e-ISSN:2320-0189
p-ISSN:2347-2308

Research & Reviews: Journal of Botanical Sciences

Estimation of Genetic Divergence in Mung Bean (*Vigna radiata* L.) under Temperate Ecology of Kashmir

Aijaz Ahmad[1], Syed Mudasir Razvi[1], Manzor Ahmad Rather[1], Mushtaq Ahmad[1], Gul Zaffar[1], Shabeer Ahmad Ganie[2], Mohmad Ramzan Mir[3] and Khalid Rehman Hakeem[4]*

[1]Division of Genetics and Pant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir Shalimar campus, Srinagar, India

[2]Division of Plant Pathology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir Shalimar campus, Srinagar -191 121, India

[3]Department of Botany, Aligarh Muslim University, Aligarh 202002, India

[4]University Putra Malaysia, Serdang-43400, Selangor, Malaysia

Research Article

Received date: 11/01/2016
Accepted date: 03/03/2016
Published date: 05/03/2016

For Correspondence: Hakeem KR, University Putra Malaysia, Serdang-43400, Selangor, Malaysia, Tel : +60 3-8946 6000

E- mail: kur.hakeem@gmail.com

Keywords: Mung bean, Divergence, Clusters, Hybridization.

ABSTRACT

Thirty five genotypes of mung bean were evaluated during kharif 2011 with the objective to work out the genetic divergence in the genotypes for future breeding studies. Significant differences were observed for all the traits studied. The material was subjected to genetic analysis and further, based on Mahalanobis D^2 statistics genotypes were grouped into seven clusters, with cluster II having maximum of 13 genotypes, cluster-I 11 genotypes and cluster IV and V, (4 genotypes each) and the rest of the cluster were monogenotypic. Inter-cluster distance was maximum between cluster VI and VII (9308.29) followed by cluster IV and VII and Cluster I and VII (5236.69) the cluster means for seed yield plant-1 revealed that the magnitude of differences among the means ranged from (4.65 g) in cluster IV to (2.83 g) in cluster V. On the basis of divergence between clusters, genotypes from cluster-VI and VII followed by cluster-IV and VII can be involved in the hybridization program for recovery of superior recombinants or transgressive segregants in segregating generations.

INTRODUCTION

Legumes constitute the third largest family of higher plants, with 20,000 species and second after cereals in agricultural importance based on area and total production (Graham and Vance, 2003). These are unique crops in having an inbuilt capacity for fixing atmospheric nitrogen. Thus, these crops meet their own nitrogen requirement to a great extent. They also leave nitrogen in the soil that enrich it and become available to the succeeding crop. They are also important constituents in the diets of a very large number of people, especially in the developing countries and are good sources of protein, which help to supplement cereal diets. Protein content of pulses is twice that of cereals (>20%), whereas their by products provide nutritious fodder for livestock. With the growing demand for nutritional security, pulses are becoming ever more important as a plant based source of protein in the human diet. Unfortunately, unlike those of cereals, the existing production levels of pulses cannot meet the emerging demands. Among pulses, mung bean (*Vigna radiata L*. Wilczek) is also known as green bean, choroko, mung, mash bean, munggo, green gram, golden gram and green soy. Mung bean is native to Bangladesh, India and Pakistan. The mung bean is one of many species recently moved from the genus *Phaseolus to Vigna*. The nutritional value of mung bean per 100 g, energy (347 kcal), carbohydrates (62.62 g), sugars (6.60 g), dietary fibre (16.3 g), fat (1.15 g), protein (23.86 g), vitamin C (4.8 mg), calcium (132 mg) and magnesium (189 mg). (USDA Nutrient Database, 1997). Mung bean is also considered as the natural source of many bioactive compounds [1].

