

Genetic Divergence Studies in Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] Genotypes

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Abstract

Forty two clusterbean genotypes collected across the country were assessed for genetic divergence using Mahalanobis D² technique. The genetic material exhibited wide range of genetic diversity for all the characters investigated and grouped into 15 different clusters. The maximum intra cluster distance was observed in cluster XIV indicated that genotypes are having diverse genetic architecture. The maximum inter-cluster distance was recorded between cluster VI and cluster XV, indicating the presence of wide range of variability among the genotypes of the cluster. The percent contribution towards genetic diversity was highest from 100 seed weight (44.48%) followed by seed yield per plant (26.25%). On the basis of inter-cluster distances and per se performance observed in the present study a hybridization programme involving genotypes for a specific character may be selected using cluster mean values.

Keywords : Clusterbean, Mahalanobis D², Cluster Analysis.

1. Introduction

Clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.) is a versatile and multipurpose legume crop of arid and semiarid regions cultivated for feed, fodder and manure. Clusterbean enhances soil productiveness by fixing atmospheric nitrogen for its own necessities and also for the succeeding crop. Although clusterbean is a minor crop but due to its better and finer guar gum qualities it is considered as an important cash crop for industrial gum production [1, 2] and for several pharmaceutical and nutraceutical products. India and Pakistan are the chief exporters of guar gum and split to different European and Gulf countries. Despite huge demand for the crop, only limited breeding work has been done and very little attention has been taken for its genetic improvement to enhance the productivity level.

Genetic diversity is an important factor and also a pre-requisite in any hybridization programme. Inclusion of diverse parents in hybridization programme serves the purpose of producing desirable recombinants. Multivariate analysis by means of Mahalanobis D² statistic is a powerful tool in quantifying the degree of divergence at genotypic level. Therefore, an attempt has been made in the present investigation to estimate genetic divergence among a set of 42 genotypes including for 12 biometrical traits.

2. Materials and Methods

Genetic evaluation of guar accessions on the basis of agromorphological traits was performed in specimen plots of Department of Plant Breeding and Genetics, Agriculture

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College and Research Institute, Madurai. Genotypes were obtained from various lead centers of clusterbean research which represents eco-geographical diverse areas of India. Experiment was conducted as per RBD with plot size of 3×3 m² during November, 2012. Three meter length row per entry with spacing of 45×15 cm followed. All agronomical practices were followed as per package of practices.

Twelve quantitative characters *viz.*, plant height, primary branches per plant, secondary branches per plant, clusters per plant, pods per cluster, pod length, seeds per pod, pods per plant, 100- seed weight, seed yield per plant, days to 50% flowering and days to maturity were taken into consideration for estimating genetic diversity. The mean values of five plants were taken for the analysis of genetic divergence following Mahalanobis [3]. The genotypes were grouped into different clusters following Tocher's method as described by Rao [4].

3. Results and Discussion

Genetic diversity is the basic requirement for successful breeding programme. Collection and evaluation of germplasm lines and genotypes of any crop is a pre-requisite for any programme and provides a greater scope for exploiting genetic diversity. The multivariate analysis (D^2) is a powerful tool to measure the genetic divergence within a set of genotypes [5]. The analysis of variance revealed significant differences among the genotypes for all the characters studied (Table 1). The genotypes were grouped into 15 clusters indicating large amount of genetic diversity among the genotypes (Table 2).

Cluster I was the largest (10 genotypes) followed by clusters IV (five genotypes), cluster XII, XIII each had three genotypes and rest of the clusters had two genotypes except cluster XV had only one distinct genotype. Grouping

Table 2. Grouping of clusterbean genotypes based on D^2 Values

Cluster	Number of genotypes	Genotypes
I	10	RGC1002, HFG119, HG884, HG16, GAU512, HG365, RGC1066, HG75, HG2-1, RGC1038
II	2	CAZG10-2, HG182
III	2	FS277, RGC197
IV	5	HG2-30, HG2-4, RGC471, RGC1003, HG832
V	2	RGM2, HG870
VI	2	RGC1017, HG563
VII	2	MRG1786, RGC1033
VII	2	HG2-20, RGC1055
IX	2	RGM1, R LOCAL
X	2	RGC936, RGC986
XI	2	HG3-52, MRSG6
XII	3	T local, Amrit 11, M local
XIII	3	SRG1058, RGC1031, HG3-20
XIV	2	HG258, GAU 513
XV	1	Pusa Navbahar

of accessions by multivariate method in the present study is of practical value to the breeders. Representative accessions may be chosen from particular cluster for genetic base enhancement. In this clustering pattern cluster XII had three genotypes *viz.*, T local, M local and Amrit 11, these genotypes mostly used as vegetable purpose on the other hand Cluster XV had a unique high yielding vegetable type variety Pusa Navbahar. This pattern of clustering mostly demarcated the gum yielding genotypes from vegetable genotypes. However majority of the genotypes from different origins are clustered into same cluster, while some other members fell into different cluster. Grouping of genotypes based on agro-morphological characters is

