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D^2 Statistic Analysis among Green gram [*Vigna radiata* (L.) Wilczek] Genotypes

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ABSTRACT: The present investigation entitled "D^2 Statistic Analysis among Green gram [*Vigna radiata* (L.) Wilczek] Genotypes" is carried out with seventy two green gram genotypes including 4 checks *viz.*, IPM 205-07, IPM 02-03, IPM 410-3 and MH 421 in RBD design with three replications during *Kharif* 2023 to study the nature and extent of diversity present among genotypes. The observations were recorded for twelve characters. Based on their level of divergence, genotypes were classified into eight distinct non-overlapping clusters using Tocher's method. Maximum intra-cluster distance showed by cluster VII followed by cluster IV and cluster VIII and highest inter-cluster distance was observed between cluster IV and VI and cluster V and VI indicates that there was greater diversity present among these genotypes. Thus, genotypes of these clusters should be used in hybridization programmes to obtain better and desirable recombinants for increasing the grain yield of green gram.

Keywords: D^2 statistic analysis, intra-cluster, inter-cluster and genetic diversity.

INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek, 2n = 2x = 22] is a self-pollinating, annual, short duration dicotyledonous legume crop belonging to the family Fabaceae and sub family Papilionaceous (Salman *et al.,* 2021). It is also known as greensoy, mungbean, mashbean and goldengram (Markam *et al*., 2018). Cultivated mungbean is believed to have been domesticated from its wild progenitor, *Vigna radiata* var. *sublobata* and believed to be originated in India (De Candole, 1886) or the Indo-Burma region (Vavilov, 1926). It is not only the primary source of protein (25-28 per cent) and carbohydrate (60-65 per cent), but it also contains fiber (3.5-4.5 per cent), minerals like calcium, iron, magnesium, zinc and some vitamin like thiamine, niacin, riboflavin, vitamin A and vitamin C (Udayasri *et al.,* 2022). Green gram is basically a warm season (*Kharif)* crop, but is also grown in *Rabi* and *Zaid* seasons in different parts of the country. In India, green gram is grown in an area 5.55 million hectares with an annual production 3.68 million tonnes and productivity 663 kg/ha. In Rajasthan, green gram occupies an area of 2.33 million hectares with annual production 1.17 million tonnes and productivity of 504 kg/ha. Genetic diversity is an essential part of any successful breeding programme as its evaluation helps in interpreting the heredity background and selection of diverse parents indirectly helping in isolation of superior recombinant. This more promising superior recombinant can also be used in further hybridization programmes to achieve higher yield of green gram. A statistical procedure (D^2) statistic was outlined by Mahalanobis (1936) to measure the genetic divergence in a given population. Estimation of degree of divergence between biological population and computation of different components to the total divergence is done completely. By keeping all these consideration in view, the present investigation was undertaken to study genetic divergence among 72 green gram genotypes for identifying diverse genotypes for the future studies and further improvement in research programmes which utilizes advanced multi-disciplinary breeding approach.

MATERIALS AND METHODS

The experiment was carried out with seventy-two genotypes of green gram along with four checks *viz.,* IPM 205-07, IPM 02-03, IPM 410-3 and MH 421 in Randomized Block Design (RBD) with three replications at experimental field of AICRP on MULLaRP, Agricultural Research Station, Ummedganj, Kota, Rajasthan, during *Kharif* 2023. The plot size for each genotype was 4×0.6 m^2 with spacing 30 ×10 cm. The observations were recorded on five

randomly selected plants per plot for characters *viz.,* plant height (cm), number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, biological yield per plant (g), 100-seed weight (g), harvest index (%), protein content (%) and seed yield per plant (g) whereas, the observations days to 50 per cent flowering and days to maturity were recorded on a whole plot basis. The documented data on various characters were subjected to analysis of genetic divergence with the help of Mahalanobis D^2 statistics based on multivariate analysis proposed in 1936 and the genotypes were grouped into different intra-cluster and inter-cluster by using Tocher's method as described by Rao (1952). It measures difference in intra and inter-cluster distance and estimates the relative contribution of individual characters to the total divergence.

