

Genetic divergence studies in dolichos bean (*L. purpureus*) genotypes through principal component analysis

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ABSTRACT

Twelve genotypes of dolichos bean collected from IIPR, Kanpur & AICRP on Pigeonpea, Bangalore were evaluated for their genetic diversity using Mahalanobis D² statistic and were grouped in to four clusters. The maximum genetic distance was observed between cluster I and cluster III followed by cluster II and cluster III. Cluster I and cluster II displayed lowest degree of divergence. The maximum intra cluster distance was exhibited by cluster III followed by cluster IV. The mean value for most of the traits was highest in cluster II. Geographical and genetic diversity were observed to be unrelated as genotypes from diverse geographical regions were placed in the same cluster, while genotypes from the same centre were grouped into different clusters.

Key words: Cluster, D², Genetic divergence, Lablab purpureus, Principal component analysis.

INTRODUCTION

Dolichos bean commonly called as Sem (Lablab purpureus L.) is an important vegetable crop widely grown in south and eastern India. Its green pods are used as vegetables and dry seeds as pulse. Success through hybridization followed by selection depends primarily on the selection of parents having genetic divergence for different characters (Murthy & Arunachalam, 2005). Information on nature and degree of divergence would help the plant breeders in choosing suitable parents for their hybridization programmes. Mahalanobis D² statistic is a valuable tool in quantifying the degree of divergence and helps the plant breeder in choosing suitable parents for hybridization programme. The importance and extent of genetic divergence have been investigated in many crops but the information generated with field bean is scanty even a great range of variation exists in the plant and pod characters among the cultivars grown all over the country. The present investigation was undertaken to elucidate information on genetic divergence so as to formulate breeding strategies to improve the yield and quality in field bean.

MATERIALS AND METHODS

The experiment was conducted at Horticultural College & Research Institute, Venkataramannagudem, West Godavari Dist. (Andhra Pradesh) during kharif season 2012. Twelve genotypes of Dolichos bean viz., Culture 4, Culture 7, Culture 47, Culture 62, GL-243, GL-388, GL-411, GL-671, GL-416, HA-4, Arka Jay (C) and Arka Vijay (C) were grown in a randomized block design with three replications. These were planted in a two row plot. The plot size and spacing were 3 × 3.6m and 60 × 30cm, respectively. Five plants were taken for recording observation on sixteen characters. The data were subjected to analysis of variance and multivariate analysis of D² statistic according to (Mahalanobis, 2008). The genotypes were further grouped into different clusters based on ward's method. PCA was conducted by using SPSS computer package. Mean values registered for each variable were used for statistical analysis. The principal components (PCs) for the dataset, eigen values (variances) for PCs, loadings (correlation of each variable with the PCs) and PC score for each genotype under the concerned PCs were used for interpretation of the analysis. PCs showing the eigen values lesser than one was considered non-significant. PC loadings greater than selection criterion (SC) were considered significant.

RESULTS AND DISCUSSION

Mahalanobis' D² **values** : The correlated unstandardized means of 18 characters studied were transformed to standardized uncorrelated set of variables by using pivotal condensation method. Based on these D² values, per cent contribution of different characters towards genetic divergence was computed.

The character, marketable pod yield per hectare ranked first for 56 times with a maximum contribution of 84.85 per cent followed by days to last pod harvest (9.09%), hundred seed weight (3.03%), days to first pod harvest (3.03) suggesting that

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Sr.	Character	No. of times	Percent
No.		ranked 1st	contribution
1.	Plant height (cm)	0.01	0.00
2.	Number of primary branches /plant	0.01	0.00
3.	Number of secondary branches	0.01	0.00
4.	Days to first flowering	0.01	0.00
5.	Days to 50% flowering	0.01	0.00
6.	Number of inflorescences per plant	t 0.01	0.00
7.	Number of pods per inflorescence	0.01	0.00
8.	Number of pods per plant	0.01	0.00
9.	Number of seeds per pod	0.01	0.00
10.	Mean pod weight (g)	0.01	0.00
11.	Pod length (cm)	0.01	0.00
12.	Pod width (cm)	0.01	0.00
13.	Days to first pod harvest	2	3.03
14.	Days to last pod harvest	6	9.09
15.	Marketable pod yield per plant (g)	0.01	0.00
16.	Hundred seed weight (g)	0.01	0.00
17.	Protein content (%)	2	3.03
18.	Pod yield/ha (q)	56	84.85

