

# Genetic Diversity Studies in Dolichos Bean [Lablab Purpureus Var. Typicus] for Growth, Yield and Quality Parameters

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**Abstract:-** Twenty-three diverse types of dolichos beans were evaluated for yield and their contributing characteristics. Genotypes were grouped into seven clusters on the basis of the relative magnitude of D<sup>2</sup> values. The maximum inter-cluster distance was observed between cluster III and cluster VI followed by clusters V and VI. The minimum inter-cluster distance was observed between cluster I and cluster VII. The maximum intra-cluster distance was in cluster VI followed by cluster IV. The mean value for most of the traits was highest in cluster V. Pod yield plant<sup>-1</sup> followed by crude fibre, crude protein and number of seeds pod<sup>-1</sup> and green pod girth contributed higher towards genetic divergence. Hence, that the genotypes from cluster V and cluster I could be selected for crop enhancement.

**Keywords:-** Dolichos bean, Hyacinth bean, genetic divergence, variability.

## I. INTRODUCTION

Dolichos bean or Indian bean (*Lablab purpureus*, var. *typicus*) generally known as hyacinth bean. Dolichos bean is an important vegetable crop of Indian origin. It occupies a unique position for vegetable purpose among the legume vegetables [1,2]. It is a multi-purpose legume crop, as it is used as a vegetable or pulse for human consumption and as green manure in agriculture and also used as cattle fodder in numerous countries, it is one of the important grain legumes extensively grown in districts of southern Karnataka and adjoining districts of Tamil Nadu, Andhra Pradesh, and Telangana states of India[11.] The population which exists in diverse environments might have been strongly diversified genetically. So, it is necessary to understand the extent of genetic divergence existing between the diversified forms. The more diverse the parents, the greater the chances of obtaining a higher amount of heterotic expression in F<sub>1</sub> and a broad spectrum of variability in segregating generations.

Genetic diversity is important to applied plant breeding as it reduces vulnerability to pests, besides accelerating progress for achieving agronomic traits such as yield. The clustering reveals the exact genetic divergence between the genotypes therefore clustering is an important tool for plant breeders to group the genotypes into different clusters based on the genetic information and to select more diverse genotypes for crop improvement programme.

## II. MATERIALS AND METHODS

The trial was conducted in the Horticulture Farm in the Department of Horticulture at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal during August-December 2022. Dolichos bean genotypes comprised twenty-three diverse genotypes collected from different geographical regions and were evaluated in a randomized block design (RBD) with two replications. Each plant is sown at a spacing of 60 x 60cm. Spacing and intercultural operations were made as per the package of practice recommended by the Horticulture farm in the Department of Horticulture.

## III. RESULT AND DISCUSSION

The genotypes were clustered based on diversity analysis. The D<sup>2</sup> values were worked out. The 23 dolichos bean genotypes by grouping them into seven clusters using clustering techniques. The constituent of different cluster is presented in the Table 1. Among seven cluster, cluster III was found to be the maximum number of genotypes (seven genotypes) out of 23 genotypes assembled from different geographical locations. The clustering pattern revealed that the genotypes did not resolve according to their geographical origin. Geographic diversity, though appears as an important factor, it seems that it is not the only factor determining the genetic divergence. This finding is in conformity with the results of Rai *et al* [2] in dolichos bean.

Seven genotypes were grouped in a single cluster (cluster III) which indicated that they are genetically related or similar in their performance. Cluster II had five genotypes, cluster VI had four genotypes, while cluster I, IV and V had two genotypes. Cluster VII was monogenotypic which indicated that these clusters contain the most diverse genotypes. The average intra-cluster distances between seven clusters revealed that cluster VI (78.30) was found to have the maximum intra-cluster distance followed by cluster III (76.42). Similarly, cluster I, II, IV, V, recorded minimum intra-cluster D<sup>2</sup> values which shows the existence of closer relation between the genotypes in these clusters. At the inter-cluster level, clusters I and VII (31.53) recorded the least inter-cluster distance revealing the closer relationship among the genotypes in the clusters and concluded that it may produce very low records during crop improvement. Greater genetic divergence between the clusters was observed between clusters III and VI (198.64) with a maximum inter-cluster distance followed by clusters VI and

V (187.61) and clusters I and VI (149.18), hence the genotypes fall under the above clusters could produce vigorous progenies and crop improvement may be rewarded. Which is presented in figure1.Hence, the selection of genotypes from cluster VI CO (GB)14 and cluster III Harit for crossing would yield superior recombinants, which is followed by VI CO(GB)14 and V Reethu genotypes are effective parents.

