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

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Abstract
Thirty-five genotypes of cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.] collected from various parts of Maharashtra and some other states of India and which were assessed for genetic divergence using Mahalanobis D^2 technique. The genetic material exhibited wide range of genetic divergence for all characters studied. All the genotypes were grouped into eight clusters. The cluster IV constituted maximum number of genotypes *i.e.* 11 followed by cluster II and III included 7 genotypes each, cluster I included 6 genotypes and rest of the clusters V, VI, VII and VIII constituted single genotype each that indicated wide divergence among the genotypes. The highest inter cluster distance was observed between cluster I and IV (D^2= 29.86, D= 5.46) while lowest between cluster V and VI (D^2= 10.35, D= 3.22). Highest intra cluster distance was found within cluster IV (D^2= 12.18, D= 3.49) while being a solitary in nature no intra cluster distance observed within clusters V, VI, VII, and VIII (D^2= 0.00). The maximum per cent contribution towards total divergence was recorded by number of primary branches per plant at 90 DAS (31.23%) while least contribution was represented by days to first harvest (0.34%). The clustering pattern revealed that genetic diversity was not parallel to the geographic distribution of the genotypes. A well-planned breeding programme in general has been suggested on the basis of inter cluster.

Keywords: Cluster bean, Genetic divergence, Mahalanobis D^2 technique

Introduction
Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.] is a versatile, multipurpose and underexploited leguminous vegetable having chromosome number 2n=2x=14. It is popularly known as khutti, guar, chavlikayi, guari etc. in different parts of country. It is a self-pollinated crop belonging to the family Leguminaceae or Fabaceae (Reddy *et al*., 2019) [9]. The long deep taproot system permits the plant to grasp all the water in the soil making it an ultimate drought resistant crop. It is mainly cultivated as a rainfed crop in arid and semiarid regions (Kumar and Ram, 2015). Cluster bean seed contains about 30-33% gum in the endosperm (Choyal *et al*., 2018 a) [1].

Tender pods of cluster bean are rich in nutrient, which contains 16 Kcal of energy, 81 g of moisture, 10.8 g of carbohydrates, 3.2 g of protein, 1.4 g of fat, 65.3 IU of Vitamin A, 49 mg of Vitamin C, 57 mg of calcium and 4.5 mg of iron per 100 g of edible portion (Kumar and Singh, 2002) [2].

Cluster bean is mainly cultivated for its tender fruits or green pods, which are used as vegetable. Cluster bean is a minor crop, but it is considered as valuable cash crop due to its superior and finer guar gum properties. Its mucilaginous seed flour is used to make guar gum (galactomannan), which is useful in paper, cosmetic, textile and oil industries all over the world as well as good absorbent for explosives (Smith, 1976). Guar gum is a cost-effective natural thickener, binder, disintegrator and stabilizer used in industry. It is leguminous plant that provides nitrogen to the soil and increases soil fertility. It is also grown as fodder crop because its residues (stubble and header rubbish) are high protein source of animal feed and useful for making high quality hay (Kapoor, 2014).

India is the major guar producer, contributing 80% of the world's production. India's total area under cluster bean is 4.25 million hectares and production is 2.41 million tonnes along with 0.57 tonnes per hectare productivity (Reddy *et al*., 2017) [9].

In any breeding programme, genetic diversity is an important aspect and a requirement. The available genetic divergence is crucial for any crop development initiative. Incorporating a variety of parents into hybridization programmes aids in the production of desired recombinants. Multivariate analysis using the Mahalanobis D^2 statistic is a strong technique

for determining the degree of genotypic divergence. The D^2 analysis-based grouping of genotypes will aid in the selection of appropriate parental lines for heterosis breeding (Rao, 1952) [8]. In general, diverse germplasm is predicted to produce high hybrid vigour, hence there is a need to investigate existing genotypes for identification of the parent for a hybridization programme. Nothing can be achieved with minimal variability; thus, the breeder must establish germplasms or genotypes for hybridization, mutation and polyploidy breeding to increase variability. Therefore, an attempt in the present investigation was made to assess the degree of genetic diversity in set of 35 genotypes collected from different geographical regions.

