



Genetic Diversity for Seed Yield and its Components in Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub]

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ABSTRACT

Background: Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] ($2n=2x=14$) is an under exploited legume belonging to family *fabaceae*. Clusterbean is a versatile legume crop cultivated mostly as animal feed, green manure green leaves as fodder, vegetable and cover crop. Clusterbean is a drought resistant, hardy, deep rooted annual legume crop. D^2 statistics provides a measure of magnitude for divergence between two genotypes under comparison. For broadening the genetic base of cultivars, the genetic diversity present in cultivated and wild relatives must be explored. Generally, diverse germplasms are expected to give high hybrid vigor and hence, it necessitates studying genetic divergence among the existing varieties and genotypes for the identification of parents for hybridization programme.

Methods: The present investigation was undertaken to study genetic variability in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub] with using a set of 40 genotypes at Agronomy Instructional Farm, Department of Agronomy, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *Kharif* 2019 in randomized block design with four replications. Mahalanobis (1928) D^2 statistic was used for assessing the genetic divergence between different populations. Grouping of the genotypes in different clusters was done by using Tocher's method. The inter-cluster distance was calculated by measuring the distance between clusters I and cluster II, between clusters I and cluster III, between clusters II and cluster III and so on. Likewise, one by one cluster was taken and their distances from other clusters were calculated.

Result: The genetic diversity analysis revealed the formation of nine clusters suggested the presence of considerable genetic diversity among the 40 genotypes. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that, the number of branches per plant followed by gum content, days to maturity, days to flowering contributed maximum towards total genetic divergence. On the basis of inter cluster distances, cluster IX was found to be more divergent. Therefore, it was concluded that the genotypes belonging to these cluster should be inter crossed in order to generate more variability.

Key words: Cluster bean, Genetic divergence, Mahalanobis D^2 technique, Variability.

INTRODUCTION

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] ($2n=2x=14$) is an under exploited legume belonging to family *fabaceae*. It is short day self-pollinated crop (Undersander *et al.*, 1991), commonly known as guar, chavli kayi, guari and khutti *etc.* Vavilov (1951) suggested India as the geographic center of variability of guar, though no wild species was reported in this region. The word "guar" represents a derivation from the Sanskrit word "Gaaahar" which means cow food or fodder of livestock (Bhosle and Kothekar, 2010). Clusterbean is a versatile legume crop cultivated mostly as animal feed, green manure (Chudzikowski, 1971 and Siddaraju *et al.*, 2010) green leaves as fodder, vegetable and cover crop (Arora and Pahuja, 2008). Clusterbean is a drought resistant, hardy, deep rooted annual legume crop. clusterbean is one of the most important and potential vegetable cum industrial crop grown for its tender pods for vegetable and for endospermic gum (30-35%). Tender pods are nutritionally rich in energy (16 kcal), moisture (81 g), protein (3.2 g), fat (1.4 g), carbohydrate (10.8 g), Vitamin A (65.3 IU), Vitamin 'C' (49 mg), calcium (57 mg) and iron (4.5 mg) for every 100 g of edible portion (Kumar and Singh, 2002).

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D^2 statistics developed by Mahalanobis (1928) provides a measure of magnitude for divergence between two genotypes under comparison. For broadening the genetic base of cultivars, the genetic diversity present in cultivated and wild relatives must be explored (Mishra *et al.*, 2010).

Generally, diverse germplasms are expected to give high hybrid vigor (Harington, 1940) and hence, it necessitates studying genetic divergence among the existing varieties and genotypes for the identification of parents for hybridization programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding programme. The D^2 statistics is a useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic diversity (Murthy and Arunachalam, 1966). Therefore, the present study was under taken to estimate the genetic divergence among 40 genotypes of cluster bean on the basis of 12 different yield and yield related traits in cluster bean.

