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Genetic Divergence Studies in Dolichos Bean (Lablab purpureus L.) Genotypes

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ABSTRACT: In the current investigation, genotypes of the dolichos bean (Lablab purpureus L.) were examined for genetic diversity. Using randomized block design (RBD), the investigation was conducted on 45 genotypes of dolichos bean, with two replications for sixteen characters. Tocher's method was used to group 45 genotypes into nine clusters by treating the estimated D² values as the square of the generalized distance.

This grouping of genotypes into clusters resulted in the formation of nine clusters. The inter cluster distance recorded was minimum between cluster I and V indicating narrow genetic diversity, whereas maximum distance recorded between clusters VI and VII indicating wider genetic diversity between these two groups. Highest contribution towards divergence in this regard was put forth by reducing sugars, total sugars, protein content, days to 50% flowering, number of pods per plant, seed length, 100-seed fresh weight, days to first harvest, Pod yield per plant, pod width, vine length, number of primary branches per plant and pod length. In contrast, the remaining traits viz., number of seeds per pod, 100-seed dry weight and seed width did not contribute to the total divergence as there is no much variation in these traits.

Keywords: Lablab purpureus, genetic diversity, percentage contribution.

INTRODUCTION

Dolichos bean, commonly referred to as the Indian bean, Hyacinth bean, sem, Egyptian kidney bean, bonavist bean, avarai, and avari chikkudu, happens to be one of the most well-known traditional vegetables that is widely grown in India. Its scientific name is Lablab purpureus L. It is mostly a crop that selfpollinates. It is one of the main vegetables and provides a good amount of calcium, phosphorus, lipids, carbohydrates, and protein, as well as iron in a vegetarian diet (Jyothireddy et al., 2018).

The crop hasn't been fully utilised despite having many beneficial attributes because of its low output, lengthy lifespan, photosensitivity, and unpredictable growth habit. The accessions grown around the nation have a wide variety of differences for the plant and pod characteristics. The success of any breeding program, including the enhancement of a trait through selection in particular, entirely depends on the genetic diversity present in available crops germplasm (Parmar et al., 2013). The size, nature, and interplay between genotypic and phenotypic variation, however, determine the extent, type, and influence of the genotypic and phenotypic variation on the development of breeding. One of the more complicated quantitative features is yield, which depends on a number of other characters that contribute to yield (Savitha, 2008). This study was undertaken to know the genetic diversity of 45 genotypes for further genetic improvement and development of new varieties by the breeders.

MATERIAL AND METHODS

The present investigation was carried out from November 2021 to March 2022 at the PG Research Block, College of Horticulture, Mojerla. The experimental material consists 45 different genotypes of dolichos bean that were obtained from NBPGR-National Bureau of Plant Genetic Resources. The divergence between the 45 genotypes was estimated using the Mahalonobis (1936) D² analysis. Based on the degree of divergence (D values) between any two genotypes, grouping of genotypes was done by using Tocher's method (Singh and Choudary 1977). In this method the populations were arranged in the order of their relative distance (D^2 values) from each other and a table was made. After establishing the clusters, the intra and inter cluster distances were worked out by taking the average of the component genotype in that particular cluster. The average inter cluster distance was obtained by considering the component D^2 values possible among the members of the two cluster considered. The square root of the average D^2 values gave the genetic distance D between clusters.

Based on the D values (inter cluster distances), the following scale of rating the distance was adopted (Rao, 1952).

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Category	D values
Less divergent (L)	Below 99
Moderately divergent (M)	Between 100 to 200
Highly divergent (H)	Above 200

Ranking was done according to the method obtained by Singh and Choudhary (1977). Each character is ranked based on the transformed correlated 'Y' values. The relative contribution towards genetic divergence was worked out by using computer software. The character contribution towards genetic divergence was computed using method given by Singh (1985). The percentage contribution of characters to divergence was estimated, together with the number of times each character appeared in the first.

RESULTS

The quantitative assessment of genetic divergence was performed by adopting Mahalonobis D^2 statistic for yield and its contributing characters. The final grouping of the genotypes was based on the D^2 values between any two genotypes, which were determined as the sum of squares of the differences between the mean values of all sixteen traits. Procedure suggested by Tocher (Rao, 1952) was used to group 45 genotypes into nine clusters by treating the estimated D^2 values as the square of the

generalized distance.