Material and Methods

The experiment was carried out during the summer season in 2021 at the Instructional-cum-Research Farm of Horticulture Section, Rajarshee Chhatrapati Shahu Maharaj College of Agriculture, Kolhapur situated at 16° 41' North latitude and 74° 16' East longitude. The altitude of Kolhapur is 548 meter above mean sea level. The experimental material (35 genotypes) of cluster bean was collected from different sources given below in (Table 1).

Thirty-five genotypes of cluster bean were grown in a Randomized Block Design with two replications. Sowing of seeds was done on 1st December, 2020 during the year of 2020-2021 in plots having 3 x 1.8 m size at the spacing of 30 x 15 cm. Five plants were randomly selected from each plot to record observations on various characters *viz.*, days to first flowering, days to 50% flowering, days to first harvest, plant height at 90 DAS (cm), No. of primary branches per plant at 90 DAS, No. of clusters per plant, No. of pods per cluster, pod length (cm), pod width (mm), pod weight (g), pod yield per plant (g), pod yield per hectare (q), No. of seeds per pod, 100 seed weight (g) and seed yield per plant (g).

Results and Discussion

Genetic divergence in 35 genotypes of cluster bean was measured by following Mahalanobis (1936) D^2 analysis. Such analysis eventually helps to choose desirable parents for recombination breeding and thus results in development of superior varieties. Quantification of genetic diversity existing within and between groups of germplasm is vital and particularly useful in proper choice of parents for understanding higher heterosis and obtaining useful recombinants. D^2 analysis is a unique method for distributing populations considering a set of parameters together rather than interring from indices based upon morphological similarities, eco-geographical diversity and phylogenetic relationships.

The D^2 values corresponding to the pair of comparison among the genotypes studied was ranged from 10.35 to 29.86, revealed a very interesting trend of genetic diversity, representing ample scope for selection of parent based on many characters at a time for further crop improvement.

The cluster formation was arrived (Tocher's method), as described by Rao (1952) [8]. Based on D^2 values 8 clusters were formed from 35 genotypes. Out of these 8 clusters, cluster IV was the largest having 11 genotypes, which was followed by cluster II and III each having 7 genotypes, cluster I having 6 genotypes and remaining clusters V, VI, VII and VIII having single genotypes each indicating wide divergence among the genotypes (Table 2).

The maximum inter cluster divergence was observed between cluster I and cluster IV (D^2= 29.86, D= 5.46) followed by cluster I and cluster VIII (D^2= 29.69, D= 5.45), cluster I and cluster III (D^2= 29.53, D= 5.43), cluster I and cluster VII (D^2= 27.61, D= 5.25), cluster I and cluster VI (D^2= 27.57, D= 5.25), cluster I and cluster II (D^2= 25.89, D= 5.09), cluster VII and cluster VIII (D^2= 24.23, D= 4.92) and cluster III and cluster VIII (D^2= 24.19, D= 4.92). Whereas, lowest between cluster V and cluster VI (D^2= 10.35, D= 3.22). Highest intra cluster distance was found within cluster IV (D^2= 12.18, D= 3.49) followed by cluster III (D^2= 11.58, D= 3.40), cluster II (D^2= 9.98, D= 3.16) and cluster I (D^2= 7.21, D= 2.69). While, being solitary in nature no intra cluster distance observed within cluster V, VI, VII and VIII (D^2= 0.00) (Table 3).

