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GENETIC DIVERSITYAND SEED SHATTERING BEHAVOUR IN GERMPLASM OF MUNGBEAN.

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ABSTRACT:

Mungbean genotypes were evaluated for thirteen yield and yield contributing characters to study the genetic diversity existing among them by using Mahalnobis D^2 statistic. The analysis of data revealed the significant difference among the genotypes for all the characters. D^2 values between all possible pairs of sixty genotypes ranged from 4.96 (LCM-4 and LCM-20) to 926.78 (LCM-26 and LCM-55). Based on genetic distance (D^2 value), sixty genotypes were grouped into seven clusters indicating wider genetic diversity in the germplasm collections of mungbean from different geographical origin. Out of seven clusters, cluster I was the largest with forty-five genotypes, followed by cluster VI, III and II with six, four and two genotypes respectively, the cluster II, IV and V were monogenotypic. The clustering pattern indicated the absence of relationship between genetic diversity and geographical origin of genotypes. Maximum inter cluster distance was observed between cluster III and V (D^2 =25.25), while lowest divergence was noticed between cluster II and IV (D^2 = 4.44). Whereas, maximum intra-cluster distance was observed for cluster VII (D^2 =11.83). Cluster V exhibited highest means for seed yield per plant.Among the thirteen characters studied, the seed shattering (56.50 %.) contributed maximum for divergence, followed by 100 seed weight (31.98%)and least by plant height (0.17%). The seed shattering behavior of 60 genotypes showed 8 resistant, 23 tolerant and 29 susceptible. On the basis of inter-cluster means, *per se* performance, the following genotypes *viz.*, LCM-25 , LCM-35, LCM-43, LCM- 47, LCM-56, LCM-46, LCM-32, LCM-23, LCM-17, LCM-34, LCM-7, LCM-48, LCM-38 may be used in breeding programme for further improvement of grain yield in mungbean under climate change.

Key words: Genetic diversity, Seed shattering, Mungbean.

INTRODUCTION:

Mungbean, (*Vigna radiata* (L.) Wilczek), commonly known as greengram, is one of the important among thirteen different seed legumes grown in India. Among pulses, mungbean holds an important position, as it contains more digestible proteins and also provides calories in Asian diets (Engel, 1978). It is easily digestible and in absence of milk, it considered as an excellent food for infants and convalescent. Mungbean is consumed in variety of ways. Sprouted mungbean are used as fresh vegetable in Chinese and Japanese diet and also used in South India for curry preparation or savory dish. Proteins isolated from it have been used for making noodles and other textured preparations (Bhumiratnam, 1978; Coffman and Garcia, 1977). It is rich in vitamin B and regarded as remedy for the disease ´Beriberi´. When it is allowed to sprout, ascorbic acid (Vit.C) is synthesized. It contains 24% proteins with all essential amino acids.

Collection of genotypes and assessment of genetic diversity is a basic step in any crop improvement programme. Consideration on geographical diversity as a reasonable index of genetic diversity may lead to erroneous conclusions. Therefore, it is necessary to use suitable technique to quantify degree of divergence between genotypes of same as well as different geographical regions.

MATERIAL AND METHODS: -

A piece of land selected for experiment was brought to fine tilt by ploughing followed

by harrowing. The 60 genotypes of mungbean were evaluated in a Randomized Block Design (RBD) with two replications. Sowing of experiment was done on 13th-June 2017 at a distance of 30 X 10 cm.The divergence analysis was carried out by D^2 statistic of Mahalanobis (1936) as described by Rao (1952). Analysis of variance for the individual characters was worked out as per RBD to test the significances among the genotypes. The characters exhibited significant differences were only used for further analysis of D^2 statistic. The analysis of covariance for pairs of characters, based on plot averages was carried out. A logical grouping of genotypes was done by following

Tocher's method described by Rao (1952). The seed shattering behavior was studied by HAO method by keeping 20 pods in hot air oven at 44°C Temperature for 6 hrs daily for seven days.

