Journal of
Current Opinion in Crop Science
Journal homepage: www.jcocs.com; ISSN(O):2583-0392

SHORT COMMUNICATION

Genetic diversity studies using Mahalanobis method in Mungbean under Acidic soils of Manipur

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Article history:

Received: November 11, 2022
Accepted: December 19, 2022
Published: December 28, 2022

Citation: Jeberson M. S., & Shashisdhar, K. S. (2022). Genetic diversity studies using Mahalanobis method in Mungbean under Acidic soils of Manipur. *Journal of Current Opinion in Crop Science, 3*(4), 173-176.

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ABSTRACT

The cultivation of mungbean is important in the NEH region. The crop's genetic improvement mostly depends on the degree of genetic variability already present in the base population, which also acts as a valuable source of the base population for a wide variety of genetic variations. The present study aimed to study the genetic diversity analysis using the Mahalanobis method in mungbean grown under acid soils in Manipur, India. The present result showed that Mungbean genotypes have differed significantly for all characters in the analysis of variance. Eleven clusters had all twenty-eight genotypes. Cluster II had the most genotypes (8), followed by cluster III (4), cluster I, V & VII (3), cluster VI (2), and clusters IV, VIII, IX, X, and XI (1 each). Furthermore, mungbean genotypes also showed significant variation in the grouping.

Keywords: genetic diversity, multivariate analysis, mungbean.

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek, 2n=22, Fabaceae) is a vital pulse crop picking cultivation in the NEH region. Genetic improvement of the crop mainly depends upon the amount of genetic variability present in the base population and serves as a valuable source of the base population for wide variability. Plant genetic diversity reveals the extent of genetic variation in populations. In the study, it was very helpful to the people who breed mung beans to group genotypes together using multivariate approaches. When it comes to generating high-yield cultivars of mung bean, it is of the utmost importance to make use of the available gene pool (Jadhav et al., 2021). Multivariate methods like D^2 and principal component analysis may help quantify genetic diversity. The multivariate method helps select divergent parents for hybridization to maximize heterosis. Multivariate analysis using Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence at the genotypic level (Jadhav et al., 2021). Therefore, the present investigation with a view to estimate genetic

divergence among a panel of 28 genotypes of mungbean has been carried out.

MATERIALS AND METHODS

The experimental materials for the present study consisted of twenty-eight mungbean genotypes (Table.1) from advanced breeding lines obtained from AICRP(MULLaRP), ICAR-IIPR, Kanpur. The experiment was conducted in randomized block design (RBD) with three replications at the Andro Research Farm, Imphal East District, CAU, Imphal, India during 2018-2019. The plants were sown with a spacing of 30 cm between rows and 10 cm between plants within row, replicated thrice (Fig.1). To raise the healthy crop recommended agronomic and plant protection measures were followed. Observations were recorded on five randomly selected plants per replication for quantitative traits namely days to fifty percent flowering (DFF), Days to maturity, plant height, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plot (g). The data were analysed using Mahalanobis D^2 statistics as per Mahalonobis (1936) method and Toucher's method as suggested by Rao (1952) was used to group the genotypes into different clusters.

RESULTS AND DISCUSSION

The results of the analysis of variance revealed that there are significant differences between the genotypes of mungbeans for all of the traits that were examined. The preceding report presented findings that were comparable to these ones (Sandhiya and Saravanan, 2018). The twenty-eight different genotypes have been organized into eleven different clusters (Table 2). Cluster II included the greatest number of genotypes (eight), followed by cluster III (four genotypes), cluster I, V, and VII (three genotypes), and cluster VI (two genotypes). Clusters IV, VIII, IX, and XI were solitary clusters, each containing only one genotype. The pattern of the mungbean genotypes grouped together showed that there is a large amount of heterogeneity between the groups.

