Genetic Diversity and Variability in Mungbean [*Vigna radiata* (L.) Wilczek]

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Fifty two genotypes of mungbean (*Vigna radiata* L.) were evaluated in randomized block design during rainy season of 2005 at Agricultural Research Station, Mandor, Jodhpur for eight characters to estimate genetic diversity, variability, heritability and genetic advance as a percentage of mean. Characters like seed yield, pod length, pods/ plant, primary branches/ plant, 100-seed weight and pod length exhibited high variability and heritability coupled with genetic advance. The hierarchical cluster analysis indicated the presence of considerable genetic divergence among the genotypes. The genotypes were grouped into eight clusters using Ward's minimum variance method. The inter-cluster Euclidean^2 distance was maximum between cluster V and VIII (54.3) followed by cluster V and VII (41.7) and cluster II and III (40.0). Cluster V showed by the maximum cluster means for plant height, primary branches/ plant, pods/ plant and days to 50% flowering, cluster II for pod length and seeds/pod, cluster VII for seed yield and cluster VIII for 100-seed weight. Contribution of different characters towards total genetic divergence revealed maximum contribution of pod length (24.5%) followed by seed yield (19.5%) and 100-seed weight (17.7%).

Key Words: Mungbean, Euclidean^2 distance analysis, Genetic divergence, Genetic variability

Introduction

Mungbean (*Vigna radiata* L.) is one of the important pulse crop grown in India. Assessment of genetic diversity in germplasm collection can facilitate classification and identification of diverse genotypes with possible utility for specific utilization in breeding programme. The hybridization between diverse lines produces a greater heterosis than those between closely related strains (Hallaur and Miranda, 1988). The utility of classifying germplasm to select diverse parents for hybridization had been appreciated (Bhatt, 1970). To increase the productivity of any crops, breeders have aimed to develop high yielding and better quality cultivars and normally it is achieved by selecting the desirable segregants from the segregating generation following hybridization. Therefore, an attempt has been made in present study to estimate genetic variability, heritability, genetic advance and genetic diversity among the genotypes of mungbean.

Materials and Methods

Fifty two genotypes of mungbean [*Vigna radiata* (L.) Wilczek] were grown in randomized block design with three replications during the rainy season of 2005 at Agricultural Research Station, Mandor, Jodhpur. Each entry was sown in a four rows of 5 m length following crop geometry of 30 x 10 cm. The crop was raised under rainfed condition and all cultural operations were done as and when necessary. The data were recorded on five competitive plants taken from each replication for plant height, primary branches/ plant, pod length (cm), pods/ plant, seeds/ pod and 100-seed weight (g) whereas seed yield, days to 50% flowering and days to maturity were recorded considering whole plot in each replication. The data were subjected to analysis of variance following standard method. Clustering was performed by procedure of Ward's minimum variance method (Ward, 1963) and the other genetic parameters such as variability, heritability and expected genetic advance as percent of mean were estimated using INDOSTAT software (Indostat Services, Hyderabad).

Table 1. Estimate of genetic parameters of seed yield and its component traits in mungbean

Characters	Mean	Range	*GCV	PCV	h^2(%)	GA
Seed yield (kg/ha)	857.0	347–1209	20.1	23.4	74	35.7
Days to 50% flowering	42.0	39–48	4.0	5.2	59	6.4
Days to maturity	66.0	63–69	2.1	2.9	54	3.2
Plant height (cm)	59.9	50–72	7.9	10.8	53	11.9
Primary branches/ plant	3.6	2.6–4.9	12.5	17.2	53	18.6
Pod length (cm)	8.1	6.8–10.2	9.4	10.9	75	16.8
No. of pods/plant	36.4	25–56	16.3	19.9	67	27.5
Seeds/pod	11.2	9.8–13.2	4.5	7.2	39	5.8
100 seed weight (g)	4.1	2.9–5.5	12.9	14.5	79	23.7

*GCV = Genetic coefficient of variation
PCV = Phenotypic coefficient of variation
h^2= Heritability, GA = Genetic Advance as percentage of mean

