Multivariate Analysis of Genetic Diversity In Mung bean [*Vigna radiata* (L.) Wilczek] Using Mahalanobis Statistic

Abstract- The present study was conducted at Norman E. Borlaug Crop Research Centre, GBPUA&T, Pantnagar, Uttarakhand, India, during the *kharif* season of 2023.Using Mahalanobis D^2 statistics, 40 mung bean genotypes were grouped into 9 distinct clusters. Cluster I was the largest, comprising 15 genotypes, followed by Cluster II with 11 genotypes. Clusters IV with 4 genotypes. Cluster V & Cluster VII each had 3 genotypes; and Clusters III, VI, VIII & IX each contained a single genotype. The greatest inter-cluster distance was observed between Cluster VII and Cluster VIII (17.12), indicating that genotypes (PM 15-12, PM 5, IPM 2-14) and (Vamban 2) can be hybridized together to produce significant genetic diversity in segregating generation among the genotypes included in these clusters. The number of pods per plant contributed the most to genetic diversity (40.26%).

INTRODUCTION

Mung bean [*Vigna radiata* (L.) Wilczek], a self-pollinated legume, belongs to the family Leguminosae and sub-family Papilionaceae, with a chromosome number 2n = 2x = 22. Mung bean is a *kharif* season crop and is the third most important pulse crop of india. The grains are consumed whole or in split form as dal. It is mainly grown in South Asia countries including India, Pakistan, Bangladesh, Sri Lanka, Cambodia, Vietnam, Indonesia and Malaysia. Notably, Asia contributes to 90% of the global mung bean production. In India, mung bean represents 10% of the total pulse production, covering an area of approximately 5.54 million hectares with an annual production of 3.67 million metric tonnes and an average yield of around 663 kg/ha (**Economic and Statistics Directorate, 2022–23)**. Genetic diversity plays a pivotal role in the collection, documentation and utilisation of germplasm for crop improvement programs. The importance of genetic diversity in different crop improvement programmes is well emphasized by Moll *et al.* (1962), De Pace *et al.* (2011), Verma *et al*. **(**2018), Bohra *et al*. (2015) and Meena *et al* (2017). Utilizing genetic diversity effectively in crops aid in selecting appropriate parents for hybridization and achieving breeding goals (Chaudhary, *et al*.2017). In the present study, the D^2 statistic, a robust method was used to access the genetic divergence among 40 elite mung been genotypes.

MATERIALS AND METHOD

Forty mung bean genotypes were evaluated during the *kharif* season of 2023 using a randomised block design (RBD) with three replications at the N.E.B. Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar. Each test genotype was grown in a two row plot of 4 meters length. A row to row spacing of 30 cm and plant to plant spacing of 10–12 cm was maintained. All the recommended agronomic practices were meticulously followed to ensure optimal crop growth.

Data were collected on ten morphological traits *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per cluster, pod length (cm), number of pods per plant, number of seeds per pod, one hundred seed weight (g), and seed yield per plant (g). Observations for all the characters were recorded on five randomly selected competitive plants from each genotype in each replication except for days to 50% flowering and days to maturity for which the data was recorded on whole plot basis. The mean value for the each replication was used for statistical analysis using the INDOSTAT statistical package.

RESULTS AND DISCUSSION

Table 1 presents the analysis of variance for yield and its related components using a randomized block design. The analysis demonstrated that significant genetic variation exists among the experimental mung bean genotypes for all studied traits. Initially, significant differences among genotypes were identified for each individual character. Subsequently, significant differences between genotypes, based on the pooled effects of all characters, were assessed using Wilk's criterion (λ). The obtained Wilk's criterion was then utilised in calculating the V statistics. The highly significant V statistic value of 1795.15, which exceeded the tabulated χ^2 value, indicated significant differences among the genotypes when all traits were considered simultaneously **(Table 2).** D^2 values were computed for all possible pairs of genotypes. Using Tocher's method **(Rao, 1952)**, the 40 mung bean genotypes were grouped into 9 distinct clusters. The distribution of genotypes into each of these 9 clusters is presented in **Table 3** and illustrated in **Fig. 1.**

