VARIABILITY AND GENETIC DIVERSITY STUDIES IN REDGRAM [*CAJANUS CAJAN* (L.) MILLSP

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ABSTRACT: An investigation was carried out with 50 accessions of pigeon pea to identify diverse genotypes. They were evaluated for ten yield and yield attributing characters using Mahalanobis D^2 statistics. The analysis of variance revealed significant differences among the genotypes for all the characters studied. Maximum range of variation was recorded for seed yield per plant. High heritability coupled with high genetic advance has been recorded for seed yield per plant and number of pods per plant, seed weight and primary branches. Based on the genetic distance all the 50 genotypes were grouped under seven different clusters. The maximum inter-cluster distance was recorded between clusters II and IV. Seed yield per plant contributed maximum to the total divergence. Seed yield, number of pods per plant and seed weight can be given due weight in selection and improvement of pigeonpea, Crossing between the genotyptes of Cluster II and IV is expected to exhibit high heterosis and give wider spectrum of variability.
Key words: Redgram-*Cajanus cajan,* Variability, Genetic diversity

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is an important food legume crop mostly cultivated in tropical and subtropical regions of the world. 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 Globally, pigeonpea is cultivated on 4.6 mha with an annual production of 3.4 mt and a mean productivity of 780 kg/ha. The area under pigeonpea in India is around 3.5 mha with a production of approximately 2.5 mt. with a productivity of 700 kg/ha. The state and national programme on the improvement of pulses emphasized the urgency of generating variability for high yield potential through genetic manipulation. The success of breeding programme lies on the fact that the parents involved in any particular cross should be genetically divergent. In the present study, an attempt was made to assess the genetic divergence using Mahalanobis D^2 statistics and clustering procedure, based on yield and yield components and assessing the relative contribution of different components to total divergence.

MATERIAL AND METHODS

The experimental material consists of forty genotypes received from NBPGR, New Delhi and ten genotypes locally maintained germplasm of AICRP pigeonpea, RARS, Warangal. The material was sown in Randomized Complete Block Design with two replications during *kharif* 2010-11 at D block farm, Regional Agricultural Research Station, Warangal. Each line was accommodated in two rows of 4 meter length spaced at 120 cm apart with plant to plant distance of 20 cm. All the recommended package of practices were 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 pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and Harvest index (%). Days to flowering and days to maturity were recorded on plot basis.

Statistical analysis

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 as per Johnson *et al*. 1955. D^2 analysis was carried by using Mahalanobis D^2 statistic and cluster analysis by Tocher method as described by Rao (1952).

RESULTS AND DISCUSSION

Genetic Variability

The analysis of variance revealed significant differences among the genotypes for all the traits. Estimates of variability (Table-1) revealed maximum range of variation for seed yield per plant (32-122), followed by number of pods per plant (98-340), days to maturity (120-210) and 100 seed weight (5-12.00). Pod length and Seeds per pod recorded moderate variability while, number of primary branches per plant recorded low range of variability. The results are in accordance to that reported by Shreelakshmi *et al*. (2011). High estimates of phenotypic and genotypic coefficient of variation were recorded for number of pods per plant, remaining traits recorded medium to low coefficient of variation at both the levels. Similar findings had been reported by Vasantha Rao (2009) and Bhadru (2010). High heritability coupled with high genetic advance were recorded for days to flowering, days to maturity, number of primary branches, number of pods per plant, 100 seed weight and seed yield per plant. Whereas moderate heritability and moderate genetic advance were recorded for the characters plant height, number of seeds per pod. Harvest index and pod length recorded low heritability and low genetic advance. It is interesting to see that genetic advance (expressed as percentage of mean) was high not only for yield itself but also for pod number, number of primary branches and 100 seed weight which are the most important component characters of pigeonpea. The association of high heritability with high genetic advance as observed in number of pods per plant, seed yield per plant, number of primary branches per plant and 100 seed weight was indicative of additive effects and consequently, high genetic gain from selection can be expected. Remaining traits showed medium to low heritability values with moderate to low genetic advance, suggesting the predominance of non additive gene action or high influence of environment and hence, their response to selection would be poor.

Table 1 :   Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for seed yield, and   Yield components in pigeonpea [*Cajanus cajan* (L.) Millsp.]

S.No	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	**125.76**	70.67	145.00	18.12	17.26	91	33.97
2	Days to maturity	**160.50**	120.00	210.67	13.69	13.52	97	27.35
3	Plant height (cm)	**175.43**	121.17	220.80	14.72	11.25	58	17.58
4	Primary branches/ plant	**15.86**	8.80	24.13	16.72	12.53	76	26.16
5	Pods/ plant	**222.51**	98.87	340.85	26.44	24.62	87	47.14
6	Pod length (cm)	**3.82**	3.53	4.50	13.66	7.19	27	7.58
7	Seeds/ pod	**4.35**	3.57	5.38	12.41	9.21	55	14.03
8	100- seed weight (g)	**8.54**	5.63	12.23	12.91	12.20	89	23.65
9	Harvest index(%)	**28.36**	21.80	35.26	12.58	7.71	37	9.58
10	Seed yield per plant (g)	**64.33**	32.19	112.97	24.23	21.53	79	39.39

PCV = Phenotypic coefficient of variation   GCV = Genotypic coefficient of variation

Genetic Divergence

Based on the relative magnitude of D^2 values 50 genotypes were grouped into seven clusters (Table-2).Thus indicating the presence of considerable diversity in pigeonpea gene pool. Cluster V was the largest (15 accessions), followed by Cluster IV & I (9 accessions), Cluster III (8 accessions), Cluster II (5 accesssions), VI (3 accessions) and VII (1 accession). The clustering pattern of genotypes revealed that there was no parallelism between clustering pattern and geographical distribution of genotypes. Similar finding were reported by Vasantha Rao et al. (2010a). The maximum intracluster distance (Table-3) was observed in cluster V (28.352) followed by cluster IV (15.912), III (12.680), VI (8.740), I (6.227), II (4.856).

