International Journal for Multidisciplinary Research (IJFMR)
E-ISSN: 2582-2160 ● Website: www.ijfmr.com ● Email: editor@ijfmr.com

Quantifying Genetic Diversity in Mothbean (Vigna AconitifoliaL.) Using Euclidean Distance and Cluster Analysis

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Abstract
The present study was carried out during late Kharif 2022-23 at 'C' block, College of Agriculture, Vijayapur (University of Agricultural Sciences, Dharwad), to assess genetic diversity among 45 Mothbean germplasm lines along with two checks (KBMB-1 and MBS-803),evaluated under an Augmented Block Design. Genetic divergence was estimated using non-hierarchical Euclideanclustering (K-means). The 45 germplasm lines weregrouped into eight distinct clusters, indicatingthepresenceofconsiderablegeneticdiversity.ClusterV wasthelargest(13 genotypes), followed by Cluster II (8 genotypes), while Cluster VI contained a single entry. The maximum intra-cluster distancewas recorded for Cluster I(3.40),while the smallest was observedin Cluster VII (2.55). Inter-cluster distance was highest between Cluster IV and V (12.07), followed by Cluster III and V (11.65), suggesting these clusters harbor the most divergent parents for hybridization. Cluster mean analysis revealed wide variation across all traits. Cluster V exhibited desirable mean values for early flowering (44days), while Cluster IV recorded the early maturity (99.57 days). The study identified genetically divergent and superior genotypes across clusters that could be effectively utilized in future Mothbean improvement programmes to generate heterotic combinations and desirable transgressive segregants.

Keywords: Mothbean, Genetic diversity, K-means clustering, Euclidean distance, Cluster analysis, Germplasm evaluation.

Introduction

Mothbean (Vigna aconitifolia) belongs to the genus Vigna, subfamily Papilionaceae, and family Leguminaceae, with a chromosome number of 2n = 2x = 22. The crop typically exhibits a bushy to semi-erect growth habit with deeply notched leaflets. Plants bearhairy, densely branched stems that may extend up to 150 cm, although the main stem height generally reaches around 40 cm. The bright yellow flowers develop on pubescent branches and later form brown pods measuring 2.5–5.0 cm in length, each containing 4–9 seeds. The seeds are smooth, sub quadrate and vary in colour-olive, black, brown, or mottled. Mothbean is well adapted to hot, arid environments and is known for its strong drought tolerance, attributed to its deep and efficient root system. It can withstand high temperatures without negatively affecting flowering or pod development, with an optimum growth temperature range of 25-

37°C. The crop thrives in dryland areas receiving 250–500 mm annual rainfall, provided adequate drainage is available. Among the kharif pulses, mothbean occupies a considerable area due to its suitability for low-rainfall regions. Nutritionally, it serves as an excellent source of easily digestible, high-quality protein and is consumed as whole grain or dal in various dietary forms.

Materialandmethods

The experiment was carried out at 'C' block, College of Agriculture, Vijayapur (University of Agricultural Sciences, Dharwad) during late Kharif 2022-23. Experimental material for the present study was comprised of 45 mothbean germplasm lines including two checks (KBMB-1and MBS-803). The seed material was collected from Regional Research Centre of IIPR, Dharwad. The experimental material was planted in anaugmented design with eight blocks which includes 8 germplasm lines. Each germplasm line was planted in two rows of 4 m length with spacing of 45 cm between rows and 10 cm between plants.

Genetic diversity which is heritable is a prerequisite for any successful breeding programme. Genetic divergence among the parents plays a vital role in cultivar improvement becauseacrossinvolvinggeneticallydiverseparents islikely toproducehighheterotic effects and more variability in segregating generations, which can be used for the desired improvement. The D^2 statistics of Mahalanobis (1936) is a powerful tool for quantifying the divergence between the two populations.