It is evident from Table 3 that Cluster I was the largest, containing 15 genotypes, followed by Cluster II (11 genotypes), Clusters IV (4 genotypes), Cluster V and Cluster VII each had 3 genotypes. Clusters III, VI, VIII and IX each contained a single genotype. The maximum intra-cluster distance was recorded for Cluster VII (6.73) followed by Cluster V (6.12), Cluster II (6.1), Cluster I (5.79) & Cluster IV (5.32) while rest of the Clusters *viz.* III, VI, VIII and IX had zero intra-cluster distances as they were solitary clusters. The highest inter-cluster distance was observed between Cluster VII and Cluster VIII (17.12) which was followed by Cluster IV & Cluster VII (14.87) and Cluster II & Cluster VIII (14.16), indicating that genotypes included in these clusters if hybridized together, they will produce wide spectrum of genetic variability in segregating generations from which desirable plants can be selected. This genetic diversity in the present investigation provides an excellent opportunity to select appropriate donors from divergent clusters that are likely to exhibit maximum heterosis and offer extensive genetic variability for yield and yield-contributing factors. Kumar *et al.* (2019), Priya *et al.* (2020), Chandra *et al*. (2021), Joshi *et al.* (2022) and Rahangdale *et al.* (2023) also obtained grouping of genotypes in to different clusters in different crops while working with different experimental material. It is also evident from the Table 4 that inter cluster distances are of high magnitude than the intra cluster distance indicating that the genotypes included in different clusters may have been adapted to different environments resulting in greater genetic divergence. The present study evaluated mung bean genotypes across several clusters to identify potential donor parents based on the cluster means for various agronomic traits (Table 5). The genotypes included in Cluster II were earliest maturing with the 50% flowering in39.79 days and maturity in 89.16 days, are ideal for breeding early maturing varieties. Cluster VIII exhibited the highest plant height (98.92 cm), while Cluster IV had the most primary branches (4.42) and the highest seed yield per plant (15.61 g). it indicated that if the genotypes from cluster II are hybridized with the genotypes included in cluster IV, the recombinant genotypes with high yield and early maturity can be obtained. Cluster V had the most pods per cluster (6.36). Cluster VI showed the longest pod length (9.42 cm), and Cluster IV had the most pods per plant (74.00). Clusters III and IX had the highest seeds per pod (12.65), and Cluster VII had the highest 100-seed weight (4.88 g). These findings highlighted specific clusters for targeted breeding programmes to improve mung bean traits. The selection and choice of parents mainly depend on the contribution of traits to total divergence (Verma *et al*. 2018, Yadav *et al*. 2024 and Bhatt *et al*. 2024). The number of times each of the 10 traits appeared in the first rank and its respective percent contribution to diversity is presented in Table 6. Among all traits, the number of pods per plant contributed the most (40.26%) to diversity, ranking first in 314 out

of 780 combinations, followed by 100-seed weight (20.77% with 162 times ranked first), days to 50% flowering (15.64% with 122 times ranked first), and plant height (12.18% with 95 times ranked first). The traits like pods per plant, 100 seed weight and pod length are important yield parameters in any pulse crop (Verma *et al*. 2018 and Naing *et al*. 2021) and in the present study these traits are contributing to the total divergence. The high contribution of pods per pant, days to 50% flowering and 100 seed weight towards total genetic diversity was also reported earlier by Priya *et al.* (2020), Joshi *et al.* (2022) and Rahangdale *et al.* (2023). It is also evident from the results that in present investigation the trait number of pods/ cluster had 0% contribution towards the total diversity indicating that this trait may have been fixed in the experimental population indicating that all the genotypes are having non-significant differences for pods per cluster resulting in no genetic variation for this trait or the trait pods per cluster may be highly correlated with other traits and the variation for pods per cluster is already captured by some other traits or the gene controlling pods per cluster has multiple effects and the variation for this trait is not contributing to the overall diversity. Similar results were previously reported by Chandra *et al.* (2017), Markam *et al.* (2018) and Sneha *et al.* (2020)**.** In the present study it was observed that the genotypes originated in different eco-geographical regions grouped together into different and in the same clusters. The grouping of genotypes originated in different geographical regions including it to same cluster may be due to their common ancestry which results in similar genetic makeup despite developed in different regions or due to the convergent evolution due to which genotypes may have evolved similar traits independently in response to similar environmental pressure or due to fact that breeding programs may have used similar parental material and breeding strategies resulting in similar kind of genotypes. (Chandra *et al.* 2021) also reported inclusion of genotypes originated in different regions in to similar cluster. Present result indicated that geographical diversity does not necessarily correlate with genetic diversity.

CONCLUSION

In the present study 40 mung bean genotypes were grouped into 9 different clusters using Tocher's method. Cluster I was the largest, comprising 15 genotypes, followed by Cluster II with 11 genotypes. Clusters IV with 4 genotypes. Cluster V & Cluster VII each had 3 genotypes; and Clusters III, VI, VIII & IX each contained a single genotype. In the present study it was observed that the genotypes originated in different eco-geographical regions grouped together in the same clusters indicating that there is no relationship between geographical and genetic diversity. Maximum inter-cluster D^2 value (17.12) was recorded between Cluster VII and Cluster VIII, indicating that crosses between these clusters would likely be most productive. The number of pods per plant contributed the most to genetic diversity (40.26%).

