Research Paper

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Genetic diversity for yield and its component traits in Mungbean [*Vigna radiata* (L.) Wilczek]

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A R T I C L E   I N F O

A B S T R A C T

Genetic diversity analysis is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components of total divergence. The present investigation was aimed to study the genetic divergence and clustering pattern of 40 genotypes of Mungbean (*Vigna radiata* L. Wilczek) for selection of suitable parents that can be utilized in hybridization programme and to study the genetic parameters attributing to yield. The crosses of genotypes from cluster II, i.e. PLM-818, PLM-829,PLM-841,PLM-884,PLM-891 with those of genotypes belonging to cluster V i.e.EC -206971,EC-206979,EC-206975,EC-206973,IC-085923,IC-10492, PLM-0003,PLM-0021, PLM-0032, IC-10497 has the highest intercluster distance and might produce high level of segregating population in regards to yield. High heritability estimates coupled with high genetic advance was observed for plant height and a number of pods per plant resembling the action of additive genes in controlling these particular characters and selection would be rewarding for yield improvement.

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1.Introduction

Pulses are extensively grown in tropical regions of the world as a major protein rich crop bringing considerable improvement in human diet. Creation of variability and selection of superior recombinants among the variants are the major objective of any plant breeding programme. As Mungbean is a self-pollinated species considerable variation exists among the green gram cultivars and also within its related species (Bisht et al. 2005). Yield components are the primary objectives for crop improvement studies as Grafius (1978) suggested that there may not be genes for yield per se but rather for the various components, the multiplicative interactions of which result in the artifact of yield. In any program aimed at genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization program between genetically diverse parents will lead to considerable amount

 of heterotic response in F1 hybrids and a broad spectrum of variability in segregating generations. The utility of multivariate analysis has greatly been emphasized (Murty and Arunachalam 1966). Even when breeding programmes emphasize to involve diverse sources as parental lines, the plant breeders generally limit their efforts to a narrow range of adapted lines for genetic improvement, leading to erosion of genetic diversity in long run. Assessment of genetic diversity in available cultivars has important implication in understanding the progress made in any breeding programme. Morphological markers are routinely used for estimating the genetic diversity (Datta et al. 2012; Sirohi et al. 2006) so, the present experiment was formulated to study the genetic divergence and clustering pattern of the Mungbean genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield.

2.Materials and Methods

The present investigation was carried out during the spring season at the Research Farms of Kisan P.G College, Simbhaoli, Hapur, Uttar Pradesh. The materials for this study consisted 40 genotypes of mungbean were obtained from NBPGR, New Delhi. The experiment was conducted in a randomized block design (RBD) with three replications. The spacing of 30 cm was maintained from plant to plant and 10 cm for the row to row. Recommended packages of practice and plant protection measures were attempted for raising a good crop. The observations were recorded on five randomly selected plants in each replication for ten characters namely; Plant height (cm), Number of branches per plant, Days to 50% flowering, Number of pods per plant, Days to maturity, Number of seeds per pod, 100-seed weight, Seed yield per plant (g), Biological yield (g) and Harvest index (%). Mahalanobis (1936) defined the distance between two populations as D^2 which was obtained by Tochers method, described by David & Rao (1954). The contribution of individual characters towards divergence was estimated according to the method described by Singh and Chaudhary (1977). The experimental data was analyzed statistically by the method of analysis of variance for single factor (Gomez and Gomez 1984).

3.Results and Discussion

The analysis of variance revealed significant difference among the accession for all the characters studied indicating the existence of a wide genetic divergence among them. Based on D^2 values, 40 genotypes were grouped into 6 clusters on the assumption that genotypes within the cluster have similar D^2 values among themselves than those from groups belonging to two different clusters (Table 1). Cluster IV has the highest number of genotypes *i.e.*, 12. Cluster V has 10 genotypes, followed by cluster I which has 6 genotypes. Clusters II have 5 genotypes. Similarly, Loganathan *et al.* (2001) grouped 42 F3 and eight varietal genotypes into seven clusters; Das *et al.* (2010) grouped 23 genotypes in 8 clusters. The clustering pattern of the genotypes showed that genetic diversity was not related to geographic diversity. Such a type of constellation of germplasm proves that the collection made were genetically viable for different characters.

The clustering pattern of the strains revealed that there was no close correspondence between geographical distribution and genetic divergence as estimated by the D^2 statistic. The intra and inter cluster D^2 value among 6 clusters are presented in table- 1. The maximum intra cluster distance was observed in the cluster II (D=2.279), followed by cluster V (D=2.054) and cluster I (D=2.002) suggesting that genotypes included in these clusters might have different genetical architecture. The maximum inter-cluster distance was observed between the cluster I and VI (D=5.530) followed by cluster I and III (D=5.449) and cluster I and II (D=5.241) indicating wide divergence among these clusters (Figure 1). This also suggests that the genetic architecture of the genotypes in one cluster differs entirely from those included in the other cluster. The minimum inter cluster distance was observed between cluster IV and V (D=2.422) followed by cluster IV and VI (D=2.712).The lower D value between their characters suggested that the genetic constitutions of these genotypes in one cluster were in close proximity to those genotypes in other clusters.

Considering the clustering pattern, presented in table 2 revealed that cluster IV has the highest number of genotypes (12) followed by cluster V having 10 genotypes, however, the minimum number of 3 genotypes were found in III clusters. The genotypes belonging to cluster I (EC-2513-3, EC-206977, IC-39327, IC-73536, PLM-759, PLM-777) and genotypes belonging to cluster V (IC-00114, IC-00557, IC-00615-5, EC-206972) has the highest intercluster distance (5.530) and can be used for hybridization programme (Table 1).

