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Assessment of genetic divergence in greengram (*Vigna radiata*) germplasm*

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The knowledge of the extent of variability prevalent in each attribute in germplasm would imply the scope for improving the character through selection. But in hybridization programme where selection of genetically diverse parent is important to get wide array of recombinants, the clear understanding of genetic diversity among the entries of germplasm is necessary. To assess the diversity in accessions, the ordination techniques like principal component analysis, followed by cluster analysis was found to be useful tool for getting multi-correlated 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 for classification of germplasm is suggested (Arunachalam 1981, Katiyar and Dixit 2009). In view of above, the present study has been taken *inter alia* to facilitate an inventory of what is available in the germplasm collection and therefore help to determine which accessions are of value.

A total of 681 accessions of greengram (*Vigna radiata* L.) from different agro-ecological regions in India were grown at Indian Institute of Pulses Research, Kanpur (26.28° N and 80.21° E), in a single replicate augmented design with two intermittent checks, namely 'Meha', and 'Narendra M 1' after every 25 row over three years (2006, 2007 and 2008) during rainy season. Each accession was grown in one row plot of 5 m length and inter and intra-row spacing of 45 and 15 cm apart. The crop was raised adopting standard cultural practices. Observations on metric and qualitative attributes were recorded but only quantitative attributes were subjected to statistical analysis. Ten distinct traits, viz days to 50% flowering, plant height (cm), number of primary branches, number of clusters/plant, number of pods/plant, number of seeds/pod, pod length (cm), 100-seed weight (g), days to maturity and yield/plant (g) were analyzed in augmented block design to get adjusted mean values (Peterson 1985).

The principal component analysis was carried out to transform the inter-dependent variables into a set of independent variables (Hotelling 1933). These principal component scores were used to compute Euclidean distance based on non-hierarchical cluster analysis through SPAR I (Beale 1969, Spark 1973). This method characterizes genetic divergence on the basis of similarity and dissimilarity denoted by aggregate effects of agronomic traits under study.

Treatment mean squares were highly significant for all the attributes indicating presence of sufficient genetic variation among genotypes.

Ten well characterized groups (A to J) of greengram accessions were derived on the basis of similarity in morphological characters from the non-hierarchical Euclidean cluster analysis. F-test showed that 10 clusters were most suited. The cluster C (108 accessions) contains the maximum number of genotypes while cluster G (24 accessions) have minimum number. These well characterized groups were obtained by transforming the metric attributes into a single index of similarity in the form of principal components which yielded 10 eigen vectors and eigen roots. Further, maximum eigen root value 3.127 was obtained by

Table 1 Eigen vectors of 10 standardized variables for the first four principal components

Variable	Principal component				
	1	2	3	4	5
Days to 50% flowering	–0.035	–0.116	0.429	0.183	0.132
Plant height (cm)	0.139	0.191	–0.080	–0.0195	0.417
Number of primary branches	–0.137	–0.039	0.191	0.376	0.160
Number of clusters/plant	0.136	0.486	0.207	–0.135	0.038
Number of pods/plant	0.481	0.003	–0.120	–0.006	–0.151
Number of seeds/pod	–0.161	0.422	0.117	0.113	0.129
Pod length (cm)	0.097	0.185	0.446	0.161	–0.205
100 seed weight (g)	0.157	0.449	–0.155	–0.017	0.183
Days to maturity	0.159	–0.192	0.143	0.488	–0.016
Yield/plant (g)	–0.218	0.024	0.204	0.421	0.118

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*Short note

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Table 2 Categorization of clusters into different groups (based on frequency distribution) for 10 metric traits in greengram

Character	Cluster group		
	High	Intermediate	Low
Days to 50% flowering	F,H,J	D,A	B,C,E,G,I
Plant height (cm)	F,G,H,J	D,E	A,B,C,I
Number of primary branches	C,A	I	B,D,E,F,G,H,J
Number of clusters/plant	F,H	C,D,G,J	A,B,E,I
Pods/plant	F,G,H	B,C,D,E,J	A,I
Seeds/pod	E,I,J	B,H	A,C,D,F,G
Pod length (cm)	A,J	B,D,F,G,H,I	C,E
100-seed weight (g)	D,F,H,J	B,C,G,I	A,E
Days to maturity	I,J	B,D,E	A,C,F,G,H
Yield/plant (g)	B,J	A,D,G,I	C,E,F,H

