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EVALUATION AND CLASSIFICATION OF URID BEAN (*VIGNA MUNGO* L.) GERMPLASM

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The evaluation and characterisation of germplasm gives considerable data to classify the material. The classification as multivariate basis rather than univariate is desirable. An attempt was made to classify 216 assessions of uridbean germplasm by cluster analysis. It gave convenient grouping of 12 clusters with like genotypes within clusters for different traits. The implications of classificatory approach have been discussed.

Key words : *Vigna mungo*, evaluation/characterisation, multivariate analysis

Urid bean (*Vigna mungo* L.) is one of the important pulse crop with its centre of diversity located in India. A thrust on its collection and evaluation is urgently needed to obtain donor parents for genetic restructuring of genotypes towards resistance to diseases, insects and abiotic stresses. Very often, in germplasm collection, many accessions are duplicate and it becomes difficult to exploit germplasm till it is aptly classified. Multivariate classification with the help of ordination methods like principal component analysis is useful tool for clustering of genotypes. The representative types from each cluster thus obtained can be earmarked for different breeding objectives. The present studies on 216 accessions were initiated to classify them through this approach.

MATERIALS AND METHODS

The experimental material for this study comprised 216 germplasm accessions having landraces, primitive cultivars and current cultivated varieties. The experiment was sown in *kharif*, 1990 at Pantnagar, in the foothills of Himalayan range, under subtropical climate. All accessions were evaluated in augmented design with three intermittent checks namely Pant U-19, Pant U-30 and Pant U-35, after every 10 rows. Each plot consisted of one row of 4 m length. Various observations on quantitative and visual traits were taken but only quantitative traits were subjected to statistical analysis. The observations on pod length, plant height, 1000 seed weight, number of pods per plant and yield per plant were analysed to get adjusted means by methods described by Federer and Raghavrao (1975) and Peterson (1985).

The value of genotypic means were adjusted for block effects on the basis of replicated check plots in every block. The number of blocks were determined by relationship

$$b > \left[\frac{10}{c-1} + 1\right]$$

so as to get atleast 10 degree of freedom for error expectations. Thus 24 blocks were used having 3 checks and 216 test accessions. The adjustment factors (r_j) were computed as under :

$$rj = (1/c)\ (Bj - M)$$

where c = number of checks; B_j = jth Block having checks c; M = grand mean

Thus, the r_j is equivalent to mean of the jth block subtraction grand mean. By subtracting these adjustment factors from observed mean, the table of adjusted means were obtained. These quantitative variable means were analysed for Principal components in the form of a multivariate matrix (S),

where $S = (X_{ij})$

i.e., a n × n symmetric semi-definite with some eigen values say r as +ve and 1 - r as zero was obtained which gave eigen values and eigen vectors of matrix S. The principal components of this eigen matrix were enumerated by taking the defined new variable as linear combination of x_i variables or a line was found in a space of x on which the projections of the data units were dispersed maximally. The first principal component would be represented by this line with largest variance of any linear combination of variables in the data matrix. Similarly, r = 5 number of principal components with orthogonality to precious components were obtained.

These components were utilized for grouping of genotypes as described by Beale (1969) and elaborated by Spark (1973). The basic assumption followed was that the euclidian distances 'D' separating 'n' points in a 'p' dimensional space are proportional to the dissimilarities between the accessions and secondly no object can belong simultaneously to two clusters. F-test was utilized for assigning appropriate number of clusters.

RESULTS AND DISCUSSIONS

The range for various characters showed wide differences in minimum and maximum values which are given in Table 1.

Table 1 : Range and checks mean of various quantitative characters in urid bean germplasm

	Pod length (cm)	Plant height (cm)	1000-seed wt. (g)	Pods per plant (no.)	Yield per plant (g)
Accessions range	3.2-5.9	19.4-33.1	17.37-70.70	3-89	2-26.0
Checks mean : PU-19	4.18	58.23	40.50	29.59	8.03
PU-30	4.30	69.27	43.04	24.84	8.88
PU-35	4.39	69.10	42.58	27.56	8.62
CV (%)	8.53	26.80	15.97	41.69	40.41

The range values indicate occurrence of wide variations for seed weight, pods per plant as well as yields, suggesting an optimistic picture for further improvement in urid bean for these traits. Variability can be incorporated in other characters by wide hybridization among distant accessions.

The classificatory procedures for earmarking distant genotypes have been emphasized by number of scientists (Griffing and Lindstrom, 1954; Moll *et al.*, 1962, Arunachalam, 1981). The D^2 statistics has been used by several workers in different crops including black gram but the limitations of this technique have also been pointed by Arunachalam (1981). The classificatory approaches like principal components and clustering of genotypes to overcome the limitations of D^2 have been advocated by Beal (1969). In the present study, all the variables were converted to single index of similarity in the form of principal component. The eigen vectors, roots and associated variance have been given in Table 2. The maximum variation of 38.15 per cent was explained by first latent vector followed by second vector (25.09%). Thus around 60 per cent variation was explained by first two vectors and rest by other three.

