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Genetic diversity analysis by D² clustering of yield and yield attributing traits in Indian bean [*Lablab purpureus* (L.) Sweet]

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Abstract
Genetic diversity analysis was conducted at Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh in 22 diverse genotypes of Indian bean for 17 yield and yield attributing traits and grouped in to five clusters through Mahalanobis' D² analysis. Out of the 5 clusters, maximum number of genotypes were accommodated in cluster I with 13 genotypes, followed by cluster II with 5 genotypes, cluster V with 2 genotypes, cluster III and IV were solitary containing single genotype each namely CHF-22 and CHF-10 respectively. Divergence study revealed pod yield per plant contributed maximum per cent to the diversity followed by number of branches per plant, plant height, number of cluster per plant, green pod crude protein, days to 50% flowering, number of flower per cluster and number of pods per cluster. Maximum inter cluster distance was observed between cluster II and V which indicated that the genotypes within these clusters were highly divergent and desirable to select for further crop improvement programme.

Keywords: Indian bean, D² analysis, cluster, divergence & Mahalanobis

Introduction

Indian bean [*Lablab purpureus* (L.) Sweet] is an annual, a self-pollinated, diploid with chromosome number 2n=22,24 belongs to the family Fabaceae. It is also known by various synonyms *viz.*, Hyacinth Bean, Country Bean, Bonavist Bean, Tonga Bean, Lablab Bean, Dolichos Bean, Butter Bean, Field Bean, Poor's man Bean and in Hindi Sem or Semi. Vavilov (1939) [1] had considered India as the primary centre of origin of Indian bean and wild forms are found in many parts of the country. In general, two cultivated types *viz.*, *Lablab purpureus* var. *typicus* and *Lablab pupureus* var. *lignosus* are under cultivation. Former is vegetable type cultivated for its soft and edible pods while the latter is cultivated as field bean for its dry seed as pulse crop. Both Varieties are cross compatible. Fresh pods are highly nutritive and contain carbohydrates (6.7 g), protein (3.8 g), fat (0.7 g), minerals (0.9 g) and fiber (1.8 g) per 100 g of edible portion (Bose *et al.,* 2000) [2]. The tender fleshy pods, shelled green seeds and also dry beans are eaten after cooking and have very good nutritive and medicinal value as it has anti diabetic property and is good for natural cure of bladder burns, cardiac problems, diarrhoea, sciatica and tenesmus (Ravinaik *et al.,* 2015) [3]. The best way to understand the potential of the available germplasm is by analysing its genetic diversity. For an outstanding breeding programme in the crop improvement, diversity analysis greatly helps the breeder in the identification and proper choice of parents for specific breeding objectives. The present study was to assess the genetic diversity among germplasm lines.

Materials and Methods

The present investigation is conducted in Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh. The experimental material for the present study comprised of 22 genotypes collected from the North Eastern states of India. The experiment was laid out in Randomized Block Design (RBD) with three replications. Seeds were sown at a depth of 2-3 cm. Spacing between row to row and plant to plant was 3 m and 1.3 m respectively. Necessary plant protection measures with intercultural operations were carried out in accordance with the recommended package of practices. Five plants were selected randomly for observation from each replication for 17 yield and yield attributing traits; the average from these fifteen plants was worked out for the statistical

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computation. Mahalanobis (1936) [4] D^2 statistical analysis was used for assessing the genetic divergence and genotypes were grouped into different clusters following Tocher's method.

Results and Discussions

The genetic diversity among 22 genotypes was measured by employing D^2 statistics and grouped in to 5 clusters using Tocher method (Rao, 1952) (Fig 1). Out of the 5 clusters, cluster I was largest group comprising of 13 genotypes, followed by cluster II with 5 genotypes, cluster V with 2 genotypes, cluster III and IV were solitary containing single genotype each (Table 1). This clearly showed that the genotypes did not cluster according to geographical distributions. These results were in concurrence with Vivek (2014) [6], Chaudhari et al. (2013) [7], Verma (2013) [8] and Singh et al. (2011) [9]. The absence of relationship between genetic diversity and geographical distance indicated that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, variation, natural and artificial selection were responsible for genetic diversity.