Based on D^2 values, the 45 genotypes, are grouped into nine highly divergent clusters, were showed in Table 1 and Fig. 1. Some genotypes were so divergent in all the characters studied, hence each single genotype formed as a separate cluster. Thus six clusters viz., III (IC-427414), V (IC-382830), VI (IC- 427436), VII (IC-261311), VIII (IC-546387) and IX (IC-598467) were solitary with one genotype in each cluster. The other three clusters were having maximum number of genotypes. The biggest cluster, Cluster I contains 32 genotypes viz., IC-261005, IC-261010, IC- 384066, IC-412977, IC-413709, IC-413710, IC-426632, IC-426957, IC-426966, IC-426970, IC-426980, IC-426983, IC-426987, IC-426988, IC-426991, IC-427417, IC-427423, IC-427424, IC-427425, IC-427428, IC-427456, IC-427462, IC-446561, IC-IC-446568, IC-446571, IC-446573, 446566, IC-446574, IC-446575, IC-446581, IC-446584 and IC-446587 followed by cluster II with 5 genotypes viz., IC-427429, IC-446585, IC-446583, IC-372119 and IC-426694 then by Cluster IV with 2 genotypes IC-261004 and Arka Adarsh are depicted in Fig. 2 in 3 dimensional plot diagram.

Table 1: Clustering pattern of 45 genotypes of dolichos bean by Tocher's method.

Cluster	Number of genotypes	Genotypes
		IC-261005, IC-261010, IC-384066, IC-412977, IC-413709, IC-413710, IC-426632, IC-426957, IC-
		426966, IC-426970,IC-426980, IC-426983, IC-426987, IC-426988, IC-426991,IC-427417, IC-
		427423, IC-427424, IC-427425, IC-427428, IC-427456, IC-427462, IC-446561, IC-446566, IC-
Ι	32	446568,IC-446571, IC-446573, IC-446574, IC-446575, IC-446581,
		IC-446584, IC-446587
П	5	IC-427429, IC-446585, IC-446583, IC-372119, IC-426694
III	1	IC-427414
IV	2	IC-261004, Arka Adarsh
V	1	IC-382830
VI	1	IC-427436
VII	1	IC-261311
VIII	1	IC-546387
IX	1	IC-598467



Fig. 1. Dendrogram showing the clustering pattern of divergence in dolichos bean genotypes.

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Fig. 2. 3D plot showing the clustering pattern of divergence in dolichos bean genotypes.

Cluster means of characters in cluster. The cluster means for the sixteen characters studied in dolichos bean genotypes revealed considerable differences among all the clusters showed in Table 2. From the present data, it is evident that the vine length was highest in cluster IX (421.56 cm), and lowest in cluster VII (222.50 cm). Maximum number of primary branches per plant was recorded in cluster IX (4.77), whereas minimum was recorded in cluster VI (3.13).

The cluster IX showed maximum number of pods per plant (149.50), whereas cluster III had minimum number of pods per plant (45.34). The cluster IX recorded maximum pod yield per plant (702.67 g) and minimum pod yield per plant (246.78g) was recorded in cluster III.

The cluster IX registered maximum number of seeds per pod (5.70), whereas cluster V observed minimum number of seeds per pod (3.30) and the cluster VIII had more 100-seed fresh weight (83.95 g), whereas cluster VII had less 100-seed fresh weight (15.35 g).

The genotypes of cluster IX recorded maximum 100seed dry weight(34.35 g), whereas genotypes of cluster VII (25.95 g) had minimum 100-seed dry weight. The highest pod length was observed in cluster VI (11.71 cm), while it was lowest in cluster VII (5.96 cm). Maximum pod width was registered in cluster V (4.74 cm), while it was minimum in cluster IX (1.34 cm). Maximum seed length was recorded in cluster VI (1.06 cm) whereas, a minimum seed length in cluster IX (0.62 cm). The highest seed width was observed in cluster VI (1.04 cm), while it was lowest in cluster VII (0.64 cm). Earlier days to 50% flowering were recorded in cluster V (55.31 days), whereas maximum days taken to 50% flowering were recorded in cluster IX (102.50 days). Earlier days to first harvest was registered in cluster IV (86.08 days), while maximum days to first harvest were recorded in cluster IX (135.92 days). Maximum protein content was recorded in cluster III (19.34%), while it was minimum in cluster VI (14.54%). Maximum reducing sugars was registered in cluster VI (1.14%), whereas it was minimum in cluster II (0.56%). Maximum total sugars were recorded in cluster VIII (1.50%), while it was minimum in cluster II (0.84%).

Cluster mean values showed a wide range of mean values among the characters studied indicating presence of wide variation among the genotypes studied.

