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

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ABSTRACT

Thirty cluster bean genotypes collected from NBPGR Regional Station, Jodhpur was assessed to estimate the genetic divergence using Mahalanobis D^2 analysis. The genotypes exhibited wide variability for all the characters studied. Thirty genotypes were grouped into V clusters. Cluster I consisted the maximum number of genotypes (12) followed by cluster II with 10 and cluster IV with 6 genotypes. Cluster III and V had only one genotype each. Intra cluster distance was maximum in cluster I with 12 genotypes indicating the high intra cluster diversity and inter cluster distance was highest between cluster V and cluster III (D^2=174782.9) followed by cluster II and V (D^2=115239.7), cluster III and IV (D^2=78577.82), cluster I and V (D^2 = 69202.2), cluster II and IV (D^2 =41433.2). Mean number of branches, number of pod clusters/plant, number of pods/plant and pod yield/plant was highest for cluster V. Pod length, pod girth and pod weight were maximum in cluster III. Cluster IV and I was earliest to attain 50% flowering, days to first fruit set. Cluster III and II took minimum days for first harvest. Traits that contributed to divergence were pod yield/plant, days to 50% flowering and days to first fruit set. Hence while designing a crop improvement programme, parents for hybridization may be selected based on the inter cluster distance, mean performance of different traits and contribution of traits to divergence.

Key words: Cluster bean, Genetic divergence, Variability.

INTRODUCTION

Cluster bean is a hardy drought tolerant crop suitable for tropical and subtropical regions. It comes up well even in those regions having marginal and submarginal soils with low rainfall. In India it is cultivated in an area of 2.20 million hectares and annual production is 0.60 million tonnes (Singh *et al*., 2009). It is popular as an industrial crop in northern parts of India particularly in states like Rajasthan, Gujarat, Haryana and Punjab. The guar gum is extracted from the seeds of cluster bean which contain galactomannan rich endosperm (Sharma *et al*., 2014) and it is used in paper, textiles and pharmaceutical industries. But in southern states, its pods are used as vegetable. These pods are rich in vitamin A, vitamin C, iron and calcium (Kumar and Singh, 2002). The plant as a whole is used as cattle feed. It improves soil fertility by fixing atmospheric nitrogen and adding organic matter.

Despite its diverse uses, very less priority is given for the genetic improvement of cluster bean. Wide variability is observed for cluster bean all over India. For a successful crop improvement programme selection of parents is of paramount importance. Genetic diversity analysis of elite germplasm provides a vast scope for selection of better parents and development of superior hybrids. D^2 analysis help to measure the magnitude of genetic divergence present in a genetic stock. The progenies developed by crossing the divergent parents would be promising genotypes with desirable quantitative and qualitative traits.

MATERIALS AND METHODS

The experiment was conducted during August- October, 2017 in randomized block design with two replications at Department of Vegetable Science, College of Horticulture, Kerala Agricultural University, Thrissur, Kerala. The experimental material consisted of thirty accessions of cluster bean collected from NBPGR, Jodhpur. The seeds were sown in plots of size 3×2.7 m^2 at a spacing of 45×45 cm. Each plot consisted of 20 plants. All the management practices were done as the Package of Practice Recommendations - Crops, KAU (2016). Observations were recorded on 10 randomly selected plants for thirteen traits plant height (cm), number of branches, days to 50% flowering (DAS), days to first fruit set (DAS), days to first harvest (DAS), number of pod clusters/plant, number of pods/cluster, number of pods/plant, pod length (cm), pod girth (cm), pod weight (g) and pod yield/plant (g). To determine the genetic diversity, D^2 statistic of (Mahalanobis, 1928) was used. The correlated unstandardized mean values for all the accessions for 13 characters under consideration was transformed into the uncorrelated standardized value. Based on the correlated squares of generalized distance (D^2 values), the grouping of the

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genotypes into clusters was done by using Tocher's method (Rao, 1952), with the help of D^2 values between and within clusters, cluster diagram showing the relationship between different population was drawn. The per cent contribution of characters towards divergence was calculated (Singh and Chaudhary, 1977).

