International Journal
of Pure & Applied
Bioscience

Genetic Divergence in Genotypes of Cluster Bean [*Cyamopsis tetragonoloba* (L.) Taub.] Under Lucknow Province

Vikas Kumar[1*], R. B. Ram[1], Sandeep Kumar Rajvanshi[1] and Omvir Singh[2]

[1]Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh - 226025, India
[2]National Bureau of Plant Genetic Resources, Regional Research Station, Jodhpur- 342003, India
*Corresponding Author E-mail: vs1744@gmail.com

ABSTRACT

A study was conducted on cluster bean to find out the genetic divergence in genotypes of cluster bean under Lucknow condition in thirty genotypes of cluster bean collected from different sources and maintained at the Horticulture Research Farm-I, of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, India. The genetic divergence studies using Mahalanobis D^2 statistics grouped thirty genotypes of cluster bean divided into 5 different clusters. The maximum intra cluster distance was observed in cluster I indicated that genotypes under this group are diverse. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive human selection for diverse adaptive complexes. The intra cluster distance varies from 3.400 in clusters I and to the maximum distance in cluster II (8.235). This reveals that presence of divergence in cluster I. The inter cluster D^2 values also ranged from 3.464 between cluster IV and cluster III, 4.218 between cluster III and V and of maximum distance of 6.625 between cluster I and cluster IV. The percent contribution towards genetic diversity was highest from days to maturity (37.87%) followed by pod yield (q/ha) (22.32%) and seed yield /plant (g). On the basis of inter-cluster distances and percent performance observed in the present study, a hybridization programme involving genotypes for a specific character may be selected using cluster mean values.

Key words: *Genetic divergence, mahalanobis $D^{2.}$ Cyamopsis tetragonoloba, intra cluster, cluster distance*

INTRODUCTION

Cluster bean is basically a crop that is diversely cultivated in the arid and semi arid areas. That is why the Southern Asian continent suits well to the cultivation of this crop especially the Indian subcontinent. The powder made after refining the gum obtained from the plant makes an important raw material in many industries. This powder has some unique characteristics like grease resistance, thickening agent, capacity to bind water, high viscosity and the capability to function in low temperatures which makes it a highly popular in those sectors. Among other by products of guar, guar gum powder is the main marketable commodity.

Cluster bean, [*Cyamopsis tetragonoloba* (L.) Taub.] usually known as Guar, is a drought and high temperature tolerant deep rooted summer annual legume of high social and economic significance. Guar is a crop of arid and semi-arid areas cultivated in north and northwest parts of India and east and south-eastern part of Pakistan. In Pakistan, Guar seed is mainly produced in Punjab and Sindh province with about 80 percent of total Guar acreage under irrigation. On the other hand production of Guar in India is mainly confined to arid zones of Rajasthan and parts of Gujarat, Haryana and Punjab. Guar in Rajasthan is mainly cultivated under rain-fed conditions[10].

Study of genetic diversity is the process by which variation among individuals or groups of individuals or populations is analyzed by a specific method or a combination of methods. Analysis of genetic relationships in crop species is an important component of crop improvement program, since it provides information about genetic diversity of the crop species which is a basic tool for crop improvement. Analysis of genetic diversity in germplasm collections can facilitate reliable classification of genotypes and identification of subsets of core genotypes with possible utility for specific breeding purpose[6].

Genetic diversity plays a very important role in survival and adaptability of a species because when a species' environment changes, slight gene variations are necessary to produce changes in the organisms' anatomy that enables it to adapt and survive. A species that has a large degree of genetic diversity among its population will have more variations from which to choose the fit alleles[7]. Genetic diversity studies in a crop are important in management of genetic resources, identification of duplicate accessions in the germplasm collection and use of genetic resources in applied breeding programs.

MATERIALS AND METHODS

Genetic evaluation of guar germplasm on the basis of agro morphological traits was performed at the Horticultural Research Farm-I, of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh during the Rabi Season of 2013-2014. Genotypes were obtained from various lead centers of cluster bean research which represents eco-geographical diverse areas of India and maintained at the Horticultural Research Farm-I. Experimental field was laid out in randomized block design with 30 genotypes and replicated thrice. Each block was further subdivided into 30 unit plots. The thirty genotypes were allotted to the 30 unit plots of each block. The plants were raised by 15 cm from the ground level to avoid water-logging, if occurred. The each plot size was 2.70 m X 1.20 m, the row to row and plant to plant spacing were kept 45 cm and 30 cm, respectively. All agronomical practices were followed as per package of practices.