Thus, it givesthe better ideaabout themagnitude of divergenceand is independent ofsize of sample and offers the basis for selection of parental lines for future breeding programme. Therefore, present investigation is proposed to assess the genetic diversity among Mothbean germplasm lines.

Results and Discussion

Unavailability of more variability is the main factor for the limited progress achieved in increasing the productivity of Mothbean. However, the current study discloses huge diversity in the Mothbean germplasm lines used under the study. The diversity among parents is an important criterion for hybridization leading to creation of new variability.

Diversity analysis helps in selection of parents to exploit maximum heterosis for higher yields and other economic traits. In the experiment total of 45 Mothbean germplasm lines which includes two checks were grouped into 8 clusters based on K-means clustering statistic (Non-hierarchical Euclidean cluster analysis) (Spark,1973).Among 8clusters, Cluster V was the biggest comprising of thirteen germplasm lines followed by Cluster II with eight germplasm lines, Cluster I and IV with seven germplasm lines, Cluster III with four germplasm lines, Cluster VIII with three germplasm lines, Cluster VII with two germplasm lines and Cluster VI containing one germplasm lines each (Table 1). Indicating that the presence of a high degree of divergence in the material used. These result are in line with Chaudhari et al.(2021) , Rasal and Parhi (2017), Janghel et al.(2020), Bandhavi et al.(2023), Kohakadeet al.(2017), Bhattacharya and Vijayalakshmi (2005). The intra- cluster distance was highest for cluster I followed by cluster VIII, cluster II, cluster III, cluster IV and cluster VI indicating that some genetic divergence still existed among the germplasm lines within the clusters. The high intra-cluster distance reveals the presence of genetic diversity between the germplasm lines that were grouped in cluster. (Table 2).

Among intra-cluster distances, Cluster I exhibited the highest value, followed by Clusters VIII, II, III, IV, and VI, indicating the existence of considerable genetic variability even within clusters. High intra-cluster distances suggest that the genotypes grouped together are not entirely similar and retain sufficient

diversity for selection and improvement. (Table 3).

All the germplasm lines were spread over 8 clusters and means were scored across the clusters for all the twenty-three characters. The maximum cluster mean was given the first rank and the clusters having next best means were given second, third and so on up to 8th rank for all the traits except for days to 50 per cent flowering and days to maturity for these three traits, the least mean was given the first rank.

Accordingly, cluster V with overall score of 56 across the twenty three traits secured first rank and it exhibited highest mean values for plant height, number of pods per plant, primary branches, secondary branches, pod yield per plant, seed yield per plant, fodder yield , Whereas, less mean values recorded for days to 50 percent flowering, followed by cluster II (73) exhibited highest mean values for number of seeds per pod, cluster IV (104) recorded highest mean values for days to maturity, cluster III (105) exhibited highest mean values for zinc content, suggesting that these are the traits which have major influence in cluster formation. Finally, the minimum ranking was recorded by cluster VII (132) with lowest mean values for majority traits.

Conclusion

The study revealed substantial genetic divergence among 45 mothbean germplasm lines, which were grouped into eight distinct clusters using K-means Euclidean analysis. Cluster V emerged as the most promising, exhibiting superior performance for several yield, physiological, and quality traits, while the highest inter-cluster distances between Clusters IV and V, and Clusters III and V, indicated the presence of highly diverse parents. These contrasting clusters offer valuable opportunities for developing heterotic and high-yielding combinations. Overall, the identified divergent genotypes represent useful parental sources for broadening the genetic base and advancing improvement programmes in mothbean.

Table1.Distribution of mothbean germplasm lines in different clusters

Cluster No.	Number of germplasm lines	Name of the germplasm lines
I	7	IC-35982, IC-39709, IC-370469, IC-39675, IC-39806, IC-39817, IC-370476.
II	8	20KR-13,IC-52149,20KR-14,IC-39817a,20KR-15,IC-102812,IC-370508,IC-39736.
III	4	IC-39686,IC-102283,IC-39702,IC-325813.
IV	7	IC-39678,IC-39668,IC-39676,20KR-1,20KR-6,IC-121015, 20KR-7.
V	13	20KR-11,20KR-12,20KR-4,IC-140727,20KR-16,20KR-2, 20KR-3,20KR-8,20KR-20,20KR-17,20KR-9,20KR-10, 20KR-19.
VI	1	IC-415164.
VII	2	IC-35955,20KR-5.
VIII	3	IC-10287,KBMB-1,MBS-803.

