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Genetic Divergence Analysis in Some Vegetable Cluster Bean Genotypes

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ABSTRACT

Background: Twenty one diverse genotypes of vegetable cluster bean collected from different geographical locations of India were evaluated under randomized block design (RBD) with 3 replications to find out the extent of genetic divergence through D^2 and PCA (Principal component analysis) studies.

Methods: The experiment was carried out at Post Graduate Research Farm under the Department of Horticulture, Centurion University, Odisha during the summer season of 2024.

Result: Collected germplasm were grouped into 6 non-overlapping clusters. Upon analysis, cluster I, III, V and VI each had 4 numbers of genotypes while cluster II and IV had 3 and 2 genotypes respectively. No monogenotypic cluster was found. Cluster I and VI had the largest inter-cluster distance, followed by cluster I and V. Cluster number VI exhibited highest mean values for most of the traits under study. So, all the genotypes which were categorized under cluster I, V and VI can effectively be utilized for hybridization purpose as there is a chance of getting maximum heterosis in the resultant hybrids. Among the traits, days to 50% flowering followed by green pod yield per plant contributed maximum towards the total divergence. From the PCA studies it is observed that first eigen root had maximum variation. First 3 PC axes collectively interpreted 96.99% variation.

Key words: Cluster bean, D^2 analysis, Genetic divergence, Genotypes, Principal component analysis.

INTRODUCTION

Cyamopsis tetragonoloba (L.) Taub, a diploid legume crop with diploid chromosome number 2n = 14, is a significant and popular vegetable in India's arid, semi-aridand coastal tropical regions. It is a member of the order *Fabales*, family *Fabaceae*, sub-family *Faboideae*, as well as the tribe *Galegae* (*Indigoferae*) (Bhatt *et al*., 2016). It is unclear where from cluster bean originated. According to Vavilov (1951), India is the geographic centre of the variability though it is not found in its wild state in this region. According to Hymowitz's (1972) trans-domestication hypothesis, *Cyamopsis tetragonoloba* evolved from the drought-tolerant wild African species *Cyampopsis senegalensis* while being transported by Arab traders to the South Asian subcontinent, most likely between the ninth and thirteenth centuries AD, for use as horse feed. Cluster bean can be used as vegetable, fodder, cattle feed and green manure crop. Its young, immature and tender pods are used as vegetables, which is also known as cheap source of energy (16 Kcal), protein (3.2 g), fat (1.4 g), carbohydrate (10.8 g), vitamin A (65.3 IU), vitamin C (49 mg), calcium (57 mg) and iron (4.5 mg) for every 100 g of edible portion. Alongside, this crop is potentially capable of fixing atmospheric nitrogen through nodule bacteria (*Rhizobium japonicum*) so that, after completion of cluster bean cultivation in 1 ha of land, the soil receives an addition of approximately 40-80 kg of N (Quin, 1997). It is mainly grown in India, Pakistan, South Africa, Morocco, Germany, Spain, Italy and United States (Ashraf and Iram, 2005; Punia *et al*., 2009). India is the major guar producer accounting for 80% of the world's production (Dodla *et al*., 2017). The majority of India's produce (>80%) comes from rainfed agriculture in Rajasthan's desert and semi-arid regions, with Gujarat, Haryana and Punjab following (Bhatt *et al*., 2017). In southern parts of Odisha, cluster bean has been under cultivation mostly in *Kharif* and summer seasons for vegetable purpose but its potentiality is not fully exploited. The present cultivars of this crop in this region exhibit lower productivity as compared to national average *i.e.* 485 kg/ha.

Genetic diversity is one of the most important components for quantification of genetic variability in self, often cross and cross pollinated vegetable crops. The concept of genetic divergence, including its nature, quantity and degree of variability is thought to be particularly helpful for a successful breeding plan in terms of choosing

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genetically diverse parents from the available genotype pool (Ullah *et al*., 2015). Important statistical tools like D^2 and Principal Component Analysis (PCA) studies can be effectively utilized in various crop species to find out genetic differences among the collected germplasm (Jatav *et al*., 2019). So, the experiment was designed to select few superior cluster bean genotypes which can be used for breeding new cultivar with high yielding ability.