The choice and selection of parental genotypes mainly depend upon the contribution of character towards divergence (Loganathan et al., 2001) and the characters, the contribution of seed yield per plot(g) was maximum (31.22 percent) followed by plant height (28.04 percent). In addition, 100 seed weight (21.96 percent), days to fifty percent flowering (7.94), and pod length (5.05 percent) also contributed towards total divergence (Table 3).

Table 1. Name and Origin of the genotypes used in the study

S.No.	Genotype Name	Origin
1	PM1511	GBUAT, Pantnagar
2	Pant M6	GBUAT, Pantnagar
3	VGG17-009	NPRC, Vamban
4	IGKM 05-6-27	IGKVV, Raipur
5	SKAU-M-365	Srinagar, J&K
6	KM 2241	CSAUA&T,Kanpur
7	SKNM 1514	SDAU, S.K. Nagar
8	MGG 399	ARS, Madhira
9	IGKM 06-18-3	IGKVV, Raipur
10	OBGG 101	OUAT, Bhubaneswar
11	Pusa 0672	IARI, New Delhi
12	SKNM 1516	SDAU, S.K. Nagar
13	DGGV-59	ARS, Dharwad
14	Pusa M 1871	IARI, New Delhi
15	OBGG 102	OUAT, Bhubaneswar
16	LGG 630	ARS, Lam
17	SVM 6262	SVHS, Hisar
18	MH1344	CCSHAU, Hisar
19	Pusa M1872	IARI, New Delhi

20	TRCM 171-B-B-12-6	Agartala,Tripura
21	ML 2483	PAU, Ludhiana
22	IPM 604-1	IIPR, Kanpur
23	AKM-1604	PDKV, Akola
24	PM 1522	GBUAT, Pantnagar
25	SML 1901	PAU, Ludhiana
26	VGG17-002	NPRC, Vamban
27	JLM 707-5	MPKV, Jalgoan
28	DGGS-4	UAS Dharwad

Table 2. Cluster composition of twenty-eight green gram genotypes (Tocher's method)

Cluster No.	No. of Genotypes	Genotypes Name
I	3	VGG17-009, VGG17-002, Pant M6
II	8	KM 2241, OBGG 101, TRCM 171-B-B-12-6, IGKM 05-6-27, PM1511, Pusa M 1871, Pusa 0672, Pusa M1872
III	4	SKNM 1514, DGGV-59, PM 1522, MH1344
IV	1	SKNM 1516
V	3	MGG 399, IGKM 06-18-3, LGG 630
VI	2	SML 1901, AKM-1604
VII	3	SKAU-M-365, DGGS-4, JLM 707-5
VIII	1	OBGG 102
IX	1	ML 2483
X	1	IPM 604-1
XI	1	SVM 6262

Table 3. Relative contribution of 9 traits towards divergence

S.No	Character	Number of First Ranks	Percentage of contribution towards Divergence
1	DFF	30	7.94
2	DM	2	0.53
3	NCP	6	1.59
4	NPP	4	1.06
5	PL (cm)	28	7.41
6	NSP	1	0.26
7	Pht (cm)	106	28.04
8	100 swt(g)	83	21.96
9	Yd/plot(g)	118	31.22

Note: DFF, Days to fifty percent flowering; DM, Days to maturity; Pht, Plant height (cm); NCP, Number of clusters per plant; NPP, Number of pods per plant, PL, pod length (cm); NSP, number of seeds per pod, 100 swt, 100 seed weight (g); Yd/plot, seed yield per plot (g).

Figure.1. Mungbean trial conducted at Andro Research Farm, CAU, Imphal

CONCLUSION

It is well known fact that crosses between contrary parents usually produce greater heterotic effect than narrowly related ones. Considering the importance of traits towards total divergence, the present investigation concluded that the parental lines selected from clusters IX, IV (ML2483, MH1344 & DGGV-59) for seed yield per plant, clusters VII (JLM 707-5) and XI (SVM6262) for 100 seed weight, cluster I (VGG17-009 and VG17-002) for plant height could be used in crossing programme to achieve desired segregants.

DISCLOSURE STATEMENT

No potential conflict of interest was reported by authors.

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