Nineteen quantitative characters viz., plant height (cm), germination (%), days taken for first flowering, days taken for 50% flowering, number of reproductive branches/plant, pod breath (cm), pod length (cm), pod width (cm), number of pods/plant, number of pods/cluster, number of clusters/plant, number of branches/plant at maturity, number of seed/pod, pod yield/plant(g), pod yield/plot(kg), 100 seed weight (g), seed yield/plant (g), days to maturity, pod yield (q/ha) and flower colour were taken into consideration for estimating genetic diversity. The mean values of five plants were taken for the analysis of genetic divergence followed by Mahalanobis[5].

The intra and inter-cluster distances were calculated by following the formula described by Singh and Chaudhary[9].

RESULTS

Thirty cluster bean genotypes were evaluated for 19 characters and the data obtained was subjected to D^2 statistics to assess the genetic divergence. Only 5 clusters were constructed using Toucher's method.

The relative contribution of different characters for genetic divergence (D^2) is given

in Table- 1. Pod yield (q/ha) (20.66%) contributed maximum to the genetic diversity among the genotypes followed by 100-seed weight (g) (20.49%), pod breadth (cm) (16.07%), number of pods/cluster (12.33%), number of pods per plant (8.42%), number of seeds/pod (6.04%) and number of clusters/plant (5.87). While there was lowest contribution found from plant height (cm) (2.47%), pod yield/plant (g) (1.96%), number of reproductive branches/plant (1.87%) and pod yield/plot (kg) (2.37%).

By adopting Toucher's method, the 30 genotypes were grouped into five clusters by treating estimated D^2 values as the square of the generalized distance. The distribution pattern of entries into various clusters is given in the Table- 2. Cluster I was the largest cluster having 8 genotypes followed by cluster II and cluster IV with six genotype each. Intra and inter-cluster average D^2 values are presented in Table- 3. The computed D^2 values for 30 genotypes had wide range showing high genetic divergence among the genotypes. Among the 5 clusters, cluster I with 8 genotypes followed by cluster II and cluster IV

with 6 genotypes each showed maximum intra-cluster diversity. The maximum intra-cluster distance was found in cluster V (D^2=6.625) closely followed by cluster II (3.813) and cluster III (3.526). Based on distance between clusters (inter-cluster), the maximum divergence was observed between cluster I and cluster II (D^2=8.235), followed by cluster II and cluster IV (D^2=6.552) and the least inter-cluster distance was found between cluster IV and cluster V (D^2=3.773).

Greatest amount of heterosis is generally accepted in cross combinations involving the parents belonging to most divergent clusters. Grouping of accessions based on morphological, phenomenal and reproductive characters is not always associated with their geographical origin.

These results are accordance with Ansari *et al.*[1] stated that the diversity range was found to be wide and the presence of six broad clusters suggests the existence of many genetic lineages that can constitute useful starting points for the use of germplasm diversity in the selection and improvement of the cluster bean crop.

Table 1: Percent contribution of different characters of the total divergence in 30 genotypes of cluster bean (2013-2014)

S. No.	Characters	Number of first rank	Rank totals	Contribution to total divergence (%)
1.	Plant height (cm)	29	3260	2.47
2.	Germination (%)	6	5961	0.51
3.	Days taken for first flowering	5	6214	0.43
4.	Days taken for 50% flowering	2	5681	0.17
5.	Number of reproductive	22	3432	1.87
6.	branches/plant	189	6047	16.07
7.	Pod breadth (cm)	5	5331	0.43
8.	Pod length (cm)	1	7157	0.09
9.	Pod width (cm)	99	4489	8.42
10.	Number of pods/plant	145	3200	12.33
11.	Number of pods /cluster	69	2265	5.87
12.	Number of clusters /plant	9	3772	0.77
13.	Number of branches /plant at	71	4673	6.04
14.	maturity	23	2417	1.96
15.	Number of seed /pod	17	3864	1.45
16.	Pod yield /plant (g)	241	3861	20.49
17.	Pod yield /plot (kg)	0.00	3718	0.00
18.	100- Seed weight (g)	0.00	3193	0.00
19.	Seed yield /plant (g)	243	4115	20.66
	Days to maturity			
	Pod yield (q/ha)			
	Total	**1176.00**		**100.00**

Table 2: Grouping of cluster bean genotypes based on D^2 values (2013-2014)

S. No.	Cluster number	Number of individual/genotypes	Name of the genotypes
1.	I	1, 2, 3, 4, 5, 8, 9, 11	IC-258087, IC-258092, IC-28272, IC-311440, IC-311441, IC-369789, IC-369868, IC-370490.
2.	II	6, 7, 12, 13, 14, 25	IC-325757, IC-329038, IC-373427, IC-373480, IC-402293, IC-421820.
3.	III	22, 23, 24, 26, 27	IC-421809, IC-421812, IC-421815, IC-421828, IC-421834.
4.	IV	10, 15, 16, 17, 18, 19	
5.	V	20, 21, 28, 29, 30	IC-370478, IC-415137, IC-415142, IC-415157, IC-415159, IC-421242. IC-421798, IC-421806, IC-421838, IC-421855, HG-365.