Inter cluster D^2 values are given in the (Table 2 and Figure 2). The intercluster D^2 value was maximum (74,427.9) between cluster II and V. The minimum (6,915.81) distance was observed between cluster I and III which indicated close relationship among the genotypes included in these two clusters. Intra cluster distance was observed only in cluster I, II and V as the remaining two clusters contained only one constituent genotype. Intra cluster distance was highest in the cluster V (8628.45), followed by cluster II (6789.03) and cluster I (2482.56). The nearest and farthest clusters from each cluster based on D2 values are represented in Table 3. It is desirable to select genotypes from clusters showing high inter-cluster distance.

Cluster means were computed in all 5 clusters for 17 characters studied and presented in Table 4. From the present data, it is evident that mean value of plant height was maximum in cluster V (375.50) and minimum in cluster II (210.60). Minimum number of branches per plant was recorded in cluster I (4.51) while maximum plant height was recorded in cluster V (8.37). The genotypes in cluster II exhibited minimum days to 50% flowering (80.53) while those in cluster V exhibited maximum days to 50% flowering (121.00). Days to maturity was recorded highest in cluster V (148.00) while minimum was recorded in cluster II (107.07). With regards to number of flowers per cluster, cluster II showed the minimum mean value (12.07), while cluster V showed the maximum (21.58). Number of cluster per plant was minimum in cluster II (7.53) and maximum in cluster IV (15.90). Cluster IV exhibited minimum to pod set (43.21) while cluster IV exhibited maximum to Pod set (48.07). Pod

length was lowest in cluster IV (9.53) while it was highest in cluster III (14.37). Pod width was observed highest in cluster III (3.97) while it was observed lowest in cluster II (2.08). The genotypes in cluster III exhibited maximum pod weight (12.30) while genotypes in cluster II exhibited minimum pod weight (5.75). The genotypes of cluster V had maximum number of pods per cluster (9.97) while genotypes of cluster II had minimum number of pods per cluster (5.18). Number of pods per plant was recorded maximum in cluster V (156.04) and minimum in cluster II (43.88). Number of seeds per pod was found maximum in cluster III (5.33) and minimum in cluster I (4.71). The genotypes in cluster IV exhibited maximum green pod crude protein (19.15) while that in cluster IV exhibited minimum green pod crude protein (15.47). Green pod crude fiber was recorded maximum in cluster V (0.32) and minimum in cluster IV (0.15). Highest pod yield per plant was found in cluster V (1882.33) while it was lowest in cluster II (226.60). Pod yield per hectare was recorded highest in cluster V (5.38) and lowest in cluster II (0.65).

In present investigation, pod yield per plant (58.87%) contributed maximum to the divergence (Table 5 & Figure 3) followed by number of branches per plant (20.78%), plant height (15.15%), number of cluster per plant (2.16%) and green pod crude protein (1.73%), Days to 50% flowering (0.43%), Number of Flowers per cluster (0.43%) and Number of pods per cluster (0.43%). Similar contributions towards diversity have also been reported by Chaudhari et al. (2013) [7] and Verma (2013) [8].

Cluster V with genotypes CHF-8 and CHF-9 were the more divergent for improving for plant height, number of branches per plant, days to 50% flowering, days to maturity, number of flowers per cluster, number of pods per cluster, number of pods per plant, green pod crude protein, green pod crude fiber, pod yield per plant and pod yield per hectare. Cluster III with single genotype (CHF-22) is found to be promising for improving pod length, pod width, pod weight and number of seeds per pod. Cluster IV with single genotype (CHF-10) is found to be promising for improving number of cluster per plant and pod set. Hence, genotypes in these clusters can be utilized in Indian bean improvement programme as donor parents for improving all these characters. Hence, apart from selecting genotypes from these clusters which have high inter-cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence in respect to a particular character of interest. This is to mean that, if breeder's intention is to improve fruit yield, they can select parents which are highly divergent with respect to these characters.

Table 1: Clustering pattern of 22 germplasm lines of Indian bean on D^2 analysis.