MATERIALS AND METHODS

The experimental material consisted of 40 clusterbean genotypes evaluated in randomized block design with four replication was conducted at Agronomy Instructional Farm, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *kharif*, 2019. The sowing was done on 5th July, 2019. Each genotype was accommodated in a single row of 4 m length with a spacing 45 cm between rows and 15 cm between plants. All the recommended crop production and protection practices were followed to raise the good crop. The

observations on twelve metric traits *viz.*, days to flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), test weight (g), protein content (%), gum content (%) and seed yield per plant (g) were recorded at appropriate crop growth stage. Five competitive plants from each genotype were selected at random for recording observations except days to 50% flowering, days to maturity and test weight which are recorded on plot basis. Mahalanobis (1928) D^2 statistic was used for assessing the genetic divergence between different populations. Grouping of the genotypes in different clusters was done by using Tocher's method (Rao, 1952). The inter-cluster distance was calculated by measuring the distance between clusters I and cluster II, between clusters I and cluster III, between clusters II and cluster III and so on. Likewise, one by one cluster was taken and their distances from other clusters were calculated.

RESULTS AND DISCUSSION

The quantitative assessment of genetic divergence was made by adopting Mahalanobis's D^2 statistics for yield and its contributing traits. Wilks test showed highly significant differences among the genotypes for the aggregate effect of 12 characters which suggested the existence of

Table 1: Distribution of genotypes evaluated for seed yield into different clusters of clusterbean.

Cluster	No. of genotypes	Name of the genotypes
I	21	GG 1806, GG 1810, IC 319038, GG 1804, GG 1703, GG 1808, IC 102828, GG 1807, IC 113432, GG 1803, GAUG 1501, GG 1805, GAUG 1304, IC 116645, IC 116629, IC 113294, GG 1709, GG 1702, GG 1809, GG 1801, IC 311444
II	8	IC 113269, IC 113298, IC 113498, IC 116633, IC 113289, IC 102853, IC 41057, IC 113537
III	2	GG 1607, GAUG1305
IV	3	GG 1612, GAUG 1507, GG 1710
V	1	IC 373497
VI	1	GG 1609
VII	2	GG 1, GG 2
VIII	1	IC 113432
Ix	1	GAUG 1502

Table 2: Average intra and inter cluster D^2 value of 40 genotypes of clusterbean.

	I	II	III	IV	V	VI	VII	VIII	Ix
I	136.42	287.92	218.82	377.13	225.06	319.08	483.95	576.22	962.95
II		154.37	361.46	425.36	215.12	263.21	845.40	649.75	758.28
III			149.89	295.99	327.98	157.16	343.69	405.54	773.96
IV				93.98	187.41	244.74	576.71	209.32	299.44
V					0	322.36	679.85	410.35	548.22
VI						0	666.84	387.31	441.95
VII							151.00	677.62	1408.24
VIII								0	460.30
Ix									0

considerable divergence in the material. This observation confirms results of Goudar *et al.* (2017),

Distribution of genotypes into clusters grouping of the genotypes was carried out by following the Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller D^2 values among themselves than those from groups belonging to different clusters. In all, nine clusters were formed from 40 genotypes. The distributions of genotypes into 9 clusters are presented in Table 1. The cluster I was the largest one contained twenty-one genotypes. Cluster II has eight genotypes, cluster III and VII contain two genotypes, cluster IV contains three genotypes and clusters V, VI, VIII and IX had a single genotype. Similar findings of Goudar *et al.* (2017), Mishra *et al.* (2019) and Remzeena *et al.* (2021) corroborated that the distribution of genotypes from different eco-geographical regions into clusters was at random, indicating geographical distribution does not necessarily exhibit genetic divergence. It was evident from the study that, there was considerable

degree of variability for seed yield and its component characters. A few of the most promising genotypes for seed yield were GG 1, GG 2, IC-41057, IC-311444 and IC-113432. The intra and inter-cluster D^2 values among nine clusters are given in Table 2 and Fig 1. Intra cluster average D^2 values ranged from 0 to 154.37. Among the clusters, cluster II had the maximum intra-cluster distance (154.37), followed by cluster VII ($D^2=151$), while the minimum intra-cluster distance was observed for cluster IV ($D^2=93.98$). The zero intra-cluster distance was observed for clusters V, VI, VIII and IX ($D^2=0$). This four clusters V, VI, VIII and IX was a solitary cluster. The present results are in conformity with the results of past worker Goudar *et al.* (2017). and Wankhade *et al.* (2017).