Table 3: Average intra and inter cluster D^2 and D values in 30 genotypes of cluster bean (2013-2014)

S. No.	Cluster distances	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
1.	Cluster I	3.400	8.235	5.327	6.552	6 .625
2.	Cluster II		3.813	4.218	5.263	6.428
3.	Cluster III			3.526	4.525	5.348
4.	Cluster IV				3.464	3.773
5.	Cluster V					5.243

DISCUSSION

Based on D^2 values 30 cluster bean genotypes were grouped into 5 clusters, 8 genotypes in cluster I and six genotypes each in clusters II and IV and five genotypes each in clusters III and V. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive human selection for diverse adaptive complexes. The intra cluster distance varies from 3.400 in clusters I and to the maximum distance in cluster II (8.235). This reveals that presence of divergence in cluster I. The inter cluster D^2 values also ranged from 3.464 between cluster IV and cluster III, 4.218 between cluster III and V and of maximum distance of 6.625 between cluster I and cluster IV. Selection of genotypes is recommended from the clusters showing higher inter cluster distance (Cluster III and V) also with higher pod yield as parents in recombination breeding programmes for obtaining desirable segregants.

Among 19 characters studied, the most important character contributing to maximum divergence was pod yield per hectare followed by other main responsible characters like 100-seed weight (g), pod breadth (cm), number of pods/cluster, number of pods per plant, number of seeds/pod and number of clusters/plant[5,8,7].

These results were supported by Singh *et al.*[8] and Henry *et al.*[4]; pods per cluster and pods per plant contribution are in accordance with Gipson and Balakrishnan[2], contribution

of plant height in accordance with Hanchinamani[3].

CONCLUSION

Basis of above finding, it can be concluded that the most important characters contributing to maximum genetic divergence was pod yield/hectare followed by other main responsible characters like 100-seed weight (g), pod breadth (cm), number of pods/cluster, number of pods/plant, number of seeds/pod and number of clusters/plant (5.87). Cluster bean germplasm is genetically diverse and possesses potential variation for morphological and yield attributing characters and hence could be extensively evaluated for greater exploitation for use in breeding programs

REFERENCES

1. Ansari, A., Sikarwar, P.S., Lade, S., Yadav, H.K. and Ranade, S.A., Genetic Diversity Clusters in Germplasm of Cluster Bean (*Cyamopsis tetragonoloba* L., Taub), an Important Food and an Industrial Legume Crop. *J. Agr. Sci. Tech.,* **18:** 1393-1406 (2016).
2. Gipson, A. and Balakrishnan, R., Genetic diversity in cluster bean. *Indian J. Hort.,* **49 (1):** 70-74 (1992).
3. Hanchinamani, N.C., Studies on genetic variability and genetic divergence in cluster bean *Cyamopsis tetragonoloba* (L.) Taub.). M. Sc. (Hort.) Thesis, Univ. Agric. Sci., Dharwad, 108 (2004).
4. Henry, A.; Mathur, B. K. and Daulay, H. S., Genetic divergence in cluster bean. *Forage Res.*, **10 (2):** 89-94 (1984).
5. Mahalanobis, P. C., On the generalized distance in statistics. *Proc. Natl. Acad. Sci. U.S.A.,* **2**: 49-55 (1936).
6. Mohammadi, S.A. and Prasanna, B.M., Analysis of genetic diversity in crop plants. Salient statistical tools and considerations. *Crop Sci.,* **43:** 1235-1248 (2003).
7. National Biological Information Infrastructure., Introduction to Genetic Diversity. *U.S. Geological Survey*, 11-16 (2012).
8. Singh, N. P.; Choudhary, A. K. and Chaudhary, S. P. S., Genetic divergence in Cluster bean (*Cyamopsis tetragonoloba*). *Indian J. Agric. Sci.,* **73 (6):** 356-357 (2003).
9. Singh, R.K. and Chaudhary, B.D., Biometrical Methods in Quantitative Genetics Analysis. *Kalyani Publishers, Ludhiana*, 288. (1977).
10. Yadav, H., Singh, S. and Haque, E., An Analysis of Performance of Guar Crop in India. *Ministry of Agriculture, Government of India*, 1-98 (2014).