RESULTS AND DISCUSSION

The genetic diversity among 30 accessions was measured by using D^2 statistic. Accessions were grouped into five different clusters (Table 1). Cluster I consisted of the highest number of accessions (12); followed by cluster II (10), cluster IV (6) respectively. Cluster III and cluster V have only one accession each, (CT-29 and CT-21) respectively. The dendrogram representing 30 genotypes depicting the spatial position of each cluster in relation to others is presented in Fig 1.

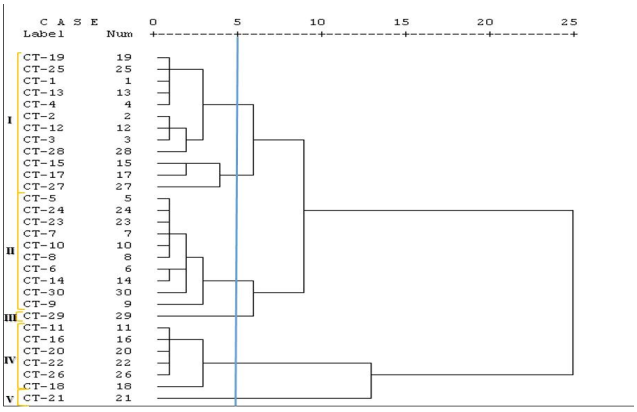

Fig 1: Dendrogram of 30 genotypes of cluster bean.

Mean values of clusters for all the thirteen characters were calculated and high magnitude of variation was there for all the characters studied (Table 3). Cluster I recorded the highest cluster mean value for plant height (149.16cm) followed by cluster IV (137.27cm) whereas, it was minimum for cluster II (129.32cm). Highest number of branches were observed in cluster IV (15.42) followed by cluster V (13.20). Cluster III recorded the minimum value (9.75). Cluster IV recorded lowest number of days to attain 50% flowering (23.67 DAS) which was immediately followed by cluster I (23.83). Maximum number of days to attain 50% flowering was found in cluster V (29.50 DAS). Days taken for first fruit set also followed a similar trend. Cluster III and II were earliest for first harvest (46.00 and 46.60 DAS). Cluster V took maximum number of days to first harvest 49.00 DAS. Number of pod clusters/plant were highest in cluster V (62.21) followed by cluster IV (49.52). It was lowest in cluster III (33.48). Cluster I recorded the highest cluster mean value for number of pods/plant (10.20) which was followed by

Table 1: Clustering pattern of 30 genotypes of cluster bean.

Cluster	Number of genotypes	Genotypes
I	12	CT-19, CT- 25, CT-1, CT-13, CT-4, CT-2, CT-12, CT-3, CT-28, CT-15,CT-17,CT-27
II	10	CT-5, CT-24, CT-23, CT-7, CT-10, CT-8, CT-6, CT-14, CT-30, CT- 9
III	1	CT-29
IV	6	CT-11, CT-16, CT-20, CT-22, CT-26, CT-18
V	1	CT-21

Table 2: Intra and inter-cluster distance among clusters in cluster bean.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	5762.028				
Cluster II	12116.44	2177.324			
Cluster III	29082.52	8370.219	0.00		
Cluster IV	17283.89	41433.2	78577.82	2254.759	
Cluster V	69202.2	115239.7	174782.9	32836.17	0.00

Table 3: Cluster means for different traits in cluster bean.

Clusters	Cluster means of traits												
	Plant height (cm)	Number of branches per plant	Days to 50% flowe--ring	Days to first fruit set	Days to first harvest	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Pod girth (cm)	Pod weight (g)	Number of seeds per pod	Pod yield per plant (g)
I	149.16	11.03	23.83	25.88	46.83	39.25	10.20	177.78	6.73	0.86	1.51	7.92	260.23
II	129.32	12.71	26.05	28.05	46.60	41.06	7.56	140.58	6.53	0.80	1.29	7.89	179.05
III	132.50	9.75	25.00	27.00	46.00	33.48	7.75	61.33	11.80	1.10	2.46	9.10	148.27
IV	137.27	15.42	23.67	25.67	47.92	49.52	8.29	271.28	6.15	0.75	1.23	8.38	330.49
V	131.90	13.20	29.50	31.50	49.00	62.21	7.25	383.62	6.28	0.71	1.07	8.90	412.83

Table 4: Contribution of different characters towards divergence.