Table 2 : Eigen vectors, eigen roots and associated variance for different components in urid bean germplasm

Characters	Eigen vectors				
	1	2	3	4	5
Pod length (cm)	0.28	0.28	0.61	0.39	0.54
Plant height (cm)	–0.24	0.62	–0.13	0.56	–0.45
1000-seed weight (g)	0.22	–0.67	0.01	0.65	–0.25
Pods per plant	–0.13	–0.003	–0.69	0.30	0.64
Yield per plant	–0.88	–0.25	0.35	0.87	0.14
Eigen roots	1.90	1.25	0.92	0.63	0.28
Variation (%)	38.15	25.09	18.47	12.62	5.64

The cluster analysis grouped 216 accessions into 12 different non-overlapping clusters. The appropriate cluster arrangement as determined by F-test revealed that the 12 clusters were most suited. The average inter and intra cluster distances are presented in Table 3 and depicted in Fig. 1. The cluster 6 and 11 were found at a maximum diverse ends. Cluster 6 with smallest number of genotypes (5) is also exclusive because of the genotypes with high values for number of pods per plant and yield per plant (Fig. 2).

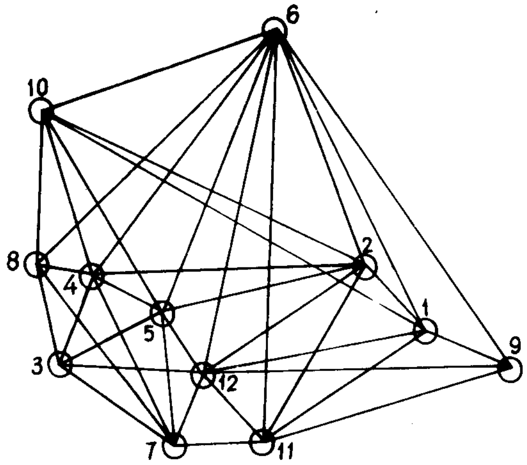

Fig. 1. Cluster diagram showing relative inter cluster distances among germplasm lines

These 12 clusters can be further grouped into four distantly related groups based on their inter- cluster distances. The biggest group consisted of 7 clusters (3, 4, 5, 7, 8, 11, 12), the next bigger group had 3 clusters (1, 2, 9) and the rest had one cluster each. This representation reflects the relative divergence of clusters and allows a convenient selection of group of genotypes with their overall phenotypic similarity for any hybridization programme facilitating better exploitation of germplasm. Although such classificatory studies are not reported in uridbean but similar studies have been done, (Negassa 1986; Ahlawat, 1987; Guo and Zhang, 1989) etc. in various other crops.

The relative superiority of different clusters for various characters is represented in the form of bar diagram (Fig. 2) which would help convenient selection of genotypes from particular clusters. The list of such possible donors has been given in Table 4 which indicate that a number of promising parents can be selected for further improvement work.

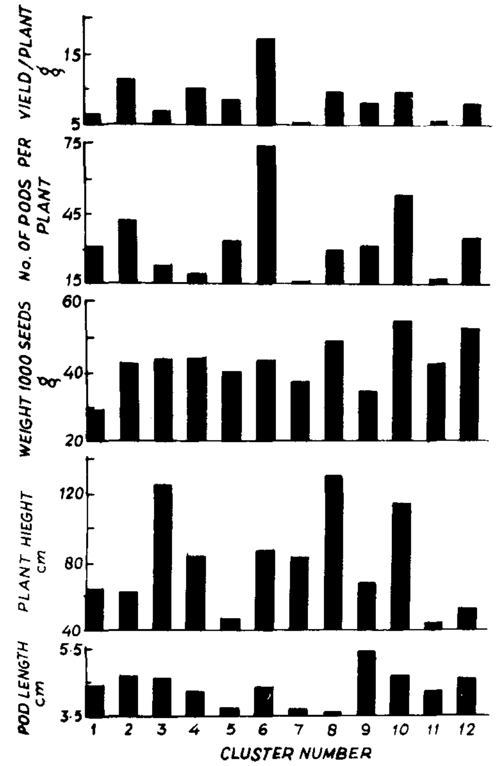

Fig. 2. Cluster mean for different characters

Table 3 : Average inter and intra cluster distances in urid bean germplasm

Cluster. No.	1	2	3	4	5	6	7	8	9	10	11	12
1.	(1.441)											
2.	2.072	(1.435)										
3.	2.393	2.526	(1.461)									
4.	2.788	1.980	2.201	(1.493)								
5.	2.162	1.986	2.894	2.341	(1.238)							
6.	3.820	2.760	4.361	4.176	3.356	(2.630)						
7.	1.938	2.833	2.151	2.304	1.794	4.465	(1.238)					
8.	3.027	3.012	2.253	2.555	2.368	3.670	1.917	(1.596)				
9.	2.175	2.216	2.631	2.980	3.587	4.517	3.522	4.283	(1.319)			
10.	3.367	2.885	2.528	3.754	3.145	3.378	3.539	2.960	3.795	(1.612)		
11.	2.173	2.221	2.328	1.934	1.785	4.627	1.861	3.093	2.776	3.450	(1.233)	
12.	2.859	2.029	2.449	2.542	2.175	4.038	2.905	3.289	2.992	2.337	1.652	(1.346)

Values in parentheses show intra cluster distances

Table 4 : Potential genetic donors for different characters in urid bean germplasm

Chatacter	Cluster number	Genotype
Grain yield per plant (g)	6	U-14/4, PLU 1064, U-3411, PLU-29, PLU-166
1000-seed weight (g)	10	PLU-573, GPU-74, U-12/12, PLU-517, U-1317, HPU-110, HPU-119
Plant height (cm)	8	PLU-640, U-12/1A, PLU-360, PLU-577 HPU-156, PLU-393, KH-1, IC-24814,
Pod length (cm)	9	PLU-317, PH-32, UPU-107, PLU-764, PLU-129, HPU-192-8, PLU-53, U-10008, IC-15790, PLU-260

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