Genetic divergence is also of utmost importance for identifying appropriate genotypes as parents with their long-term potentialities. Mahalanobis D^2 statistics is a powerful tool in quantifying the degree of divergence at the genotypic level with

e-ISSN:2320-0189
p-ISSN:2347-2308

regard to characters which needed to be improved and provides an opportunity to identify putative parents for executing an effective breeding strategy [1]. Till date limited efforts have been made in characterizing mung bean accessions in India in general and in the Kashmir valley in particular. Precise information about genetic divergence is critical for productive breeding programs as genetically diverse parents are known to produce high heterotic effects consequently increasing yield in desirable segregants. D^2 statistics, it has now become possible to quantify the degree of genetic divergence among the biological population [2]. Therefore, the present investigation was aimed at ascertaining the nature and magnitude of genetic diversity among 35 mung bean genotypes for morphological yield and yield attributing traits to identify suitable parents for hybridization program.

MATERIALS AND METHODS

An experiment was carried out at experiential farm of Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir (SKUAST-K) Shalimar campus, Srinagar. Overall, 35 genotypes **(Table 1)** of mung bean including Shalimar mung-1 as check were evaluated in a randomized complete block design (RBD) with 3 replications during kharif 2011. Each experimental plot comprised two rows each of 3 m length, with 30 and 10 cm inter- and intra-row spacing. Recommended agronomic package of practices were followed to raise a healthy crop.

Table 1. List of germplasm lines, their source and pedigree.

S. No.	Name of Genotype	Source	Pedigree
1	SKUM-101	TNAU Coimbatore	COGWG 923 × VC 6040A
2.	SKUM-102	Mad hive	MGG 295 × MGG 341
3.	SKUM-103	ARS, Durgapura	ML 613 × BDYER-2
4	SKUM-105	CSAU, Kanpur	Samrat × ML-13
5	SKUM-106	PAU, Ludhiana	M1 267 × ML 949
6	SKUM-107	PAU, Ludhiana	NO 54 × HY 645
7	SKUM-108	S.K. Nagar	GM 9303 × PB-1
8	SKUM-109	CSAU Kanpour	PDM 54 × Pusa 9872
9	SKUM-110	CCSAU, Hissar	CO-6 × BDYR-1
10	SKUM-111	IIPR Kanpur	PBM 139 × PB2
11	SKUM-112	Shillong	PDM 84-143 × ML 337 × SGI
12	SKUM-113	IARI, New Delhi	IPM 99-125 × IM P02-1
13	SKUM-114	PAU Ludhiana	ML 267 × ML 955
14	SKUM-115	CSAUA&T Kanpur	Samrat × PDM 54
15	SKUM-116	IARI, New Delhi	Pusa Bald 2 × SEL.11
16	SKUM-117	CCSAU,Hissar	Aisha × MH 98-7
17	SKUM-118	NDUAT, Faizabad	NDM1 × NDM Sel 11
18	SKUM-119	IIPR, Kanpur	PPM 139 × PB-2
19	SKUM-120	PAU, Ludhiana	5145 / 87 × ML 267
20	SKUM-121	S.K. Nagar.	GM 9402 × E92-3
21	SKUM-122	Berhampur (0)	Mutant of Sujata
22	SKUM-123	Madhira	MGG 295 × MGG 332-2
23	SKUM-124	Shillong	T44 × AAU 34
24	SKUM-125	Shillongani	PDM 91-243 × WGG 62
25	SKUM-126	S.K. NAGAR	GM3 × TM 96-1
26	SKUM-127	CSAUA&T kanpur	Samrat × PDM 54
27	SKUM-130	GBPUA&T	Pant Mung 2 × AMP-36
28	SKUM-131	BARC Jabalpur	Kopergnon × TARM-B
29	SKUM-132	BARC Mumbai.	Mutant of 96-2
30	SKUM-133	Jalgaon.	Vaibhav × Tata Mung
31	SKUM-134	Akola	JLM 3 × Kopergoon
32	SKUM-135	PAU Ludhiana	No 54 × HY 645
33	SKUM-136	NDUAT Faizabad.	NDM -70-2 × NDM-1
34	SKUM-137	PAU Ludhiana	MC 1020 × UPM 98
35	Shalimar mung-1	SKUAST-K	Sel-2 × local

Observations were recorded on eleven morpho-agronomic, yield and quality traits viz., days to 50% flowering, number of clusters plant-1, number of primary branches plant-1, number of pods plant-1, Pod length (cm), days to 80% maturity, plant height (cm), number of seeds pod-1, 100-seed weight (g), Seed yield plant-1 (g) and protein content (%).