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Table 1: Analysis of variance for ten different characters among 40 mung bean genotypes

S.no.	Characters	Mean sum of squares		
		Replication	Treatment	Error
	Degree of freedom	2	39	78
1.	Days to 50% flowering	5.00	36.44	2.31
2.	Days to maturity	21.78	120.63	11.25
3.	Plant height (cm)	23.23	416.37	29.38
4.	No. of primary branches	0.60	0.77	0.40
5.	No. of pods/ cluster	1.04	1.18	1.03
6.	Pod length	0.24	1.32	0.15
7.	No. of pods/plant	18.96	589.19	18.19
8.	No. of seeds/pod	0.32	2.68	0.76
9.	100 seed weight	0.11	0.92	0.05
10.	Seed yield/plant	1.28	22.09	3.40

*Significance at 5% and **Significance at 1%

Table 2: Wilks Test for 40 mung bean genotypes for yield and its attributes

S.No.	Content	Value
1.	Determinate of error matrix	23556.30868E-3
2.	Determinate of error + variety matrix	86983.081E+5
3.	Wilks criterion	27081.48344E-13
4.	M	91
5.	Degree of freedom	390
6.	V statistic	1795.15

Table 3: Clustering of 40 mung bean genotypes (Tocher's method) for yield and related attributes

Cluster	Number of genotypes		Genotypes included	Place of Origin
I	15	13	PM 3, PM 15-19, PM 15-13, PM 4, PM 15-7, PM 15-8, PM 7, PM 8, PM 15-15, PM 15-10, PM 9, PM 2, PM 15-21	GBPUA&T
		1	IPM 02-3	IIPR, KANPUR
		1	LGG 460	RARS, LAM
II	11	6	PM 15-5, PM 15-6, PM 15-17, PM 15-3, PM 15-18, PM 15-9	GBPUA&T
		3	SML 1082, SML 1808, ML 818	PAU, LUDHIANA
		1	HUM 12	VARANASI
		1	Pusa Vishal	IARI, NEW DELHI
III	1	1	PM 15-20	GBPUA&T
IV	4	3	PM 15-14, PM 15-2, PM 15-4	GBPUA&T
		1	SML 1815	PAU, LUDHIANA
V	3	2	IPM 02-19, IPM 02-13	IIPR, KANPUR
		1	Sona Mung 1	IIPR, KANPUR
VI	1	1	PM 15-16	GBPUA&T
VII	3	2	PM 15-12, PM 5	GBPUA&T
		1	IPM 2-14	IIPR, KANPUR
VIII	1	1	Vamban 2	NPRC, VAMBAN
IX	1	1	PM 15-11	GBPUA&T

Table 4: Average intra and inter-cluster distances (D^2 values) for 9 clusters of mung bean genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	**5.79**	8.12	7.44	8.05	9.6	7.1	11.51	9.19	8.08
Cluster II		**6.1**	7.85	11.08	10.06	9.01	8.43	14.16	10.12
Cluster III			**0**	7.89	12.24	6.4	11.28	12.4	8.19
Cluster IV				**5.32**	12.84	8.55	14.87	10.49	9.08
Cluster V					**6.12**	10.86	12.03	12.98	9.42
Cluster VI						**0**	11.44	11.43	6.68
Cluster VII							**6.73**	17.12	11.11
Cluster VIII								**0**	11.05
Cluster IX									**0**

* Highlighted values indicated intra cluster distances

Table 5: Cluster means for different character of mung bean genotypes

Cluster	DFF	DM	PH	NPB	PPC	PL	NPP	NSP	HSW	SYP
Cluster I	43.71	94.78	80.56	3.91	5.92	7.7	53.62	11.76	3.49	13.35
Cluster II	39.79	89.16	71.06	4	5.55	8.08	42.61	11.61	3.95	11.45
Cluster III	42.32	101.63	68.98	4.33	5.67	8.31	61	12.65	4.06	13.76
Cluster IV	42.74	92.32	67.44	4.42	5.98	7.68	74	11.91	3.67	15.61
Cluster V	44.89	95.36	57.19	3.56	6.36	7.45	30.11	11.24	2.81	7.36
Cluster VI	46.65	104.32	69.11	4	5.66	9.42	61.33	9.65	3.72	12.09
Cluster VII	45.12	96.22	67.5	3.56	6.25	8.25	30.78	11.66	4.88	10.62
Cluster VIII	49.67	104.34	98.92	4	4.66	6	58.67	12.34	3.08	12.74
Cluster IX	51.32	109.97	55.03	4.33	5.4	8.33	51	12.65	3.95	14.25

DFF- Days to 50% flowering, **DM-** Days to maturity, **PH-** Plant height (cm), **NPB-** Number of primary branches per plant, **PPC-** Number of pods per cluster, **PL-** Pod length, **NPP-** Number of pods per plant, **NSP**-Number of seeds per pod, **HSW**- One hundred seed weight (g) and **SYP-** Seed yield per plant (g).