MATERIALS AND METHODS

Twenty-one cluster bean germplasm were evaluated at the Post Graduate Research Farm, Ranadevi for genetic divergence studies during February-May of 2024 under the supervision of Horticulture Department, MSSSoA, CUTM (Centurion University of Technology and Management), Odisha. The experimental field is falling under the north eastern ghat agro-climatic zone with a typical sub-tropic and sub-humid climate.

The research work was carried out with 3 replications in randomized complete block design (RCBD) to evaluate the performance of cluster bean genotypes. The plants were planted in distinct plots measuring 2.25 m by 1.2 m, with a distance between plants of 15 cm and rows separated by 45 cm. The "Manual on Agricultural Production Technology" (Anonymous, 2008) recommended several cultural techniques and preventative measures for the development of vegetable cluster bean, all of which were followed to ensure a strong crop stand. The information was collected on 14 quantitative characteristics *viz*., plant height (cm), days to first flowering, days to 50 % flowering, number of cluster on main shoot, number of clusters per plant, cluster length (cm), green pod length (cm), 10 green pod weight (g), number of green pod per plant, number of seeds per pod, 100 seed weight (g), pod width (cm), green pod yield per plant (g), protein content of green pods (%). Data from ten plants per genotype were averaged replication-wise and statistical analysis was performed using the resulting mean data.

Following Mahalanobis D^2 statistics (1936), a genetic divergence investigation was conducted. Genotype clustering was accomplished using Tocher's approach which Rao (1952) detailed further. The Ward's technique (1963) was also executed to construct one dendrogram (Fig 1). SAS Professional Version 9.3 and SPSS 13.0 Professional Version were used for the statistical analysis for D^2 and principal components.

RESULTS AND DISCUSSION

All of the genotypes were accommodated into 6 groups based on the degree of divergence by using computed D^2 values as the square of the generalized distance (Table 1). Each of cluster I, III, V and VI had 4 numbers of genotypes while cluster II and IV had 3 and 2 genotypes respectively. The grouping sample of genotypes turned into random that's indicating that there was no direct relationship among geographical distribution and genetic distance. Therefore, the choice of genotypes for hybridization ought to be based on genetic divergence in preference to geographic diversity. Numerous previous research mentioned that vegetable cluster bean genotypes under study were grouped under