Table 1. Mean squares for analysis of variance among various characters in clusterbean genotypes

	d.f	PH	B/P	2B/P	C/P	P/C	PL	S/P	P/P	DDF	DTM	100 SW	SPY
Replication	1.00	992.75	4.62	4.81	195.35	3.01	0.04	0.03	699.81	0.30	24.07	0.02	10.52
Genotypes	41.00	185.61**	10.84**	2.37*	64.52*	4.71**	5.72**	0.53**	1010.86*	17.91**	68.80**	0.25**	31.39**
Error	41.00	79.36	2.01	1.38	34.00	1.62	0.20	0.24	547.18	0.44	5.99	0.05	15.01

* Significant at 5% level of probability ** Significance at 1% level of probability

Traits - **PH** (Plant height), **B/P** (Primary branches per plant), **2B/P** (Secondary branches per plant), **C/P** (Clusters per plant), **P/C** (Pods per cluster), **PL** (Pod length), **S/P** (Seeds per pod), **P/P** (Pods per plant) **DDF** (Days to fifty percent flowering), **DTM** (Days to maturity), **100 SW** (100 seed weight), **SPY** (Seed yield per plant)

not always associated with their geographical origin. Our results are in accordance with the findings of Brahmi et al. [6], Pervaiz et al. [7], Pathak et al. [2], Rai et al. [8], Sultan et al. [9], Grish et al. [10] and Kumar et al. [11] whose results given conclusion that there is no or less correlation between geographic location and genetic diversity in guar.

Average intra- and inter-cluster distances (D^2 values) among 15 clusters are given in Table 3. The value of intra-cluster distance for cluster XV was zero as it had only one genotype in the cluster. In this cluster prominent ruling vegetable purpose variety Pusa Navbahar was a lone member. While considering the other clusters, the intra-cluster distance varied from 2.75 to 14.36 and did not transgress the limits of any of the inter-cluster distances. Cluster II had lowest intra-cluster distance of 2.75 and cluster XIV accounted for highest intra-cluster distance of 14.36.

The highest inter cluster distance was found between cluster VI and cluster XV (27.66) followed by cluster XI and XV (26.58), cluster VII and XV (25.96) and cluster V and XV (25.77). The inter cluster distance of all other clusters with cluster XV showed higher values when compared to the inter cluster distances between other clusters. The

least inter cluster distance was found between cluster V and X (4.46).

The maximum distances between clusters are the right choice of diverse parents for hybridization programme (10, 14). The contribution of various traits to the genetic diversity worked out from their rank, maximum contribution (44.48%) was from 100 seed weight followed by seed yield per plant (26.25%) and least contribution of 0% from plant height, secondary branches per plant and pods per plant (Table 4). The mean value for all the characters are presented vide Table 5. Cluster III had highest mean value for plant height (91.5 cm) and lowest value was from (62.34 cm) cluster VII. The highest mean value for number of primary branches per plant was recorded by cluster VI (7.30) and the lowest was recorded by XV and III (0). Cluster XIV had the maximum mean value for secondary branches per plant (3.68) and the minimum was recorded by cluster XV and III (0). The highest mean value was recorded for the character of clusters per plant from cluster XIV and the lowest value of 11.65 recorded from cluster III. Maximum number of pods per cluster was observed from cluster III and minimum of 3.6 from cluster XV. The highest mean

Table 3. Average intra (in bold) and inter cluster D^2 distances

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	7	6.91	8.29	11.50	7.16	6.51	12.71	6.34	10.13	7.13	6.27	17.28	11.04	16.25	25.72
II		2.75	6.72	11.13	4.13	7.90	11.21	3.77	7.94	5.58	6.74	15.88	8.80	16.12	24.77
III			2.87	12.14	8.09	8.25	13.16	7.23	10.26	8.11	7.13	16.63	11.19	16.64	25.12
IV				12.04	11.02	12.83	9.92	11.44	9.16	9.75	11.32	15.54	11.50	12.85	21.58
V					3.43	8.71	9.94	4.52	7.75	4.46	7.00	17.10	7.75	15.43	25.77
VI						3.85	15.09	6.73	12.01	8.65	5.09	18.89	13.00	18.07	27.66
VII							3.99	11.81	5.61	8.57	12.46	16.13	8.53	9.68	21.54
VII								4.06	8.56	5.20	5.90	17.04	9.46	16.17	25.96
IX									4.38	6.37	9.69	15.10	8.04	10.97	21.72
X										4.75	6.67	16.13	7.58	13.45	24.28
XI											6.59	18.10	10.89	15.94	26.58
XII												12.17	16.71	18.08	13.21
XIII													10.06	14.25	24.00
XIV														14.36	21.50
XV															0.00

