

RESEARCH ARTICLE

Genetic diversity studies in pigeonpea (*Cajanus cajan* L. Millsp.)

■ S. D. Atkare, S. B. Sarode, S. G. Gawai and S. L. Haloli

SUMMARY

Genetic diversity using Mahalanobis D-square (D^2) techniques was studied for yield and yield contributing traits of 100 genotypes of pigeonpea. These genotypes were grouped into nine clusters. The greatest distance between two clusters was existed between cluster VII and III (727.38) indicating greatest divergence, followed by cluster VIII and III (630.51), cluster IX and V (604.66), cluster V and III (580.32) and cluster VIII and V (573.60). Whereas the least distance was recorded between cluster V and IV (71.57) followed by cluster III and II (122.10), cluster IV and I (217.85), cluster II and I (219.33) indicating least genetic divergence among genotypes. The intra cluster values varied from 0.00 to 139.00. The maximum intra-cluster distance was noticed in cluster I (139.00).

Key Words : Pigeonpea, Genetic diversity, Clustering pattern, D^2 statistics

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Pigeonpea (*Cajanus cajan* L.) is an important grain legume of the Indian sub-continent, Southern Asia, Africa and Central America. It is the most widely grown legume after chickpea in India covering an area of 3.6 million hectares in the states of Maharashtra, Karnataka, Andhra Pradesh, Uttar Pradesh, Madhya

Pradesh and Gujarat. In order to improve the production, a large number of varieties have been released for different agro climatic zones. According to Vavilov, 1949, genus *Cajanus* originated in the Hindustan. As per Van Der Maesen, 1980 also, the centre of origin of the crop is India. Pigeonpea are extensively grown throughout the tropics, subtropics and warmer equatorial regions of Asia, East Africa and Central America between 30 N and 35S latitude.

Pigeonpea is a protein rich food. It contains about 22 per cent protein, which is almost three times that of cereals. Pigeonpea supplies a major share of protein requirement of vegetarian population of the country.

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Pigeonpea is mainly consumed in the form of split pulse as *Dal*, which is an essential supplement of cereal based diet. The combinations of *Dal-Chawal* (pulse-rice) or *Dal-Roti* (pulse-wheat bread) are the main ingredients in the average Indian diet. The biological value improves greatly, when wheat or rice is combined with pigeonpea because of the complementary relationship of the essential amino acids. It is particularly rich in lysine, riboflavin, thiamine, niacin and iron. In addition to being an important source of human food and animal feed, pigeonpea also plays an important role in sustaining soil fertility by improving physical properties of soil by fixing atmospheric nitrogen. Every Pigeonpea plant is a minifertilizer factory as the crop has unique characteristics of restoring and maintaining soil fertility through fixing atmospheric nitrogen in symbiotic association with *Rhizobium* bacteria present in the root nodules. Being a drought tolerant crop because of its deep penetrating root system, it is suitable for dryland farming particularly in the rainfed area and predominantly used as an intercrop with other crops. Pigeonpea crop is suitable for inter-cropping, with different crops (Cotton Sorghum, Pearl millet, Green gram, Black gram, Maize, Soybean, Groundnut) for increasing production and maintaining soil fertility. The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability.

Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programmes. D^2 analysis has been found most effective and therefore, widely used for the classification of parental lines. A thorough knowledge of existing genetic variation between yield and yield contributing traits is essential for developing high yielding genotypes in pigeonpea. The observed variability is a combined measure of genetic and environment causes. Assessment of divergence or similarity among the genotypes would help in identification of genotypes that could be used in cross breeding programme for producing transgressive segregants. Limited systematic breeding programme for breeding superior high yielding genotypes in pigeonpea have been initiated.

MATERIAL AND METHODS

The present investigation on pigeonpea for studying genetic diversity was conducted at College of Agriculture,

Badnapur, during *Kharif* season of 2019-20. Experimental material comprising 100 genotypes lines with wider variability for different characters received from Agricultural Research Station, Badnapur. Hundred genotypes of pigeonpea were evaluated in a Randomized Block Design with two replications during *Kharif* season of 2019-20. Each genotype was sown in two rows of 4 m length with spacing of 90 cm between rows and 20 cm within rows. The data were recorded on five randomly selected plants of each replication for all characters such as days to 50% of flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, harvest index, test weight, and seed yield.