The maximum inter cluster distance was recorded between cluster VII and cluster IX ($D^2=1408.24$) followed by that between I and IX ($D^2=962.95$), while the minimum inter-cluster distance was observed between clusters III and VI ($D^2=157.16$). Cluster I had the largest distance from cluster

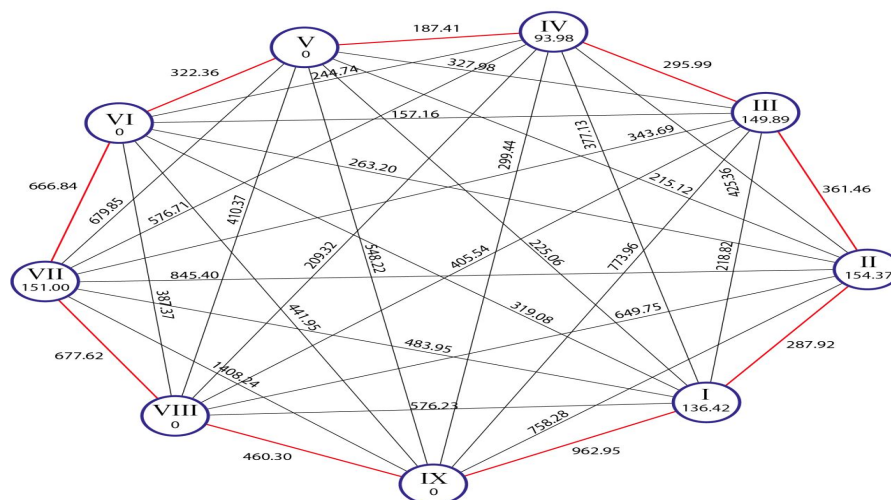


Fig 1: Cluster diagram.

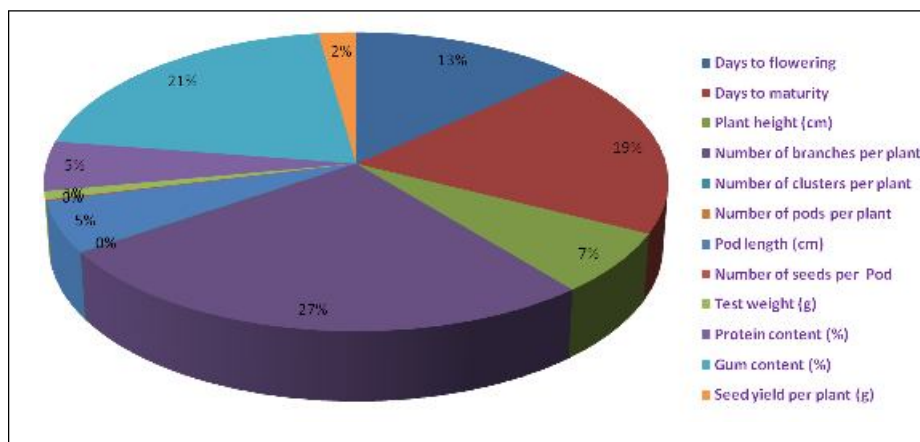


Fig 2: Per cent contribution of different characters to genetic divergence in clusterbean.

Table 3: Cluster mean for seed yield and its component in clusterbean.

Clusters	Days to Flowering (1)	Days to maturity (2)	Plant height (cm) (3)	Number of branches per plant (4)	Number of clusters per plant (5)	Number of pods per plant (6)	Pod length (cm) (7)	Number of seeds per pod (8)	Test weight (g) (9)	Protein content (%) (10)	Gum content (%) (11)	Seed yield per plant (g) (12)
I	30.59	74.49	71.52	3.66	4.76	13.49	5.01	7.14	2.39	23.38	26.14	2.35
II	29.75	81.75	84.25	2.04	4.55	13.31	4.80	7.19	2.57	23.82	25.31	2.49
III	32.38	80.88	67.46	3.53	4.68	13.20	5.37	7.40	2.29	25.48	28.26	2.48
IV	44.00	96.08	60.63	3.30	5.05	13.98	5.31	7.45	2.49	23.58	26.72	2.76
V	36.50	89.25	85.18	3.30	5.20	14.20	5.32	7.20	2.17	22.44	24.71	2.20
VI	33.75	87.25	60.43	2.25	4.25	11.33	4.91	7.10	2.52	25.13	28.26	2.02
VII	30.00	80.38	69.78	5.58	6.78	16.54	5.55	7.83	3.31	25.41	28.72	4.31
VIII	52.50	87.75	72.58	2.25	5.45	14.85	5.64	7.80	2.73	23.45	28.45	3.16
XI	55.25	112.75	58.43	2.45	4.55	12.75	4.35	6.48	2.20	24.55	26.76	1.81

Table 4: Relative per cent contribution of different characters towards genetic diversity in clusterbean genotypes evaluated for seed yield.