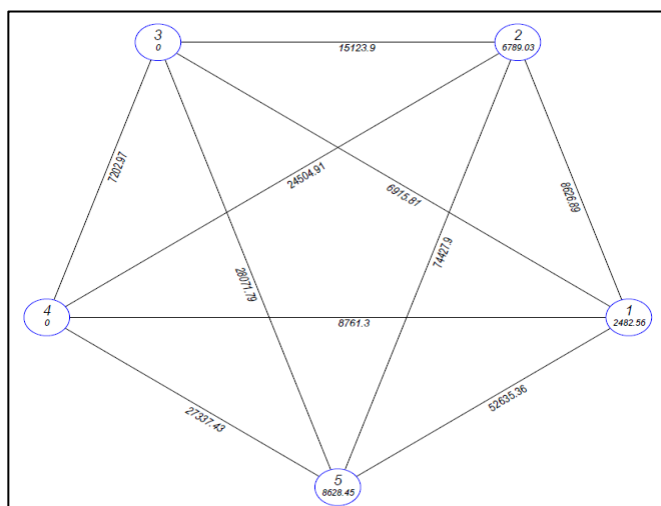| Sl. No.	Cluster	Number of genotypes	Genotypes
1.	Cluster I	13	CHF-13, CHF-14, CHF-16, CHF-5, CHF-7, CHF-12, CHF-19, CHF-1, CHF-16, CHF-17, CHF-4, CHF-18, CHF-15
2.	Cluster II	5	CHF-11, CHF-21, CHF-3, CHF-2, CHF-20
3.	Cluster III	1	CHF-22
4.	Cluster IV	1	CHF-10
5.	Cluster V	2	CHF-8, CHF-9
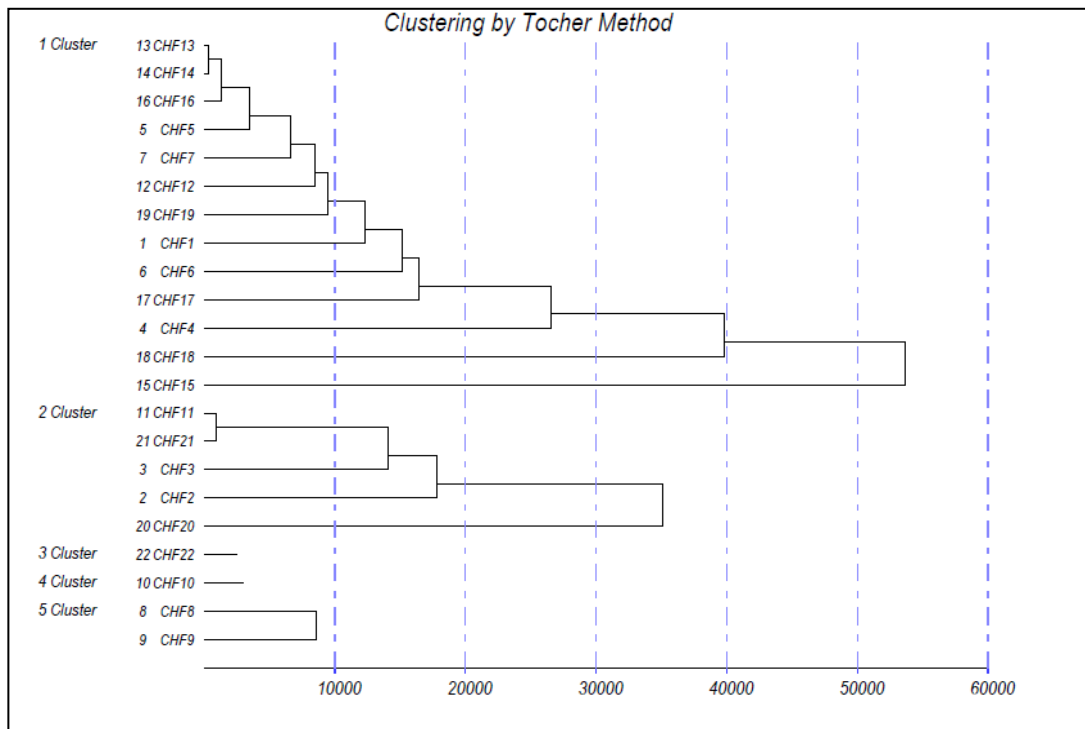
Fig 1: Clustering pattern of 22 genotypes of Indian bean for seventeen studied characters using Tocher's method

**Table 2:** Average intra and inter cluster D² values of clusters in Indian bean

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	2482.56	8626.89	6915.81	8761.30	52635.36
Cluster II		6789.03	15123.90	24504.91	74427.90
Cluster III			0.00	7202.97	28071.79
Cluster IV				0.00	27337.43
Cluster V					8628.45

Table 3: The nearest and farthest clusters from each cluster based on D² values in Indian bean.