According to the present results, Cluster analysis was unable to discriminate accessions based on their geographic origin an indication that no relationship exists between geographic origin and the genetic diversity of lablab species [4]. Existing variations could be attributed to genotype, environment and the interaction of genotype and environment. Hence, the crossing of genotypes from the genetically divergent clusters produces transgressive segregants in advanced generations and hence it would be useful in hybridization programmes. Similar reports were proposed by Singh *et al.* [5] in cowpea.

The cluster mean values for all 15 characters of 23 Dolichos bean genotypes are presented in Table 3 and the cluster mean values serve for selection of parents for recombination breeding. The cluster V (Reethu and Green long) recorded the highest mean performance for most characters viz., plant height (116.93), days to first flowering (49.59), number of pods plant-1(101.35), individual pod weight (7.19), crude fibre (7.35), crude protein (10.51) and pod yield plant-1(761.50) whereas, mean performance number of branches plant-1 (6.92), days to 50 per cent of flowering (54.56), number of pods cluster-1 (10.62) and number of seeds pod-1 (4.42), were found to be maximum in cluster I Hritu Ankur and cumbum local.

The cluster mean for yield plant-1 (761.5 g) was maximum in cluster VI followed by cluster II. The genotypes in cluster I recorded early performance for days to first flowering. Hence, these genotypes Hritu Ankur, Cumbum local would be used for selection for earliness in crop improvement programmes. It is interesting to note that the pod yield plant-1 obtained in the present study was

(761.5g) cluster V followed by cluster II (746.8g) is three-fold higher values than the results obtained by Hossain *et al.* [6] and reflects the greater scope for identifying superior genotypes for the coastal region.

Therefore, genotypes from these clusters can be selected for a hybridization programme to get desirable recombinants. The cluster means revealing the best cluster for various characters. Depending upon the aim of breeding, potential lines can be selected from different clusters as parents in a hybridization programme.

The number of times that each character appeared first rank is presented in Table 4. The character pod yield plant-1 contributed the maximum of (47.04 per cent) towards the genetic divergence followed by crude fibre (43.09 per cent), crude protein (8.30), number of seeds pod-1 (1.19), green pod girth (0.40), individual pod weight (1.58 per cent), pod yield plant-1 (1.58), number of seeds pod-1 (1.18 per cent) and green pod girth (0.79 per cent). All the other characters exhibited very low contributions towards genetic divergence which is presented in figure 2. Similar results in dolichos beans have been reported by Pandey *et al.* [7] and Ganesh [8].

The relative contribution of plant height, number of branches plant-1, days to first flowering, days to 50 per cent flowering, number of flowers inflorescence-1,number of pods plant-1, pod set per cent, number of pods cluster-1 and green pod length for divergence among the genotypes were found nil. It indicated that the genotypes from cluster V ( Plant height, days to first flowering, number of pods plant-1, individual pod weight, crude fibre, crude protein and pod yield plant-1) and cluster I (days to 50 per cent flowering, number of branches plant-1, number of pods cluster-1, and number of seeds pod-1) could be selected for crop improvement in dolichos bean as they recorded higher cluster mean values for traits contributing maximum towards genetic divergence. Similar findings were earlier reported by Mahalingam *et al.* [9] and Rai *et al.* [10] in dolichos bean.

Table 1: Clustering pattern of 23 genotypes of Dolichos bean.

Cluster number	Total numbers of genotypes	Genotypes
I	2	Hritu Ankur
		Cumbum Local
		Ankur Goldy
		DolichosNandhini
II	5	Splendour
		Trichy Local
		ArkaSambhram

		Theni local (Black)
		Arka Jay
		Eesanya
III	7	Green Lady
		Harit
		Paravi Local
		Theni Local (Red)
		Villupuram Local
IV	2	ArkaAmogh
		Reethu
V	2	Green Long
		Soamnath
		Samrat
VI	4	Thekkady Local
		CO(GB)14
VII	1	Salem Dwarf

Table 2: Mean intra cluster (diagonal) and inter cluster D<sup>2</sup> and D values

Cluster	I	II	III	IV	V	VI	VII
I	<b>267.74</b> <b>(16.36)</b>	9148.05 (95.64)	5522.21 (74.31)	1517.84 (38.95)	2464.85 (49.64)	22256.90 (149.18)	994.19 (31.53)
II		<b>3877.26</b> <b>(62.27)</b>	20905.72 (144.58)	12457.97 (111.61)	17293.71 (131.50)	7136.40 (84.47)	5772.49 (75.97)
III			<b>5840.13</b> <b>(76.42)</b>	3659.12 (60.49)	3606.40 (60.05)	39459.19 (198.64)	7218.84 (84.96)
IV				<b>864.86</b> <b>(29.41)</b>	1762.28 (41.97)	27945.77 (167.17)	2333.50 (48.30)
V					<b>1188.63</b> <b>(34.48)</b>	35198.48 (187.61)	4376.60 (66.15)
VI						<b>6130.75</b> <b>(78.30)</b>	1635.16 (129.364)
VII							<b>0.000</b> <b>(0.000)</b>

