

Genetic divergence in lablab bean [*Lablab purpureas* (L.) Sweet]

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The lablab bean [*Lablab purpureas* (L.) Sweet] is an important leguminous vegetable grown for its nutritious tender pod. It is a self pollinated crop but cross pollination (25-30%) has also been reported. Hence, over long period of time, a high degree of genetic diversity has been emerged within the species [4]. The yield improvement in this crop can be achieved through selection of superior genotypes with desirable traits existing in nature. Mahalanobis [1] D^2 statistics which is based on the multivariate analysis of quantitative trait is a powerful tool for measuring divergence among a set populations. Therefore, an attempt was made to study the multivariate analysis of genetic divergence in local landraces of lablab bean.

The experimental material comprised of 31 landraces of lablab bean belonging to different geographical regions of Tripura were evaluated during 2005 and 2006. The mean data of quantitative traits were replicated. The analysis of genetic divergence was carried out by using Mahalanobis D^2 statistics. The genotypes were grouped in to clusters as per Tochar's method [3].

The analysis of variance for 9 quantitative characters showed significant differences among 31 landraces indicating the existence of genetic diversity. These 31 landraces were grouped in to 6 clusters as presented in Table 1. It was apparent that 24 landraces were in cluster 1, 3 landraces in cluster 2 and rest of the clusters had one landrace each. The pattern of distribution of landraces in different clusters indicated that genetic divergence was related to geographical differentiation. Clustering genotypes from different eco-geographic locations in to one cluster can be attributed to the possibility of free exchange of seed materials. However, the unidirectional selection practiced for a

particular trait (or) a group of linked traits in several places may produce similar phenotype, which can be aggregated in to one cluster irrespective of their geographic origin [5].

The yield and yield related parameters are presented in Table 1. In general all collected genotypes were pole type and photosensitive in nature. The yield/plant ranges from 1.48 kg to 10.30 kg among the germplasm evaluated. The analysis of variance showed significant differences indicating existence wide genetic diversity. All genotypes were grouped in to 6 clusters as presented in Table 2. It was apparent that 24 landraces were in cluster 1, 3 in cluster 2 and rest of the clusters had one genotype.

The pattern of distribution of genotypes in different clusters indicated that genetic divergence was related to geographical differentiation. Clustering of genotypes from different eco-geographical locations showed the possibility of free exchanging seed materials. However, the unidirectional selection practiced for particular trait or a group of linked traits in several places may produce similar phenotype, which can be aggregated in to one cluster irrespective of their geographic origin [2]. The maximum inter cluster distance value was obtained between clusters VI and V (Table 3). These two cluster may be utilized in the hybridization programme due to wide variability and transgressive segregants [6-7]. The minimum distance was noticed between clusters IV and V, which reveals that the landraces belonging to these clusters are relatively closer. Selection of parents from genetically closer clusters, may be due to narrow genetic base and inbreeding depression.

The comparison of cluster means revealed that cluster II gave exceptionally high values for yield and

