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Multivariate diversity analysis of quantitative traits of mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficit moisture stress

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Abstract

Genetically diverse parents give an increased chance of genetic recombination and superior expression of hybrid vigour. Mahalanobis D^2 statistics is an important tool for calculating the amount of genetic diversity in the populations and for assessing the relative contribution of various components to the total genetic divergence. The present experiment comprised of fifty five mungbean germplasm lines tested over two years in a randomized block design with two replications to study genetic diversity. D2 analysis indicated that material was genetically diverse. five clusters were formed by dividing the genotypes. The highest intra-cluster distance was associated with Cluster I, II found appropriate for within group hybridization due to the presence of most heterogeneous genotypes indicating high intra-cluster value. To become highly genetically diverse, the inter-cluster distance should be high (the most divergent clusters were Cluster II and Cluster IV followed by Clusters II and Cluster V , Cluster II & Cluster III, which can be used for hybridization programme. Cluster data revealed that genotypes in cluster VI and V had desirable traits for yield improvement. These clusters could be directly selected for breeding programme. Among the yield attributing traits, the maximum contribution towards divergence was made by seed yield/plant, followed by no. of pods per plant & hundred seed weight.

Introduction

Mungbean is also called greengram, goldengram, greenbean, greensoy, moong and mashbean. Mungbean is a diploid which has $2n = 22$ chromosomes and it is a self-polinating crop. The center of origin for mungbean is not known exactly, but it might have originated in Hindustan and Central Asiatic region. Mungbean farming is practised worldwide, including in nations like India, Pakistan, Burma, Nepal, Bangladesh, Sri Lanka, Thailand, Indonesia, the Philippines, and the African continent. The Indian states that grow mungbean include Maharashtra, Gujarat, Andhra Pradesh, Tamil Nadu, Uttar Pradesh, and Bihar (Singh *et al.,* 2010; Inbasekar, 2014; Kumar and Kumar, 2014) [20, 8, 10]. The major limiting factors for mungbean production and productivity in our country are the different abiotic, biotic stresses and non-availability of high yielding varieties which can tolerate environmental fluctuations to greater extent. Therefore, plant breeders has to study the genetic diversity in the varieties/germplasm. Mostly diverse parents generally produce high heterotic effects (Griffing and Lindston, 1954) [5]. To increase the likelyhood of producing a wide range of diversity in segregating generations and to bring together a higher frequency of desirable genes in a strain, various genotypes with broad genetic backgrounds should be chosen as parents for hybridization programmes. For the purpose of enhancing complicated quantitative features like seed production, the choice of parents should be based on a number of significant traits taken as a whole rather than separately. The coefficient of racial similarity (Pearson, 1926) [13], Discriminant function (Fisher, 1936), multiple regression (Hotelling, 1936) [7], and D^2 statistics are methods to evaluate population divergence using multivariate analysis (Mahalanobis, 1936) [7]. These include the Mahalanobis (1936) [7] D^2 statistics, which measure the extent of genetic diversity in populations and evaluate the extent of diversity.

Materials and Methods

The experiment was laid out in randomized block design (RBD) in two replications with fifty five genotypes. The deficit moisture stress condition induced by withholding the irrigation for

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fifteen days prior to the flowering. The trial was sown on 13th February of 2019-20 and 2020-21 at EB-II section of OUAT Bhubaneswar to expose the crop to low moisture stress at the early growth stage. Each genotype was represented by two rows with spacing of 30cm×10cm. Fertilizers were applied @ 20:40:20 kg of N: P_2O_5: K_2O along with 300 cft. of farm yard manure (FYM) per hectare. Half of nitrogenous and whole of phosphatic and potassic fertilizers were applied in lines as basal at the time of sowing. The rest amount of nitrogen was applied after 25 days of sowing as top dressing. Weeding was done before top dressing of nitrogenous fertilizer. Other management practices were followed as per recommended package of practices.

Five randomly selected plants of each genotype per replication were used for the collection of data on ten quantitative traits including single plant seed yield. Mahalanobis' D^2-statistic (Rao, 1952) [16] was used for estimation of D^2 distances among the 55 genotypes with respect to ten quantitative characters. The relative contribution of individual characters to overall genetic divergence among the cultures was assessed by rank average method. Constellation of genotypes into different clusters were done using Tocher's method.

Results and Discussion

Mahalanobis's D^2 statistics computed for fifty five genotypes by using data of ten morphological characters. Total five clusters are formed and they are given in table 1. Under deficit moisture stress average intra- and inter-cluster distance (D^2) values among the clusters were calculated and are presented in (Table:2). The highest intra-cluster distance was associated with Cluster I (2.74) and the lowest intra-cluster distance was associated with Cluster II (2.55). cluster III,IV and V showed the zero inter cluster distance due to the existence of one genotype each. From the average inter-cluster distance, it was evident that the most divergent clusters were Cluster II and Cluster IV (16.95) followed by Clusters II and Cluster V (13.73) , Cluster II & Cluster III (12.62). On the other hand the least inter-clusters distance was observed between Cluster I & Cluster III (4.42) followed by Clusters I & Cluster III (4.42). Basnet et al. (2014) [2] reported that the multivariate analysis involving the qualitative traits clearly showed the alignment of the different genotypes into different clusters according to the similarity indices. The use of diverse parents to increase the chance of getting superior varieties has been reported by (Katiyar et al., 2015; Piyada et al., 2010; Narasimhulu et al., 2013) [20, 14, 12]. Similarly, Behl et al. (1985) [3] suggested that increment in heterosis occurs within a restricted range of diversity.The mean performances of different clusters for different characters were estimated and are presented in (Table: 4). The highest cluster mean for days to 50% flowering was obtained in Cluster-III (32.25), days to maturity was obtained in Cluster-I (46.11), plant height(30.8), number of pods/cluster(3.28) , pod length (6.10) and hundred seed weight (2.67) was noticed in Cluster-V. Cluster-IV showed the highest cluster mean for seed yield/plant (2.65). These type of findings have been earlier confirmed by Gokulakrishnan et al. (2012) [4], Abna et al. (2014) [1] and Razzaque et al. (2016) [17].