Characters	Time ranked 1 st	Contribution to divergence %
Days to flowering	104	13.33
Days to maturity	149	19.10
Plant height (cm)	52	6.67
Number of branches per plant	206	26.41
Number of clusters Per Plant	1	0.13
Number of pods per plant	0	0
Pod length (cm)	42	5.38
Number of seeds per pod	1	0.13
Test weight (g)	7	0.89
Protein content (%)	42	5.38
Gum content (%)	159	20.38
Seed yield per plant (g)	17	2.18

Ix ($D^2=962.95$) followed by cluster VIII ($D^2=576.22$), cluster VII ($D^2=483.95$) and cluster IV ($D^2=37.13$). The D value between cluster I and III ($D^2=218.82$) and cluster I and V ($D^2=225.06$) were comparatively of two magnitude. The distance between clusters II and VII ($D^2=845.40$) was highest followed by cluster Ix ($D^2=758.28$) and cluster VIII ($D^2=649.75$). The closest cluster from cluster II was cluster V ($D^2=215.12$). The cluster Ix ($D^2=773.96$) was far away from cluster III followed by cluster VIII ($D^2=405.54$) and cluster VII ($D^2= 343.69$). Cluster VI ($D^2= 157.16$) was nearest to cluster III. Cluster IV depicted maximum distance from cluster VII ($D^2= 576.71$), which was followed by cluster Ix ($D^2= 299.44$). Whereas, it had minimum D^2 value with cluster V ($D^2= 187.41$). Cluster VIII ($D^2= 677.62$) and cluster Ix ($D^2= 1408.24$) were distantly placed away from cluster VII. Inter-cluster distances were higher than intra-cluster distances which indicated the existence of substantial diversity among the genotypes. The same results were also obtained by Goudar *et al.* (2017), Wankhade *et al.* (2017) and Remzeena *et al.* (2021). The selection of parents for crossing from divergent clusters may result in heterotic expression for yield and quality traits.

The mean performance of clusters for twelve characters is presented character wise in Table 3. Wider ranges of mean values among the clusters were recorded for different traits. The cluster I and II had the highest mean values and desirable rating for earliness on the basis of days to maturity (74.49 days) and days to flowering (29.75). The cluster III had the highest mean values and desirable rating for protein content (25.48%). The cluster V had the highest mean values for plant height (85.18). The cluster VII had the highest mean values for the number of clusters per plant (6.77), number of branches per plant (5.57), number of pods per plant (16.53), seed yield per plant (4.30 g), test weight (3.30 g), gum content (28.72%) and number of seeds per pod (7.82). Cluster VIII had a desirable rating for pod length (5.64 cm). The cluster Ix had a desirable rating for dwarfness

(58.42 cm). Similar findings also observed by Remzeena *et al.* (2021).

Relative Contribution of each character towards diversity are presented in Table 4 and Fig 2. Among all the characters, number of branches per plant (26.41%) contributed maximum to the diversity by taking the first rank 206 times out of 780 combinations, followed by gum content (20.38%) with 159 times, days to maturity (19.10%) with 149 times, days to flowering (13.33%) with 104 times. While, plant height (6.67%) with 52 times, pod length (5.38%) with 42 times, protein content (5.38%) with 42 times and seed yield per plant (2.18%) with 17 times, number of clusters per plant (0.13%) with 1 time, number of seeds per pod (0.13%) with 1 time and test weight (0.89%) with 7 times contributed minimum towards total genetic divergence. While characters like the number of pods per plant contributed null towards the total genetic divergence as depicted in Table 4.

CONCLUSION

Ranking based on both mean performance and contribution of characters towards divergence resulted in the identification of GG 1, GG 2, IC-41057, IC-311444 and IC-113432 as genotypes and can be utilized as parents in the selection programme for the improvement of seed yield.

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