Cluster VII consisted of only one genotype, hence lack intra cluster distance (0.00). The relative divergence of each cluster from other cluster (inter cluster distance) indicated greater divergence between cluster II and cluster IV (2620.10), followed by cluster II and III (1525.13) and Cluster II and VII (1082.11). The selection of divergent genotypes from cluster II and III, IV and VII would produce broad spectrum of variability for yield and yield traits, which may enable further selection and genetic improvement. The average cluster wise mean values presented in Table-4 assist to assess the superiority of clusters which could be considered for improvement of various characters through hybridization programme. Cluster I had desirable mean for pod number and seed yield per plant. Cluster II exhibited better mean for early flowering and maturity, also high mean for pod length, seed per pod and seed weight. Cluster III showed superior mean for number of pods per plant and better seed yield per plant. Cluster V had desirable mean for harvest index. Among the ten characters studied seed yield contributed the most (20.2 %) towards genetic divergence (Table-4) followed by days to flowering, days to maturity, pods per plant, 100 seed weight. Plant height, number of branches, pod length, seeds per pod and harvest index contributed the least towards divergence indicating narrow divergence for these traits among the genotypes under study. Singh et al. (2010) and Shree lakshmi et al. (2010) also reported that seed yield per plant contributed maximum towards genetic diversity. Rekha et al. (2011) reported 100 seed weight and number of pods per plant contributed maximum towards total genetic divergence.

Table 2: Clustering pattern of 50 pigeonpea [*Cajanus cajan* (L.) Millsp]. genotypes by Tocher's variance method.

Cluster No.	No. of genotypes	Name of the genotypes
I	9	IC – 525402, IC – 525409, IC-525410, IC-73791 , IC-525571, IC- 385885, WRG – 27, LRG- 41, WRG- 55.
II	5	IC-525520, IC-525529, IC-525521, IC-73868, WRGE-90.
III	8	IC – 383168, IC – 361457, IC – 525407, IC –73871, IC – 525572, IC-525465, IC- 525509, IC – 525584.
IV	9	IC – 525570, IC – 525522, ICPL- 96053, IC- 525412, , LRG – 52, IC- 525529, ICP-7035, ICPL-99004, IC-525581.
V	15	ICPL 87119, BSMR – 853, ICP-72751, IC-525408, IC-525408, IC-525411, IC-73322, IC-525418, IC-525423, IC-525526, IC-525567, IC-525573, WRG-65, WRG-79, IC-525477
VI	3	IC- 525574, IC- 525466, IC-525528.
VII	1	IC-73752

Table 3: Average intra-and inter-cluster distance (D^2) values of seven clusters in pigeonpea [*Cajanus cajan* (L.) Millsp.]

Cluster No	I	II	III	IV	V	VI	VII
I	6.227	962.270	101.220	409.214	27.786	116.546	49.416
II		4.856	1525.126	2620.106	936.400	438.852	1082.115
III			12.680	105.220	137.883	525.730	29.716
IV				15.912	450.422	942.841	225.404
V					29.352	107.986	62.793
VI						8.740	294.998
VII							0.000

Note: Bold and diagonal values indicate intra-cluster D^2 distance

Table 4.: Mean values of seven clusters estimated by Tocher's method from 50 genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.]

Cluster No	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Pods / plant	Pod length (cm)	Seeds/ pod	100 seed weight (g)	Harvest Index (%)	Seed yield/ plant (g)
I	122.026	166.125	198.126	18.224	268.225	3.914	4.826	8.652	28.022	62.090
II	75.000	102.000	148.251	10.022	168.830	4.520	5.618	9.825	25.225	35.892
III	135.381	192.528	182.926	19.256	260.012	3.924	4.882	8.296	27.959	58.256
IV	158.393	205.672	201.523	20.656	258.921	3.867	3.922	8.729	28.925	55.625
V	122.177	166.226	188.231	18.454	243.397	3.888	4.455	8.988	29.743	59.114
VI	114.600	149.267	180.445	17.283	228.156	4.022	4.878	8.122	27.012	45.244
VII	137.869	182.333	190.212	18.122	212.235	3.825	4.000	8.670	28.824	48.922
% Contribution towards genetic divergence	13.9	12.2	5.30	5.30	8.23	0.80	0.80	6.04	0.75	20.2

Based on the above studies, crosses between genotypes from cluster II and cluster I would result in high yielding early pigeonpea varieties, crosses between genotypes from Cluster II and Cluster IV the most distant clusters are expected to exhibit high heterosis and might result in high yielding segregants with desirable traits.

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