Among the yield attributing traits, the maximum contribution towards divergence was made by seed yield/plant (21.41%) (Table: 3), followed by no. of pods per plant (17.7) & hundred seed weight (12.59%). According to this study So in deficit moisture stress condition emphasis should be given to these characters for better improvement. According to Gupta et al. (2019) [6] characters giving the highest contribution towards the diversity could be used further in the identification of the parents for the hybridization programme. The results were in affirmation with the reports of Rahim et al. (2010) [1], Tiwari et al. (2000) [22], Kumararathna et al. (2013) [11], Singh et al. (2014) [19], Rekha et al. (2015) [18] and Sofia et al. (2017) [21].

Table 1: Clustering of 55 mungbean genotypes by Torcher's method pooled over 2 years under stress condition

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	46	Dhaul, HUM-10, LGG-460, ML-729, OUM-11-5, OUM-31-1, OUM-99-4, OUM-132, OBGG-152, OBGG-173, OBGG-282, Pant-M-5, Pant-M-6, PDM-154, Pusa bold, Pusa ratna, pusa-9631, pusa-9632, Pusa-9772, pusa-2072, RCM-3, RCM-14, OGG-56, TM-98-2, T-2-1, T-27-1, T-3-2-2, T-7-1, T-7-3, T-30-7-1, T-34-1-5, T-32-23, T-34-1, Tarm-1, Visasmart-c, GC-69-3358, SC-693360, EC-693363, EC-693363, EC-693365, ML-1299, GOP-A, Jain mung baraghar, Jagath singh pur, Kalakandi-A, Phulbani- B.
2 Cluster	6	ML-613, T-34-1-3, OBGG-194, B-10-33-1, BGG-40 & V-461
3 Cluster	1	SML-668
4 Cluster	1	PUSA-9672
5 Cluster	1	RCM-4

Table 2: Average intra and inter-cluster distance values for 4 clusters in 55 mungbean genotypes pooled over 2 years under stress condition

Cluster No:	I	II	III	IV	V
I	2.74	6.80	4.42	5.59	6.15
II	6.80	2.55	12.62	16.95	13.73
III	4.42	12.62	0.00	1.53	8.10
IV	5.59	16.95	1.53	0.00	8.88
V	6.15	13.73	8.10	8.88	0.00

Table 3: Cluster wise mean value of ten morphological characters in 55 genotypes of mungbean pooled over 2 years under stress condition

	Days to fifty percent flowering	Days to maturity	Plant height (cm)	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
Cluster 1	29.95	46.11	28.39	3.58	2.62	9.37	5.18	8.40	2.50	2.02
Cluster 2	29.78	45.31	26.34	2.78	2.42	6.72	5.14	8.00	2.21	1.15
Cluster 3	32.25	43.00	28.03	4.26	2.84	12.06	4.88	7.45	2.64	2.41
Cluster 4	30.25	44.75	29.25	4.88	2.57	12.51	5.20	8.05	2.66	2.65
Cluster 5	30.68	45.75	30.80	2.93	3.28	9.54	6.10	9.38	2.67	2.47

Table 4: Relative contribution of different characters to genetic divergence among 55 greengram genotypes pooled over 2 years under stress condition

SL. No.	Source	Contribution %
1	Days to fifty percent flowering	03.3
2	Days to maturity	03.91
3	Plant height (cm)	11.58
4	Number of clusters per plant	03.23
5	Number of pods per cluster	07.47
6	Number of pods per plant	17.71
7	Pod length (cm)	12.05
8	Number of seeds per pod	06.73
9	100 seed weight (g)	12.59
10	Seed yield per plant (g)	21.41

Conclusion

Genetic diversity using D2 analysis indicated that material studied under deficit moisture stress showed some divergence. The genotypes were partitioned into five clusters. Considering the highest inter-cluster distance between cluster II and IV. which can be used for hybridization programme. Intra-cluster value was highest for cluster I followed by cluster II which indicated that genotypes of these clusters were most heterogeneous and these clusters were the best for within group hybridization, and remaining clusters with only one genotype so there is no intra cluster distance. Cluster data revealed that among the yield attributing traits, the maximum contribution towards divergence was made by seed yield/plant, followed by no. of pods per plant & hundred seed weight . Cluster-IV showed the highest cluster mean for seed yield/plant among all other clusters, such divergent cluster may serve as useful materials for deficit moisture tolerance breeding.

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