Influence of parents and their habit on genetic diversity among hybrids of pigeonpea (*Cajanus cajan* (L.) Millsp.)

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Abstract : Twenty-seven pigeonpea genotypes consisting of 18 hybrids and their parents were evaluated for 11 traits to quantify the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into 14 clusters. Cluster size varied from single genotype (Cluster IX to XIV) to four genotypes (Clusters I and II). In general, hybrids with same habit were grouped into same cluster. Though the present results indicated the influence of parental genotype on the clustering, it could not confirm the influence of cytoplasm. Hence it might be concluded that the clustering pattern was influenced by the parents involved and habit of the genotypes than geographical origin. Number of seeds per pod, which contributed for maximum genetic distance (15.10), followed by plant height and number of branches per plant (11.40) and days to maturity (10.54). Among these characters, plant height, number of branches and days to maturity related to habit of the plants. This indicated the influence of habit on clustering through the related characters. Hence, the present study clearly indicated the influence of parents and their habit in the clustering pattern. Though the parents created variability in their crosses, the diversity of hybrids from parents was limited.

Key words : Pigeonpea, diversity analysis, genetic divergence, heterosis.

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is an important pulse crop of Indian cropping system because of its ability to produce protein rich seeds and large amount of quality biomass. India is the largest producer of pigeonpea accounting for over 80% of the world production. Genetic diversity is an important factor and also prerequisite in any hybridization programme. Hybrids between genetically diverse parents manifest greater heterosis than those closely related parents (Arunachalam, 1981). Earlier reports of the genetic improvement for yield are generally at the cost of genetic diversity among the related varieties, which cause narrowing down of the genetic base and in turn yield plateau in crops. Many breeding efforts have been carried out to improve the yield of this crop and to break the yield plateau by accumulation of desirable traits spread over the diverse genotypes. In order to choose diverse parental genotypes for hybridization programme, the existing genotypes are needed to classify into clusters based on genetic divergence. Mahalanobis generalized distance (D^2) has been very often used by crop breeders to measure the nature and magnitude of diversity. In view of these, 27 genotypes were evaluated in this study to determine the grouping pattern of genotypes and to identify genetically diverse genotypes for exploitation in a breeding program.

Table 1. Mean performance of phenology, seed yield and their component traits of pigeonpea genotypes

Genotypes	Habit	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches/ plant	Number of clusters/ plant	Number of pods/ plant	Number of seeds/ pod	Pod length (cm)	100 seed weight (g)	Seed protein content (%)	Seed yield/ plant (g)
CO 5	IDT	80.67	137.33	118.63	11.73	85.07	187.67	3.53	5.55	8.45	20.63	52.60
VBN 1	DT	73.33	124.00	88.87	9.07	55.07	175.00	3.62	4.51	8.41	18.91	44.29
CORG 9407	DT	78.33	122.33	81.27	7.53	30.13	103.67	4.40	5.81	10.37	21.13	35.98
CORG 9701	IDT	78.00	129.33	119.37	12.40	81.13	162.47	3.37	5.19	8.51	20.12	38.51
ICPL 87	DT	73.00	120.67	75.43	8.00	34.53	123.77	4.08	6.11	9.51	18.05	44.26
CORG 990IDT4	IDT	64.67	115.33	100.83	11.07	58.93	126.33	3.35	4.88	8.54	21.28	26.86
APK 1	DT	73.33	130.67	100.27	8.67	27.33	84.93	4.55	6.15	10.36	21.32	38.94
ICPL 83024	DT	68.00	122.00	72.37	7.67	28.47	90.47	3.80	5.47	12.42	21.05	39.73
ICPL 83027I	DT	84.33	135.00	129.97	11.80	74.27	169.07	3.56	5.17	8.95	19.56	53.16
CO 5 x APK 1	IDT	69.00	122.67	125.20	12.20	64.73	165.60	3.99	6.07	10.62	20.92	57.62
CO 5 x ICPL 8302I4	IDT	73.67	119.67	127.63	11.33	87.73	175.00	3.81	5.85	9.97	21.11	51.15
CO 5 x ICPL 83027	IDT	82.33	136.33	141.63	13.27	125.80	253.53	3.81	5.57	8.09	20.19	65.82
VBN 1 x APK 1	DT	63.00	121.00	90.43	11.27	73.20	175.13	4.21	5.31	8.77	19.92	50.09
VBN 1 x ICPL 83024	DT	72.33	119.67	87.33	10.93	50.67	134.73	3.04	5.06	9.17	19.71	35.45
VBN 1 x ICPL 83027	IDT	84.33	138.33	151.60	13.10	159.13	293.13	3.85	4.97	8.33	18.89	88.56
CORG 9407 x APK 1	DT	62.67	120.67	82.23	10.13	48.80	138.00	4.31	5.33	10.05	19.62	45.61
CORG 9407 x ICPL 83024	DT	75.00	122.67	83.30	8.00	39.87	125.00	4.34	5.38	10.37	20.65	43.07
CORG 9407 x ICPL 83027I	IDT	80.33	132.67	80.73	9.00	52.53	134.67	4.44	5.49	11.42	19.91	56.54
CORG 9701 x APK 1	IDT	69.67	123.33	103.99	11.73	111.00	197.20	3.59	5.37	9.73	18.51	56.26
CORG 9701 x ICPL 83024	IDT	74.33	126.67	99.47	9.40	54.80	153.73	3.91	4.98	9.18	18.89	39.53
CORG 9701 x ICPL 83027	IDT	80.67	130.33	109.00	10.07	78.53	208.93	3.63	4.67	7.37	18.31	41.70
ICPL 87 x APK 1	DT	62.67	117.67	78.03	8.73	37.27	129.87	4.04	5.26	10.72	18.77	42.73
ICPL 87 x ICPL 83024	DT	76.33	125.67	77.67	9.60	45.87	153.67	4.79	6.03	9.75	18.37	57.12
ICPL 87 x ICPL 83027	IDT	78.00	127.33	121.60	11.00	83.93	175.80	3.93	4.87	9.32	18.93	55.49
CORG 9904 x APK 1	IDT	69.33	118.67	102.40	8.90	49.00	125.03	4.03	5.30	9.48	20.11	34.83
CORG 9904 x ICPL 83024	IDT	76.67	120.33	104.57	10.47	48.67	136.60	4.00	5.02	8.90	21.83	33.50
CORG 9904 x ICPL 83027	IDT	76.67	123.67	123.27	13.00	110.40	244.60	3.68	4.84	8.10	20.95	62.61