Table 6: Contribution of different characters towards total divergence

S. No.	Characters	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	122	15.64
2	Days to maturity	28	3.59
3	Plant height (cm)	95	12.18
4	No. of primary branches	3	0.38
5	No. of pods/ cluster	0	0
6	Pod Length (cm)	33	4.23
7	No. of pods/plant	314	40.26
8	No. of seeds/pod	11	1.41
9	100 seed weight	162	20.77
10	Seed yield/plant	12	1.54

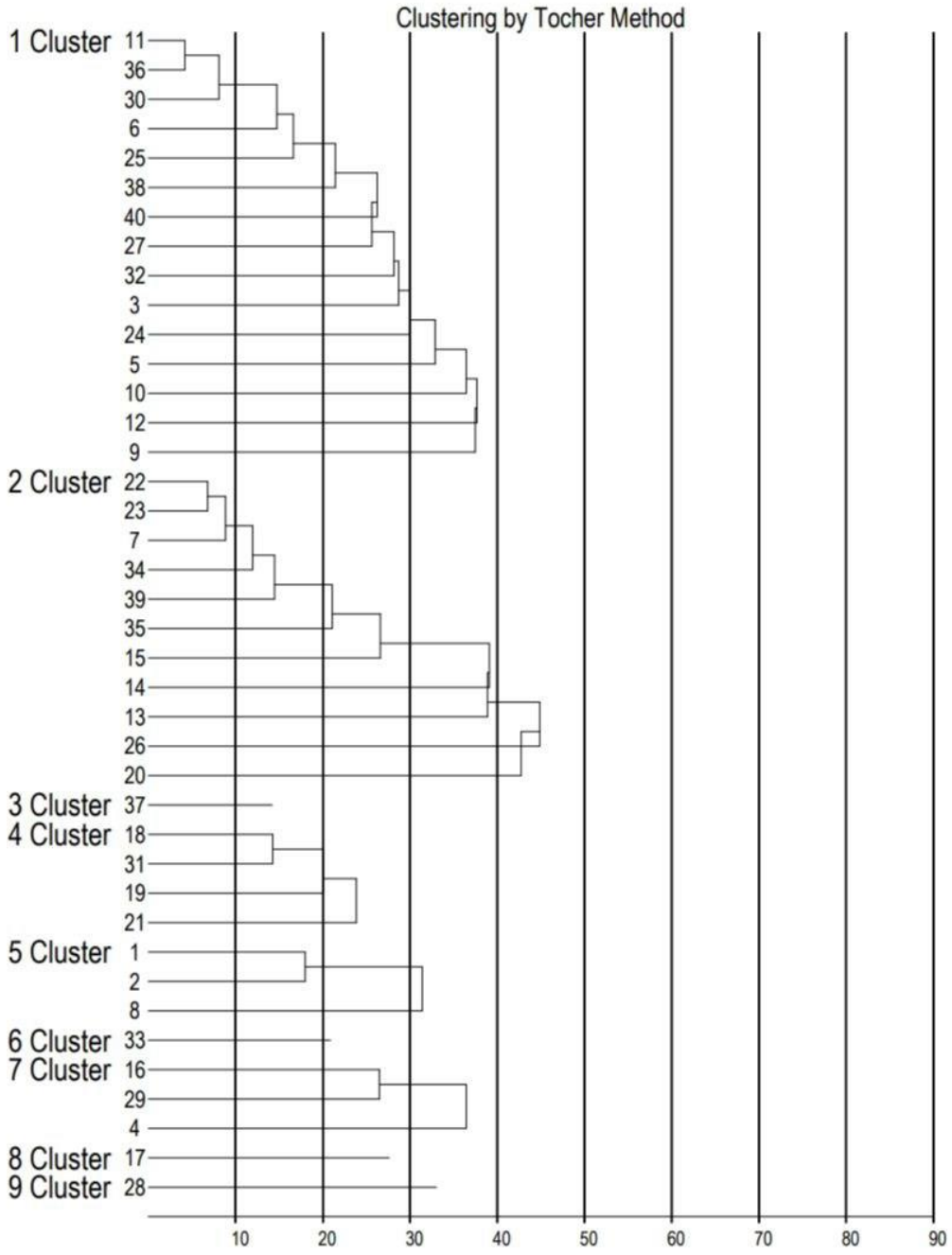

Fig. 1: Dendrogram showing the clustering pattern of 40 mung bean genotype