Int.J.Curr.Microbiol.App.Sci (2018) *7*(7): 1101-1108

International Journal of Current Microbiology and Applied Sciences
***ISSN: 2319-7706* Volume 7 Number 07 (2018)**
Journal homepage: http://www.ijcmas.com

Review Article https://doi.org/10.20546/ijcmas.2018.707.134

Tailoring the Genetic Diversity of Mung Bean through Cluster Analysis for Yield Attributing Traits to Obtain Efficient Hybrids

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Keywords

Diversity, Plant height, Selective breeding, Pods plant^{-1}, Early maturity

Article Info

Accepted:
08 June 2018
Available Online:
10 July 2018

A B S T R A C T

Through hierarchical clustering method, 27 genotypes were confined to VII clusters. Cluster I encompasses of three genotype accessions Basanti, TM-99-50, Sublobata-02 and it showed high cluster mean for plant height, days to maturity, number of pods plant^{-1}. Lower plant height was observed in genotypes under Cluster IV, clusters I and clusters V consisted of high plant height. Early maturity genotypes were under cluster V and late maturity genotypes were under cluster I. Cluster IV showed highest mean in protein content and seed yield plant^{-1} among all clusters. Highest pod width was recorded by cluster VII (0.470) and lowest pod width was recorded in cluster I (0.250). Genotypes in cluster IV and cluster VII (56.321) was found very diverse clusters. High yielding genotypes with high mean value seed weight and protein content was found in cluster IV. With the selection of most diverse plants with high mean performance for many characters cluster analysis can be applied inbreeding program for mung bean improvement.

Introduction

Genetic diversity is one of the criteria of parent selection in the hybridization program. The availability of transgressive segregant in any breeding program depends upon the diversity between the parents involves. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D2-statistic and Canonical Variate Analysis (CVA) has made possible to choose genetically diverged parents. Recent works indicated that the Mahalanobis generalized distance (D2-statistic) may be an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936). The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis. The present study was undertaken to select the divergent parent for future hybridization program.

Sasma *et al.*, (2008), observed hybridization is one of the important tools for crop improvement. Genetic divergence plays a vital role in the choice of parents to be used in hybridization programme. An experiment was

conducted among mung bean genotypes. The grouping of genotypes into four clusters, indicated the presence of wide range of genetic variability. Cluster III was evolved as a largest cluster and comprised seven genotypes and maximum inter-cluster distance was observed between cluster I and IV. Hybridization between clusters I and IV was expected to generate a wide range of variability and will facilitate the isolation of desirable genotypes. Characters, 100-seed weight, plant height and seed yield plant-1 contributed maximum to genetic divergence and needs due consideration while selecting the parents for hybridization for yield improvement.

Lavanya *et al.,* (2010), conducted an experiment with an objective to study genetic diversity available in mung bean. The mung bean genotypes were distributed into five and six clusters based on Euclidean distances under two environments, respectively. Cluster IV evolved as a major cluster in one environment and clusters III, IV as large clusters in other environment. Distribution of genotypes into different clusters, suggested the presence of substantial genetic divergence among the germplasm. Inter cluster distance was found maximum between clusters I and II during kharif, 2005. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement in mung bean. Mean performance of different clusters were variable, suggesting wide range of differences between clusters. Ghulam-Abbas *et al.*, (2010), studied different morphological and economic traits like plant height, clusters plant-1, pods plant-1, hundred seed weight, biological yield, seed yield and harvest index exhibited considerable genetic variability in mung bean genotypes. Metroglyph analysis distributed mung bean genotypes into 8 groups. Group I and II, consisted of only one genotype each and were found to be distant from all other groups. Groups VII and VIII were the largest groups consisting of 10 genotypes each. On the basis of this grouping it may be concluded that an effective hybridization program may include the genotypes of group I, II, VII and VIII to produce better segregants that may be used for the development of high yielding mung bean varieties. Rahim *et al.,* (2010), grouped twenty six genotypes were grouped into III clusters. Maximum number of genotypes (12) was grouped into cluster II. The maximum range of variability was observed for number of pods plant-1 (12.22-20.55) among all the characters in III clusters. Crosses involving cluster I and III may exhibit high heterosis for yield as well as earliness.