Table 2. Composition of clusters in pigeonpea

Clusters	No. of genotypes	Genotypes
I	4	CORG 9407 x ICPL 83024, CORG 9904 x APK 1, CORG 9904 x ICPL 83024, CORG 9407 VBN 1 x APK 1,
II	4	CORG 9407 x APK 1, ICPL 87 x APK 1, CORG 9904 CORG 9701 x ICPL 83024,
III	3	CORG 9701 x ICPL 83027, CORG 9701 VBN 1 x ICPL 83024,
IV	2	ICPL 87 x ICPL 83024 ICPL 87 x ICPL 83027,
V	2	ICPL 83027
VI	2	CORG 9407 x ICPL 83027, ICPL 83024
VII	2	CO 5 x ICPL 83024, CO 5 x ICPL 83027 CORG 9904 x ICPL 83027,
VIII	2	VBN 1
IX	1	CO 5
X	1	VBN 1x ICPL 83027
XI	1	APK 1
XII	1	CORG 9701 x APK 1
XIII	1	CO 5 x APK 1
XIV	1	ICPL 87

Table 3. Estimates of average Intra (diagonal) and Inter cluster D² values

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	9.39	18.38	42.10	81.32	101.52	122.18	138.79	157.32	338.40	364.43	383.46	410.03	438.20	464.44
II		14.04	20.43	50.26	73.87	98.24	121.54	140.95	304.32	332.71	355.48	377.24	402.39	431.63
III			12.64	19.93	39.64	65.14	83.43	106.16	232.15	263.11	289.80	312.21	341.92	372.83
IV				13.53	20.54	45.89	69.70	93.00	213.17	247.03	277.16	300.94	328.20	351.85
V					10.41	25.37	51.22	74.39	174.00	193.99	219.12	247.99	273.24	302.51
VI						15.44	27.31	53.00	128.72	159.88	189.50	214.03	245.68	282.56
VII							15.40	24.30	69.49	92.91	119.17	139.29	158.63	189.21
VIII								15.29	20.63	43.91	81.44	114.31	142.41	170.97
IX									0.00	27.95	47.54	76.39	105.66	131.37
X										0.00	31.85	57.18	95.93	133.26
XI											0.00	39.60	70.95	105.67
XII												0.00	38.99	67.34
XIII													0.00	36.02
XIV														0.00

