



Research Note

Studies on genetic diversity for yield, quality and yield attributing traits in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.] genotypes

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Abstract

The study was carried out to assess the genetic divergence among 56 cluster bean genotypes using Mahalanobis D^2 . Fifty-six genotypes were grouped into 8 clusters based on 11 characters. The intra-cluster distances were seen to be lower than the inter-cluster distances. The maximum inter-cluster distance was noticed between cluster VI and VII whereas, inter-cluster D^2 value was least between cluster I and V. The maximum intra-cluster distance was observed in cluster IV. Clusters V, VII and VIII had only one genotype each and hence intra-cluster distance was 0.00. The per cent contribution towards genetic diversity was maximum in 100 seed weight (52.08%) followed by the protein content of pods (45.19%). On the basis of inter-cluster distances observed, the genotypes with specific characters can be utilized for the hybridization programme.

Keywords

Genetic divergence, cluster bean, Mahalanobis D^2 , cluster distance

Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub] is a versatile, multipurpose and underexploited leguminous vegetable crop of the arid and semi-arid region belonging to the family *Leguminosae*. It is a drought-tolerant, hardy and deep-rooted summer annual legume cultivated for its green pods, fodder and manure. Although cluster bean is a minor crop due to its better and finer guar gum qualities, it is considered as an important cash crop for industrial gum production and for several pharmaceutical and nutraceutical products. It has been reported that the cultivated species *C. tetragonoloba* was developed from a drought-tolerant wild African species *C. senegalensis* (Mudgil *et al.*, 2014), while Vavilov (1951) suggested India be the centre of variability for cluster bean. The crop is widely grown in countries like India, Pakistan, Indonesia and other parts of Southern and Southeastern Asia as a vegetable and fodder crop for a long time

Despite the importance of this crop, only limited breeding work has been done and very little attention has been given for its genetic improvement in the past, to enhance

the productivity levels of *Kharif* cluster bean. Information on the nature and magnitude of genetic diversity present in the genotypes is a prerequisite. The availability of genetic diversity is essential for any crop improvement programme. The inclusion of diverse parents in hybridization programme serves the purpose of producing desirable recombinants. Multivariate analysis of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence at the genotypic level. The grouping of the genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. (Rao, 1952). Therefore, an attempt in the present investigation was made to study the degree of genetic diversity in cluster bean genotypes.

An investigation was carried out at the College of Horticulture, Dr Y. S. R. Horticultural University, Venkataramannagudem, West Godavari district during the *Kharif* season of 2018 using 56 cluster bean genotypes (table 1). Genotypes were evaluated with two replications with the spacing of 45 cm x 15 cm. Optimum management

practices were followed uniformly for raising the crop. Observations were recorded on the individual plot basis for days to 50% flowering, 100 seed weight (g), the average weight of 50 pods (g) and protein content of pods (%). Characters viz., plant height (cm), the number of branches per plant, internodal length (cm), the number of

pods per cluster, pod length (cm), the number of seeds per pod and pod yield per plant (g) were recorded on five randomly selected plants and then averaged. Mahalanobis D^2 statistic, as suggested by Rao (1952) was used to measure genetic divergence.