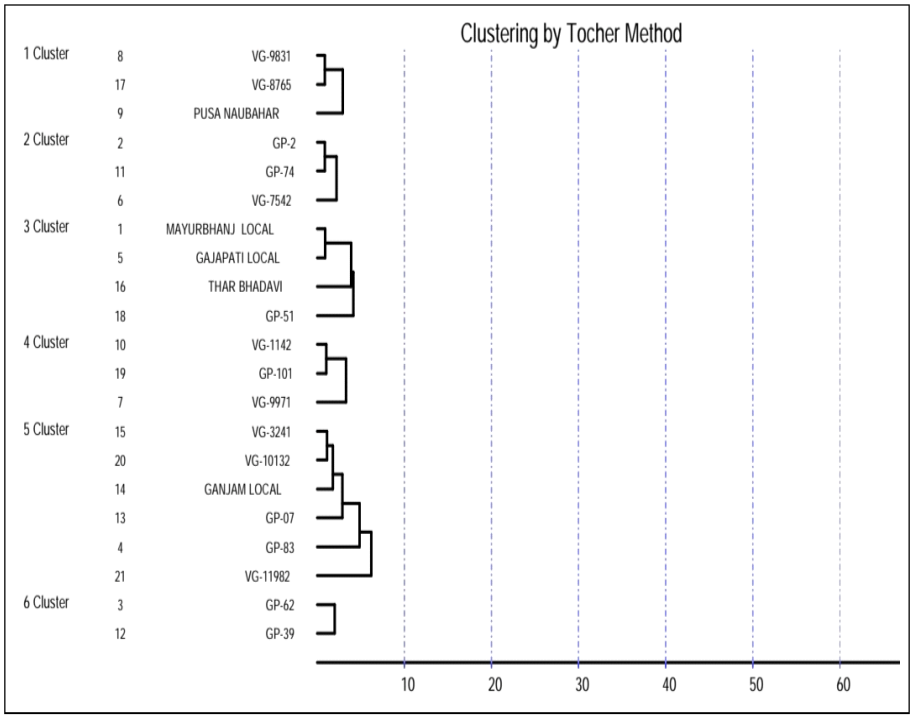


Fig 1: Dendogram of 21 genotypes of vegetable cluster bean by Tocher's method.

Table 1: Genotype clustering of vegetable cluster bean.

Number of cluster	Name of the genotype
I (4)	Mayurbhanj Local, Gajapati Local, Thar Bhadavi, GP 51
II (3)	VG 1142, GP 101, VG 9971
III (4)	GP 2, GP 74, VG 7542 , PusaNaubahar
IV (2)	VG 9831, VG 8765
V (4)	GP 62, GP 39, GP 83, VG 11982
VI (4)	VG3241, VG 10132, Ganjam Local, GP 07

Figures in parentheses indicate number of genotypes.

5-6 clusters (Henry and Mathur, 2005; Anil *et al*., 2014; Kumar *et al*., 2014; Vishnoi *et al*., 2017; Patel *et al*., 2019; Remzeena *et al*., 2021; Mehta *et al*., 2022).

Cluster I followed by cluster V had the highest intra-cluster value compared to the other clusters, which suggests that there is a lot of genetic variation among the component germplasm, according to the results. Cluster IV followed by cluster VI, II and III had the lowest intra-cluster distance. The largest value between clusters I and VI was seen at the inter-cluster level, with clusters I and V and clusters II and VI following closely after. The highest level of divergence was evidently exhibited by the genotypes within these clusters. The lowest inter-cluster value was found between cluster III and IV, followed by cluster V and VI and cluster IV and V, indicating a close link between the genotypes contained in these clusters. In Table 2, the average intra as well as inter cluster distances have been presented whereas Fig 1 and Fig 2 are depicting cluster dendogram and Mahalanobis distance respectively. The genotypes found in the Ist , IInd , Vth and VIth cluster can be utilized as parental materials in a hybridization programme to produce hybrids with considerable heterosis, as evidenced by the highest inter-cluster value between those. In the advanced generation, the segregating population is also expected to give transgressive segregates. Girish *et al*. (2012), Manivannan and Anandakumar (2013), Rai and Dharmatti (2013), Goudar *et al*. (2017) and Masal *et al*. (2022) also found similar kind of findings earlier and they hypothesized that crossing the genotypes selected from distant clusters would likely result in desirable recombinants in cluster bean.

Contribution of characters towards genetic divergence is the main factor on the basis of which parents are selected for a hybridization programme. The character that contributed the most towards diversity was days to 50% flowering (13.80%) followed by green pod yield per plant (12.00%), green pod length (10.48%), number of clusters on main shoot (10.00 %), plant height (10.00%) and number of seeds per pod (7.86%) presented in Table 3. Therefore, these previously mentioned traits can be considered as the most fruitful traits for choosing different genotypes in vegetable cluster bean breeding programme. Previously, high contribution towards the divergence through days to 50% flowering (Patel *et al*., 2019; Remzeena *et al*., 2021; Mehta *et al*., 2022), green pod yield per plant (Goudar *et al*., 2017; Remzeena *et al*., 2021; Masal *et al*., 2022; Susmitha *et al*., 2024), green pod length (Manivannan and Anandakumar, 2013; Rai and Dharmatii, 2013; Mishra *et al*., 2019; Masal *et al*., 2022), number of clusters on main shoot (Mishra *et al*., 2019), plant height (Rai and Dharmatii, 2013; Vishnoi *et al*., 2017; Mishra *et al*., 2019) and number of seeds per pod (Choyal *et al*., 2017) was reported by several researchers. The qualitative trait *i.e*. protein content of green pod had very little contribution towards divergence which corroborated the previous finding by Mehta *et al*. (2022).