Table 3 Frequency distribution of qualitative attributes of 681 accessions of mungbean

Plant descriptor	Range of expression	No. of accessions
Growth habit	Erect	598
	Semi erect	83
	Spreading	0
Plant habit	Determinate	609
	Indeterminate	72
Stem colour	Green	536
	Green with purple splashes	145
Stem pubescence	Absent	3
	Present	678
Leaflet lobes	Absent	677
	Present	4
Leaf shape (terminal)	Deltoid	11
	Ovate	656
	Cunate	6
	Lanceolate	8
Leaf colour	Green	568
	Dark green	113
Leaf vein colour	Green	13
	Purple	29
	Greenish purple	639
Petiole colour	Green	15
	Green with purple splashes	659
	Purple	7
Flower colour	Yellow	173
	Light yellow	508
Pod colour (premature)	Green	550
	Green with pigmented sutures	131
Pod position	Above canopy	465
	Intermediate	216
Pod colour (mature)	Brown	12
	Black	669
Pod curvature	Straight	393
	Curved	288
Seed colour	Yellow	1
	Green	663
	Black	17
Seed lusture	Shiny	533
	Dull	148
Seed shape	Oval	577
	Drum	104

eigen vector 1, followed by 1.753, 1.309, 1.111, 0.817, 0.983, 0.600, 0.462, 0.261 and 0.215, respectively for rest of the vectors. The first five principal components calculated by using standard variables accounted for 26.01, 20.56, 16.29, 11.72 and 8.74% of the variation, respectively (total = 83.32%). The first component was a measure of pods/plant as the coefficients associated with these traits have the maximum magnitude (Table 1). The second principal component was determined by clusters/plant, 100-seed weight and no. of seeds/pod. Days to 50% flowering and pod length were represented by third principal component, whereas fourth principal component was a measure of days to maturity, number of primary branches and yield/plant. Fifth component was a measure of plant height.

Average distance of clusters from cluster centroids ranged from 1.327 to 2.652. It was maximum in cluster C and minimum in cluster H. Therefore, utilizing the cultivars from these cluster in hybridization programme may result in the putative transgressive segregants. So for as inter-cluster distance is concerned, cluster B and F centriods were the farthest (3.891) from each other. The minimum distance was observed between D and I (1.004). These observed distances reflect the genetic diversity in cultivars and their linkage with respect to one another.

Categorization of clusters into groups (high, medium, low based on frequency distribution) for relative superiority of different attributes are presented in Table 2. The frequency distribution of qualitative attributes of mungbean accessions is depicted in Table 3. The potential donors for plant height (<45 cm) were 'CN 8067', 'CN 8074', 'CN 8052', 'CN 8096', 'IC 39396', 'DMG 1125', 'ML 584'; for early flowering (<35 days) 'EC 319049', 'BDYR 2', 'CN 9042', 'DMG 1103', 'PM 6'; for number of primary branches (>4) 'EC 470090', 'GP 274', 'DMOI 1125', 'LM 34', 'IC 20305'; for number of cluster/plants (>10) 'K 369760', 'STV 3714', 'Kopergaon 1', 'LM 58; for pod length (>10 cm) 'EC 30401', 'EC 470096', 'IC 325823'; for number of seeds/pod (>12) 'AKP/NP/8/9', 'DRA 24', 'AKP/NP/8/63', 'EC 30400', 'LM 1510', 'IC 325823', 'ML 490'; and for 100-seed weight (>5 g) 'EC 398886', 'BRS 2435', 'IPOI 359', 'GG 1990', 'EC 407077', 'PLM 531', 'CN 8082', 'GP 205'. The accessions included in a particular group exhibited more or less similar characteristics but differed from those included in other groups. Selecting genotypes from these groups and using them in hybridization would prove fruitful in mungbean improvement programme.

SUMMARY

The genetic divergence analysis was carried out in 681 mungbean [*Vigna radiata* (L.) Wilczk] germplasm based on Euclidean distance for the identification of genetically diverse and agronomically superior accessions which may generate putative transgressive segregates on hybridization. Principal component and non-hierarchical Euclidean cluster analysis were used to compare the genotypes. Based on first five principal components which accounted for 83.32% of the total variation, non-hierarchical Euclidean cluster analysis grouped the accessions into 10 well characterized clusters based on aggregate effects of similarity in traits. There is no parallelism between genetic diversity and geographical origin of accessions.

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