Original Research Article

Assessment of genetic diversity in greengram (*Vigna radiata* L. Wilczek)

ABSTRACT

The experiment was conducted in a Randomized Block Design with three replications during the *Zaid* season 2023 at field experimentation centre, Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj, U.P. The aim of experimentation was to analyse genetic diversity present among green gram germplasms. Plant to plant distance was 10 cm and row to row distance was 30 cm. the data were recorded from randomly selected five plants for each genotypes for each replications for thirteen characters *viz.* days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed index (g), biological yield (g), harvest index and seed yield per plant (g).From the present investigation it was concluded that among 31 genotypes of greengram on the basis of mean performance3 genotypes were found to be superior for seed yield per plant over check variety Samrat*viz.*,IC-76569, IC-121220 and IC-119006. On the basis of Mahalanobis' D^2 statistics 31 genotypes of greengram were grouped into five clusters. Maximum numbers of 13 genotypes were included in cluster 1 followed by cluster 2 with 7 genotypes, cluster 3 with 5 genotypes, cluster 4with only single genotypes in each cluster. The highest intra cluster D^2 value was recorded for cluster 5 (43.09) with 5 genotypes followed by cluster 2 (30.45) with 7 genotypes. The maximum inter cluster value of 153.82 was recorded between cluster 3 and cluster 5. It was also reported that the characters like seed yield per plant, biological yield, number of pods per plant, number of clusters per plant, number of seeds per pod, pod length and harvest index contributed about 71.13% towards total divergence alone. Therefore, selection should be done based on these characters considering the diversity and genetic variability present in greengram.

Keywords: *Vigna radiata*,Geneticdiversity, clusters.

INTRODUCTION

Green gram also called mungbean is botanically referred to as *Vigna radiata* (L.) Wilczek is a member of the Papillionaceae sub-family of the Leguminosae family. With

chromosome number 2n=2x=22, it is a diploid self-pollinating species (Karpechenko, 1925). According to Vavilov (1935), the Indo-Burma region of central Hindustan is most likely where mungbean originated. It is mostly grown in south-east Asia, including China, India, Burma, and other regions. *Vigna radiata sublobata* is the mungbean's wild ancestor. In India, 40.38 lakh hectares are used for green gram production, and 3.15 million tonnes were produced in 2021–2022. (*Source:* DES, Government of India, Ministry of Agriculture & Farmers Welfare, 2022-23). In terms of green gram production and area, Rajasthan leads Maharashtra and Karnataka in 2019–20. In Uttar Pradesh, green gram is grown on 0.58 lakh hectares of land, with a projected production of 0.36 million tonnes in 2021–2022. Because of its high protein content (25–28%) and exceptional digestibility, green gram is regarded as a high-quality pulse. Green gram is an excellent source of high-quality, readily digestible protein for the majority of vegetarians in India. It contains 334–344 kcal of energy per serving, with a dry weight of 59–65% carbohydrates, 22–28% total protein, 21–25% amino acids, 1.5–2.63% lipids, 1.0–1.5% fat, 3.5–4.5% fibre, and 4-5% ash. It meets the protein needs of the nation's vegetarian population. Compared to most other legumes, green gram seeds have higher levels of iron and folate and are a good source of dietary protein (Keatinge*et al.* 2011). Many essential amino acids are present in it, such as lysine, leucine, isoleucine, and phenylalanine (Lambrides and Godwin, 2007). To estimate the degree of divergence at genotypic level and to assess the relative contribution of different characters to the total divergence, multivariate analysis, by means of Mahalanobis'D^2 statistic, has been used as a powerful tool. This analysis provides the basis for grouping the germplasm collections into different more or less homogenous groups and therefore it is helpful in reducing the size of germplasm collection to be evaluated. The D^2 statistic for multivariate analysis has been successfully used to select divergent genotypes in order to exploit heterosis and for bringing together higher frequency of desirable genes in the segregants(Mahalanobis', 1936).The success of the hybridization largely depends on the selection of parents showing high genetic diversity for traits of interest. The genetic variability present among different genotypes of a species may arise either due to geographical separation or due to genetic barriers to cross ability. This potent techniques of assessing genetic divergence is D^2 statistic technique measures the forces of differentiation at two levels viz., intra cluster and inter cluster that helps selection of genetically divergent parents for exploitation in hybridization programmes.