Values in parenthesis indicate 'D' values  
 Bold diagonal values indicate intra cluster value



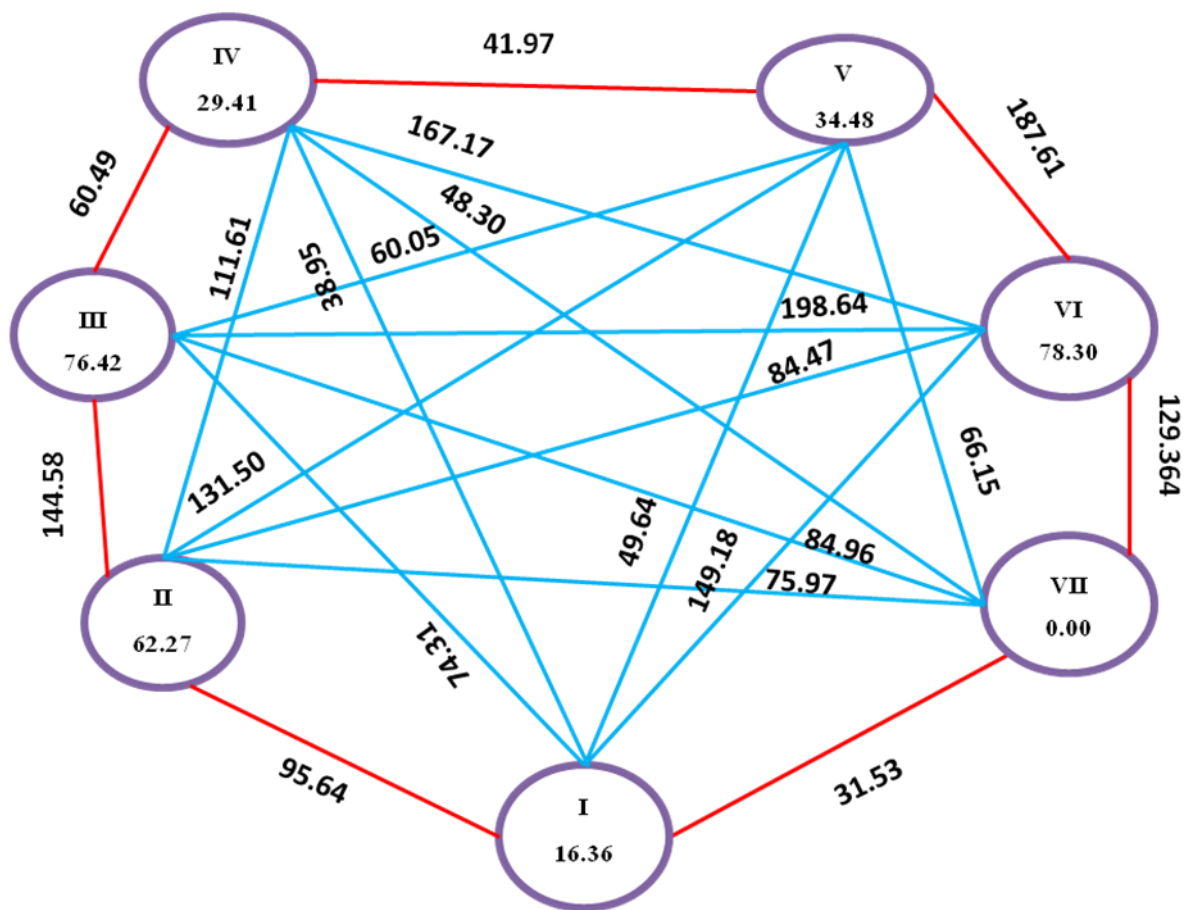


Fig. 1: Mean intra cluster and inter cluster distances (D values) (not to scale)