Yadav *et al.,* (2011), evaluated 135 mung bean genotypes and observations were recorded on seed yield plant-1 and 11 other yield associated traits. Data were subjected to Non-hierarchical Euclidean Cluster Analysis. 135 genotypes were grouped in to IX distinct clusters indicating existence of high degree of genetic diversity in the germplasm collection. The maximum intra-cluster distance was recorded in clusters VIII (3.106) while, the lowest value was found in cluster VI (2.027) indicating the genotype of same cluster have little genetic divergence from each other. Maximum intra cluster distance was observed between cluster-IV and IX (5.722) followed by cluster III and IX (5.352). The crosses between genotypes of clusters separated by high intra-cluster distance are likely to throw desirable segregants. It is most desirable to attempt crossing between the genotypes separated by high inter clusters value. Katiyar *et al.,* (2011), carried out genetic divergence analysis was carried out in 681 mung bean germplasm based on Euclidean distance for the identification of genetically diverse and agronomically superior accessions which may generate putative transgressive segregates on hybridization. Principal component and non-

hierarchical Euclidean cluster analysis were used to compare the genotypes. Based on first five principal components which accounted for 83.32% of the total variation, non-hierarchical Euclidean cluster analysis grouped the accessions into 10 well characterized clusters based on aggregate effects of similarity in traits. There is no parallelism between genetic diversity and geographical origin of accessions.

Singh *et al.,* (2012), grouped thirty genotypes were grouped into six. Clusters and cluster II comprised of 19 genotypes, evolving as the largest cluster, followed by cluster III with four genotypes, cluster II, IV and IV with two genotypes each and cluster V comprised a single genotype. Inter-cluster distance (D2) was found maximum between clusters II and IV, II and V and clusters III and V. Mean performance of different clusters was variable, suggesting wide range of differences between clusters. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement in mung bean.

Shweta *et al.,* (2013), evaluated seventy seven genotypes of mung bean for ten different characters to estimate for genetic diversity. The genotypes were grouped into IX clusters. Cluster III had maximum intra-cluster distance while inter-cluster distance was highest between clusters VIII and IX. Cluster means indicated that none of the cluster was superior for all the characters studied. Therefore, hybridization between genotypes belonging to different clusters is suggested for development of superior genotypes. Sonu *et al.,* (2013), from analysis of variance revealed significant differences among 50 mung bean genotypes for 11 characters studied. Fifty genotypes were grouped into eight different clusters. Cluster II comprised maximum nine genotypes, cluster VII comprised eight genotypes and cluster IV included three genotypes. Cluster VIII registered maximum cluster mean value for number of pods plant-1 and seed yield plant-1. Maximum inter-cluster distance was observed between cluster V and VIII. Seed yield plant-1 contributed maximum to genetic diversity. Therefore, for hybridization between genotypes in clusters V and VIII should be selected for development of superior genotypes. Shahin-uz-Zaman *et al.,* (2013), evaluated thirty one genotypes of mung bean to estimate the genetic diversity among genotypes. All genotypes that was significantly differed with these characters belonged to 6 groups (Clusters I to VI) as recorded from principal component analysis. Maximum intracluster distance was observed in Cluster IV (9.28) followed by Cluster VI (8.70) indicating the wide genetic variability within the genotypes belonging to the two clusters. Cluster III exhibited the highest mean value for nodes of 1st peduncle, cluster plant-1, cluster on main stem, and cluster on branches, primary branches plant-1 and pods plant-1. Whereas cluster I had the lowest days to maturity and maximum pods cluster-1 as well as the highest grain yield plant-1.

Mahalanobis' D2 – Statistics

Mahalanobis (1936) defined the distance between two populations as:

$D2= \Sigma\Sigma WijPj=1Pi=1didj$ …… (i)

Where,

Wij is the (ij) th element in the inverse matrix of estimated within population variance covariance matrix, 'p' is the number of characters involved, di and dj are the differences in the means of two populations for the ith and jth characters. If't' is the number of populations, the total number 'n' of the pairs of population is t (t – 1)/2.