Table 1. List of cluster bean genotypes used in the present study

Treatment	Genotypes	Source	Treatment	Genotypes	Source
T ₁	IC-113272	NBPGR, Jodhpur	T ₂₉	IC-116626	NBPGR, Jodhpur
T ₂	IC-113277	NBPGR, Jodhpur	T ₃₀	IC-116652	NBPGR, Jodhpur
T ₃	IC-113278	NBPGR, Jodhpur	T ₃₁	IC-116660	NBPGR, Jodhpur
T ₄	IC-113281	NBPGR, Jodhpur	T ₃₂	IC-116779	NBPGR, Jodhpur
T ₅	IC-113308	NBPGR, Jodhpur	T ₃₃	IC-116705	NBPGR, Jodhpur
T ₆	IC-113374	NBPGR, Jodhpur	T ₃₄	IC-116825	NBPGR, Jodhpur
T ₇	IC-113376	NBPGR, Jodhpur	T ₃₅	IC-116925	NBPGR, Jodhpur
T ₈	IC-113377	NBPGR, Jodhpur	T ₃₆	IC-116930	NBPGR, Jodhpur
T ₉	IC-113378	NBPGR, Jodhpur	T ₃₇	IC-116932	NBPGR, Jodhpur
T ₁₀	IC-113379	NBPGR, Jodhpur	T ₃₈	IC-384974	NBPGR, Jodhpur
T ₁₁	IC-113380	NBPGR, Jodhpur	T ₃₉	IC-384986	NBPGR, Jodhpur
T ₁₂	IC-113382	NBPGR, Jodhpur	T ₄₀	IC-522399	NBPGR, Jodhpur
T ₁₃	IC-113383	NBPGR, Jodhpur	T ₄₁	IC-522389	NBPGR, Jodhpur
T ₁₄	IC-113390	NBPGR, Jodhpur	T ₄₂	IC-522511	NBPGR, Jodhpur
T ₁₅	IC-113393	NBPGR, Jodhpur	T ₄₃	IC-522421	NBPGR, Jodhpur
T ₁₆	IC-113394	NBPGR, Jodhpur	T ₄₄	IC-522487	NBPGR, Jodhpur
T ₁₇	IC-113395	NBPGR, Jodhpur	T ₄₅	IC-522506	NBPGR, Jodhpur
T ₁₈	IC-113396	NBPGR, Jodhpur	T ₄₆	IC-52249	NBPGR, Jodhpur
T ₁₉	IC-113399	NBPGR, Jodhpur	T ₄₇	RGC-986	NBPGR, Jodhpur
T ₂₀	IC-113503	NBPGR, Jodhpur	T ₄₈	PLG-85	NBPGR, Jodhpur
T ₂₁	IC-113506	NBPGR, Jodhpur	T ₄₉	RGC-1038	NBPGR, Jodhpur
T ₂₂	IC-113523	NBPGR, Jodhpur	T ₅₀	IC-421850	NBPGR, Jodhpur
T ₂₃	IC-113568	NBPGR, Jodhpur	T ₅₁	IC-421855	NBPGR, Jodhpur
T ₂₄	IC-113513	NBPGR, Jodhpur	T ₅₂	IC-51063	NBPGR, Jodhpur
T ₂₅	IC-116569	NBPGR, Jodhpur	T ₅₃	Thar Bhadavi	CIAH, Bikaner, Rajasthan
T ₂₆	IC-116607	NBPGR, Jodhpur	T ₅₄	MDU-1	TNAU, Coimbatore
T ₂₇	IC-116608	NBPGR, Jodhpur	T ₅₅	Chitra Gold	Vagro seeds Pvt. Ltd, Hyderabad
T ₂₈	IC-116619	NBPGR, Jodhpur	T ₅₆	Pusa Navbahar (Check)	IARI, New Delhi

The analysis of variance showed significant differences among the genotypes for all 11 characters studied in 56 cluster bean genotypes. This suggested the presence of an appreciable amount of diversity among the genotypes under study. Fifty-six genotypes were grouped into eight clusters presented in **table 2**. Cluster I was the largest with 33 genotypes followed by cluster III with eight genotypes, cluster IV with six genotypes, cluster II with four genotypes and cluster VI with 2 genotypes. Cluster V, cluster VII and cluster VIII were monogenotypic. Clustering between genetic diversity was in agreement with Singh *et al.* (2003), Pathak *et al.* (2009) and Girish *et al.* (2012). Cluster mean values of eleven characters are presented in **table 3**. The highest mean for plant height (105.73 cm) was shown by cluster V, while the lowest

was seen in cluster VII (75.81 cm). Cluster VII had the maximum cluster mean for the number of branches per plant (11.70) and cluster V and VI (0.00) had the minimum value. Cluster II exhibited the maximum mean value (6.04 cm) for internodal length and minimum value in VIII (4.50cm). The minimum mean value for days to 50% flowering was seen in cluster IV (25.92) and maximum value in cluster V (29.00). Cluster V showed a maximum mean value for the number of pods per cluster (10.90) and a minimum value in cluster II (7.53). The maximum mean value for an average weight of 50 pods was observed in cluster VI (173.50 g) and minimum mean value in cluster VIII (51.00 g). Maximum mean values for pod length was exhibited in cluster VI (10.35 cm). The minimum mean value was in cluster III and VII (6.25 cm).