Character	Times ranked Ist	Contribution (%)
Plant height (cm)	0	0
Number of branches	0	0
Days to 50% flowering	1	25%
Days to first fruit set	1	25%
Days to first harvest	0	0
Number of pod clusters/plant	0	0
Number of pods/cluster	1	25%
Number of pods/plant	0	0
Pod length (cm)	0	0
Pod girth (cm)	0	0
Pod weight (g)	0	0
Number of seeds/pod	0	0
Pod yield/plant (g)	1	25%

cluster IV (8.29) wheras, it was lowest in cluster V (7.25). Highest number of pods/plant was found in cluster V (383.62), which consist of sole member CT-21 which is highest pod yielder. Lowest number of pods/cluster was observed in cluster III (61.33). It had only one accession CT-29, which is the lowest pod yielder. Pod length was highest in cluster III (11.80cm), followed by cluster I (6.73cm) and lowest pod length was observed in cluster IV. The pod girth was highest in cluster III (1.10cm) followed by cluster I (0.86 cm). It was lowest in cluster V (0.71cm). Highest pod weight was observed in cluster III (2.46g) followed by cluster I (1.51g) and cluster V (1.07g) recorded the lowest value for pod weight. Number of seeds/pod was highest in cluster III (9.10) followed by cluster V (8.90). It was minimum in cluster II (7.89). The cluster V, consisting of single genotype CT-21 recorded the highest pod yield/plant (412.83g/plant) followed by cluster IV (330.49g/plant) and lowest pod yield/plant was observed in cluster III (148.27g/plant).

Average intra and inter- cluster D^2 values (Table 2) revealed that intra-cluster distance ranged from 0 to 57 62. 028. Cluster I with 12 genotypes showed maximum intra cluster diversity (D^2= 5762.028) followed by cluster IV (D^2 = 2254.759), cluster II (D^2 = 2177.324) indicating presence of diverse genotypes in these clusters. Cluster III and Cluster V had only one genotype, hence intra cluster distance was zero.

Based on the distance between clusters, maximum divergence was observed between cluster III and cluster V (D^2=174782.9) followed by cluster II and V (D^2=115239.7), cluster III and IV (D^2=78577.82), cluster I and V (D^2 = 69202.2), cluster II and IV (D^2 =41433.2). It indicated that selection of genotypes from these clusters for hybridization may give hybrids with high heterosis. The hybridization between genotypes of cluster III and V,cluster II and V and cluster III and IV would be very useful for generating highly diverse recombinant lines. This indicated that presence of diversity and crossing between genotypes belonging to clusters having high inter cluster distance will help in the development of heterotic hybrids as reported by Singh *et al*. (2005) and Pathak *et al*. (2010). Distance between clusters was minimum between cluster II and III (D^2 = 8370.22) which indicated that the genotypes of these clusters were less divergent.

Contribution of characters towards divergence is presented in Table 4. Among the thirteen characters studied the main contributors to divergence are days to 50% flowering (25%), days to first fruit set (25%) and pod yield/plant (25%). Greater emphasis is given to those characters which contribute to divergence during the further selection process.

CONCLUSION

Hence, it can be concluded that, elite germplasm collection can be utilized for developing genotypes with high yield and other economic attributes. To develop early varieties, genotypes belonging to cluster IV and cluster I can be used. High yielders can be developed by selection from cluster V and cluster IV and yield attributing traits like number of pod clusters/plant and number of pods/plant were also high for these clusters. When traits like pod length, pod girth, fruit weight is considered genotype belonging to cluster III can be selected, but yield is less for this genotype so it has to be used in hybridization programme with high pod yielders to get progenies having desirable traits. Inter cluster distance was also maximum between cluster III and cluster V hence, maximum heterosis can be expected in crosses involving the genotypes of this two divergent clusters as parents. High pod yielders can also be developed by crossing between genotypes of clusters having high mean pod yield and inter cluster distance. This will help in broadening the genetic base for improvement of yield in cluster bean.

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