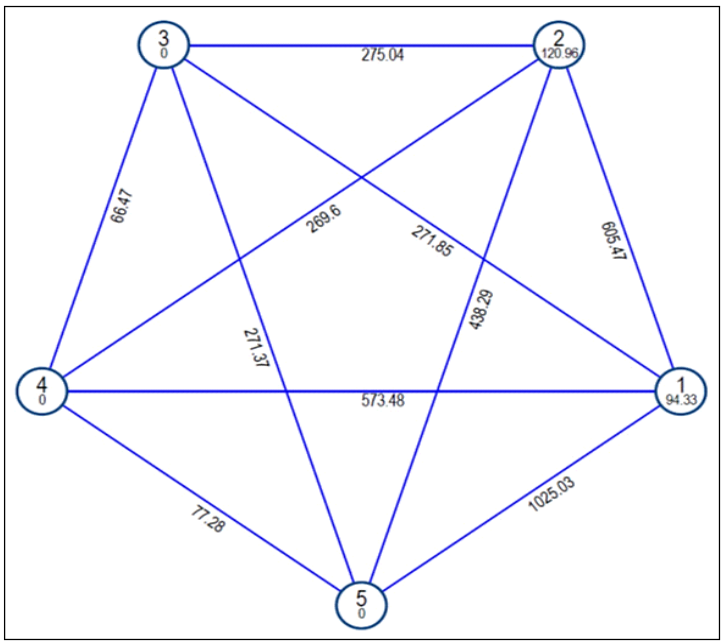


Fig 2: Mahalanobis Euclidean distance of 21 genotypes of vegetable cluster bean.

The cluster means of twenty one genotypes showed that for every character under investigation, the cluster mean values differed in magnitude (Table 3). For all the traits under study except protein content of green pod, cluster VI had the highest cluster mean. Cluster I had the highest cluster mean for protein content of green pod. Cluster VI and I disclose the minimum and maximum number of days to first and 50% flowering respectively. Cluster V also had mean values towards higher sides for almost all the traits. These clusters could act as useful sources of genes for improvement regarding earliness, green pod yield and quality characters. It is possible to bred early bearing, high yielding hybrids with superior pod quality by using genotypes from cluster I, V and VI as parents. Similar divergence investigations have been conducted in the past by Manivannan and Anandakumar (2013), Goudar *et al*. (2017); Mishra *et al*. (2019); Remzeena *et al*. (2021); Masal *et al*. (2022) and Susmitha *et al*. (2024).

Based on the correlation matrix of yield and yield-attributing variables of twenty one cluster bean genotypes, three eigen values were derived from the principal component analysis. Eigen roots and the amount of variance accounted for by each eigen root are shown in Table 4. The greatest eigen value was observed for the first principal component. Approximately 88.75% of total variance was accounted by the eigen root of PC1 followed by PC2 and PC3 which accounted 6.76% and 1.47% of total variance present among genotypes respectively. 96.99 % of all variations were described by the first three principal components, indicating that these components are sufficient to account for variances in the reduced dimension. They were perceived to indicate the relative importance of the factors in each component. Table 4 indicates factors are significant based on their relative weight values, which might be positive or negative. First component (PC1) had high positive weight to plant height, number of clusters on main shoot, number of clusters per plant, cluster length, number of green pods per plant, green pod length, 10 green pod weight, number of seeds per pod, 100 seed weight, pod width, protein content of green pod and green pod yield per plant while second component had high positive weight to plant height, number of clusters per plant, cluster

Table 2: D values within and between clusters.

Clusters	I	II	III	IV	V	VI
I	38.84	197.43	615.90	1125.19	1932.93	2837.47
II		29.17	150.96	434.06	984.56	1658.93
III			31.74	99.70	414.73	876.04
IV				6.91	128.28	418.18
V					35.44	119.57
VI						24.09

Table 3: Cluster mean for fourteen traits in vegetable cluster bean genotypes.