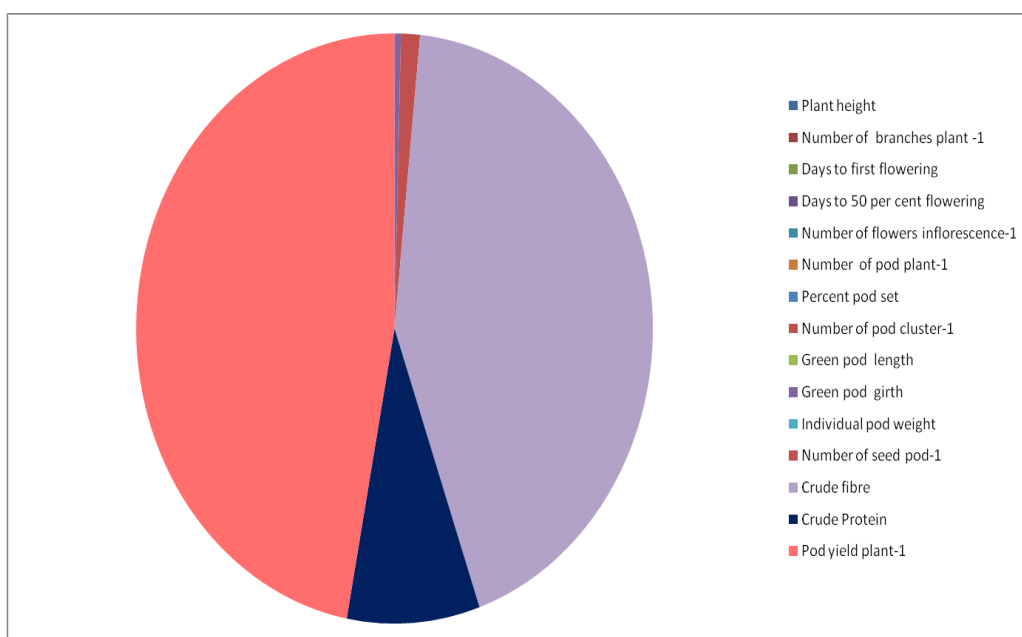


Fig. 2: Per cent contribution of different traits to the total divergence in dolichos bean genotypes

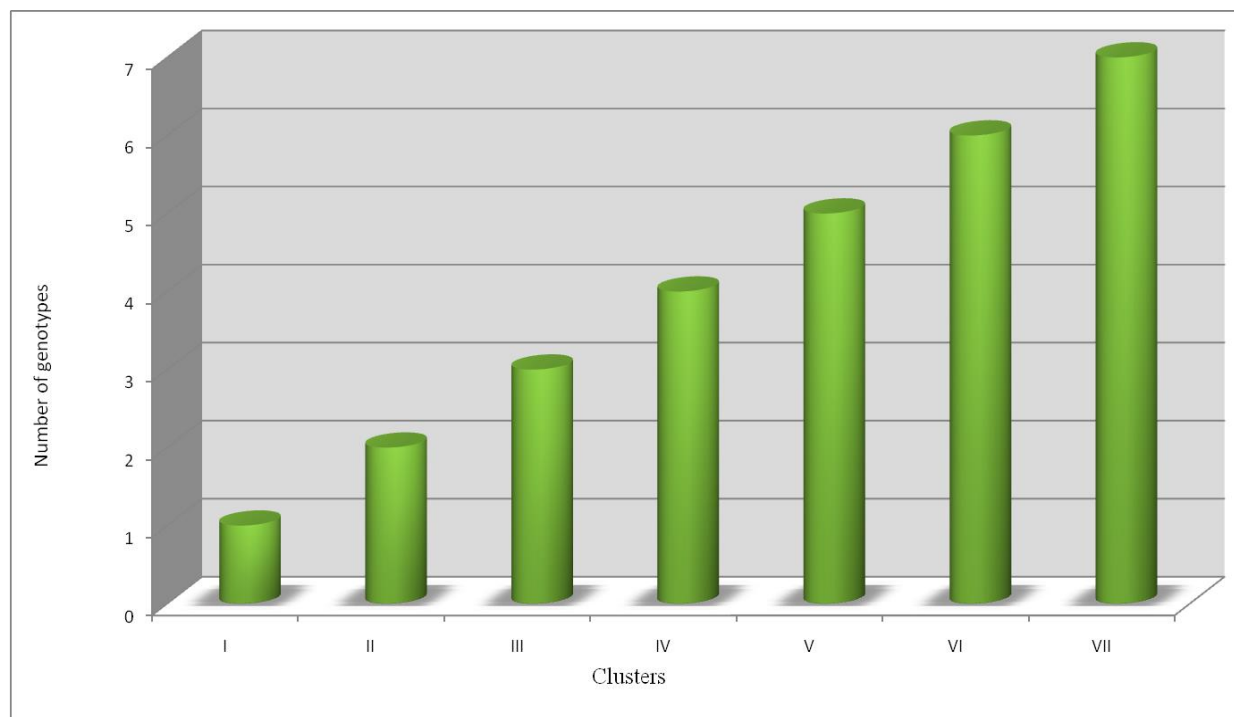


Fig. 3: Genotypic composition of D2 clusters in dolichos bean genotypes

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