Since the numerical evaluation of D2, using equation (i), would involve the inversion of a P×P matrix and the summation of P2 products, a simpler method of using transformed uncorrelated variables has been followed. The

transformation of correlated variables to uncorrelated ones is done by using pivotal condensation method. The coefficients for the transformation are obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements (only the absolute values of these elements are considered). By using this method, given by Rao (1952), the D2 value is obtained as a sum of squares of P values of the uncorrelated variables.

Thus,

$D2=\Sigma fi2Pi=1$ …….. (ii)

Where,
fi is the difference between yi means of the transformed uncorrelated variables.

Grouping of genotypes into separate clusters by Tocher's method

Arranging the populations in order of increasing magnitude of D2 value from each individual population, various clusters are formed following the method suggested by Tocher (Rao, 1952) as follows:

The populations having smallest distance from each other are considered first to which a third population having smallest average D2 value from the first two populations is added. Then comes nearest forth populations and so it goes on. At certain stage when it is felt that after adding a particular population, there is abrupt increase in the average D2, this population is not added in that cluster. Generally, this level should be approximately near the maximum D2 value between any two populations in the first row of the table where D2 values are arranged in increasing order of magnitude. Similarly, a second cluster was formed. Thus, the process was continued till all the populations were included into one or other cluster.

Average intra-cluster distance

Average intra-cluster distance is estimated as:

$$= \Sigma Di \div 2n$$

Where,
ΣDi2 is the sum of distance between all possible combinations (n) of the population included in the cluster and 'n' is the total number of all possible combinations.

Average inter-cluster distance

Average inter-cluster distance is estimated as:

$$= \Sigma D2 \div ninj$$

Where,
ΣD2 = sum of distance between the populations of ith and jth cluster.
ni = number of population in the ith cluster
nj = number of population in the jth clusters

Diversity (D) 2 cluster analysis

In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extent of available genetic diversity (Mohammadi, 2003). Lee *et al.*, (2004) considered morphological characterization as an important step in description and classification of crop germplasm because a breeding program mainly depends upon the magnitude of genetic variability (Piyada *et al.*, 2010)

Through hierarchical clustering method, 27 genotypes were confined to VII clusters. Maximum number of genotypes under study belongs to Cluster VI with 8 accessions each followed by Cluster III and Cluster V with 8 accessions, Cluster I with 3 accessions and Cluster II, Cluster IV, Cluster VII consists of 2 accessions each respectively. Cluster I encompasses of three genotype accessions Basanti, TM-99-50, Sublobata-02 and it showed high cluster mean for plant height, days to maturity, number of pods plant-1. Cluster II consists of two genotypes Tarm-02, WBM 04-05. Cluster III composed of 5

genotypes Bireswar, HUM-12, PS-16, IPM-2-3, and Malda-95-13. Cluster IV includes two genotypes K-851, Midnapur local and cluster V composed V genotypes WBM-314, Kopergaon, Meha, Pant mung-5, and PDM-54. Cluster VI composed of VIII genotypes Pusa vishal, Samrat, Sonali, Sublobata-14, TM-99-21, TM-99-30, TM-99-37, and WBM-220. Cluster VII composed of 2 WBM-4131, WBM-611-3 genotypes.

Table.1 Cluster no. of members

CLUSTER I	**BASANTI, TM-99-50, SUBLOBATA-02**
CLUSTER II	TARM-02, WBM 04-05
CLUSTER III	BIRESWAR, HUM-12, PS-16, IPM-2-3, MALDA-95-13
CLUSTER IV	K-851, MIDNAPUR LOCAL,
CLUSTER V	WBM-314, KOPERAGON, MEHA, PANTMUNG-5, PDM-54
CLUSTER VI	PUSAVISHAL, SAMRAT, SONALI, SUBLOBATA-14, TM-99-21, TM-99-30, TM-99-37, WBM-220
CLUSTERVII	WBM-4131, WBM-611-3

Table.2 Contribution of each charactto divergence

Sl.No	Character	No. of first rank	% contribution
1	Plant height	0	0.000
2	Days to 50% flowering	8	2.2792
3	Days to maturity	23	6.5527
4	Number of branches plant^{-1}	38	10.8262
5	Number of seeds pod^{-1}	31	8.8319
6	Pod length	10	2.8490
7	Pod width	1	0.2849
8	Number of pods plant^{-1}	44	12.5356
9	Seed weight (100 seeds)	21	5.9829
10	Protein content	30	8.5470
11	Seed yield plant $^{-1}$	145	8.5470
TOTAL		351	41.3105