Cluster	Nearest cluster	Farthest cluster
Cluster I	III (6,915.81)	V (52,635.36)
Cluster II	I (8,626.89)	V (74,427.9)
Cluster III	I (6,915.81)	V (28,071.79)
Cluster IV	III (7,202.97)	V (27,337.43)
Cluster V	IV (27,337.43)	II (74,427.9)

Fig 2: Intra and inter-cluster distances among five clusters of Indian bean genotypes
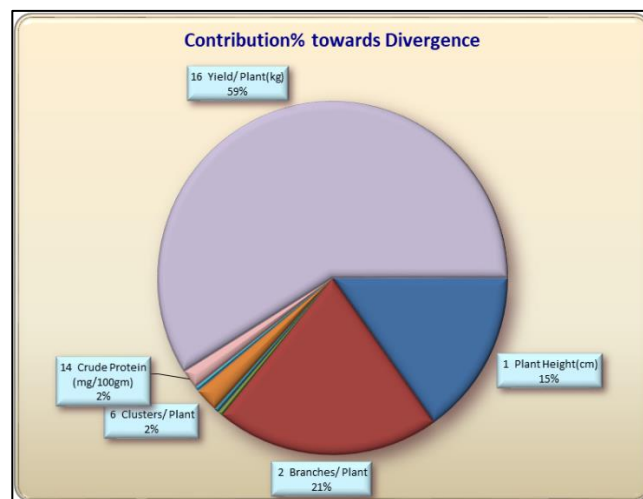
Fig 3: Percent contribution of 17 characters towards diversity in Indian bean

Table 4: Cluster mean analysis

Cluster Number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Cluster I	311.28	4.51	107.31	135.21	16.23	12.22	44.13	10.26	2.46	7.15	7.10	87.44	4.71	17.85	0.29	607.53	1.74
Cluster II	210.60	4.96	80.53	107.07	12.07	7.53	43.21	9.93	2.08	5.75	5.18	43.88	4.72	15.79	0.21	226.60	0.65
Cluster III	344.33	6.32	119.67	146.33	16.17	12.63	45.83	14.37	3.97	12.30	5.50	69.49	5.33	15.63	0.29	854.42	2.44
Cluster IV	318.33	4.64	105.33	132.67	19.77	15.90	48.07	9.53	2.63	8.13	9.13	145.22	4.83	15.47	0.15	1180.87	3.37
Cluster V	375.50	8.37	121.00	148.00	21.58	15.62	46.19	11.00	3.15	12.02	9.97	156.04	4.75	19.15	0.32	1882.33	5.38

Where,
1. Plant height (cm)
2. Number of branches per plant
3. Days to 50% flowering
4. Days to maturity
5. Number of flowers per cluster
6. Number of cluster per plant
7. Pod Set (%)
8. Pod length (cm)
9. Pod width (cm)
10. Pod weight (g)
11. Number of pods per cluster
12. Number of pods per plant
13. Number of seeds per pod
14. Green pod crude protein (mg/100g)
15. Green pod crude fiber (%)
16. Pod yield per plant (kg)
17. Pod yield per ha (q)

Table 5: Percentage contribution of seventeen characters towards diversity in Indian bean genotypes

Character	Contribution (%)
Plant Height(cm)	15.15%
Number of branches/ plant	20.78%
Days to 50% flowering	0.43%
Days to maturity	0.00%
Number of flowers per cluster	0.43%
Number of cluster per plant	2.16%
Pod set%	0.00%
Pod length (cm)	0.00%
Pod width (cm)	0.00%
Pod weight(gm)	0.00%
Number of pods per cluster	0.43%
Number of pods per plant	0.00%
Number of seeds per pod	0.00%
Green pod crude protein	1.73%
Green pod crude fiber	0.00%
Yield per plant (Kg)	58.87%
Yield per hectare (q)	0.00%

Conclusion
Genetic divergence among 22 genotypes revealed that cluster V with genotypes CHF-8 and CHF-9 were the more divergent for improving plant height, number of branches per plant, days to 50% flowering, number of flowers per cluster, green pod crude protein and pod yield per plant. Cluster III with single genotype (CHF-22) is found to be promising for improving pod length, pod width, pod weight and number of seeds per pod. Cluster IV with single genotype (CHF-10) is found to be promising for improving number of cluster per plant and pod set. Hence, genotypes in these clusters can be utilized in Indian bean improvement programme as donor parents for improving all these characters. Moreover, out of 17 characters studied; pod yield per plant contributed maximum percent to the diversity followed by number of branches per plant, plant height, number of cluster per plant, green pod crude protein, days to 50% flowering, number of flowers per cluster and number of pods per cluster. Hence, the above characters are to be taken into consideration while attempting crop improvement studies in Indian bean.

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