



Research Paper

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Genetic diversity in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub]

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ABSTRACT : Fifty genotypes of cluster bean [*Cyamopsis tetragonoloba* (L.) Taub] with a broad spectrum of variation were assessed for genetic divergence using Mahalanobis D² technique. The genetic material exhibited wide range of genetic divergence for all the 16 characters investigated. All the genotypes were grouped into ten different clusters. Among the ten clusters it was observed that cluster X had the maximum of 11 accessions followed by cluster V, IV, III, VIII, IX, and II, which had 10, 7, 5, 4, 4, 3, accessions, respectively. Cluster I, VI, and VII exhibited two accessions each in a cluster. The intra and inter cluster distance revealed that the lowest mean intra cluster distance of 27.53 was exhibited by cluster I, while the highest intra cluster distance was recorded by the cluster IX (235.85). It was followed by cluster X with a distance of (233.67). The highest inter cluster distance of 374.88 was recorded between cluster II and VIII, followed by 366.77 between clusters II and VII, whereas the clusters I and VI were the least divergent (94.82) followed by clusters I and III showing a distance of 140.59 between them. On the basis of inter – cluster distances and *per se* performances observed, the genotypes with specific characters can be utilized for hybridization programme.

KEY WORDS : Cluster bean, Genetic divergence, Mahalanobis D² technique

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Cluster bean belongs to the family Fabaceae and is a drought tolerant crop. It is cultivated as a rainfed crop in arid and semi-arid regions during rainy season for vegetable, forage and green manure. Seeds of cluster bean have a large endosperm when compared to other legumes, and contains galactomannan type of gum, which forms a viscous gel and has diversified industrial applications viz., paper, food, cosmetics, mining, petroleum, well drilling, pharmaceuticals etc. (Pathak *et al.*, 2009). In order to enhance the productivity, information on the nature and magnitude of genetic diversity present in the genotypes is a pre-requisite. The D² statistics is found to be an effective tool among the various techniques available for genetic differentiation among population (Rao, 1960). Therefore, an attempt was made to study the degree of genetic diversity in 50 genotypes of cluster bean and to identify suitable parents having wider genetic divergence for formulating the crossing programme.

RESEARCH METHODS

An investigation was carried out in the Department of

Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, U.T. of Puducherry during *Kharif* 2008. The genotypes were replicated thrice. Seeds were sown at a spacing of 45 x 15cm. Management practices were followed uniformly for raising the crop. Observations were recorded for quantitative characters like plant height (cm), number of branches per plant, days taken to first flowering, number of clusters per plant, number of pods per cluster, pod length (cm), pod yield per plant (fresh and dry) (g), seed yield per plant (g), number of seeds per pod, 100 seed weight (g), days to maturity, harvest index (%), and qualitative characters like crude fibre, crude protein and guar gum content were also recorded from five randomly selected plants. Mahalanobis D² statistics as suggested by Rao (1952) was used to measure the genetic divergence.

RESEARCH FINDINGS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all 16 characters studied. This suggested the presence of appreciable amount of diversity

among the genotypes under study. The computed D² values for 50 genotypes had wide range showing high divergence among the genotypes. The D² values were worked out for 1225 pairs of combinations. By the application of clustering technique, all 50 accessions were grouped into ten different clusters. The constituents of different clusters are presented in Table 1. Among the ten clusters, it was observed that cluster X had the maximum of 11 accessions followed by cluster V, IV, III, VIII, IX, and II, which had 10, 7, 5, 4, 4, 3, accessions, respectively. Cluster I, VI, and VII exhibited two accessions each in a cluster. The use of Mahalanobis D² statistics for estimating genetic divergence have been emphasized by many workers like Henry and Krishna (1990), Narsinghani *et al.* (1988), Sankaran *et al.* (2008) and Singh and Ram (1985) in peas and beans since, it permits precise comparison among

all possible pairs of population in any given group effecting actual crosses.

Intra and Inter cluster distance:

The intra and inter cluster distance among 10 clusters are presented in Table 2. The lowest mean intra cluster distance of 27.53 was exhibited by cluster I, while the highest intra cluster distance was recorded by the cluster IX (235.85). It was followed by cluster X with a distance of (233.67). The highest inter cluster distance of 374.88 was recorded between cluster II and VIII, followed by 366.77 between clusters II and VII, whereas the clusters I and VI were the least divergent (94.82) followed by clusters I and III showing a distance of 140.59 between them. Selection of genotypes belonging to clusters with maximum inter cluster distance

Table 1 : Clustering pattern of 50 accessions in cluster bean

Cluster	No. of accessions	Accessions
I	2	CT 22, CT 32.
II	3	CT 1, CT 18, CT 49.
III	5	CT2, CT 3, CT 4, CT 5, CT 28.
IV	7	CT 6, CT 7, CT 8, CT 9, CT 10, CT 12, CT 17.
V	10	CT 11, CT 13, CT 14, CT 15, CT 16, CT 19, CT 20, CT 21, CT 26, CT 27.
VI	2	CT 24, CT 45.
VII	2	CT 25, CT 46.
VIII	4	CT 23, CT 29, CT 30, CT 43.
IX	4	CT 31, CT 33, CT 42, CT 50.
X	11	CT 34, CT 35, CT 36, CT 37, CT 38, CT 39, CT 40, CT 41, CT 44, CT 47, CT 48.