RESULTS AND DISCUSSION

Based on their level of divergence, genotypes classified into eight distinct non-overlapping clusters and presented in Table 1. The discrimination of genotypes into discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Out of all cluster, cluster II had maximum number of genotypes *i.e.,* twenty three namely BCM 20-1, BCM 20-45, BCM 06-2, HUM 16, IPM 1604-1, IPM 1704- 14, IPM 205-7, IPM 02-3, IPM 410- 3, IPM 512-1, KM 2421, MH 18- 100, MH 18- 181, MH 18- 189, MH 1918, MH 421, MML 2552, MML 2556, Pusa M 22-42, OBGG 111, MH 1850, MH 1762 and IPMD 101-2 followed by cluster V contain nineteen genotypes *viz*., JLPM 818- 8, PMD 14, Pusa M 22- 31, Pusa M 23- 31, Pusa M 23-41, Pusa M 23- 42, RMG 1169, RMG 1186, SML 1082, SML 2108, SVM 88, TRM 146, TRM 230, VGG 20-153, MH 1703, MHBC 20- 14 and OBGG 105, cluster VIII contain nine genotype namely BCM 14-2, GM 6, IPM 1707- 1, IPM 2- 14, JLPM 707- 27, Pusa M 23-32, PMS 13, Pusa M 21- 31 and Pusa M 19111, cluster I contain eight genotypes PM 1803, RMG 1148, SML 1115, TMB 233, Pant M- 2, OBGG 110, PMS 9 and Pusa M 22- 31, cluster IV contain five genotypes BCM 20-55, SKNM 2006, SVM 66, MHBC 20- 8 and PMS 12, cluster VII contain four genotypes PM 1711, Pusa M 9531, TCA- DM- 1 and VGG 20- 255, cluster III contain three genotypes BCM 20-50, MHBC 20- 13 and MH 1762 and cluster VI contain only one genotype CO 7. This indicates the presence of diversity among the genotypes under study.

The average D^2 values of intra and inter-cluster distance and the nearest and farthest cluster from each other based on D^2 Values are presented in the Table 2. The intra-cluster distance was varied from 0 to 12.32. The maximum intra-cluster distance was recorded in cluster VII (12.32) followed by cluster IV (8.63), cluster VIII (7.28), cluster II (6.81), cluster V (6.13) and cluster I (5.27) while no intra-cluster distance was recorded in cluster VI (0). Maximum intra-cluster distance showed that there was greater diversity present among the genotypes assigned to those respective clusters and minimum intra-cluster distance indicating that genotypes present in cluster were closely related to each other. Similarly, the inter-cluster distances ranged from 8.84 to 36.34. Highest inter-cluster distance was observed between cluster IV and VI (36.34), followed by cluster V and VI (32.20), cluster II and VI (29.96), cluster III and VI (29.35), cluster IV and VII (29.96) and cluster I and VI (26.57). Inter-cluster distance was minimum between cluster I and II (8.84). Greater inter-cluster distance between two clusters indicates wider genetic diversity among genotypes of these clusters. Thus, a high heterotic combination would arise from hybridization between genotypes having the high inter-cluster distance. These results concur with the prior results of Talukdar *et al.* (2020); Bindu *et al.* (2023).

The mean values of twelve characters for eight clusters are presented in Table 3. The cluster IV with genotypes BCM 20-55, SKNM 2006, SVM 66, MHBC 20- 8 and PMS 12 was found earliest days to 50 per cent flowering, days to maturity, dwarf plant height and higher cluster mean values for harvest index, 100-seed weight, number of seeds per pod and pod length, while cluster III (BCM 20-50, MHBC 20- 13 and MH 1762) had higher cluster mean for number of clusters per plant, number of pods per plant, biological yield and seed yield per plant and cluster I (PM 1803, RMG 1148, SML 1115, TMB 233, Pant M- 2, OBGG 110, PMS 9 and Pusa M 22- 31) was found promising for higher protein content. Therefore, it is vital pre-requisite for a breeder to wisely combine all the desired traits of diverse genotypes with high cluster mean values for hybridization programmes to obtain better and desirable recombinants. Sneha *et al.* (2020); Sridhar *et al.* (2022); Bindu *et al.* (2023); Jadhav *et al.* (2023) also recorded similar types of findings conform to the prior results.

Table 1: Distribution of green gram genotypes into different eight clusters.