Table 2. Distribution of cluster bean genotypes into clusters, as per Mahalanobis D² values

Cluster	Count	Genotype	Source
I	33	IC-113568	
		RGC-986	
		IC-113374	
		IC-116607	
		IC-113394	
		PLG-85	
		IC-116705	
		IC-116825	
		IC-522511	
		IC-113378	
		IC-113379	
		IC-51063	
		IC-52249	
		IC-116608	
		IC-116779	
		IC-113277	
		IC-113523	
		IC-384974	
		IC-116569	
		IC-522399	
		IC-116652	
		IC-421855	
		IC-113395	
IC-113272			
IC-113506			
IC-116626			
IC-522389			
IC-113396			
IC-421850			
IC-113382			
IC-522487			
IC-113308			
IC-116660			
IC-113377			
IC-113383			
II	4	IC-116619	
		IC-113399	
		IC-113390	
		IC-113513	
III	8	RGC-1038	
		IC-113376	
		IC-116930	
		IC-113278	
		IC-113380	
		IC-113393	
		IC-384986	
		IC-522421	
IV	6	IC-522506	
		IC-113503	
		Chitra Gold	
V	1	Pusa Navbahar	
VI	2	IC-116932	
		Thar Bhadavi	
VII	1	MDU-1	
		IC-116925	
VIII	1	IC-113281	

Table 3. Cluster mean values for different characters of cluster bean genotypes

Characters	Clusters							
	I	II	III	IV	V	VI	VII	VIII
Plant height (cm)	91.87	96.87	88.68	102.83	105.73	98.50	75.81	77.31
Number of branches per plant	7.62	5.85	6.21	5.45	0.00	0.00	11.70	9.60
Internodal length (cm)	5.09	6.04	5.38	5.66	4.70	5.58	5.25	4.50
Days to 50 % flowering	27.03	27.50	27.31	25.92	29.00	26.75	26.50	26.00
Number of pods per cluster	8.82	7.53	8.37	7.98	10.90	8.90	7.56	7.56
Average weight of 50 pods (g)	78.89	80.63	70.94	126.83	111.00	173.50	76.00	51.00
Pod length (cm)	6.55	6.60	6.25	7.93	7.73	10.35	6.25	6.34
Number of seeds per pod	7.84	8.13	7.55	8.07	6.20	8.80	9.40	7.80
100 seed weight (g)	3.32	3.98	3.17	4.25	2.78	4.72	2.45	3.69
Pod yield per plant (g)	202.30	208.15	199.15	262.28	182.70	224.60	152.10	191.10
Protein content of pods (%)	14.95	14.93	23.45	21.40	15.49	14.56	20.53	29.15

Cluster VII had the maximum mean value for the number of seeds per pod (9.40), the minimum value was in cluster V (6.20). The highest mean value for 100 seed weight was in cluster VI (4.72 g) and the minimum value was in cluster VII (2.45 g). The highest mean value for pod yield per plant was in the cluster IV (262.28 g) and the minimum was in cluster VII (152.10 g). The maximum mean value of protein content of the pods was in cluster VIII (29.15%) and the minimum was in cluster VI (14.56%). Mean values of clusters could be utilized based on the objective of the breeding program. That is, if the breeder's aim is to improve the earliness of the crop one must choose the genotypes from characters which have a minimum cluster to mean values such as days to flower initiation, days to 50% flowering and days to first harvest. For other parameter selection might be considered from the clusters

having maximum cluster mean value. Similar results were obtained by Singh *et al.* (2003), Pathak *et al.* (2009) and Girish *et al.* (2012).

Cluster distances presented in table 4, showed maximum intracluster distance in cluster IV (2063.90). Clusters V, VII and VIII had only one genotype each and hence intra cluster distance was 0.00. The maximum inter-cluster distance was noticed between cluster VI and VII (39402.44) indicating that these two clusters show the maximum genetic divergence which can be utilized in hybridization programs to get the heterotic advantage as reported by Singh *et al.* (2003) and Rai and Dharmatti (2014). However, inter-cluster D² value was least between cluster I and V (2793.31) clearly indicating that they are genetically similar.