MATERIALS AND METHODS

To better understand the genetic diversity presentamonggreen gram genotypes, the current study was conducted. The investigation, which took place at Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj, during the *Zaid*season of 2023, at Field Experimentation Centre, Department of Genetics and Plant breeding.Approximately 5 kilometres from Prayagraj City, the University is located on the left side of the Prayagraj–Rewa National Highway. Field preparation, inputs, irrigation facilities, labour, and other resources required for the successful cultivation of a crop were all provided by the Department of Genetics and Plant Breeding at the Naini Agricultural Institute of Sam Higginbottom University of Agriculture, Technology, and Sciences in Prayagraj, Uttar Pradesh.Prayagraj is located in the central plain sub-zone of Agro-climatic zone V. Naini is located between latitudes 20° 33' 40" to 21".50' N and longitudes 73° 27' 58" to 73° 56' 36" E. This region has a tropical climate with warm, humid monsoons, reasonably hot summers, and mildly cold winters. This area typically experiences heavy rainfall from June to September. The majority of the precipitation falls during the south-west advancing monsoon, which is most noticeable in July and August.The experimental site consisted of levelled land with a uniformly fertile sandy loam soil that has a high percentage of sand and little clay. Randomly selected soil samples were taken between 0 and 30 cm in depth. The soil was then analysed for pH (7.1); organic carbon (0.52%); available nitrogen (142.33 kg/ha); available phosphorus (4.56 kg/ha); and available potassium (206.11 kg/ha).Plant spacing was set at 10 cm between plants and 30 cm between rows. Data were collected from five randomly selected plants for each genotype in each replication, focusing on thirteen different traits including days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed index (g), biological yield (g), harvest index, and seed yield per plant (g). The experiment was set up using a Randomized Block Design (RBD). The Fisher and Yates, 1936 method was used to statistically analyse the data. The D^2 statistic proposed by Mahalanobis, 1936 measures the divergence at two levels, namely intra cluster and inter cluster levels. Henceforth, it helps in selection of genetically divergent parents for exploitation in hybridization programmes.Grouping of the genotypes was done by Tocher’s method (Rao, 1952).The details of genotype used in experiment has been enlisted below in table 1.

RESULTS AND DISCUSSION

Analysis of Variance

For the purposes of the experimental design, analysis of variance was performed on the mean sum squares data for 13 characters. Table 2 displays the variance analysis for the various characters that was calculated. For all the studied characters, the analysis of variance revealed highly significant differences (=0.01 & 0.05) among 31 genotypes, indicating that there is a sizable amount of genetic variation among the green gram germplasms. Additionally, it demonstrated the range of green gram genetic improvement through selection. The data on the values of different characters and the analysis of variance showed significant differences among genotypes for all 13 characters indicating that the material has adequate genetic variability to support the breeding programme for improving the pod yield of green gram. The findings are consistent with research by Das and Barua (2015), and Joshi *et al.* (2022).

Genetic diversity

Genetic diversity plays a vital role in plant breeding because hybrids between lines of diverse origin generally manifest a greater heterosis than those with closely related strains. The D^2 statistic proposed by Mahalanobis in 1936 measures the divergence at two levels, namely intra cluster and inter cluster levels. Henceforth, it helps in selection of genetically divergent parents for exploitation in hybridization programmes. D^2 analysis (Mahalanobis, 1936) was accomplished to predict genetic divergence among 31 genotypes of greengram. Grouping of the genotypes was done by Tocher's method (Rao, 1952). The test of significance for multiple measurements using "V" statistics (0.0009) which utilized Wilke's 'V' (statistic) criterion that confirmed significant differences among greengram genotypes for all nineteen characters. The significance of 'V' (statistic) values was tested by "Chi-square" at 390 degrees of freedom. In addition to aiding in the selection of divergent parents for hybridization, D^2 statistic measured the degree of diversification and determined the relative proportion of each component character to the total divergence. The genotypes grouped in single cluster are less divergent than ones which are placed in different clusters. The clusters, which are separated by the greatest statistical distances, show maximum divergence.On the basis of Mahalanobis' D^2 statistics and Tocher's method (Rao, 1952) 31 genotypes of greengram were grouped into five clusters [Table 3& Fig 1]. Maximum numbers of 13 genotypes were included in cluster 1 followed by cluster 2 with 7 genotypes, cluster 3and 5 with 5 genotypes, cluster 4with only single genotypes. Similar results were

concluded by Joshi*et al.* (2022) reported 12 clusters from 435 genotypes; Kumar*et al.* (2022) reported 5 clusters from 23 genotypes in greengram in their work done.