Table 1. Mean performance of different traits of lablab bean genotypes

S.No.	Variety	No.of flowers/ spike	No.of fruits/ spike	No.of spikes/ plant	Pod length (cm)	Pericarp thickness (cm)	Pod breadth (cm)	No.of seeds/ pod	Pod weight (g)	Yield/ plant (kg)
1	TRC- D1	45.67	17.33	105.33	10.66	0.26	1.66	4.66	6.20	10.33
2	TRC-D2	35.33	16.33	96.33	10.93	0.15	2.20	4.66	7.55	9.46
3	TRC-D3	32.33	16.66	81.33	14.66	0.18	2.30	5.66	5.96	10.10
4	TRC-D4	32.33	11.66	107.33	15.16	0.15	2.16	5.66	9.30	8.10
5	TRC-D5	33.67	13.00	111.66	6.73	0.26	2.53	4.66	6.26	9.03
6	TRC-D6	33.00	13.33	20.66	8.00	0.17	2.56	4.33	4.45	8.23
7	TRC-D7	24.66	9.00	18.66	6.73	0.20	2.13	5.33	5.93	2.30
8	TRC-D8	27.33	12.66	111.33	8.00	0.16	1.86	4.00	4.73	1.42
9	TRC-D9	37.66	18.66	99.66	8.83	0.11	2.10	5.33	6.58	10.12
10	TRC-D10	39.33	11.00	67.33	8.83	0.11	2.06	5.33	6.66	4.36
11	TRC-D11	32.33	9.66	85.66	14.00	0.18	2.56	4.33	9.70	6.80
12	TRC-D12	37.33	11.66	112.00	14.33	0.15	2.60	4.33	10.20	10.03
13	TRC-D13	25.66	8.66	98.00	13.66	0.15	2.33	4.66	6.06	5.23
14	TRC-D14	29.33	8.33	84.33	13.66	0.13	1.76	4.33	9.06	6.40
15	TRC-D15	35.33	9.33	83.66	12.16	0.18	1.80	3.66	7.63	5.98
16	TRC-D16	39.66	13.66	93.33	11.03	0.18	1.80	4.33	7.80	8.10
17	TRC-D17	28.66	7.66	110.33	10.06	0.11	1.76	4.66	5.93	7.53
18	TRC-D18	42.00	16.66	84.33	11.40	0.11	1.43	5.33	7.53	7.40
19	TRC-D19	23.66	8.00	107.33	10.06	0.13	1.63	4.66	4.83	8.76
20	TRC-D20	32.00	9.00	110.00	18.50	0.16	3.03	3.66	12.76	5.05
21	TRC-D21	29.33	9.33	88.66	7.66	0.38	2.23	5.66	5.46	5.02
22	TRC-D22	23.33	5.66	110.00	8.00	0.66	1.76	3.33	5.01	5.02
23	TRC-D23	28.67	9.00	86.66	9.13	0.20	2.40	3.66	8.52	5.93
24	TRC-D24	28.66	8.33	115.33	6.96	0.19	2.10	3.66	4.44	4.28
25	TRC-D25	33.66	9.00	109.67	8.36	0.18	2.26	4.00	5.30	5.37
26	TRC-D26	27.66	9.33	92.00	8.96	0.20	2.20	5.00	6.77	6.31
27	TRC-D27	31.33	10.66	104.66	7.23	0.18	2.70	4.66	5.97	5.33
28	TRC-D28	29.33	6.33	74.66	9.13	0.19	2.56	4.00	8.16	8.72
29	TRC-D29	33.00	9.00	105.33	10.60	0.14	1.93	4.66	5.73	3.20
30	TRC-D30	29.33	8.66	90.33	8.13	0.14	2.20	4.33	8.63	5.20
31	TRC-D31	31.33	11.00	90.00	8.16	0.17	2.06	5.33	6.80	5.80
	C.D. at 5%	8.77	4.53	14.78	1.52	NS	0.50	1.4	0.91	1.62

Table 2. Distribution of 31 genotypes in different clusters pooled over environment

S.No.	Clusters	Genotypes included in the clusters	Seed source	Genotypes in the clusters
1	I	26, 31, 10, 21, 25, 27, 29, 24, 22, 17, 30, 23, 5, 13, 15, 16, 28, 19, 2, 9, 18, 14, 1, 11	West Tripura South Tripura West Tripura South Tripura West Tripura	24
2	II	4, 12, 13	South Tripura	3
3	III	8	West Tripura	1
4	IV	7	West Tripura	1
5	V	20	South Tripura	1
6	VI	6	West Tripura	1

Table 3. Inter and intra cluster distances (D^2) in lablab bean

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	7.602	10.751	10.159	12.943	17.569	12.444
Cluster II		8.227	16.500	18.666	13.930	15.898
Cluster III			0.000	11.586	20.972	15.370
Cluster IV				0.000	24.061	9.762
Cluster V					0.000	25.063
Cluster VI						0.000

Table 4. Cluster mean for different traits in lablab bean

Trait/ Cluster No.	No. of flowers/ spike	No. of fruits/ spike	No. of spike/ plant	Pod length (cm)	Pericarp thickness (cm)	Pod breadth (cm)	No. of seeds/ pod	Pod weight (g)	Yield/ plant (kg)
I	32.194	10.611	95.694	9.768	0.199	2.087	4.542	6.777	6.656
II	34.000	13.333	100.22	14.722	0.161	2.356	5.222	8.489	9.411
III	27.333	12.667	111.33	8.000	0.167	1.867	4.000	4.733	1.420
IV	24.667	9.000	18.667	6.733	0.203	2.133	5.333	5.9333	2.300
V	32.000	9.000	110.00	18.50	0.167	3.033	3.667	12.767	5.057
VI	33.00	13.333	20.667	8.00	0.177	2.567	4.333	4.453	8.233

other yield contributing traits followed by cluster VI (Table 4). Cluster mean for fruit weight was highest for cluster V followed by cluster II. Therefore, these genotypes can be used in hybridization programme to get recombinations with highest value for the all the traits under study. Further, in the cluster II selection can be practiced as it contains highest number of flowers/spike and number of spike/plant, which are directly contributing to the yield.

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