Table 2 : Mean intra-cluster (diagonal) and inter-cluster D² and D values

I	757.85 (27.53)	59387.13 (243.69)	19765.86 (140.59)	34316.09 (185.25)	26229.24 (161.95)	8991.15 (94.82)	39501.74 (198.75)	45153.82 (212.49)	27797.29 (166.72)	42822.34 (207.08)
II		17949.28 (133.97)	86743.47 (294.52)	125189.50 (353.82)	78454.28 (280.10)	32576.28 (180.49)	134523.51 (366.77)	140536.70 (374.88)	65497.41 (255.92)	122146.62 (349.49)
III			35175.49 (187.55)	36693.70 (191.56)	38895.73 (197.22)	27705.36 (166.45)	34277.79 (185.14)	43855.69 (209.41)	41784.30 (204.41)	45303.19 (212.84)
IV				37165.23 (192.78)	49616.68 (222.75)	49258.09 (221.94)	29957.37 (173.08)	32151.91 (179.31)	53549.30 (231.40)	42432.30 (205.99)
V					48087.10 (219.29)	28140.56 (167.75)	56961.47 (238.67)	52920.51 (230.04)	44688.19 (211.40)	54897.14 (234.30)
VI						3889.07 (62.36)	58665.45 (242.21)	56784.96 (238.30)	26638.70 (163.21)	51750.63 (227.49)
VII							4217.09 (64.94)	41862.21 (204.60)	60669.82 (246.31)	45857.51 (214.14)
VIII								26140.45 (161.68)	58418.97 (241.70)	38778.37 (196.92)
IX									55624.50 (235.85)	58358.09 (241.57)
X										54602.51 (233.67)

Intra cluster divergence - diagonal values, Inter cluster divergence - off diagonal values, D values - values in parenthesis

Table 3 : Cluster mean values for 16 characters in cluster bean

Clusters and characters	I	II	III	IV	V	VI	VII	VIII	IX	X
Plant height (cm)	122.83	132.44	114.33	107.29	113.90	108.00	93.33	110.92	122.33	114.73
Number of branches per plant	8.33	4.11	5.40	7.24	5.77	2.50	7.67	6.67	5.08	6.45
Days taken to first flowering	28.83	25.67	30.07	31.29	29.93	28.00	32.17	31.75	27.92	31.18
Number of clusters per plant	28.33	19.00	23.93	29.43	24.73	18.17	24.00	25.42	22.25	27.00
Number of pods per cluster	5.00	13.22	8.27	5.62	7.90	9.50	7.33	6.33	9.25	6.30
Pod length (cm)	6.29	6.27	5.90	5.50	5.69	5.91	6.14	4.69	5.75	5.21
Fresh pod yield per plant (g)	264.33	348.44	236.67	216.12	261.05	287.00	199.00	208.67	273.50	225.09
Dry pod yield per plant (g)	184.00	268.00	180.93	167.86	185.03	207.17	161.50	163.42	204.42	171.00
Number of seeds per pod	8.67	8.44	7.47	8.24	7.87	8.67	7.50	7.17	7.92	7.67
Seed yield per plant (g)	33.02	40.46	31.00	28.71	30.74	35.25	27.10	27.26	34.04	29.91
Hundred seed weight (g)	3.83	5.50	4.29	3.70	4.19	4.61	4.40	3.59	4.11	3.96
Days taken to maturity	59.00	55.67	60.07	61.38	60.00	58.00	62.17	61.58	57.92	61.30
Harvest index (%)	21.02	23.11	23.10	21.98	22.72	22.56	21.33	23.33	21.99	23.35
Crude fibre content (%)	21.47	22.34	22.52	23.74	22.48	21.74	25.36	23.92	23.04	23.63
Crude protein content (%)	16.90	16.71	19.41	18.04	19.80	19.03	17.03	16.58	19.49	18.10
Gum content (%)	26.20	25.69	21.67	21.89	25.35	21.33	20.30	29.44	20.79	22.50

has been proposed by Henry and Krishna (1990), Singh *et al.* (2003) in cluster bean, Narayanankutty *et al.* (2005), Borah and Khan (2001) in vegetable cow pea.