The average intra and inter cluster D^2 values have been presented in Table 4 and Fig 2. Average intra cluster D^2 values of greengram genotypes ranged from 0.00 to 43.09. The highest intra cluster D^2 value was recorded for cluster 5 (43.09) with 5 genotypes followed by cluster 2 (30.45) with 7 genotypes; cluster 3 (28.3) with 5 genotypes and cluster 1 (23.6) with 13 genotypes. However, intra cluster D^2 values for cluster 4 was zero because of single genotype.The average inter cluster D^2 values for greengram genotypes ranged from 31.79 to 153.82. The maximum inter cluster value of 153.82 was recorded between cluster 3 and cluster 5. It was followed by 118.71 between cluster 2 and cluster 5. Another pair of cluster 2 and cluster 1 had D^2 value of 49.12. Cluster 3 and cluster 1 had D^2 value of 59.32. Cluster 3 had D^2 value of 46.06 with cluster 1. Cluster 2 had D^2 value of 68.85 with cluster 4. Cluster 3 had D^2 value of 59.70 with cluster 4. Cluster 1 and cluster 5 had D^2 value of 58.22. Cluster 4 and cluster 5 had D^2 value of 66.63. However, the minimum value (31.79) was recorded between cluster 1 and cluster 4.

CONCLUSION

From the present investigation itwas concluded that analysis of variance showed significant variation among different genotypes for all characters studied.On the basis of Mahalanobis' D^2 statistics 31 genotypes of greengram were grouped into five clusters. Maximum numbers of 13 genotypes were included in cluster 1 followed by cluster 2 with 7 genotypes, cluster 3 with 5 genotypes, cluster 4with only single genotypes in each cluster. The highest intra cluster D^2 value was recorded for cluster 5 (43.09) with 5 genotypes followed by cluster 2 (30.45) with 7 genotypes. The maximum inter cluster value of 153.82 was recorded between cluster 3 and cluster 5.

Table 1 Genotypes Details

S. No	Genotypes	S. No	Genotypes	S. No	Genotypes	S. No	Genotypes	S. No	Genotypes	S. No	Genotypes	S. No	Genotypes
1	IC- 332327	6	IC- 119048	11	IC- 121224	16	IC- 76414	21	IC- 76464	26	IC-121220	31	Samrat (Check)
2	IC- 249567	7	IC- 39280	12	IC- 121221	17	IC- 76569	22	IC- 119005	27	IC-282079		
3	IC- 39294	8	IC- 332181	13	IC- 76378	18	IC- 76599	23	IC-43600	28	IC-22456		
4	IC- 305291	9	IC- 305241	14	IC- 76418	19	IC- 333090	24	IC-9887	29	IC-103979		
5	IC- 119006	10	IC- 119027	15	IC- 11468	20	IC- 11604	25	IC-249656	30	IC-38995		

Table 2 Analysis of Variance (ANOVA) for 13 characters in green gram.

Characters	**Mean sum of Squares**		
	Replication(*df*=2)	**Genotypes(*df*=30)**	**Error (*df*=60)**
Days to 50% Flowering	31.37	6.62*	3.84
Days to 50% pod setting	5.03	7.79*	2.24
Days to maturity	4.05	8.97**	2.29
Plant Height (cm)	0.59	291.11**	7.22
No of Primary Branches	0.39	0.69**	0.16
No of Clusters per Plant	2.43	7.50**	1.47
No of Pods per plant	5.59	41.05**	3.57
No of seeds per pod	12.05	11.52**	0.12
Pod length (cm)	0.14	0.65**	0.19
Biological yield (g)	9.44	100.38**	4.09
Seed Index (g)	0.35	0.99**	0.10
Harvest Index (%)	324.65	494.28**	33.41

