Volume : 4 | Issue : 6 | June 2015 • ISSN No 2277 - 8179

Research Paper

Multivariate analysis for genetic divergence in Mungbean (*Vigna radiata L. wilczek*)

Botany

KEYWORDS : Mungbean, Cluster, Diversity, Variability

***Manoj Katiyar** — Legume Section Department of Genetics and Plant Breeding C.S. Azad University of Agril. & Technology, Kanpur. *Corresponding author

Sachin Kumar — Legume Section Department of Genetics and Plant Breeding C.S. Azad University of Agril. & Technology, Kanpur

ABSTRACT

The objective of this study was to assess the genetic divergence available in mungbean accessions, based on Euclidean distances for the identification of genetically diverse and agronomically superior accessions. Wide physio-morphological divergence was obtained for all the traits under study. Principal component analysis, which transformed for all the metric traits into single index of similarity, yielded ten eigen vector and roots. Based on first seven principal components (which accounted for 93.57% of the total variation), non-hierarchical Euclidean cluster analysis grouped the fourty five mungbean accessions into seven well characterized groups.

INTRODUCTION

Mungbean (Vigna radiata L. Wilczek), also known as green gram is one of the most important pulse crops of Asia. In countries like India, food legumes, commonly known as pulses, are major source of dietary (24-27%) protein, which is 2 to 2.5 times higher than that of cereals. Its productivity is low which may be improved through employing the genetic variability appropriately. Magnitude of genetic divergence among different genotypes of a species determines the spectrum of variability expected in segregating generation. The variability offers a working bench for selection intensity and direction which is determined by the crop breeders according to breeding objectives of crop improvement. Genetic diversity is generally considered as an important criterion for choosing diverse for obtaining high yielding line for efficient and hybridization programme greater the diversity in crop species, better is the chance of evolving promising and desired types . The ordination technique like principal component analysis followed by cluster analysis has been found to be useful tool for getting multi-coorelated variables into another set of uncorrelated variables which can be utilized for classification of genotypes into homogenous groups. Hence the genotypes from diverse clusters can be earmarked for different objectives.

The use of non-hierarchical Euclidean cluster analysis to estimate genetic divergence and of classification of germplasm has been suggested (1) In view of the above, the present studies were taken up with fourty five genotypes of mungbean to (i) assess variability in the germplasm based on morphological attributes and (ii) perform natural classification in the germplasm accessions for their characterization based on cluster analysis for identification of genetically diverse and agronomically superior genotypes. In a present study, the classification of fourty five genotypes of mungbean into different clusters through D^2 analysis are determination of genetic closeness and for assessing diversity among the genotypes.

MATERIALS AND METHODS

The experimental material consisted of fourty five genotypes of mungbean. These strain was collected from germplasm pool of mungbean maintained at Legume Section of C.S. Azad University of Agriculture and Technology, Kanpur. The experiment was carried out in a complete randomized block design with three replications during currently two years pooled data. Each plot consisted of six rows of four meter length, and spaced 30 cm apart, maintaining plant to plant distance of 10 cm. Observation were recorded on randomly chosen ten competitive plants in each genotype in each replication. Data were recorded for ten characters viz., days to 50 per cent flowering, plant height (cm), number of branches per plant, number of pods per plant, number of pods per cluster,pod length, number of seeds per pod, 100-seed weight (g), days to maturity and grain yield per plant(g). D^2 analysis was carried out as given by Mahalanobis's (1928).

RESULTS AND DISCUSSION

The need of parental diversity in optimum magnitude to obtain superior genotypes for recovery of transgressive segregants has also been repeatedly emphasized. Hence characterization of genetic divergence for selection of suitable and diverse parents should be based on sound statistical procedures, such as D_2 statistics and non-hierarchical Euclidean cluster analysis. These procedures characterized genetic divergence using the criteria of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters. The analysis of variance was highly significant among the divergent genotypes for all the 9 traits under study, which revealed the presence of considerable variability among the genotypes. This suggested that adequate scope is available for selection of superior genotypes aimed at enhancing genetic yield potential of lentil. Based on this, 45mungbean accessions were grouped into seven well-characterized groups (I-VII) based on the similarity in traits (Table1). The maximum number of genotypes (13) fell in cluster V, namely, KM 2325, KM 2326, KM 2327, KM 2341, KM 2360, K 2361, SML 1123, SML 1127, IP 117, IP 1142 and ND 1239 while, minimum number (2) was observed in cluster VI, i.e., SML 1120 and SML 1109. This grouping indicated considerable diversity in the germplasm. (Table 1). Pattern of distribution of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. The maximum numbers of genotypes were comprised into cluster V (13), followed by cluster I (8), cluster VII (8), cluster II (5), cluster IV (5). The minimum genotypes (2) comprised in to cluster VII. This finding is in agreement with the report advocating lack of definite relationship between genetic and geographic diversity in mungbean. Similar reports were made by Singh et.al. 2009, Lavanya et.al. 2008, Shweta 2013.

