Indian J. Pl. Genet. Resources 12(3): 366-370, 1999

CLASSIFICATION OF URIDBEAN GERMPLASM FROM DIVERSITY ZONES OF UTTAR PRADESH

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The landraces in Urid bean (*Vigna mungo* L.) were collected from diversity rich zones in Uttar Pradesh, India. The collections were characterized for visual traits and quantitative characters. The ordination of genotypes were done by principal component analysis. The classification gave 13 clusters. Many resistant genotypes for viral diseases were identified. The genetic donors for yield, pod and flowering traits were isolated along with green seeded erect types which are not found frequently.

Key words : Uridbean, *Vigna mungo* L., landraces, classification

Uridbean [*Vigna mungo* (L.)] Hepper is an important pulse crop of Indian sub-continent. India being one of the important centre of diversity, a thrust for germplasm collection, evaluation and conservation is a desired necessity to keep pace with increasing population. Keeping this in view, explorations were conducted in the districts of Uttar Pradesh namely Hardoi, Barabanki, Bareilly, Sitapur and eight districts in Kumaon and Garhwal which were reported to be rich in diversity for local types in this crops (Paroda and Arora, 1991). For estimation of diversity within the germplasm, the classification of germplasm accessions into homogenous groups is utmost desirable practice using multivariate parameters instead of using univariate methods. It was presumed that the genotypes originated from distantly separated regions of the world are likely to be different in their genetic make up. However, several scientists for different crop species have supported no parallelism in geographical distribution and genetic diversity (Malhotra and Singh, 1971).

A number of classificatory approaches based on multivariate analysis have been postulated by several workers. The D^2 statistics has been given by Mahalanobis (1936). In case of germplasm collection, which are characterized in large numbers involving various characters, the use of D^2 becomes very limited and goes beyond practical reach (Arunachalam, 1981). The classificatory approaches like principal component, factor analysis and clustering of genotypes overcome these limitations of D^2 statistics (Beale, 1969). In principal component analysis, the observable variates are presented as a function of smaller number of latent vectors, so that few orthogonal variates are obtained (Morrison, 1976). The cluster analysis is utilized for further classification. The collected 150 accessions of uridbean were subjected to such classification in the present study.

MATERIAL AND METHODS

The 150 uridbean accession collected from diversity zones of Uttar Pradesh were sown in the month of July at Crop Research Station, Pantnagar in augmented design with four checks namely Narendra Urid-1, Pant Urid-35, Type-9, and Pant Urid-19 after every 10 plots of new accessions. Each plot of accession as well as checks consisted of 2 rows of 4m length. The row spacing was 30 cm and plant spacing was kept 10 cm. All accessions were assigned in 15 blocks with 4 repeated checks in every block. Observations for characters such as, plant height (cm), days to 50 per cent flowering, days to maturity, pods per plant, pod length (cm), seeds per pod, 100 seed weight (g) and yield (kg/ha) were subjected to statistical analysis. The analysis of variance was performed in augmented design using by Federer and Raghav Rao (1975) and Peterson (1985). The genotypic means were adjusted for the block effects as measured by the check plots. The total number of block were determined by relationship

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

where, b = number of blocks
c = number of checks

The adjustment factor rj = (1/C) (Bj–M) = Mean of j^{th} block minus grand mean. The adjusted yields were calculated by substracting rj from actual observations.

$$y_i = y_{ij} - r_j$$

where, Y_{ij} = yield of i^{th} variety occurring in j^{th} block.

This analysis gave adjusted values for all characters in each accessions. Further classificatory analysis was done on these adjusted values of variables. For extracting the principal components, correlation matrix was obtained by adjusted means of variable as matrix following Mardia *et al.* (1980). The matrix of r non zero eigen values was utilized to extract r principal components. Thus from a matrix of 6 non-zero eigen values, 6 principal components (PCP) were extracted. Here the 1st PCP represented largest variance of random linear combination of variables represented in data matrix. The other PCPs were orthogonal axis of 1st PCP. The measure of degree of fit or fraction of total variance explained by 6 principal components were obtained as fraction of non zero eigen values and total R eigen values.

The genetic divergence among genotypes was studied using method of non hierarchical euclidian, cluster analysis (Beale, 1969; Spark, 1973). The PCPs obtained from original variables were utilized for this analysis. The assumption for this method was that the euclidian distances 'D' separating 'n' points in a 'P' dimensional space are proportional to the dissimilarities between the objects and secondly, that no object can belong simultaneously to two clusters.

RESULTS AND DISCUSSION

The analysis of variance performed for augmented designs revealed sufficient differences among checks. The results for mean and range in various characters has been given in Table 1. The range of characters is indicative of high amount of variability as the plant height ranged from 125-184 cm and maturity ranged from 58 days to 116 days. The pods per plant showed tremendous variability with minimum of 9.9 up to 116.6 pods. The pod length varied from 2.9 to 7.12 cm and seed weight varied from 1.32 to 4.72 g. The maximum yield was obtained in accession ShU 96133 which was a local collection from district Nainital. The earliest accession in flowering and maturity was ShU 9547 which had different foliage and pod characters. Accession ShU 9534, a collection from district Hardoi had the highest number of pods and found resistant to both yellow mosaic and leaf crinkle virus.