Materials and Methods

The genetic materials used in the present study consisted of 27 genotypes which included 18 hybrids and their 9 parental genotypes. All the 27 genotypes were evaluated in a Randomized Block Design with three replications at Millet Breeding Station, Tamil Nadu Agricultural University, Coimbatore during *kharif* 2003. Each genotype was sown in 5-m row plot with 75 and 30 cm spacing maintained between rows and plants, respectively. All recommended practices were followed for raising good crop to evaluate phenotypic performance precisely. Observations were recorded on five randomly selected plants per entry per replication. The biometrical traits chosen for the study were days to 50% flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100 seed weight, seed protein content and seed yield per plant. The Mahalanobis (1936) D² statistic was used to estimate the divergence and Tocher's method as given by Rao (1952) was used to cluster the genotypes.

Results and Discussion

The mean performance of all the genotypes for 11 characters including phenological and yield and its component traits were presented in Table 1. D² values were computed for all pair wise combinations. By the application of clustering technique, all the genotypes were grouped into 14 clusters (Table 2), which revealed that the genotypes studied were highly divergent. The number of genotypes per cluster varied from four (Clusters I and II) to one (Cluster IX to XIV). All nine parental genotypes were placed in different clusters due to the higher genetic divergence between them. The clustering pattern revealed that genotypes derived from one common parent grouped into the same cluster *viz.*, hybrids (CORG 9904

x APK 1 and CORG 9904 x ICPL 8302) involving CORG 9904 were grouped into cluster 1, hybrids (VBN 1 x APK 1; CORG 9407 x APK 1; ICPL 87 x APK 1) involving APK 1 were grouped into cluster II, hybrids involving CORG 9701 (CORG 9701 x ICPL 83024; CORG 9701 x ICPL 83027) grouped into cluster III, hybrids involving ICPL 83024 (VBN 1 x ICPL 83024; ICPL 87 x ICPL 83024) grouped into cluster IV and hybrids involving CO 5 (CO 5 x ICPL 83024; CO 5 x ICPL 83027) grouped into cluster VII. In general, hybrids with same habit were grouped into same cluster as above.

Parents and some of their hybrids were clustered into same cluster as in the case of CORG 9407 (cluster I), CORG 9701 (cluster III) and ICPL 83027 (cluster V). Influence of female parents in the clustering pattern is evident in cluster 1 (CORG 9904), cluster III (CORG 9901), cluster VII (CO 5) and male parent in cluster 1 (ICPL 83024), cluster II (APK 1) and cluster IV (ICPL 83024). Though the present results indicate the influence of parental genotype on the clustering, it could not confirm the influence of cytoplasm. Hence it may be concluded that the clustering pattern is influenced by the parents involved and habit of the genotypes than geographical origin. Murthy and Arunachalam (1966) reported that genetic drift and selection in different environments could cause greater diversity than geographic distance. The present result was in concordance with the reports of Henry and Krishna (1992) and Sandhu et al. (1993) on pigeonpea. They observed that apart from single genotype cluster, all the other clusters included genotypes from different geographical regions. This indicated that the genetic diversity was not parallel to the geographical diversity.

The average intra and inter-cluster distances are given in Table 3. The intra-cluster distance ranged from 0.00 (Cluster IX to XIV) to 15.44 (Cluster VI). It indicated that the genotypes of the cluster VI, VII and VIII were highly divergent among them. The maximum inter-cluster distance (464.44) was noted between cluster I and XIV followed by clusters I and XIII (438.20), while the clusters I and II were closely related (18.38) followed by cluster III and IV (19.93). The genotypes of distant clusters were expected to be genetically divergent. In general, the inter cluster distance between parents and their hybrids were minimum to average with few exceptions. Hence the influence of parents was also seen in the inter cluster distance.

In addition to classifying the genotypes into clusters based on genetic divergence, the amount of contribution made by 11 traits towards divergence was also estimated. Number of seeds per pod, which contributed for maximum genetic distance (15.10), followed by plant height and number of branches per plant (11.40) and days to maturity (10.54). Among the characters, plant height, number of branches and days to maturity were related to habit of the plants. Hence the influence of habit through the related characters was clearly expressed in the study. Singh and Gumber (1996) reported that the 100 seed mass, days to maturity and biological yield were major contributing traits towards the total divergence. Contrary to these results, Patel et al. (1988) reported that secondary branches, number of pods per plant, number of clusters per plant were major contributing traits. Hence, the present study clearly indicated the influence of parents and their habit in the clustering pattern. Though the parents created variability in their crosses, the diversity of hybrids from parents was limited.

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