Cluster	Vine length (cm)	Number of primary branches per plant	Days to 50% flowering	Days to first harvest	Number of pods per plant	Pod length (cm)	Pod width (cm)	Number of seeds per pod	Seed length (cm)	Seed width (cm)	100- seed fresh weight (g)	100- seed dry weight (g)	Pod yield per plant(g)	Protein content (%)	Reducing sugars (%)	Total sugars (%)
I	364.28	3.56	74.62	101.29	57.83	9.71	1.70	4.58	0.89	0.86	61.55	28.69	307.35	17.35	0.87	1.07
II	378.69	3.84	73.62	104.07	66.08	8.35	1.95	4.38	0.96	0.94	68.28	30.27	384.61	18.62	0.56	0.84
ш	362.59	3.36	84.28	106.88	45.34	11.59	2.30	4.50	0.95	0.98	57.50	31.13	246.78	19.34	0.66	1.33
IV	409.47	3.96	55.53	86.08	123.73	10.34	1.85	4.85	0.88	0.89	61.10	33.22	640.97	19.16	0.88	1.04
v	376.12	3.64	55.31	91.08	58.50	10.27	4.74	3.30	0.88	0.86	27.75	32.13	345.61	16.49	0.63	0.95
VI	372.05	3.13	66.00	91.41	62.00	11.71	1.91	4.40	1.06	1.04	70.50	27.88	350.56	14.54	1.14	1.36
VII	222.50	3.84	65.79	88.26	93.65	5.96	1.88	3.90	0.80	0.64	15.35	25.95	345.17	18.96	0.58	1.04
VIII	370.36	4.16	97.49	121.43	116.50	6.93	1.62	5.40	0.77	0.76	83.95	31.83	448.45	18.71	0.66	1.50
IX	421.56	4.77	102.5	135.92	149.50	10.28	1.34	5.70	0.62	0.92	70.15	34.35	702.67	18.10	0.92	1.06

Table 2: Mean values of clusters for sixteen characters in 45 genotypes of dolichos bean.

Average intra and inter cluster distances. The mean intra and inter cluster D^2 values among the nine clusters were given in the Table 3. The intra cluster D^2 value ranged from nil (cluster III, V, VI, VII, VIII and IX) to 199.15 (cluster II). The cluster II had maximum D^2

value (199.15) followed by Cluster I (177.39) and Cluster IV (119.41) $\,$

The inter cluster D^2 values of nine clusters recorded that the highest inter cluster generalized distance (1542.14) was between cluster VI & cluster VII

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followed by the inter cluster distance between cluster VI and IX (1455.57), while the lowest (279.05) was between cluster I and cluster V.

The inter cluster distance was minimum between cluster I and V indicating narrow genetic diversity, whereas maximum recorded between clusters VI and VII indicating wider genetic diversity between these groups. The closest and farthest clusters from each of the cluster based on D^2 values are depicted in Table 4. Cluster I was nearest to cluster V (279.05) and farthest from cluster IX (812.76). Cluster II noticed close proximity with cluster III (324.53) and maximum divergence with cluster VI (1173.63). Cluster III was

nearest to cluster I (284.15), whereas it was farthest from IX (944.20). Cluster IV was nearest to cluster I (387.65) and distant from cluster VI (740.81).

Cluster V observed intimate relation with cluster I (279.05), while it was wide diversity with cluster IX (1089.05). Cluster VI was nearest to cluster I (518.88) and farthest from cluster VII (1542.14). Cluster VII was nearest to cluster II (426.74) and distant from cluster VI (1542.14). Nearest and farthest clusters for cluster VII (1542.14). Nearest cluster VII (1542.14). Nearest and farthest clusters for cluster VII (1542.14). Nearest cluster VII (1542.14). Nearest NII (1542.14). Nearest

Table 3: Average intra ((bold) and inter-cluster D	values for nine clustersin 45	genotypes of dolichos bean.

Cluster	Ι	II	III	IV	V	VI	VII	VIII	IX
Ι	177.39	341.3	284.15	387.65	279.05	518.88	611.34	488.74	812.76
Π		199.15	324.53	426.5	366.15	1173.63	426.74	567.69	717.49
III			0	652.32	405.22	923.6	522.33	352.51	944.2
IV				119.41	455.86	740.81	524.08	555.33	569.15
V					0	688.18	532.37	795.16	1089.05
VI						0	1542.14	995.35	1455.57
VII							0	577.6	943.29
VIII								0	483.78
IX									0

Bold diagonal values indicate intra cluster distance, rest of the values show theinter cluster distances.





Fig. 3. Cluster diagram showing average intra and inter cluster D2 of dolichos bean genotypes.