Ten competitive representative plants were selected at random from each experimental plot in each replication and tagged for recording the observations. The genetic divergence was computed using the procedure as described by Rao, Singh and Choudhary.

e-ISSN:2320-0189
p-ISSN:2347-2308

RESULTS AND DISCUSSION

Estimation of Genetic Divergence

Analysis of variance for dispersion revealed that the genotypes tested expressed significant variability for the morphological, maturity, quality, yield and yield component traits. The 'V' statistics, which is a measure of Wilk's criterion was significantly higher than the corresponding chi-square value (3245.05) revealing thereby that the genotypes possessed a significant diversity and thus, could be studied for divergence studies.

Based on the performance of the genotypes the 35 genotypes, including a check got grouped into 7 clusters **(Table 2)** as per the Mahalanobis D^2 analysis employing Tocher's method (Rao). Cluster-II comprised maximum genotypes (13) followed by cluster-I (11), cluster-IV and cluster-V (4) each. The rest of the cluster was mono-genotypic. The check Shalimar mung bean-1 got grouped in cluster-IV. Similar results have been reported by Rahim et al. and Katiyar et al. [3,4].

Table 2. Distribution of different Mung bean (*Vignaradiata* L. Wilczek), Genotypes into clusters based on D^2 statistics.

Cluster No.	No. of Genotypes in the cluster	Variety/accession No. of the genotypes
I	11	SKUM-112, SKUM-118, SKUM-133, SKUM-123, SKUM-111 SKUM-119, SKUM-137. SKUM-120, SKUM-114, SKUM-134, SKUM-122.
II	13	SKUM-109, SKUM-117, SKUM-127, SKUM-125, SKUM-130. SKUM-126, SKUM-108, SKUM-110, SKUM-102, SKUM-113, SKUM-115, SKUM-105, SKUM-106.
III	1	SKUM-136.
IV	4	SKUM-131, Shalimar mung-1, SKUM-101, SKUM-132.
V	4	SKUM-103, SKUM-135, SKUM-107, SKUM-124.
VI	1	SKUM-121.
VII	1	SKUM-116.

Checks : Shalimar mung-1

The mean intra and inter-cluster distance (D^2) values **(Table 3)** revealed that cluster-V had the highest estimate of intra cluster distance (D^2) 947.96 followed by cluster-II (490.84), cluster-I (421.86) and cluster-IV (378.90). The estimate for inter-cluster distance (D^2) was found highest between cluster-VI and cluster-VII (9308.29) followed by the distance between cluster-IV and cluster-VII (8708.22), cluster-I and cluster-VII (5236.69), cluster-IV and cluster-V (4782.11), cluster-V and cluster-VI (4209.98), cluster-III and cluster-VII (3194.89), cluster-II and cluster-VI (3006.26). The minimum inter-cluster distance was observed between cluster-III and cluster-V (784.32), followed by cluster-I and cluster-III (819.31) and cluster-II and cluster-III (987.29). The classification of genotypes into different clusters have been reported in different studies [5,6]. Recently, Singh et al. have grouped drought tolerant genotypes of Lentil (Lens culinaris Medik.) in different clusters based on their sensitivity to drought stress [7]. Wild accessions were separated from cultivars on the basis of both population structure and cluster analysis [8].

Table 3. Average inter cluster (above diagonal) and intra cluster (diagonal) D^2 values among mung bean (*Vignaradiata* L. Wilczek).

Clusters ↓→	I	II	III	IV	V	VI	VII
I	**421.86**	1048.39	819.39	1250.57	2084.22	973.88	5236.69
II		**490.84**	987.29	2199.61	1335.80	3006.26	2817.10
III			**0.00**	2911.82	784.32	1880.00	3194.89
IV				**378.90**	4782.11	1477.65	8708.22
V					**947.96**	4209.98	1702.56
VI						**0.00**	9308.29
VII							**0.00**