Table.3 Inter and intra cluster distance

CLUSTERS	CLUSTER I	CLUSTER II	CLUSTER III	CLUSTER IV	CLUSTER V	CLUSTER VI	CLUSTER VII
CLUSTER I	**18.660**	25.324	30.352	44.152	24.335	19.405	35.364
CLUSTER II		**25.689**	20.899	20.814	34.230	23.734	24.092
CLUSTER III			**4.331**	23.085	45.645	25.115	20.142
CLUSTER IV				**22.307**	25.212	44.162	56.321
CLUSTER V					**24.029**	24.910	35.649
CLUSTER VI						**4.993**	25.196
CLUSTER VII							**24.332**

Table.4 Cluster means

Sl. No	CLUSTERS	CHARACTERS										
		plant height	Days to 50% flowering	Days to maturity	No. of branches plant^{-1}	No. of seeds pod^{-1}	Pod length	Pod width	Pods plant^{-1}	Seed weight (100 seeds)	Protein content	Seed yield plant^{-1}
1	CLUSTER I	41.350	48.600	79.133	1.783	11.550	6.383	0.250	33.433	3.733	21.683	8.300
2	CLUSTER II	40.600	48.525	78.850	2.325	9.125	7.425	0.265	23.550	3.525	22.675	7.675
3	CLUSTER III	35.00	49.660	77.930	2.590	9.980	8.370	0.310	24.000	4.250	19.580	7.250
4	CLUSTER IV	29.700	48.850	77.925	3.400	9.275	9.375	0.300	23.500	4.500	23.175	8.475
5	CLUSTER V	41.250	48.860	76.070	2.010	10.160	11.360	0.450	32.620	3.060	17.090	7.090
6	CLUSTER VI	35.100	48.488	78.262	2.450	9.588	10.363	0.469	26.587	4.581	20.806	7.806
7	CLUSTER VII	34.400	49.100	78.850	2.400	9.175	6.300	0.470	23.600	3.250	19.275	7.275

The mean performance of all the characters in different clusters is presented in Table 4.13. Lower plant height was observed in genotypes under Cluster IV, clusters I and clusters V consisted of high plant height. Early maturity genotypes were under cluster V and late maturity genotypes were under cluster I. Cluster IV showed highest mean in protein content and seed yield plant-1 among all clusters. Highest pod width was recorded by cluster VII (0.470) and lowest pod width was recorded in cluster I (0.250). The inter-cluster distance value showed that the genotypes most diverse in cluster IV and cluster VII (56.321) followed by Cluster III and VI (44.645), Cluster IV and VI (44.162) is presented in table 4.13. Genotypes in cluster IV and cluster VII (56.321) was found very diversed clusters.

High yielding genotypes with high mean value seed weight and protein content was found in cluster IV. Similarly genotype in cluster I was found superior for plant height, number of pods plant-1 and number of seeds plant-1, and genotypes in cluster V for early maturity and pod length. So selective breeding can be approached considering all these genotypes scattered in different cluster to bring improvement in plant architecture yield and protein content in seed.

Studies conducted by Bisht *et al.,* 1998, showed that 111 mung bean accessions were grouped into six discrete and well-defined clusters. Pandiyan *et al.,* (2012), subjected 646 green gram accessions into hierarchical cluster analysis which revealed eight distinct clusters. Similar results were reported by Rahim *et al.,* (2008) and Abna *et al.,* (2012). Parents with more genetic distance can create higher variation which can increase of genetic gain in selection. With the selection of most diverse plants with high mean performance for many characters cluster analysis can be applied for crossing program for mung bean improvement. High yielding genotypes with high mean value seed weight and protein content was found in cluster IV. Similarly genotype in cluster I was found superior for plant height, number of pods plant^{-1} and number of seeds plant^{-1}, and genotypes in cluster V for early maturity and pod length. So selective breeding can be approached considering all these genotypes scattered in different cluster to bring improvement in plant architecture yield and protein content in seed.