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters. The range,

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mean, coefficient of variability, heritability in broad sense and genetic advance for yield and its component characters are presented in Table 1. High magnitudes of phenotypic as well as genotypic coefficient of variation observed for seed yield, number of pods per plant, 100-seed weight and primary branches/ plant showed ample amount of variation for these characters. The heritability was high (range 53-79%) for all the characters except seeds/ pod (39%). Traits like 100-seed weight, pod length, seed yield and pod length had high estimate of heritability along with high genetic advance as percent of mean, suggesting the probability of a greater amount of additive gene action for these characters. Thus, selection of these traits would be effective for crop improvement. These results are in agreement with those reported earlier (Lal and Mishra, 2006; Sirohi and Kumar, 2006; Samad and Lavanya, 2005; Khairnar *et al.*, 2003; Reddy *et al.*, 2003; Yadav *et al.*, 2001).

A hierarchical cluster analysis of Ward's minimum variance method produced a dendrogram showing successive fusion of individuals which clearly partitioned the genotypes into eight clusters (Fig. 1). The genotypes within each cluster were closer to each other than the genotypes grouped in to different clusters. Maximum number of genotypes (14) were included in cluster I followed by 10 in cluster VII, seven each in cluster VI

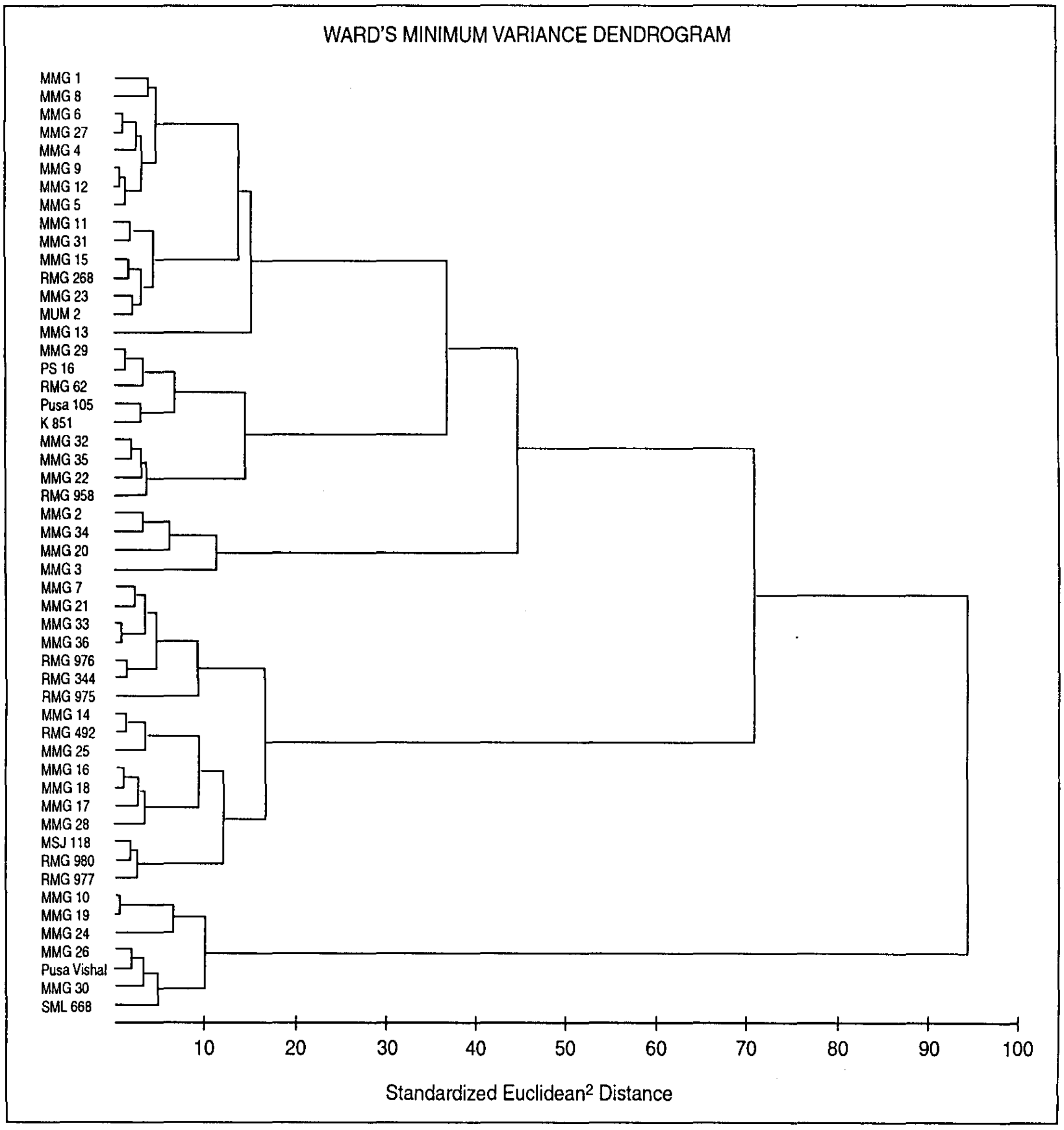

Fig. 1: Dendrogram showing different clusters of mungbean

Table 2. Average intra- and inter- cluster values among eight clusters in mungbean

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	6.7	18.8	14.2	10.7	22.5	10.8	13.8	18.4
Cluster II		0.0	40.0	31.3	33.3	30.9	37.1	29.4
Cluster III			6.9	11.2	28.3	20.1	17.8	28.4
Cluster IV				5.3	17.8	11.2	15.7	35.1
Cluster V					13.5	27.2	41.7	54.3
Cluster VI						7.0	10.6	28.8
Cluster VII							8.1	22.5
Cluster VIII								9.0

Table 3. Cluster means and percent contribution of different characters in mungbean

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Contribution to diversity (%)
Seed yield (kg/ha)	849.0	583.0	677.0	823.0	674.0	993.0	994.0	832.0	19.5
Days to 50% flowering	42.7	42.7	44.3	44.2	45.4	40.9	41.1	41.3	7.2