Cluster Group	No. of Genotypes	List of Genotypes
Cluster I	8	PM 1803, RMG 1148, SML 1115, TMB 233, Pant M- 2, OBGG 110, PMS 9 and Pusa M 22- 31
Cluster II	23	BCM 20-1, BCM 20-45, BCM 06-2, HUM 16, IPM 1604-1, IPM 1704- 14, IPM 205- 7, IPM 02-3, IPM 410- 3, IPM 512-1, KM 2421, MH 18- 100, MH 18- 181, MH 18- 189, MH 1918, MH 421, MML 2552, MML 2556, Pusa M 22-42, OBGG 111, MH 1850, MH 1762 and IPMD 101- 2
Cluster III	3	BCM 20-50, MHBC 20- 13 and MH 1762
Cluster IV	5	BCM 20-55, SKNM 2006, SVM 66, MHBC 20- 8 and PMS 12
Cluster V	19	JLPM 818- 8, PMD 14, Pusa M 22- 31, Pusa M 23- 31, Pusa M 23- 41, Pusa M 23- 42, RMG 1169, RMG 1186, RMG 1196, SML 1082, SML 2108, SVM 55, SVM 88, TRM 146, TRM 230, VGG 20-153, MH 1703, MHBC 20- 14 and OBGG 105
Cluster VI	1	CO 7
Cluster VII	4	PM 1711, Pusa M 9531, TCA- DM- 1 and VGG 20- 255
Cluster VIII	9	BCM 14-2, GM 6, IPM 1707- 1, IPM 2- 14, JLPM 707- 27, Pusa M 23- 32, PMS 13, Pusa M 21- 31 and Pusa M 19111

Table 2: Inter and Intra-cluster distance among different clusters of mungbean genotypes.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**5.27**	8.84	15.66	20.06	10.38	26.57	17.52	10.03
Cluster II		**6.81**	11.13	12.15	9.73	29.96	21.60	11.69
Cluster III			**5.21**	14.97	14.84	29.35	24.14	16.62
Cluster IV				**8.63**	15.47	36.34	26.96	22.45
Cluster V					**6.13**	32.20	20.24	18.57
Cluster VI						**0.00**	17.86	23.98
Cluster VII							**12.32**	21.69
Cluster VIII								**7.28**

Table 3: Cluster mean values of seed yield and its contributing traits.

Cluster Means : Tocher's Method												
Cluster	**Days to 50 per cent flowering**	**Days to maturity**	**Plant height (cm)**	**Number of clusters per plant**	**Number of pods per plant**	**Pod length (cm)**	**Number of seeds per pod**	**Biological yield per plant**	**Harvest index (%)**	**100-seed weight**	**Protein content (%)**	**seed yield per plant (g)**
Cluster I	38.50	62.67	57.74	4.44	15.38	7.58	7.59	19.55	10.80	2.02	20.84	2.11
Cluster II	35.49	60.51	54.63	4.70	16.57	7.67	8.17	20.00	17.83	2.70	19.95	3.54
Cluster III	36.11	60.67	55.17	7.25	25.96	7.64	8.12	25.00	19.21	2.79	20.00	4.78
Cluster IV	35.47	60.13	46.33	5.25	18.95	8.15	8.72	18.34	26.05	2.96	20.63	4.72
Cluster V	36.89	62.72	47.88	4.95	16.81	7.41	7.62	21.67	11.71	2.35	20.60	2.51
Cluster VI	51.00	80.33	69.67	5.53	20.13	7.10	7.64	24.77	17.03	2.69	20.15	4.22
Cluster VII	52.58	72.50	55.70	4.30	16.63	7.27	6.43	19.88	12.88	2.34	20.81	2.57
Cluster VIII	36.00	63.48	65.70	4.33	15.52	7.97	7.51	19.78	16.11	2.52	20.11	3.19

CONCLUSIONS

From the current experiment, it can be suggested that genotypes from cluster IV should be selected for developing early maturity varieties of green gram while genotypes from cluster III should be selected for selection as parent in hybridization programmes for improving seed yield in green gram and cluster I should be selected for improving protein content of green gram. Maximum intra-cluster distance showed by cluster VII followed by cluster IV and cluster VIII indicates that there was greater diversity present among genotypes of these clusters. Highest inter-cluster distance was observed between cluster IV and VI and cluster V and VI which indicating wider genetic diversity among genotypes. Thus, these cluster's genotypes should be used in hybridization programmes to obtain better and desirable recombinants for increasing the seed yield of green gram.

FUTURE SCOPE

Based on D^2 statistics, the current investigation helps to identification of diverse germplasm line and gene stock which is pre-requisite for any successful breeding programmes for improving yield and its contributing traits.

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