The cluster means for different traits **(Table 4)** revealed that the magnitude of differences among the mean of traits for different clusters was significant. The range of variation in cluster means for days to 50 per cent flowering was 43.25 (cluster-IV) to 53.21 (cluster-I). Mean of days taken to 80 per cent maturity ranged from 93.33 (cluster-III) to 110.00 (cluster-VI). The lowest mean of clusters plant^{-1} were expressed by cluster-VII (3.97) and highest by cluster-III (5.57). The minimum mean number of primary branches plant^{-1} were expressed by cluster-VII (2.57) and highest by cluster-III (3.47). Maximum mean number of pods plant^{-1} were recorded in cluster-III (22.30) and minimum in cluster-VII (16.00). Mean pod length (cm) ranged from 6.72 in cluster-III to 7.86 in cluster-IV. Plant height recorded lowest mean of 66.03 in cluster -VI and highest mean of 118.60 in cluster-V. Maximum mean of seeds pod^{-1} were recorded in cluster-IV (8.17) and minimum in cluster-V (7.05). Cluster-I had maximum 100-seed weight of 3.24 g and cluster-III with minimum of 2.20 g. The mean seed yield plant^{-1} ranged from 4.65 g in cluster-IV to 2.83 g in cluster-V. Maximum and minimum mean protein content was expressed by cluster-IV (22.41) and cluster-VI (20.59), respectively.

Analysis of genetic diversity is a platform for stratified sampling of breeding population and to identify the genotypes for hybridization [8]. Involving genetically diverse parents is known to provide an opportunity for bringing together gene constellation yielding desirable transgressive segregants in advanced generations. In order to classify large number of potential genotypes into few numbers of homogenous clusters, the D^2 statistic of (Mahalanobis) is now well established in plant breeding [1]. The use of

Mahalanobis D^2 statistic for estimating genetic divergence have been emphasized by many workers because it permits precise comparison among all the possible pair of populations in any group before effecting actual crosses [9]. Murthy and Arunachalam hypothesized that (Mahalanobis,) generalized distance as a measure of metric distance between population centroids could be very useful multivariate statistical tool for effective discrimination among parents, as high yield parents, with greater genetic diversity and expected to develop productive hybrids [10,11]. Multi-variate analysis quantifies the degree of divergence between populations so as to understand the trend of their evolutionary pattern and to assess the relative contribution of different components to the total divergence together with nature of forces operating at intra and inter-cluster levels.

Table 4. Cluster means for quality yield and yield component traits in mung bean (*Vignaradiata L*. Wilczek).

Cluster	Days to 50% flowering	Days to 80% maturity	No. of clusters plant $^{-1}$	No. of primary branches plant $^{-1}$	No. of pods plant $^{-1}$	Pod length (cm)	Plant height (cm)	No. of seeds pod $^{-1}$	100- seed weight (g)	Seed yield plant^{-1}(g)	Protein content (%)
I	53.21	105.27	4.38	2.70	16.36	7.65	86.73	7.40	3.24	3.86	21.43
II	52.10	96.92	4.58	2.64	16.54	7.29	104.88	7.52	2.78	3.54	22.17
III	46.67	93.34	5.57	3.47	22.30	6.72	103.25	7.36	2.20	3.64	20.81
IV	43.25	93.33	4.27	2.83	17.70	7.86	70.44	8.17	3.21	4.65	22.41
V	48.83	96.00	4.16	2.99	16.70	6.81	118.60	7.05	2.22	2.83	21.14
VI	52.00	110.00	4.60	2.83	16.77	7.24	66.03	7.72	2.94	4.19	20.59
VII	50.00	102.00	3.97	2.57	16.00	7.33	148.01	7.66	2.88	3.57	21.85

The pattern of group constellations in the present study, suggested that geographical diversity was not an essential factor to group the genotypes from a particular source or origin into one particular cluster. This means that, geographical diversity, though important, was not the only factor in determining the genetic divergence. Earlier workers have discussed genetic drift, selection pressure and environment as major factors that could cause greater diversity than geographical distance [12]. Genetic diversity is the outcome of several factors, including geographical diversification. Therefore, selection of parents should be based on genetic diversity rather than geographical diversity and statistical distance D^2, presented the index of genetic diversity among these clusters.