value of 12.88 cm for pod length was recorded in cluster XV and lowest of 5.53 cm from cluster XI. Cluster XII had maximum number of seeds per pod, while cluster VI, XI each recorded minimum number of seed. Cluster XIV recorded highest number of pods per plant with the mean value of 125.15 and cluster XV showed lowest of 29.7. Maximum days to attain fifty percent flowering was recorded from cluster XV (33.5 days) and lowest from cluster V and VI each with the value of 23.5 days. Cluster XIII took maximum days for maturity (104.5 days) and cluster VI was recorded with minimum days (89.25 days). Maximum 100 seed weight of 4.79g was recorded in the cluster of XV and cluster XIII was recorded minimum of 3.54g. Cluster XIV had highest mean values of seed yield per plant (24.87g) and lowest was observed from cluster XV (8.3g). Cluster XIV had maximum cluster mean values for number of characters viz., number of secondary branches per plant, number of clusters per plant, number of pods per plant and seed yield per plant showing the its superiority over other clusters. Greater manifestation of heterosis is expected in cross combinations involving the parents from the most divergent clusters. Similar results were obtained by Singh et al. [12], Pathak et al. [13], Girish et al. [10] and Rai et al. [14]. Cluster bean which is a self-pollinated crop though

Table 4. Per cent contribution of the different characters to the total divergence in cluster bean genotypes

Characters	No. of First Rank	% Contribution
Plant height	0.00	0.00
Primary branches per plant	35.00	4.07
Secondary branches per plant	0.00	0.00
Clusters per plant	1.00	0.12
Pods per cluster	0.00	0.00
Pod length	71.00	8.25
Seeds per Pod	4.00	0.46
Pods per plant	5.00	0.58
Days to 50% flowering	72.00	8.36
Days to maturity	64.00	7.43
100-Seed weight	383.00	44.48
Seed yield per plant	226.00	26.25
Total	861.00	100.00

there is a potential for obtaining hybrid vigor by implementing hybridization programme between the genotypes of distinct group to obtain superior genotypes from the segregating generation.

Table 5. Cluster mean values for 12 biometrical characters in clusterbean

Cluster	PH	B/P	2B/P	C/P	P/C	PL	S/P	P/P	DFF	DTM	100SW	SPY
I	68.41	6.08	1.07	24.60	7.37	6.17	8.06	85.91	24.05	94.15	3.90	16.40
II	71.86	4.60	0.40	23.20	7.18	6.32	8.10	73.40	24.00	103.00	4.07	14.85
III	91.50	0.00	0.00	11.65	9.55	5.65	8.05	65.75	24.00	101.00	4.09	13.80
IV	66.32	4.90	0.72	21.84	7.46	6.55	8.16	77.20	27.70	96.30	4.03	14.92
V	66.85	5.00	0.15	21.30	7.05	5.76	8.20	75.90	23.50	103.25	3.59	14.74
VI	64.80	7.30	1.85	24.80	7.80	5.92	7.90	89.95	23.50	89.25	4.08	14.40
VII	62.34	4.40	0.60	19.13	7.95	5.63	8.10	71.05	28.50	104.00	3.59	13.41
VII	67.34	6.40	2.20	25.50	7.05	6.16	8.05	82.20	24.00	100.25	3.93	17.89
IX	73.29	5.99	1.71	26.11	7.51	6.04	7.98	78.25	27.75	102.75	3.80	14.43
X	69.40	6.15	1.28	22.45	8.10	6.21	8.60	77.15	25.00	100.25	3.66	16.92
XI	70.80	5.95	1.10	22.15	8.65	5.53	7.90	84.25	24.25	93.25	3.87	15.15
XII	70.71	1.40	0.00	13.53	4.73	10.69	9.00	36.23	28.50	99.00	4.66	9.74
XIII	64.53	3.97	0.47	17.17	9.10	6.01	8.27	68.20	25.33	104.50	3.54	13.65
XIV	76.10	6.78	3.68	30.68	8.98	5.99	8.23	125.15	31.25	100.00	3.87	24.87
XV	80.30	0.00	0.00	15.10	3.60	12.88	8.90	29.70	33.50	96.00	4.79	8.30

Traits - **PH** (Plant height), **B/P** (Primary branches per plant), **2B/P** (Secondary branches per plant), **C/P** (Clusters per plant), **P/C** (Pods per cluster), **PL** (Pod length), **S/P** (Seeds per pod), **P/P** (Pods per plant) **DFF** (Days to fifty percent flowering), **DTM** (Days to maturity), **100 SW** (100 seed weight), **SPY** (Seed yield per plant)

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