Cluster mean values for different clusters:

The data on the means of all the 16 characters in respect of 10 clusters are summarized in Table 3. Cluster I exhibited the lowest mean values for number of pods per cluster (5.00), harvest index (21.02), and crude fibre content (21.47). The same cluster possessed highest mean values for number of branches per plant (8.33), pod length (6.29) and number of seeds per pod (8.67). Cluster II possessed highest mean values for plant height (133.44), number of pods per cluster (13.22), fresh pod yield (348.44), dry pod yield (268.00), seed yield per plant (40.46), hundred seed weight (5.50). This cluster also possessed lowest mean value for days taken to first flowering (25.67), and days to maturity (55.67). Cluster IV and cluster V exhibited highest mean values for only one trait *viz.*, number of clusters per plant (29.43), and crude protein content (19.80).

Two lowest mean values was exhibited by cluster VI *viz.*, number of branches per plant (2.50), and number of clusters per plant (18.17) and also it recorded a highest mean value of 8.67 for the trait number of seeds per pod. Cluster VII exhibited three highest cluster mean for days taken to first flowering (32.17), days to maturity (62.17) and crude fibre content (25.36). Further Cluster VII recorded the lowest mean for the characters plant height (93.33), fresh pod yield (199.00), dry pod yield (161.50), seed yield per plant (27.10), and gum content (20.30). One highest mean value for gum content (29.44) and four lowest mean values for pod length (4.69), number of seeds per pod (7.17),

hundred seed weight (3.59) and crude protein content (16.58) was observed in cluster VIII. Cluster X exhibited highest mean value for the trait harvest index (23.35). In general cluster II recorded highest mean for six characters namely plant height, number of pods per cluster, fresh pod yield, dry pod yield, seed yield per plant, and hundred seed weight followed by cluster I and VII which recorded highest mean values for number of branches per plant, pod length, number of seeds per pod, days taken to first flowering, days

Table 4 : Character contribution to divergence in cluster bean accessions

Characters	No. of first rank	Contribution to divergence (%)
Plant height (cm)	0	0.00
Number of branches per plant	0	0.00
Days taken to first flowering	0	0.00
Number of clusters per plant	0	0.00
Number of pods per cluster	0	0.00
Pod length (cm)	147	12.00
Fresh pod yield per plant (g)	249	20.33
Dry pod yield per plant (g)	36	2.94
Number of seeds per pod	7	0.57
Seed yield per plant (g)	1	0.08
100 seed weight (g)	164	13.39
Days taken to maturity	1	0.08
Harvest index (%)	7	0.57
Crude fibre content (%)	284	23.18
Crude protein content (%)	68	5.55
Gum content (%)	261	21.30
Total	1225	100

taken to maturity and crude fibre content.

Relative contribution of each character:

The relative contribution of each character towards genetic divergence was estimated by the individual characters. The number of times each character appeared in first rank is presented in Table 4. The character crude fibre contributed the maximum percentage of 23.18 towards genetic divergence followed by gum content (21.30), fresh pod yield (20.33), hundred seed weight (13.39), pod length (12.00), crude protein content (5.55), and dry pod yield (2.94). Characters like number of seeds per pod, harvest index, seed yield per plant and days taken to maturity showed negligible contribution to divergence.

The ranking of genotypes based on the method suggested by Nadarajan and Gunasekaran (2005), indicated that the genotypes could be ranked more appropriately than done by the commonly employed method of using mean and critical difference for all the traits, without considering their magnitude of contribution towards total genetic divergence. This method relies on the contribution of characters to genetic diversity for ranking of genotypes. Hence, the combined ranking, results in the identification of superior genotypes for further exploitation as potential parents for hybridization programme. Combined ranking based on five characters, viz., crude fibre content, gum content, fresh pod yield per plant, 100 seed weight, and pod length which had contributed maximum to genetic divergence resulted in the identification of IC- 373467 (CT 13) and IC- 311392 (CT 1) as the best accessions followed by IC- 415156 (CT 31), IC- 415163 (CT 37), IC- 402295 (CT 18), IC- 370509 (CT 11), IC- 421812 (CT 41), IC- 421823 (IC- 49). The importance of hundred seed weight was observed by Singh and Mishra (2008) and Sulanthi *et al.* (2007) for pod length. The above superior accessions were identified as desirable ones, for further utilization as parents for hybridization programme.

Conclusion:

Ranking based on both mean performance and contribution of characters towards divergence resulted in

the identification of CT 1 (IC- 311392), CT 13 (IC- 373467), and CT 31 (IC- 415156) as better genotypes and can be utilized as parents in the hybridization programme for the improvement of pod yield and quality.

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