	26.09	21.15	11.82
7.	Number of pods per cluster	2.89	2.4	3.6	0.003	0.12	2.08	11.82	3.08	0.74
8.	Pod length (cm)	5.54	4.8	6.4	0.04	0.10	3.61	5.59	41.49	4.75
9.	Number of seeds per pod	3.66	1.3	4.6	0.52	0.60	20.04	21.22	87.39	37.42
10.	Days to maturity	206.25	201	245	104.12	104.5	4.95	4.95	99.63	9.95
11.	100 seed weight (g)	9.67	7.90	12.90	1.44	1.52	12.41	12.73	94.99	24.38
12.	Seed yield per plant (g)	12.16	5.72	21.25	3.67	10.65	26.84	31.11	74.37	47.09

High heritability coupled with high genetic advance was found for seed yield, number of seeds per pod and number of secondary branches per plant which indicated that the predominance of additive gene action in the expression of these characters which could be utilized through selection for the genetic improvement of these characters. The traits number of pods per plant, number of primary branches per plant and pod length showed moderate heritability estimates coupled with moderate to low genetic advance as percentage of mean indicated the role of non additive genetic variance or high influence of environment in their expression. These findings are in general agreement with the findings of Deshmukh *et al.*, (2000), Singh *et al.*, (2003), Mahamad *et al.*,

(2006), Kalaimagal *et al.*, (2008), Bhadru (2010) and Vanisree *et al.*, (2013),

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