RESULTS AND DISCUSSION:

Genetic divergence which is due to genetic factors is the basis for heritable crop improvement. The plant breeders have always, therefore been fascinated by great amount of diversity in crop plants. The precise information about the genetic divergence is therefore, crucial for productive breeding program. The genetically diverse parents are known to produce high heterotic effects and consequently give desirable recombinants in the breeding material or wide spectrum of transgressive sergeants in segregating generations. The material used in present study comprised of diverse sixty genotypes from different eco-geological origin were therefore, assessed for genetic diversity for a set of thirteen characters. In the present study, analysis of variance revealed highly significant differences due to genotypes for all the characters under study. On the basis of D^2 values, all sixty genotypes were grouped into seven clusters with substantial genetic divergence between them [Table I]. The cluster I was the largest having 45 genotypes, followed by clusters VI, III, VII with 6, 4 and 2 genotypes, respectively, while clusters II, IV, V were solitary[Fig. I]. These findings indicated the presence of genetic distance among the genotypes, which provide the choice of selection of diverse genotype in breeding programme for improvement of specific traits. The clustering pattern showed that genotypes from different sources were clubbed into one group and also genotypes of same source forming different clusters indicated no relationship between geographical diversity and genetic divergence.

The D^2 values between all possible pairs of sixty genotypes studied for seed yield per plant ranged from 4.96 (LCM-4 and LCM-20) to 926.78 (LCM-26 and LCM-55). The significant differences due to genotypes with high range in D^2 value clearly indicated the presence of adequate diversity among the genotypes studied. The wide range of diversity was also reported by Ahmed et al.(2016) and Keerthiga et al.(2017)

The maximum inter-cluster distance was found between cluster III and V(25.44) followed by cluster III and IV(25.25), whereas minimum between cluster ii and IV(4.44).This was revealed by the fact that the genotypes from different origin were grouped into same cluster, as they had low genetic distance (D^2 values) from each other. This was evident from cluster VII which had high intra-cluster distance (D^2 =11.83), followed by cluster I (D^2 = 9.78), cluster V (D^2 = 9.36) and cluster IV (D^2 =8.75). Cluster II, IV and V being monogenotypic had zero intra-cluster distances[Table II & Fig. II]. These observations confirming the results of Gadakh et al.(2013) and Keerthiga et al.(2017).

The variance of cluster means provides information on relative importance of characters towards the divergence. All the sixty genotypes of mungbean were studied for thirteen characters and the data collected was used to determine degree of divergence. Out of thirteen characters studied, the characters seed shattering (56.5%) contributed maximum in divergence followed by 100 seed weight (31.98%) and pod length (3.28%). However, the contribution of number of seeds per pod (0.28%) and plant height (0.17%) were minimum. (0.17%). Gadakh *et al.*(2013) observed the major contribution of protein content and 100 seed weight in the divergence. This suggested that seed shattering, 100 seed weight and pod length were the major contributor in the divergence.

The seed shattering behaviour of 60 genotypes showed 8 resistant, 23 tolerant and 29 susceptible. The genotypes showed 0-10% seed shattering are treated as resistance. These will be tested for their consistency in the performance and if found superior may be used in breeding programme for improvement of mungbean in relation to quality and climate change. Similar observation was also made by Girase et al.(2018)

On the basis of inter-cluster means, *per se* performance, the following genotypes *viz.*, LCM-25 , LCM-35, LCM-43, LCM- 47, LCM-56, LCM-46, LCM-32, LCM-23, LCM-17, LCM-34, LCM-7, LCM-48, LCM-38 may be used in breeding programme for further improvement of grain yield in mungbean. Intercrossing among them would lead to upgrade base in the base population and opportunities for obtaining the high heterotic effect and also to recover desirable transgressive

segregants and wide spectrum of variability in subsequent generations which may be suitable under climate change.

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Table.1. Distribution of sixty mungbean genotypes intodifferent clusters:

Clusters	Number of genotypes in cluster	Name of genotypes
I	45	LCM-1, LCM-2, LCM-3, LCM-4, LCM-5, LCM-6, LCM-8, LCM-9, LCM-10, LCM-11, LCM-12, LCM-13, LCM-14, LCM-15, LCM-16, LCM-18, LCM-19, LCM-20, LCM-21, LCM-22, LCM-23, LCM-24, LCM-25, LCM-27, LCM-28, LCM-29, LCM-30, LCM-31, LCM-33, LCM-34, LCM-36, LCM-37, LCM-40, LCM-41, LCM-44, LCM-45, LCM-47, LCM-48, LCM-49, LCM-50, LCM-51, LCM-52, LCM-54, LCM-58, Naval.
II	1	LCM-17
III	4	LCM-26, LCM-32, LCM-56, LCM-57
IV	1	LCM-42
V	1	LCM-46
VI	6	LCM-7, LCM-35, LCM-39, LCM-43, LCM-53 and LCM-55
VII	2	LCM-38 and Vaibhav

Fig. 1. Cluster formation of sixty genotypes by Tocher`s thod in mungbean.