The principal component analysis was carried out to transform the interdependent variables into a set of dependent variables. These principal component scores were used to compute Eucildan distances based on non-hierarchical cluster analysis. This method characterizes genetic divergence on the basis of similarity and dis-similarity denoted by aggregate effects of agronomic traits under study.

The D^2 analysis showed intra and inter-cluster distance (Table 2). The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity ex-

Volume : 4 | Issue : 6 | June 2015 • ISSN No 2277 - 8179

isted among the genotypes belonging to distantly spaced groups. The maximum inter-cluster distance (297.39) existed between cluster II and V followed between cluster II and IV (280.37) and between cluster II and III (250.26), suggesting wide diversity between them and the genotypes in these cluster could be used as parents in hybridization programme for isolating transgressive segregates. The highest intra-cluster distance was observed in cluster V (17.24) and the lowest in cluster VII (5.08). The crosses between genotypes belonging to the cluster separated by low inter cluster distances are unlikely to generate promising recombinants in segregating generations (Shweta 2013, Gokulakrishan 2012, Singh et.al. 2012 Singh et.al. 2009, Lavanya et.al. 2008). The genotypes grouped into same cluster displayed the lowest degree of divergence from one another, and when crosses are made among the genotypes of the same cluster, no transgressive segregant is expected from such combinations. Therefore, hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants. The genotypes for hybridization may be chosen from widely separated clusters.

The variance for the cluster means were calculated for quantitative characters of mungbean. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objectives is not only high heterosis but also reduction of duration. The mean performance of clusters, for ten characters is presented in Table 3. The genotypes of clusters VI were early flowering (x=30.16) followed by cluster III (x=32.16). The highest and lowest cluster mean for plant height at maturity was observed for cluster VI (x=41.45 cm) and cluster VII (x=35.15 cm) respectively. The highest number of branches per plant was found in cluster VII (x=3.29). the highest cluster mean for number of pods per plant was observed for cluster VI (x=25.83). The highest cluster mean for number of pods per cluster was exhibited by cluster IV (x=7.86). The genotypes representing the maximum cluster mean for number of seeds per pod were present in cluster I (x=8.41). 100-seed weight was highest in the genotypes of cluster I (x=4.02). The entries represented in cluster VI were comparatively early maturing (x=66.50). The highest cluster mean for grain yield per plant was observed in case of cluster I (x=6.07), which indicates that lines having very high seed yield were concentrated in this cluster. Similar results were made by Kumar et.al. 2010, Arshad et.al. 2009 and Khedar et.al. 2006. The greater the distance between two clusters, the wider genetic diversity between genotypes. Keeping this in view, the cluster I, VI, and III were among the most divergent clusters having high grain yield performance along with its contributing traits could be utilized in hybridization programme for getting desirable transgressive segregants and high heterotic response.

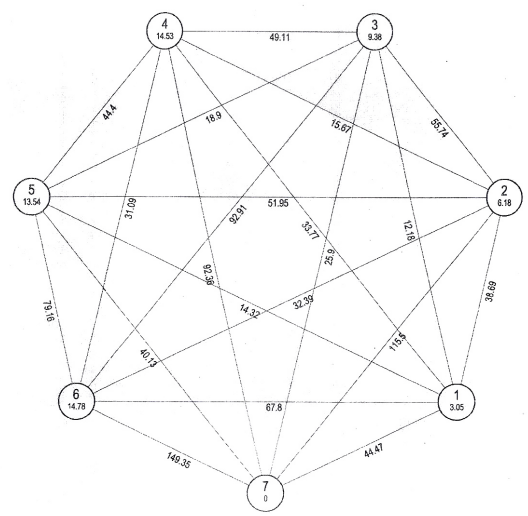
Table 1: Distribution of genotypes in different clusters

Cluster Number	Number of Population	Genotypes
I	8	KM 2320, KM 2321, IP 1118.,IP 1139, IP 1141, PDM 163, PDM 167, PDM 168
II	5	IP 1145, KM 2342, NDM 1238, KM 2352, KM 2357
III	4	IP 1090, IP 1131, NDM 1237, KM 2351
IV	5	KM 2328, IP 1121, KM 2339, KM 2340, NDM 1231
V	13	KM 2325, KM 2326, KM 2327, SML 1123, SML 1127, IP 1117, IP 1142, IP 1143, KM 2341, NDM 1239, KM 2360, KM 2361
VI	2	SML 1120, SML 1109
VII	8	KM 2324, IP 1121, NDM 1235, NDM 1243, KM 2353, KM 2365, KM 2356, KM 2359

Table- 2: Estimates of average intra and inter-cluster distances for the seven clusters in lentil