The maximum *per cent* contribution towards total divergence was recorded by number of primary branches per plant at 90 DAS (31.23%) while least contribution was represented by days to first harvest (0.34%) (Table 4). Cluster means for different characters are presented in below Table 4. According to the cluster mean performance, cluster VIII for first flowering and cluster V for 50% flowering were earliest while cluster III was late for both first flowering and 50% flowering; cluster VI was earlier for first harvest while cluster VII was late; cluster VIII had tallest plant height at 90 DAS while cluster VI had dwarfest; highest number of primary branches per plant was recorded by cluster IV while least by cluster I; cluster IV showed highest number of clusters per plant while cluster V showed lowest clusters per plant; clusters VIII and I recorded maximum and minimum number of pods per cluster, respectively. Cluster I recorded maximum pod length, pod width and pod weight while minimum pod length, pod width and pod weight were observed in clusters IV, III and VII, respectively. Maximum and minimum pod yield per plant and per hectare was recorded by cluster I and III, respectively. Cluster II recorded highest and cluster III recorded lowest number of seeds per pod; highest 100 seed weight was found in cluster I while lowest in cluster III. Cluster VIII produced highest seed yield per plant while cluster VII produced lowest.

Table 1: Different genotypes of cluster bean and their source

Sr. No.	Genotype No.	Source	Sr. No.	Genotype No.	Source
1	ACKCB-1	Rajasthan-1	19	ACKCB-19	Junnar, Pune
2	ACKCB-2	Rajasthan-2	20	ACKCB-20	Indapur, Pune
3	ACKCB-3	Rajasthan-3	21	ACKCB-21	Mangalwedha
4	ACKCB-4	Rajasthan-4	22	ACKCB-22	Khatav, Satara
5	ACKCB-5	Andhra Pradesh	23	ACKCB-23	Parbhani
6	ACKCB-6	Mul, Chandrapur	24	ACKCB-24	Tembhurni, Solapur
7	ACKCB-7	Naghbhir, Chandrapur	25	ACKCB-25	Shrirampur, A. Nagar
8	ACKCB-8	Shirol, Kolhapur	26	ACKCB-26	Shirur, Pune
9	ACKCB-9	Hatkanangale, Kolhapur	27	ACKCB-27	Karveer, Kolhapur

10	ACKCB-10	Bhokar, Nanded	28	ACKCB-28	Pandharpur, Solapur
11	ACKCB-11	Rahata, Ahmednagar	29	ACKCB-29	Bihar
12	ACKCB-12	Latur	30	ACKCB-30	Daund, Pune
13	ACKCB-13	Karad, Satara	31	ACKCB-31	Purandar, Pune
14	ACKCB-14	Satara	32	ACKCB-32	Hinganghat, Wardha
15	ACKCB-15	Morgaon, Gondia	33	ACKCB-33	Madha, Solapur
16	ACKCB-16	Phaltan, Satara	34	ACKCB-34	Mohol, Solapur
17	ACKCB-17	Sangola, Solapur	35	Phule Guar (C)	MPKV, Rahuri
18	ACKCB-18	Niphad, Nashik			

Table 2: Distribution of 35 cluster bean genotypes into different clusters

Cluster Number	Total number of genotypes included	Genotype number
I	6	ACKCB-6 (Mul, Chandrapur), ACKCB-7 (Naghbhir, Chandrapur), ACKCB-5 (Andhra Pradesh), ACKCB-32 (Hinganghat, Wardha), ACKCB-15 (Morgaon, Gondia), ACKCB-29 (Bihar)
II	7	ACKCB-11 (Rahata, Ahmednagar), Phule Guar (Rahuri), ACKCB-25 (Shrirampur, Ahmednagar), ACKCB-13 (Karad, Satara), ACKCB-22 (Khatav, Satara), ACKCB-14 (Satara), ACKCB-16 (Phaltan, Satara)
III	7	ACKCB-31 (Purandar, Pune), ACKCB-30 (Daund, Pune), ACKCB-24 (Tembhurni, Solapur) ACKCB-34 (Mohol, Solapur), ACKCB-33 (Madha, Solapur), ACKCB-21 (Mangalwedha, Solapur), ACKCB-17 (Sangola, Solapur)
IV	11	ACKCB-8 (Shirol, Kolhapur), ACKCB-19 (Junnar, Pune), ACKCB-4 (Rajasthan), ACKCB-1 (Rajasthan), ACKCB-26 (Shirur, Pune), ACKCB-27 (Karveer Kolhapur), ACKCB-3 (Rajasthan), ACKCB-9 (Hatkanangale, Kolhapur), ACKCB-28 (Pandharpur, Solapur), ACKCB-20 (Indapur, Pune), ACKCB-2 (Rajasthan)
V	1	ACKCB-18 (Niphad, Nashik)
VI	1	ACKCB-10 (Bhokar, Nanded)
VII	1	ACKCB-12 (Latur)
VIII	1	ACKCB-23 (Parbhani)