Table2. Cluster means of mothbean germplasm lines for seed yield and yield attributing traits.

Cluster no.	No. of germplasm lines	DFF	DM	PH (cm)	NPP	PL (cm)	PB	SB	NSP	PYP P(g)	SYP P(g)	FYP P(g)	TW (g)
I	7	60.00 (8)	124.25(8)	26.29 (5)	35.70 (5)	3.81 (5)	2.50 (4)	5.20 (6)	5.80 (6)	8.84 (5)	4.29 (6)	10.27 (6)	59.56 (1)
II	8	57.69 (6)	120.90 (6)	37.45 (2)	55.60 (2)	3.97 (2)	2.73 (3)	6.44 (2)	6.43 (1)	14.42 (2)	6.59 (2)	16.72 (3)	18.24 (6)
III	4	51.00 (4)	104.00(3)	32.26 (3)	37.93 (3)	3.42 (8)	2.27 (7)	5.60 (4)	5.20 (8)	11.22 (3)	4.96 (3)	15.37 (4)	19.00 (4)
IV	7	45.86 (2)	99.57 (1)	24.61 (8)	34.69 (6)	3.77 (6)	2.80 (2)	5.37 (5)	6.03 (5)	9.65 (4)	4.37 (5)	9.32 (7)	20.03 (3)
V	13	44.00 (1)	101.00(2)	43.32 (1)	89.80 (1)	3.52 (7)	3.50 (1)	8.70 (1)	5.50 (7)	25.28 (1)	11.71 (1)	27.69 (1)	18.55 (5)
VI	1	57.88 (7)	121.38(7)	28.92 (7)	37.24 (4)	3.95 (3)	2.45 (6)	4.76 (7)	6.38 (2)	8.38 (6)	4.39 (4)	18.52 (2)	17.92 (8)
VII	2	47.33 (3)	104.33(4)	26.38 (6)	25.70 (8)	3.88 (4)	2.20 (8)	4.50 (8)	6.17 (3)	6.87 (7)	2.88 (8)	7.46 (8)	17.95 (7)
VIII	3	56.75 (5)	112.00 (5)	25.44 (4)	30.20 (7)	4.07 (1)	2.45 (5)	5.70 (3)	6.05 (4)	5.98 (8)	3.87 (7)	13.59 (5)	20.04 (2)

Figures in the parenthesis, indicate the ranks based on cluster mean. Overall score is the sum of rank numbers for all traits DFF-Days to 50% flowering, DM- Days to maturity, PH-Plant height(cm), NPP- Number of pods per plant, PL - Pod length (cm), PB- Primary branches, SB- Secondary branches, NSP - Number of seeds per pod, PYPP- Pod yield per plant (g), SYPP- Seed yield per plant (g), FYPP – Fodder yield per plant, TW - Test weight (g).

Table3. Average intra (diagonal and bold) and intercluster distances in mothbean germplasm lines for seed yield and yield attributing traits

Cluster no.	I	II	III	IV	V	VI	VII	VIII
I	**3.40**	4.60	4.88	3.91	11.32	6.90	5.50	4.02
II		**3.32**	5.10	3.81	10.55	5.58	5.51	4.27
III			**3.29**	5.38	11.65	7.54	6.21	5.87
IV				**3.27**	12.07	6.78	6.19	4.54
V					**0.00**	8.14	7.87	9.477
VI						**2.75**	5.91	5.60
VII							**2.55**	5.07
VIII								**3.34**

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