Table 4. Cluster distances of cluster bean genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	1450.32	4098.81	7394.82	8261.03	2793.31	13525.31	9232.92	15132.91
II		1663.19	12966.99	4499.08	10119.42	4421.65	20215.20	17492.31
III			1752.70	9834.25	5726.05	26252.39	4177.35	4040.50
IV				2063.90	14556.70	7043.25	20704.45	8631.06
V					0.00	24742.77	3473.37	15826.42
VI						708.70	39402.44	27572.32
VII							0.00	12194.60
VIII								0.00

Apart from genetic divergence, due importance should be given to the performance of character with a maximum contribution towards divergence. The number of times each of the 11 characters appeared in the first rank and its respective per cent contribution towards diversity was worked out and presented in fig.1. Hundred seed weight contributed the maximum (52.08%) towards genetic divergence followed by the protein content of pods (45.19%), number of seeds per pod (1.69%), number of branches per plant (0.84%), number of pods per cluster

(0.13%) and pod length (0.06%). In the same manner, these characters ranked 802, 696, 26, 13, 2 and 1 a number of times, respectively. On contrary plant height, internodal length, days to 50% flowering, the average weight of 50 pods and pod yield per plant did not contribute towards genetic divergence. These results were in accordance with the findings of Choyal *et al.* (2017), Wankhade *et al.* (2017) and Rishita (2018) in cluster bean genotypes.

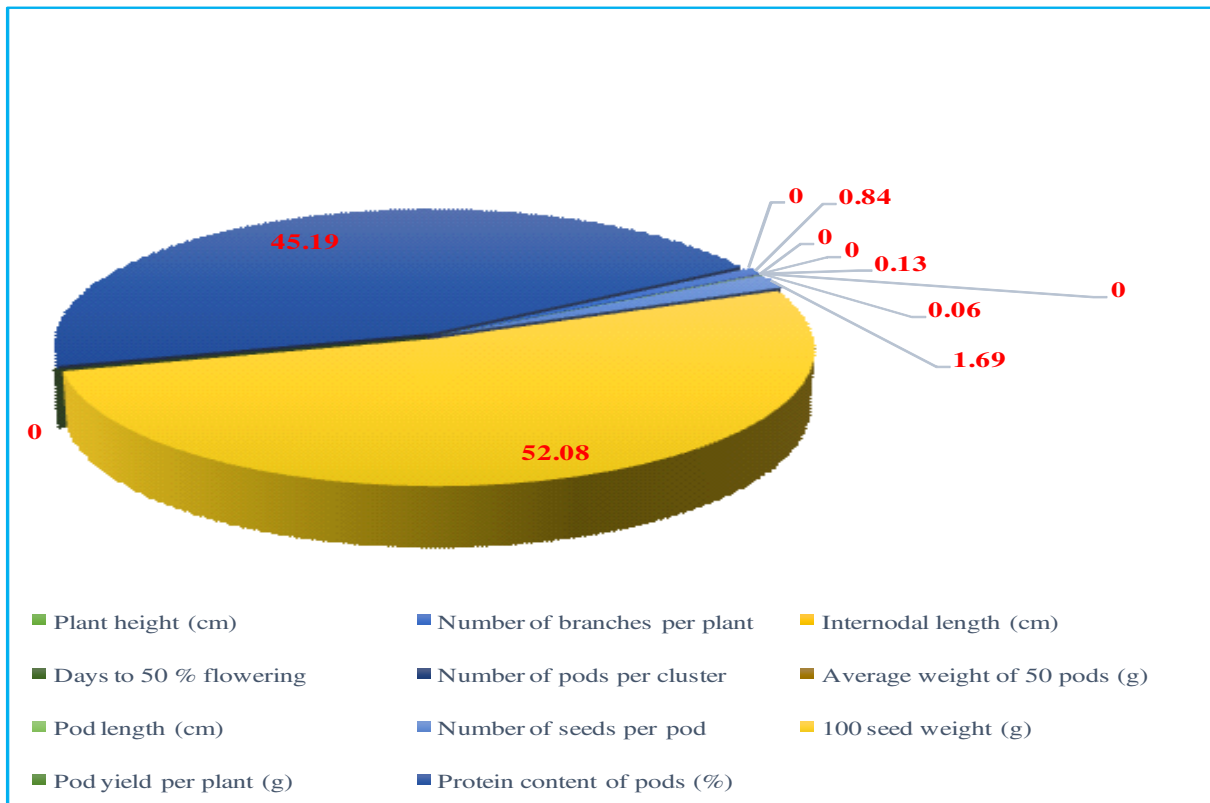


Fig. 1 Per cent contribution of different characters towards diversity in different cluster bean

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Based on the results of the present investigation, an extensive range of genetic diversity has been explored in cluster bean genotypes. It is suggested that hybridization programme between the genotypes of the distinct group to obtain superior genotypes from the segregating generation to overcome the yield constraints in the *Kharif*

cluster bean can be performed. Cataloguing and documenting the diversity of genotypes is essential for future cluster bean breeding programme.

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