 Table 1. Per cent contribution of different characters towards diversity in dolichos bean genotypes

these are potent factors in differentiating the germplasm of dolichos bean **(Table 1)**. Plant height (cm), number of primary branches, number of secondary branches, days to first flowering, days to 50% flowering, number of inflorescences per plant, number of pods per inflorescence, number of seeds per pod, pod length (cm), pod width (cm), mean pod weight (g) and hundred seed weight (g) did not contribute anything towards the genetic diversity.

PCA analysis : About 95.67 % of total variance of the observations was explained by the first 4 principal components (Table 2). Component loadings of 18 guantitative traits are also given in Table 2. The significance of variables in each PC was determined by comparing the loading with corresponding SC. The days to first harvest (-0.311), pod yield per ha (0.307), and pod yield per plant (0.303) explained maximum variance in PC 1. Positive correlation was observed among 100 seed weight and pod yield per plant. Negative value was observed with days to first harvest in PC 1, which explained 55.42 % of the total variance. So there is great scope of improvement of these traits through selection (Pan et al., 2009). The PC 2 which accounted for 20.51 % of total variance showed a higher value of 0.386 for pod length signifying its importance in pod yield of lablab bean. Significant negative loading (-0.349) was obtained from 100 seed weight. PC 3 that explained 15.89 % of total variance reflected significant loading of traits like plant height (0.498) and significant negative loading was obtained from pods per inflorescence (-0.559). PC 4 which explained 3.83% of total variation reflected significant negative loadings of traits like protein content (-0.580), inflorescence per plant (-0.441) and number of primary branches/plant (-0.395).

Table 2.Component loading of 18 traits, eigen values,
proportion of total variability, represented by
four principal components (PC), cumulative
per cent variability and selection criterion (SC)
in 12 dolichos bean genotypes

Trait	Р	Principal components			
	1	2	3	4	
Plant height (cm)	0.024	0.273	0.498	0.060	
Primary branches/ Plant	-0.213	-0.238	-0.262	-0.395	
Secondary branches / Plant	0.278	0.024	-0.266	0.039	
Days to first flowering	-0.219	0.350	-0.019	0.227	
Days to 50% flowering	-0.227	0.343	-0.017	0.120	
Inflorescence / Plant	0.239	0.080	0.289	-0.441	
Pods/ Inflorescence	0.050	-0.123	-0.559	0.101	
Pods/ Plant	0.294	0.174	-0.084	-0.032	
Seeds/ Pod	-0.179	-0.287	0.265	-0.233	
Mean pod weight (g)	-0.216	-0.349	-0.018	0.001	
Pod length (cm)	-0.017	0.386	-0.328	-0.156	
Pod width (cm)	-0.272	-0.245	0.042	-0.045	
100 seed weight (gm)	0.299	-0.072	-0.004	0.182	
Protein content %	-0.147	0.367	-0.112	-0.580	
Pod yield/ Plant (gm)	0.303	-0.076	0.094	0.125	
Pod yield/ ha (q)	0.307	-0.086	0.025	-0.100	
Days to first pod harvest	-0.311	0.016	0.081	0.094	
Days to last harvest	-0.291	0.103	-0.017	0.286	
Eigene value (Root)	9.977	3.693	2.862	0.691	
% Var. exp.	55.428	20.517	15.897	3.837	
Cum. var. exp.	55.428	75.945	91.842	95.679	

Clustering of D² values : Twelve dolichos bean genotypes were grouped into four clusters by treating estimated D² values as the square of the generalized distance (**Table 3**). Cluster I consisting of four genotypes, Cluster II having only one genotype, Cluster III with three genotypes and Cluster IV comprising four genotypes. The genotypes collected from same geographical location fall in different clusters, revealed that geographical distance do not contribute to genetic divergence. These results are in general agreement with the findings of (Golani *et al.*, 2006).