Future scope

Genetic diversity studies at molecular and biochemical levels and also for other important morphological and physiological characters may be carried out to help selection of most diverse genotype accompanied by desirable attributes for development elite lines following combination breeding

References

Abna, F., Golam, F. and Bhassu S. 2012. Estimation of genetic diversity of mung bean (*Vigna radiata* L. Wilczek) in Malaysian tropical environment. *Afrin. Jrnl. of Mirbilgy. Res.*, 6(8): 1770-1775.

Bisht I.S., Mahajan R.K., Kawalkar T.G. 1998. Diversity in green gram (*Vigna radiata* (L.) Wilczek) germplasm collection and its potential use in crop improvement. *Annuals of Applied Biol.*, 132(2): 301–312.

Ghulam-Abbas, 2010. Genetic diversity in mung bean (*Vigna radiata* L.) Wilczek *Pakistan. Jrnl. of. Bot.,* 42(5): 3485-3495.

Katiyar, 2011. Assessment of genetic divergence in green gram (*Vigna radiata*) germplasm. *Indian J. of Agri. Sci.,* 81(1): 79-81.

Lavanya, 2010. Genetic divergence in mung

bean under two environments. *Trends-in-Biosci*., 3(2): 127-129.

Lee, Y.S., Lee, J.Y., Kim D.K., Yoon C.Y., Bak, G.C., Park, I.J, Bang, G.P., and Moon. 2004. A new high-yielding mung bean cultivar, "Samgang" with lobed leaflet. *Korean J. Breed.,* 36: 183-184.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of the Nat. Insti. Sci. India*. 12: 49–55.

Mohammadi S. 2003. Analysis of genetic diversity in crop plants-salient statistical tools and Considerations. *Crop Sci.*, 43(4): 1235.

Pandiyan M, Senthil N, Packiaraj D, Thanga Pandian R, Suresh R, Jagadeesh S. 2012. Characterization and evaluation of 646 green gram (*Vigna radiate* L.) genotypes for constituting core collection. *Wudpecker J. Agri. Res.*, 1(8): 294 – 301.

Piyada T, Juthamas T, Thongchai P, Thanawit T, Chutamas P, Worapa S, Thitiporn M. 2010. Variety identification and genetic relationships of mung bean and black gram in Thailand based on morphological characters and ISSR analysis. *Afr. J. Biotechnol*. 9(27): 4452-4464.

Rahim, M.A. 2010. Genetic variability, character association and genetic divergence in mung bean (*Vigna radiata* L. Wilczek). *Plant omics journal.* 3(1): 1-6.

Rahim, M.A., Mia, A.A., Mahmud, F. Afrin, K.S. 2008. Multivariate analysis in some mung bean accessions on the basis of agronomic traits. *American-Eurasian J. Sci. Res.,* 3(2): 217-221.

Rao, C.R. 1952. Advanced Statistical Methods in Biometric Research. John Wiley Sons, New York, 390p.

Sasma, 2008. Studies on genetic divergence in mung bean (*Vigna radiata* L. Wilczek). Mysore *J. Agri. Sci.,* 42(2): 206-208.

Shahin-uz-Zaman, 2013. Genetic divergence in mung bean. *Bulletin-of-the-Institute of Tropical Agriculture,-Kyushu-Univ.,* 36: 79-84.

Shweta, 2013. Genetic diversity analysis in mung bean (*Vigna radiata* L. Wilczek). *Inter. J. Plant-Sci. Muzaffar.,* 8(1): 64-66.

Singh, 2012. Selection of diverse mung bean genotypes for seed yield improvement: *New-Agr.,* 23(1): 5-9.

Sonu, 2013. Genetic divergence in mung bean (*Vigna radiata* L. Wilczek) germplasm. *J. Agri. Res. Technol.*, 38(2): 241-245.

Yadav, 2011. Genetic divergence analysis in mung bean (*Vigna radiata* (L.) Wilczek). New- Agri., 22(2): 159-163.

How to cite this article:

Umesh Kumar, V. and Sarkar, K.K. 2018. Tailoring the Genetic Diversity of Mung Bean Through Cluster Analysis for Yield Attributing Traits to Obtain Efficient Hybrids. *Int.J.Curr.Microbiol.App.Sci.* 7(07): 1101-1108. doi: https://doi.org/10.20546/ijcmas.2018.707.134