Table 4: The nearest and farthest clusters from each cluster based on D²values in dolichos bean genotypes

Cluster	Nearest cluster with D^2 values	Farthest cluster with D ² values
Ι	279.05 (V)	812.76 (IX)
II	324.53 (III)	1173.63 (VI)
III	284.15 (I)	944.20 (IX)
IV	387.65 (I)	740.81 (VI)
V	279.05 (I)	1089.05 (IX)
VI	518.88 (I)	1542.14 (VII)
VII	426.74 (II)	1542.14 (VI)
VIII	352.51 (III)	995.35 (VI)
IX	483.78 (VIII)	1455.57 (VI)

Relative Contribution of different characters towards divergence. Table 5 illustrates the frequency with which sixteen traits were ranked first, along with their corresponding percentage contributions to genetic divergence. The results depicted that reducing sugars contributed maximum (28.28%) towards diversity by taking 280 times first ranking followed by total sugars (20.10%) by 199 times, protein content (13.64%) by 135 times, days to 50% flowering (10.70%) by 107 times, number of pods per plant (7.47%) by 74 times, seed length (4.75%) by 47 times, days to first harvest (4.05%) by 40 times, 100- seed fresh weight (3.03%) by 30 times, pod width (2.50%) by 25 times, pod yield per plant (2.32%) by 23 times, vine length (1.52%) by 15 time, number of primarybranches per plant (1.21%) by 12 time, pod length (0.30%) by 3 time. On the other

hand, traits like the number of seeds per pod, 100-seed dry weight, and seed width did not play a role in the total divergence. Besides the significant high divergence, the performance of the genotypes and the characters with maximum contribution towards divergence should also be given due consideration which appears as desirable for inclusion in dolichos bean improvement.

 Table 5: Percent contribution of different characters towards geneticdivergence in 45 genotypes of dolichos bean.

Sr. No.	Character	Number of times ranked 1 st	Percent contribution
1.	Vine length (cm)	15	1.52%
2.	Number of primary branches perplant	12	1.21%
3.	Days to 50% flowering	107	10.70%
4.	Days to first harvest	40	4.05%
5.	Number of pods per plant	74	7.47%
6.	Pod length (cm)	3	0.30%
7.	Pod width (cm)	25	2.50%
8.	Number of seeds per pod	0	0%
9.	Seed length (cm)	47	4.75%
10.	Seed width (cm)	0	0%
11.	100-seed fresh weight(g)	30	3.03%
12.	100-seed dry weight (g)	0	0%
13.	Pod yield per plant (g)	23	2.32%
14.	Protein content (%)	135	13.64%
15.	Reducing sugars (%)	280	28.28%
16.	Total sugars (%)	199	20.10%



Fig. 4. Percent contribution of different characters towards genetic divergence in 45 genotypes of dolichos bean.

DISCUSSION

Mahalanobis (1936) D^2 statistics, a powerful tool was utilized to quantify the genetic divergence between the genotypes and to identify diverse parents for crossing. This approach also aids in relating clustering pattern with the geographical origin. In the present study, 45 germplasm lines of dolichos bean were grouped into nine clusters. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated.

The Statistical distance represents the extent of genetic diversity among clusters. The inter cluster distance was minimum between cluster I and cluster V indicating close relationship and similarity for most of the characters of the genotypes included in these clusters. The maximum inter cluster distance observed was between clusters cluster VI and VII, indicating wider genetic diversity among the genotypes included in these

groups.

Maximum intra cluster distance was noticed in cluster II, which might be due to limited gene exchange or selection practices among the genotypes for diverse characters.

Emphasis should be laid on characters contributing maximum D^2 values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. Highest contribution towards divergence in this regard was put forth by reducing sugars, total sugars, protein content, days to 50% flowering, number of pods per plant, seed length, days to first harvest, 100-seed fresh weight, pod width, Pod yield per plant, vine length, number of primary branches per plant and pod length. Thus, these were the major traits contributing to divergence.

Therefore, selection for divergent parents based on these characters would be beneficial for future breeding

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programmes in dolichos bean. Chaitanya *et al.* (2013); Dhillon *et al.* (2015); Jyothireddy *et al.* (2018); Gamit (2019); Geetha and Divya (2021); Shibli *et al.* (2021); Magalingam *et al.* (2013); Golani *et al.*(2006) conducted similar studies.

CONCLUSIONS

The utmost importance may be given for highly divergent clusters for further selection of genotypes for hybridization programmes. Selection of parents from the diverse clusters for hybridization programme would help in achieving novel recombinants.

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