	I cluster	II cluster	III cluster	IV cluster	V cluster	VI cluster	VII cluster
I cluster	33.864 (5.81)	87.541 (9.35)	159.83 (12.64)	188.23 (13.71)	223.68 (14.95)	62.55 (7.90)	100.58 (10.02)
II cluster		43.501 (6.59)	250.26 (15.81)	280.37 (16.74)	297.39 (17.24)	132.40 (11.50)	167.23 (12.93)
III cluster			30.65 (5.53)	56.91 (7.54)	61.31 (7.83)	75.99 (8.71)	50.73 (7.12)
IV cluster				45.20 (6.72)	70.60 (8.40)	81.08 (9.00)	77.21 (8.78)
V cluster					29.92 (5.46)	131.06 (11.44)	62.64 (7.91)
VI cluster						32.77 (5.72)	55.35 (7.43)
VII cluster							25.84 (5.08)

Bold figures represent intra-cluster distances



Diagrammatic reperesentation of Cluster Diagramme (Distances are exactly according to Scale)

Table-3: Cluster mean of fourty five genotypes of mungbean for ten characters

Cluster	Days to 50 per cent flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Pod Length (cm)	Number of seeds per pod	100- seed weight (g)	Grain yield per plant (g)
I	35.25	68.83	35.32	3.25	7.08	19.29	7.33	8.41	4.02	6.07
II	33.06	67.73	40.74	3.00	7.13	19.80	7.36	8.00	3.21	4.68
III	32.16	67.75	38.72	2.75	7.75	23.00	7.40	7.75	3.27	4.93
IV	36.46	70.13	35.87	3.13	7.86	26.13	6.68	7.40	3.14	4.90
V	32.89	68.33	39.63	3.07	6.64	18.66	7.08	7.79	3.80	4.56
VI	30.83	66.50	41.45	3.16	7.50	25.83	6.78	7.16	3.04	5.02
VII	34.70	69.25	35.15	3.29	6.66	20.95	7.16	7.83	3.39	4.58

REFERENCE

Mahalanobis, P.C. (1928) .A statistical study at Chinese head measurement. Journal Asiatic, Soc Bengal 25:257-287. | Lavanya, G. R.; Srivastava, Jyoti . and Ranade, S. A. (2008). Molecularassessmentof genetic diversity in mung bean germplasm. Journal of Genetics; 87(1):65-74. | Gokulakrishnam, J.; Kumar, B.S. and Prakash, M. (2012). Studies on genetic diversity in mungbean (Vigna radiata L. Wilczek). Legume Research, 45(1): 50-52. | Ghulam Abbas.; Asghar, M. J.; Shah, T. M. and Atta, B. M. (2010). Genetic diversity in mungbean (Vigna radiata L. Wilczek) germplasm. Pakistan Journal of Botany; 42(5):3485-3495. | Katiyar, P K. and Dixit, G. P. (2011). Assessment of genetic divergence in green gram (Vigna radiata L. Wilczek) germplasm. Journal of Agricultural Sciences.81(1):79-81. | Prakash, Vijay (2007). Genetic divergence and correlation analysis mungbean (Vigna radiata (L.) Wilczek. Crop Improvement society of india Ludhiana 33:2, 175-180. | Rao, G. R.; Rao, Y. K. and Rao, C. M. (2006). Genetic divergence in mungbean. Indian Journal of Pulses Research; 19(1):61-63. | Singh, S.K.; Singh, I.P.; Singh, B.B. and Onkar, Singh. (2009). Genetic divergence in mungbean (Vigna radiata (L.) Wilczek). Agricultural Research Communication Centre; 32(2): 98-102. | Shweta (2013). Genetic diversity analysis in mungbean [Vigna radiata (L.) Wilczek]. International Journal of Plant Scinces (Mujaffarnagar); 8(1):64-66. | Singh, S.K.; Lavanya, G.R.; Krupakar, A. and Babu, G.S. (2012). Selection of diverse mungbean genotypes for seed yield improvement. New Agriculturist; 23(1):5-9. | Arshad, Muhammad. and Aslam, Irshad. (2009). Journal of Agricultural Research (Lahore). 47: 2, 121-126. | Babu, G.S.; Sasmal, Narendranath. and Lavanya, G.R. (2012). New Agriculturist; 23(1) : 31-33. | Begum, Sabra.; Noor, Muhammad.; Hidayat-ur-Rahman.; Hasan, Ghulam.; Durrishawar.; Ullah, Hidayat . and Ali, Farhan. (2013). Britis Journal of Applied Science & Technology; 3(3):472-481. | Dhananjay.; Rama Kant.; Singh, B.N. and Singh, G. (2009). Crop Research Hisar; 38(1/3): 176-178. | Henry, A. and Mathur, B.K. (2007). Journal of Arid Legumes; 4(1): 43-46. | Khedar, O.P.; Singh, R.V. and prakash, Ved (2006). Journal of Arid Legumes;3(2): 68-70. | Kumar, N. V.; Lavanya, G. R.; Singh, S. K. and Pandey, Praveen. (2010). AAB Bioflux. 2: 3, 251-257. | Nand, M. J. and Anuradha, C. (2013). Journal of Research ANGRAU; 41(3): 31-39. | Prasanna , B. L.; Rao, P. J. M .; Murthy, K.G.K.; Prakash, K.K. (2013). Environment and Ecology; 31(4) : 1782-1788. | |