Cluster means of different clusters identify the characters to be chosen for hybridization. Hence in the present set of material, genotypes in cluster IV represent highest cluster means for most of the traits, so genotypes from cluster IV should be used for hybridization program should be selected from this cluster for the improvement of these traits. Sardana et al. observed that cluster means and coefficient of variation are an interesting picture of the nature of diversity [13].

Improvement over existing germplasm is a continuous process in plant breeding. Any successful hybridization program for varietal improvement depends mainly on the selection of parents with high genetic variability so that desirable character combinations could be selected for the target traits to be improved upon. Maurya and Singh suggested that more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining the higher magnitude of heterotic expression in F_1's and subsequently result in the release of broad spectrum of genetic variability in the segregating generations [14].

The results obtained in present investigation indicate that considerable variability and diversity is available in the experimental material for converging the elite allelic resources though a systemic breeding and selection approach to recover high yielding segregates that possess good quality characteristics as well. Therefore, selection of parents for hybridization should be done form different clusters having wider inter-cluster distance. The parents to be selected form such clusters should also have high per se performance for traits. In general, combining high yielding potential with wide genetic diversity is emphasized for further selection and choice of parents for hybridization. Thus, crosses between genotypes of the cluster IV and cluster VII are likely to exhibit high heterosis and produce superior recombinants with desired traits.

CONCLUSION

Average inter-cluster D^2 value was maximum between cluster-VI and cluster-VII, followed by cluster-IV and cluster-VII. Minimum intra-cluster distance was observed in cluster-V followed by cluster-II. The cluster means for different morphological, yield and quality traits revealed substantial genetic variability for all the traits. In the present set of material, genotypes in cluster IV represent highest cluster means for most of the traits, so genotypes from cluster IV should be selected to use in the hybridization programme for the improvement of these traits and further indicated that crosses between genotypes in cluster-VI and cluster-VII are likely to produce superior recombinants for yield and yield contributing traits.

REFERENCES

1. Silva LR, et al. Glycine max (L.) Merr., Vigna radiata L. and Medicago sativa L. sprouts: A natural source of bioactive compounds. Food Research International. 2013;50:167-175
2. Mahalanobis PC. On the generalized distance in statistics. Proceedings of National Academy of Science (India). 1936;2:49-55.

3. Rahim MA, et al. Multivariate analysis in some mung bean (Vigna radiataL. Wilczek) accessions on the basis of agronomic traits. International Journal of Agricultural, Environment and Biotechnology. 2009;2:230-234.
4. Katiyar PK, et al. Non-hierarchical Euclidean cluster analysis for genetic divergence in mung bean cultivars. Journal of Food Legumes. 2009;22:34-36.
5. Neelavathi S and Govindarasu R. Analysis of variability and diversity in rice fallow blackgram [Vignamungo (L.) Hepper]. Legume Research. 2010;33:206-210.
6. Abbas G, et al. Genetic diversity in mung bean (Vigna radiata L.) Pakistan Journal of Botany. 2010;42: 3485-3495.
7. Singh D, et al. Molecular Assortment of Lens Species with Different Adaptations to Drought Conditions Using SSR Markers. Plos One. 2016;11:e0147213.
8. Mohammadi SA and Prasanna BM. Analysis of genetic diversity in crop plants – salient statistical tools and considerations. Crop Science. 2003;43:1235-1248.
9. Chohata RK, et al. Genetic divergence in micro sperma lentil. Legume Research. 1994;17:132-134.
10. Murthy BR and Arunachalam V. The nature of divergence in relation to breeding system in some crop plants. Indian Journal of Genetics. 1966;26:188-198.
11. Mahalanobis PC. A Statistical Study at Chinese head measurement. Journal of Asiatic Society Bengal. 1928;25:301-377.
12. Bhat GM. Multivariate analysis approach for selection of parents for hybridization aiming at yield improvement in self-pollinated crops. Australian Journal of Agricultural Research. 1970;21:1-7.
13. Sardana S, et al. Genetic divergence in rice germplasm of Tripura. Oryza. 1997;34:201-208.
14. Maurya DM and Singh DP. Genetic divergence in rice. Indian Journal of Genetic and Plant Breeding. 1997;37:403-410.