The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster mean for different characters (Table 3). The maximum number of pods per plant was noticed in cluster IV (59.97) while the minimum was observed in cluster I (49.10). The maximum number of seed yield per plant was recorded by the genotypes in cluster VI (70.71) and minimum in cluster III (16.39). So from the above result, it can be concluded that the genetic diversity was not related to geographic diversity.

Among the 40 genotypes, the genotypes from cluster I, i.e. EC-2513-3, EC-206977, IC-39327, IC-73536, PLM-759, PLM-777 with those of genotypes belonging to cluster VI i.e. IC-00114, IC-00557, IC-00615-5, EC-206972 has the highest inter cluster distance and might produce a high level of segregating population with regards to yield. Two

characters *viz*., plant height and number of pods per plant exhibited high heritability estimates coupled with high genetic advance which resembles the action of additive genes in controlling these particular characters. These characters should be given importance for the further improvement of yield and its components. The present findings are conformity with the findings of Gadakh et al. 2013.

Table 1: Estimates of average inter and intra clusters (bold values) involving 40 genotypes.

I	II	III	IV	V	VI
2.002	5.241	5.449	5.074	3.095	5.530
	2.279	4.782	4.001	4.362	4.494
		1.496	3.066	3.856	3.748
			1.733	2.422	2.712
				2.054	3.208
					1.936

Table 2: Distribution of 40 genotypes of Mungbean for six clusters.

Clusters	No. of genotypes	Name of genotypes
I	6	EC-2513-3,EC-206977,IC-39327,IC-73536,PLM-759,PLM-777
II	5	PLM-818,PLM-829,PLM-841,PLM-884,PLM-891
III	3	IC-08917,PLM-924,PLM-953
IV	12	EC-206976,EC-206978,EC-206974, EC-206980,IC-11303-3,PLM-0345 PLM-0380,PLM-391-A,PLM-726,PLM-748,PLM-904, IC-02056-2
V	10	EC-206971,EC-206979,EC-206975,EC-206973,IC-08592-3,IC-10492 PLM-0003,PLM-0021, PLM-0032, IC-10497
VI	4	IC-00114,IC-00557,IC-00615-5,EC-206972

Table 3: Average performance of different clusters for yield contributing traits in Mungbean

Cluster	Days to 75% flowering	Days to Maturity	Plant Height (cm)	Number of branches per plant	Number of pods per plant	Number of seeds per plant	Seed yield per plant (g)	Biological yield per plant (g)	Seed weight (g)	Harvest index
I	37.42	8.39	54.68	11.73	49.10	9.43	15.38	47.53	3.17	32.19
II	43.99	48.14	59.75	17.2	53.15	10.24	22.14	73.88	3.44	31.8
III	36.08	87.77	65.32	18.17	58.3	11.29	16.39	53.71	3.7	30.35
IV	37.75	88.07	67.95	16.69	59.97	9.78	19.06	57.8	3.37	33.05
V	36.65	85.78	62.49	14.92	53.5	9.6	17.65	52.72	3.09	33.68
VI	35.24	87.52	61.55	17.16	59.39	10.66	70.71	58.03	3.67	35.8

Figure 1: Cluster diagram showing intra and inter cluster distances for six clusters
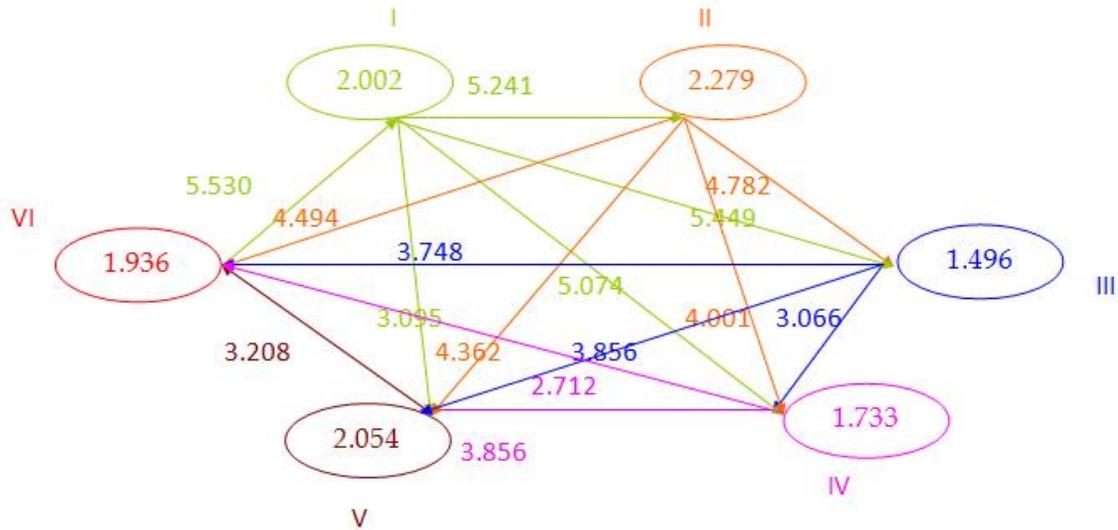
4. Conclusion

The major finding of this study was genetic divergence was estimated and intra, as well as inter cluster distance, was found for cluster II, while cluster III showed minimum inter cluster distance. Inter cluster distance was noted between cluster I and cluster VI, indicating relationship between these clusters (environment I) while in environment II the inter cluster distance was maximum for cluster II and minimum inter cluster distance was observed between cluster IV and VI, indicating the divergence and resembles, whereas, in environment III and IV, maximum intra cluster distance was for cluster III and I and lowest inter cluster distance was observed between cluster IV, VI and III clusters, respectively.

5. Acknowledgements

6. References

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