RESULTS AND DISCUSSION

The D^2 values for all comparisons between pairs of genotypes are calculated. On the basis of divergence 100 genotypes under investigation have been grouped into nine distinct clusters (Table 1) indicating wide diversity in the experimental materials for majority of the characters. Distance between all pairs of genotypes was calculated using squared Euclidean distance method and the genotypes were clustered based on Tochar's method. The cluster mean values were estimated over genotypes for ten yield attributing characters in pigeonpea related to yield, which revealed that a widerange of variation (Table 2). Minimum mean for days to 50% flowering was reported in cluster VIII (97.00) comprised by early flowering genotypes. While maximum mean was recorded in cluster II (132.00) which comprised late

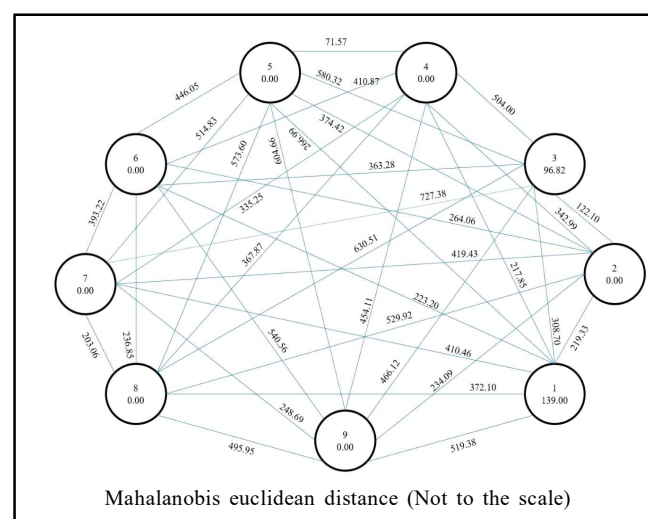


Fig. 1: Diagram showing the cluster distance

Table 1: Composition of hundred pigeonpea genotypes into different cluster by Tocher's method

Cluster number	No. of strains	Genotype included in the cluster
I	90	BSMR-1, BWR-23, BDN-716, BSMR-26 ,BSMR-175 ,BSMR-579, ICP-939, BWR-254 ,ICP-387, RAJESHWARI, BSMR-74, BSMR-316 ,ICP-2376 ,BPG-58-1, ICP-2248 ,ICP-1136, ICP-2746, BPG-58-4, ICP-1535, BPG-51-3-1 ,ICP-2178 ,ICP-476, ICP-1691, ICP-3099, ICP-3451, ICP-3328, ICP-3498, ICP-2698, ICP-1126, ASHA, ICP-1650, BPG-75-3, ICP-1083, BSMR-553, BPG-55-3, ICP-624, ICP-2223, BPG-38-6, ICP-1105, ICP-163, BPG-72-2, BWR-133, VIPULA, ICP-1615, ICP-1838, BPG-72-1 ICP-2372, ICP-655 ,BPG-23-1,BPG-59-2, BSMR-243, ICP-1005, ICP-1514, BSMR-203, BPG-59-4, ICP-228, BSMR-65, ICP-633, BPG-74-2-1, ICP-995, ICP-3235, ICP-1071, ICP-426, ICP-2698 ,BPG-33-2, BSMR-79, ICP-2391, ICP-29, ICP-1209, ICP-348 ,BSMR-853, BSMR-736, ICP-1053, ICP-1008, WRG-65, ICP-3287, BWR-153, BPG-69-2 ,BDN-711, ICP-1117 ,BWR-134 ,ICP-709,ICP-3230, ICP-178 ,ICP-28, BRG-4, BWR-164, ICP-1136, ICP-1208.
II	1	ICPL-871119
III	3	ICP-3855, BPG-37-4, BPG-38-3-1
IV	1	BDN-708
V	1	BSMR-846
VI	1	BWR-24
VII	1	BPG-74-4-1
VIII	1	ICP-369
IX	1	BPG-61-1

Table 2: Cluster means for seed yield and its components in pigeonpea

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches /plant	Number of secondary branches /plant	Number of pods /plant	Number of seeds /pod	Test weight (gm)	Harvest index	Seed yield /plant
I	113.62	167.87	200.25	10.36	22.59	238.25	3.90	10.05	28.55	89.81
II	132.00	180.00	219.70	13.90	29.20	285.70	3.70	9.55	27.17	99.59
III	125.00	189.38	226.75	7.75	15.93	204.10	3.20	7.54	36.95	52.45
IV	119.00	162.00	192.84	7.50	19.20	294.10	4.30	14.08	36.34	172.82
V	126.00	159.50	181.00	11.60	26.30	168.90	4.90	15.25	37.43	120.23
VI	110.00	174.00	212.00	13.20	19.90	413.60	4.90	10.23	26.92	92.17
VII	115.00	164.50	250.50	16.50	36.90	632.40	3.00	13.73	19.72	237.01
VIII	97.00	173.00	205.70	8.70	18.50	582.10	2.45	12.50	32.83	160.12
IX	130.00	185.00	255.01	8.90	37.00	501.20	3.10	14.49	18.27	215.83

flowering genotypes. Minimum mean for days to maturity was recorded in cluster IV (159.50) comprised by early maturing genotypes. While maximum mean was reported in cluster III (189.38) which comprised late maturing genotypes. Highest cluster mean for plant height was showed by cluster IX (255.01) followed by cluster VII (250.50) while, lowest mean for plant height recorded in cluster V (181.00). The cluster mean for primary branches was highest in cluster VII (16.50) followed by cluster II (13.90). However least number of primary branches mean was reported in cluster IV (7.50). The maximum cluster mean for secondary branches was