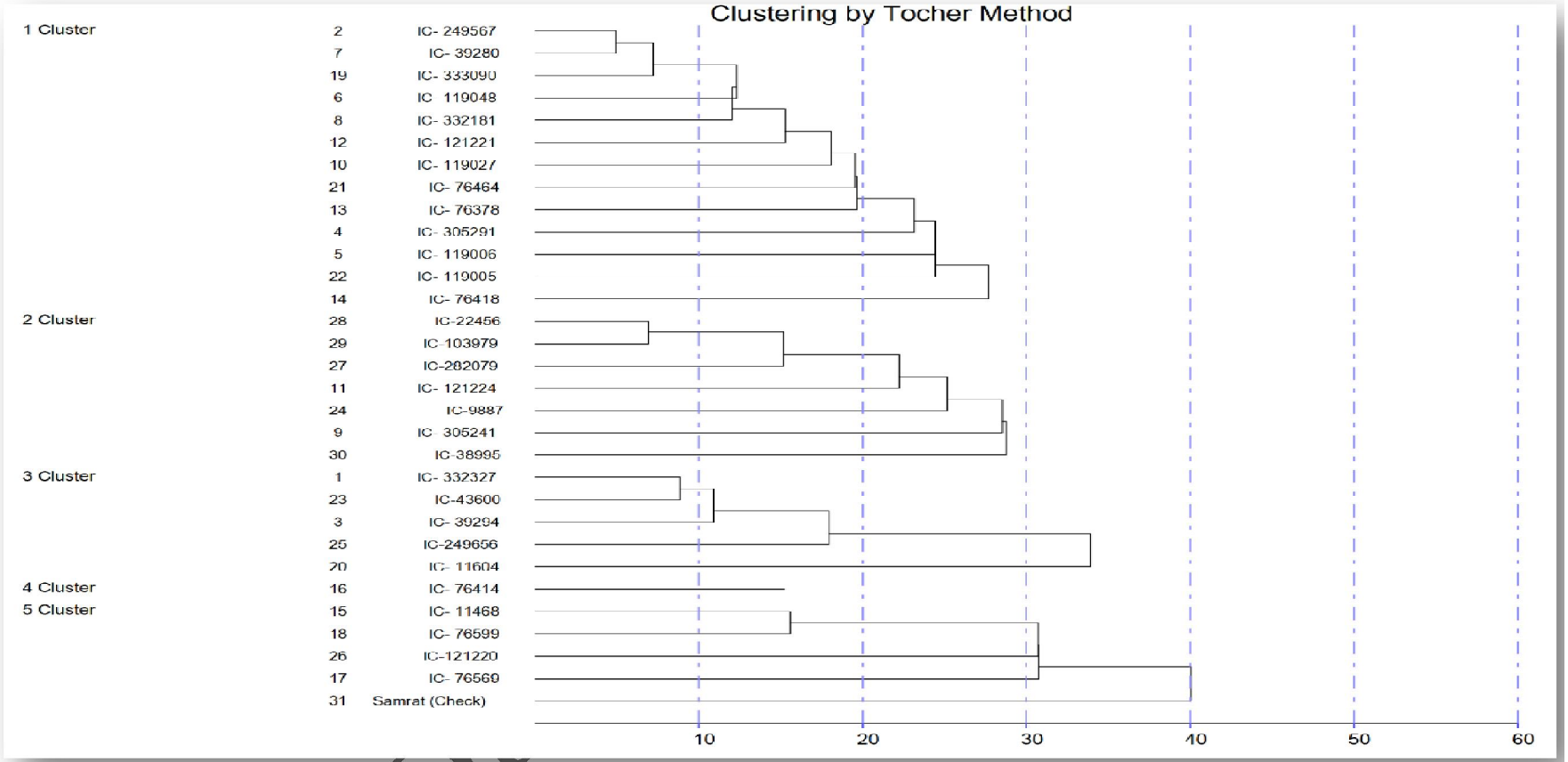
Seed yield per plant (g)	2.35	6.93**	0.53
****,* Significant at 1% and 5% level of significance respectively**			

Table 3. Composition of clusters in greengram genotypes

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	13	IC-249567, IC-39280, IC-333090, IC-119048, IC-332181, IC-121221, IC- 1 19027, IC-76464, IC-76378, IC-305291, IC-119006, IC-119005 and IC-76418
2 Cluster	7	IC-22456, IC-103979, IC-282079, IC-121224, IC-9887, IC- 305241 and IC-38995
3 Cluster	5	IC-332327, IC-43600, IC-39294, IC-249656 and IC- 11604
4 Cluster	1	IC-76414
5 Cluster	5	IC-11468, IC-76599, IC-121220, IC-76569 and Samrat (Check)

Table 4Average Intra Cluster (Bold) and Inter Cluster D^2 value in greengram genotypes