Days to maturity	65.8	65.0	67.5	67.8	68.1	65.5	65.0	64.0	6.1
Plant height (cm)	61.3	52.1	62.3	62.7	69.9	61.8	56.2	52.9	3.1
Primary branches/plant	3.8	4.5	3.5	3.6	4.8	3.8	3.2	3.2	4.8
Pod length (cm)	8.3	9.4	7.7	7.2	8.2	7.5	7.6	9.4	24.5
Pods/plant	36.0	39.2	28.4	40.6	45.7	41.8	35.6	30.4	13.5
Seeds/pod	11.6	13.2	10.6	11.3	11.5	11.2	10.8	11.1	3.0
100 seed weight (g)	4.3	4.1	3.98	3.69	3.92	3.74	3.73	5.2	17.7

and cluster VIII, five in cluster III, four each in cluster IV and cluster V whereas cluster II was having only a single genotype.

Average intra- and inter-cluster Euclidean^2 distances are sown in Table 2. Maximum intra-cluster distance was observed in cluster V (13.52) followed by cluster VIII (8.99) indicating wide genetic variability within the genotypes of these two clusters. The highest inter-cluster distance was observed between clusters V and VIII (54.3) followed by clusters V and VII (41.7), and clusters II and III (40.0), suggesting wide diversity between genotypes of these clusters. Therefore, genotype belonging to these clusters may be used in hybridization programme for improvement of mungbean. The least inter-cluster distance was observed between clusters I and IV (10.7) indicating close relationship between the genotypes of these two clusters.

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 3). Cluster V showed by the maximum cluster means for plant height, primary branches/ plant, pods/ plant and days to 50% flowering; cluster II for pod length and seeds/ pod; cluster VII for seed yield (kg/ha) and cluster VIII for 100-seed weight (g). These results showed that different clusters were superior for different characters. Amongst the characters, pod length contributed maximum towards genetic divergence (24.5%) followed by seed yield (19.5%) and 100-seed weight (17.7%). These results are in conformity with those reported by Sandhu and Brar (2002).

In the present study, the maximum inter-cluster distance observed between clusters V (genotypes MMG 2, MMG 34, MMG 20 and MMG 3) and VIII (genotypes MMG 10, MMG 19, MMG 24, MMG 26, Pusa Vishal, MMG 30 and SML 668) would be resulted into transgressive segregation. As seed yield, pod length and 100-seed weight contributed maximum towards the divergence, direct selection of these traits help in crop improvement.

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