 Table 3. Clustering pattern of twelve genotypes of dolichos bean

Cluster	No. of genotypes	Genotypes
I	Four	Culture-4, Culture-7, GL-416, HA-4
II	One	GL-411
111	Three	Culture-47, GL-243, GL-671
IV	Four	Culture-62, GL-388, Arka Jay, Arka Vijay

Average intra and inter cluster distances : The intra cluster distance ranged from 16052.400 (cluster I) to 27745.960 (Cluster III). The inter cluster D² values varied from 64494.990 to 531230.700 and maximum genetic divergence existed between clusters I and III (531230.700) followed by cluster II and III (255649.300) indicating wider genetic diversity

Table 4. Average intra and inter-cluster D² values for four clusters in twelve genotypes of dolichos bean

Clusters	Ι	Ш	III	IV
I	16052.400	64494.990	531230.700	252919.000
II		0.000	255649.960	79936.230
			27745.960	75971.380
IV				17175.630

among the genotypes included in these groups (**Table 4**). The minimum genetic divergence was registered between clusters I and II (64494.990) followed by clusters III and IV (75971.380). Cluster IV was the most diverse as many clusters showed high inter cluster distances with it. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated (Biju *et al.*, 2004).

Statistical distance represents the extent of genetic diversity among clusters. Cluster-II displayed minimum intra cluster distance, while the maximum intra cluster distance was recorded in cluster- III which may be due to limited gene exchange or selection practices among the genotypes for diverse characters. In this experiment, inter cluster distance was always higher than intra-cluster distance. Similar results were found by (Nandi et al., 2003, Sureja and Sharma, 2009, Singh and Mishra, 2010 and Savitha, 2011). Maximum inter cluster distance was observed between cluster -I and cluster -III followed by cluster -II and cluster -III indicating wider genetic diversity among the genotypes included in these groups. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Similar results in dolichos bean have been reported by (Pandey et al. 2006 and Ganesh, 2007).

Cluster means for different characters showed considerable differences between the clusters for all the characters (Table 5). Among four clusters, the genotypes

 Table 5. Mean values of clusters for 18 characters in twelve genotypes of dolichos bean

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Cluster	I	II	III	IV
Plant height (cm)	87.33	75.63	89.80	83.27
No. of primary branches/plant	3.82	2.92	2.66	3.38
No. of secondary branch/plant	8.34	12.26	14.56	11.66
Days to first flowering	58.39	55.39	46.75	48.89
Days to 50% flowering	61.12	58.42	48.75	51.65
No. of inflorescence /plant	7.42	10.46	12.97	11.50
No. of pods /inflorescence	4.72	6.86	7.47	5.83
Number of pods per plant	31.08	68.38	82.37	65.35
Number of seeds per pod	3.72	3.63	4.03	3.92
Mean pod weight (g)	3.67	2.42	3.47	3.44
Pod length (cm)	6.20	4.73	5.94	6.39
Pod width (cm)	1.76	1.52	1.85	1.91
Days to first harvest	83.23	83.13	73.19	76.44
Days to last harvest	135.83	146.29	171.02	145.23
Pod yield per plant (g)	102.00	166.11	273.09	223.13
Hundred seed weight (g)	29.41	33.83	56.63	34.22
Protein content (%)	24.94	25.64	19.30	23.82
Pod yield per ha (q)	56.60	92.39	151.79	123.87

present in the cluster- III showed higher marketable yield per plant followed by the genotypes present in cluster –IV, which is due to the fact that the genotypes present in cluster –III recorded more number of pods per plant, inflorescence per plant, pods per inflorescence and hundred seed weight. Hence, these genotypes can be utilized in crop improvement programme as donor parents for improving the respective characters.

CONCLUSION

Hence, apart from selecting genotypes from the 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 pod yield, he can select parents which are highly divergent with respect to these characters.

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