Cluster Distances					
	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**
Cluster 1	**23.6**	49.12	59.32	31.79	58.22
Cluster 2		**30.45**	46.06	68.85	118.71
Cluster 3			**28.30**	59.70	153.82
Cluster 4				**0.00**	66.63
Cluster 5					**43.09**



Fig

1Cluster composition of 31 genotypes represented in Dendrogram using Tocher's Method

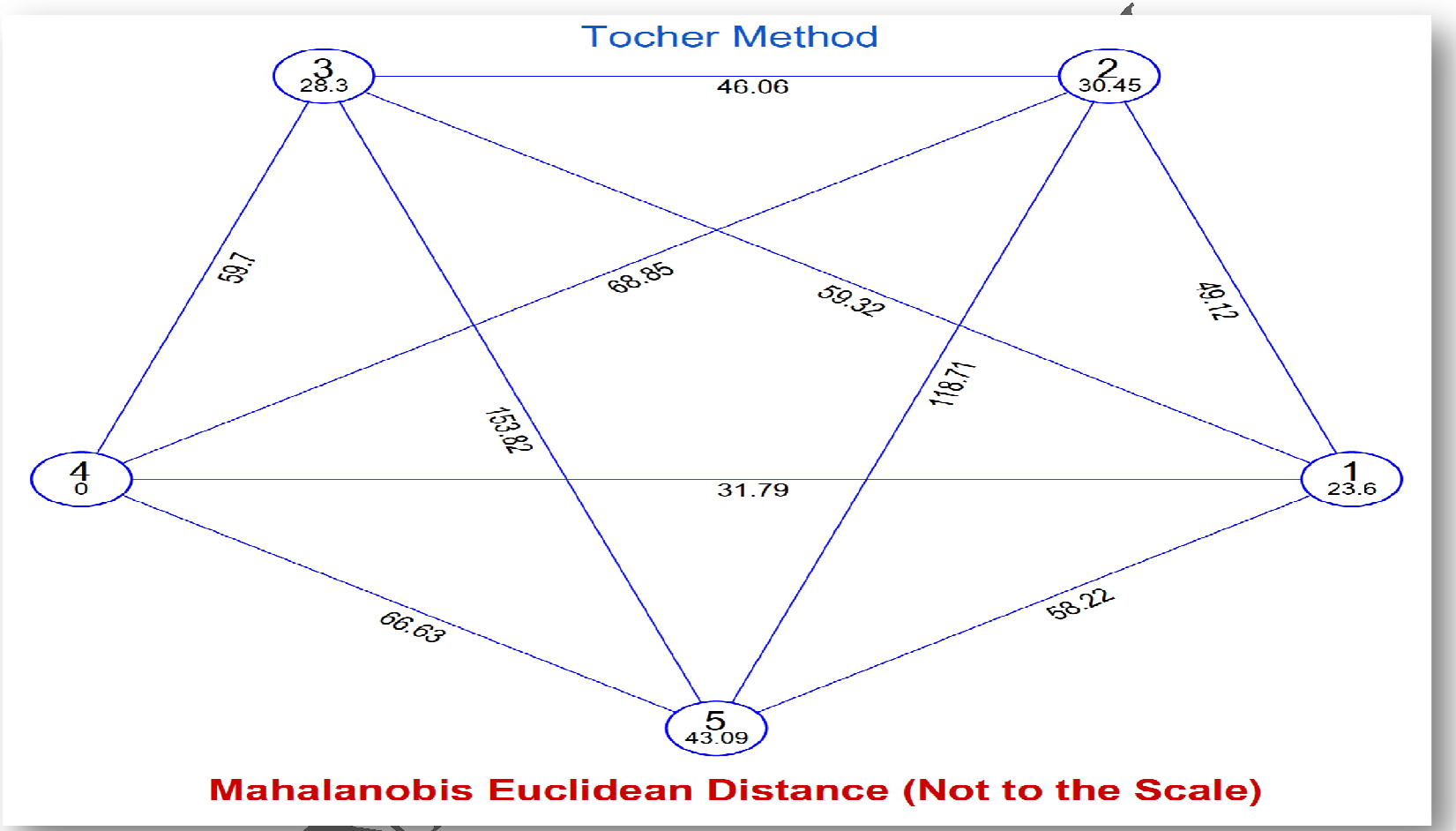


Fig 2. Cluster Diagram using Tocher's method

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