Table 3: Average inter and intra cluster values of eight clusters of 35 cluster bean genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	7.21 (2.69)	25.89 (5.09)	29.53 (5.43)	29.86 (5.46)	23.86 (4.88)	27.57 (5.25)	27.61 (5.25)	29.69 (5.45)
II		9.98 (3.16)	18.35 (4.28)	21.57 (4.64)	13.27 (3.64)	17.00 (4.12)	17.72 (4.21)	13.62 (3.69)
III			11.58 (3.40)	21.22 (4.61)	15.43 (3.93)	20.29 (4.50)	14.57 (3.82)	24.19 (4.92)
IV				12.18 (3.49)	18.84 (4.34)	18.74 (4.33)	23.31 (4.83)	20.73 (4.55)
V					0.00	10.35 (3.22)	14.61 (3.82)	15.37 (3.92)
VI						0.00	18.87 (4.34)	13.33 (3.65)
VII							0.00	24.23 (4.92)
VIII								0.00

Table 4: *Per cent* contribution of 15 characters towards divergence in cluster bean

Sr. No.	Source	Times ranked 1st	Contribution %
1	Days to first flowering	4	0.67%
2	Days to 50% flowering	5	0.84%
3	Days to first harvest	2	0.34%
4	Plant height at 90 DAS (cm)	41	6.89%
5	No. of primary branches per plant at 90 DAS	187	31.23%
6	No. of clusters per plant	4	0.67%
7	No. of pods per cluster	5	0.84%
8	Pod length (cm)	26	4.37%
9	Pod width (mm)	4	0.67%
10	Pod weight (g)	127	21.21%
11	Pod yield per plant (g)	59	9.93%
12	Pod yield per hectare (q)	50	8.40%
13	No. of seeds per pod	4	0.67%
14	100 Seed weight (g)	24	4.03%
15	Seed yield per plant (g)	55	9.24%

Table 5: Cluster mean of various characters in different cluster bean genotypes

Character Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
I	35.42	42.75	52.58	77.18	1.00	16.38	3.93	8.50	6.80	1.92	104.88	100.51	5.97	4.34	7.89
II	35.71	42.29	55.00	93.59	1.43	15.23	8.61	6.07	5.40	0.82	102.94	94.32	7.19	3.61	14.07
III	39.36	45.86	56.00	64.37	1.84	12.21	5.17	5.23	4.77	0.67	71.80	61.19	5.71	3.23	8.28
IV	35.82	42.68	51.14	70.65	4.78	19.16	6.26	5.02	5.13	0.67	96.42	80.62	6.25	3.45	11.87
V	35.00	41.50	53.00	63.78	1.40	9.40	7.90	5.30	5.40	0.85	95.90	81.46	6.10	3.60	10.60
VI	36.00	44.00	49.50	63.15	1.30	18.20	5.70	5.26	4.65	0.77	98.80	73.60	6.60	3.40	14.90
VII	38.50	43.00	58.00	69.41	1.30	10.70	5.10	6.96	5.78	0.65	96.80	72.89	5.80	3.45	8.10
VIII	34.00	44.00	53.50	98.50	2.00	16.90	8.90	5.04	5.34	0.80	99.90	78.27	6.60	3.60	17.10

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