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	% contribution towards divergence
PH (cm)	82.18	85.66	87.88	90.90	93.33	102.75	10.00
DFF	31.16	29.88	28.75	26.50	25.75	23.83	7.62
D50F	35.41	33.88	32.58	31.66	30.00	28.25	13.81
NCMS	14.43	16.94	19.04	20.13	22.16	25.56	10.00
NCPP	23.39	29.95	34.91	41.33	43.56	45.83	0.95
CL (cm)	4.96	6.62	7.84	8.26	8.85	9.80	8.57
NGPPP	128.42	176.78	210.60	233.51	260.89	287.35	2.86
GPL (cm)	6.29	7.56	8.82	9.93	10.97	13.35	10.48
10 GPW(g)	16.54	18.95	22.80	27.76	29.48	32.47	4.76
NSPP	5.56	5.17	5.50	6.10	6.96	7.11	7.86
100SW(g)	4.97	5.22	5.77	6.10	6.46	6.58	7.76
PW (cm)	0.55	0.57	0.68	0.78	0.84	0.98	2.38
PCGP (%)	3.90	3.73	3.53	3.33	3.14	3.17	0.95
GPYPP	269.03	309.47	355.55	397.40	451.28	500.92	12.00

Where, PH- Plant height; DFF- Days to first flowering; D50F- Days to 50% flowering; NCMS- Number of cluster on main shoot; NCPP- Number of cluster per plant; CL- Cluster length (cm); NGPPP- Number of green pods per plant; GPL- Green pod length (cm); 10 GPW- 10 Green pod weight(g); NSPP- Number of seeds per pod; 100 SW-100 Seed weight(g); PW- Pod width (cm); PCGP- Protein content of green pod (%); GPYPP- Green pod yield per plant (g).

Table 4: Results of principal component analysis (PCA) for characters contributing to divergence in cluster bean.

Canonical roots analysis (P.C.A.)	PC1	PC2	PC3
Eigene value (Root)	12.42556	1.94717	1.20598
% var. exp.	88.75401	6.76553	1.47129
Cum. var. exp.	88.75401	95.51955	96.99083
Plant height (cm)	0.27104	0.00058	0.56844
Days to first flowering	-0.27976	-0.02042	-0.28004
Days to 50% flowering	-0.28181	-0.03674	-0.16311
Number of cluster on main shoot	0.26400	-0.03409	-0.30112
Number of cluster per plant	0.27062	0.07432	-0.36136
Cluster length (cm)	0.27652	0.0954	-0.0406
Number of green pods per plant	0.28032	0.01683	-0.26715
Green pod length (cm)	0.28252	-0.00729	-0.0959
10 green pod weight (g)	0.27664	0.04497	0.26537
Number of seeds per pod	0.28034	0.03387	-0.20159
100 seed weight (g)	0.27949	-0.02808	-0.28436
Pod width (cm)	0.26938	0.00855	0.27649
Protein content of green pod (%)	0.0764	-0.98893	0.00327
Green pod yield per plant (g)	0.28184	0.00994	-0.00011

length, number of green pods per plant, 10 green pod weight, number of seeds per pod, pod width and green pod yield per plant. Third component (PC3) exhibited high positive weight to plant height, 10 green pod weight and pod width. The choice of lines for the characters under PC1 may be preferable since it had the biggest percentage deviation and was the most prominent.

CONCLUSION

The principal component analysis led to the conclusion that days to 50 % flowering, plant height, number of clusters on main shoot, number of green pods per plant, green pod length, number of seeds per pod, pod width and green pod yield per plant were significant variables in cluster bean genotypes with respect to yield contributing traits. The aforementioned factors could be taken into account while choosing parents for a hybridization scheme. Similar selection indices for cluster bean improvement have previously been reported by Susmitha *et al*. (2024). Based on D^2 statistics and principal component analysis genotypes like VG3241, VG 10132, Ganjam Local, GP 07, GP 62, GP 39 and Thar Bhadavi can be considered good for utilization in future breeding programme.

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Conflict of interest

The authors are declaring that no conflicts of interests are associated with this research.

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