reported in cluster IX (37.00) followed by cluster VII (36.90) while minimum cluster mean was recorded in cluster III (15.93). The highest cluster mean for no. of pods per plant in cluster VII (632.40) followed by cluster VIII (582.10) whereas least mean was observed in cluster V (168.90). The maximum mean for no. of seed per pod was reported in cluster V, VI (4.90) while minimum mean recorded in cluster VIII (2.45). The cluster mean for test weight was highest in cluster V (15.25) followed by cluster IX (14.49) while, least mean was recorded in cluster III (7.54). The highest cluster mean for harvest index was reported in cluster V (37.43)

Table 3: Average intra and inter cluster D² values in pigeonpea

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX
I	139.00	219.33	308.70	217.85	266.99	233.20	410.46	372.10	519.38
II		0.00	122.10	342.99	374.42	264.06	419.43	529.92	234.09
III			96.82	504.00	580.32	363.28	727.38	630.51	466.12
IV				0.00	71.57	410.87	335.25	367.87	454.11
V					0.00	446.05	514.83	573.60	604.66
VI						0.00	393.22	236.85	540.56
VII							0.00	203.06	248.69
VIII								0.00	495.95
IX									0.00

Table 4 : Per cent contribution of different characters to genetic diversity

Sr. No.	Characters	No. of times appearing I in ranking	% Contribution
1.	Days to 50% flowering	594	12.00
2.	Days to maturity	1665	33.64
3.	Plant height (cm)	153	3.07
4.	Number of primary branches per plant	27	0.55
5.	Number of secondary branches per plant	142	2.87
6.	Number of pods per plant	793	16.02
7.	Number of seeds per pod	192	3.88
8.	Test weight (g)	567	11.45
9.	Harvest index (%)	302	6.10
10.	Seed yield per plant (g)	516	10.42
11.	Total	4951	100

followed by cluster III (36.95) whereas least mean was observed in cluster IX (18.27). The maximum cluster mean for seed yield was recorded in cluster VII (237.01) followed by cluster IX (215.83) while minimum mean was recorded in cluster III (52.45). The clustering pattern of genotypes also confirmed the present of wide diversity. Among the nine clusters, the cluster I was the largest comprising 90 genotypes, followed by cluster III (3 genotypes) and cluster II, IV, V, VI, VII, VIII, IX had one genotype each, respectively. The divergence within the cluster indicates the divergence among the genotypes in the same cluster. On the other hand, inter cluster divergence suggests the distance (divergence) between the genotypes of different clusters. Inter and intra cluster D² values were worked out from divergence analysis. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relation. The composition of cluster and values of inter and intra cluster distances are given in Table 3. A cluster diagram was constructed

showing the relationship between the different populations. The greatest distance between two clusters was existed between cluster VII and III (727.38) indicating greatest divergence, followed by cluster VIII and III (630.51), cluster IX and V (604.66), cluster V and III (580.32) and cluster VIII and V (573.60). Whereas the least distance was recorded between cluster V and IV (71.57) followed by cluster III and II (122.10), cluster IV and I (217.85) cluster II and I (219.33) and indicating least genetic divergence among genotypes. The average intra distance D² values of various clusters were furnished in Table 3. The intra cluster values varied from 0.00 to 139.00. The maximum intra-cluster distance of 139.00 was noticed in cluster I. It was 96.82 in cluster III suggesting that the genotypes belonging to these cluster may further be used as parents for hybridization programme to develop desirable types because crosses between genetically divergent parents will generate transgressive segregants. The characters contributing maximum divergence needs greater

emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times each of the yield component characters appeared first in rank and its respective per cent contribution towards genetic divergence was presented in Table 4. The days to maturity (33.64%) has the major contribution to total genetic diversity, number of pods per plant (16.02%), days to 50 % flowering (12.00%), test weight (11.45%), seed yield per plant (10.42%), harvest index (6.10%), number of seeds per pod (3.88%), plant height (3.07%), number of secondary branches per plant (2.87%), number of primary branches per plant (0.55%), negligible contribution towards the total genetic divergence. From the above study it can be concluded the diversity in pigeonpea genotypes for yield and yield attributing characters may be due to days to maturity, number of pods per plant, days to 50% flowering, test weight, harvest index. Similar result also observed by Baskaran and Muthiah (2008) and Sreelakshmi *et al.* (2010). Pandey *et al.* (2013) observed highest contribution was exhibited by 100 seed weight followed by pods per plant, days to maturity, harvest index, and days to 50% flowering. Prasad *et al.* (2013) reported maximum contribution by seed yield, 100 seed weight, grain per pod, days to maturity and plant height.

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