The evaluation data obtained as adjusted means for various characters were converted to single index of similarity in the form of principal component. The values of eigen vectors, roots and variation explained has been given in Table 2. The maximum value of eigen roots 2.89 was obtained by 1st eigen vector followed by 1.85, 1.08, 0.833, 0.69, 0.42, 0.18, 0.33 by other corresponding seven vectors. The different vectors associated with various characters have shown positive and negative values as contribution obtained for vectors. The contribution of positive and negative values is based on relative proportion of multivariates in the formation of orthogonal vectors as the observable variates are presented as a function of smaller number of latent vectors so that few orthogonal variates are obtained (Morrison, 1976).

The maximum variation of 36.13 per cent was explained by 1st vector and rest of the variation 23.20, 13.54, 10.42, 8.63, 5.36, 2.27 and 0.41 were explained by other seven vectors. The maximum variation contributed for first vector is from characters plant height, pods per plant and yield kg/ha. The first six-principal components explained 97.31 per cent variation which were utilized for clustering purpose.

The cluster analysis grouped 154 accessions into 13 clusters which was found appropriate as determined by F test. The non-hierarchical clustering procedures followed, allows solution to large data problems because it is not necessary to calculate and store the similarity matrix every time. The inter and intra cluster distance between and within clusters have been given in Table 3.

The maximum intra cluster distance 1.976 was found in cluster 8 and minimum in cluster 6. This distance is indicative of relative divergence among similar genotypes within a group. The maximum inter cluster distance was between cluster 13 and 10. These clusters had accessions collected from various different localities. The arrangement of accessions in between clusters was found independent of their locality of collections indicating that pattern of diversity in uridbean is not location specific.

The cluster means as depicted in Fig. 2 revealed that within clusters, the accessions with distinct characters, clustered together making a particular cluster distinct. The tallest accessions were recorded in cluster 10 which had the highest mean of 139.27 cm, cluster 8 had early flowering

Table 1. Mean and range of various quantitative characters in uridbean germplasm

Particulars	Characters							
	Plant height (cm)	Days to 50% flowering	Days to maturity	Pods/plant	Pod length (cm)	Seed/pod	100 seed weight (g)	Yield (kg/ha)
Accessions	90.83 (125.5-183.8)	54.93 (18.4-79.7)	86.37 (58- 116)	30.20 (9.9-116.6)	4.22 (2.90-7.12)	6.67 (3.42-7.61)	3.24 (1.32-4.72)	1057 (709-2839)
Check 1 (Narendra Urid 1)	191.5	42.93	75.53	44.87	4.567	6.507	3.175	2301
Check 2 (PU-35)	112.3	42.73	74.67	42.93	4.567	6.780	3.039	1602
Check 3 (T-9)	93.87	43.20	76.00	35.53	4.380	6.820	3.197	1371
Check-4 (PU-19)	101.6	43.93	75.00	39.07	4.300	6.593	2.984	1709
CV %	16.13	3.773	4.164	26.80	5.263	6.321	8.858	18.63

(Range in parenthesis)

Table 2. Showing eigen vectors, eigen roots and associated variance for different components in urid germplasm

Particulars	Characters							
	Plant height (cm)	Days to 50% flowering	Days to maturity	Pods/plant	Pod length (cm)	Seed/pod	100 seed weight (g)	Yield (kg/ha)
Plant height (cm)	0.38	0.40	–0.14	–0.23	–0.16	0.51	0.56	–0.027
Days to 50% flowering	–0.35	0.57	–0.039	0.050	0.19	–0.026	–0.048	0.71
Days to maturity	–0.33	0.58	–0.02	0.07	0.21	–0.032	–0.09	–0.69
Pods/plant	0.42	0.28	0.10	0.06	–0.14	–0.80	0.23	0.002
Pod length (cm)	0.35	–0.08	–0.21	–0.30	0.84	–0.065	–0.064	0.01
Seeds/pod	0.15	–0.016	–0.68	0.70	0.01	0.04	–0.003	0.003
100 seed weight (g)	0.22	0.009	0.66	0.57	0.31	0.23	0.13	0.03
Yield (kg/ha)	0.48	0.28	0.06	–0.04	–0.22	0.18	–0.76	0.03
Eigen roots	2.89	1.85	1.08	0.833	0.69	0.42	0.18	0.033

Table 3. Average inter and intra cluster distances in uridbean germplasm

Cluster No.	1	2	3	4	5	6	7	8	9	10	11	12	13
1.	(1.106)												
2.	1.791	(1.212)											
3.	1.687	1.550	(1.239)										
4.	3.379	3.085	2.541	(1.566)									
5.	2.283	2.601	2.467	1.939	(1.023)								
6.	3.156	2.601	2.966	3.995	3.143	(1.030)							
7.	2.742	2.238	3.057	3.175	1.916	2.158	(1.340)						
8.	5.493	4.010	4.716	4.068	4.962	5.367	4.500	(1.976)					
9.	4.402	3.976	3.946	4.436	4.220	4.635	4.506	6.166	(1.412)				
10.	3.140	3.117	2.409	2.545	2.261	2.389	2.906	5.582	4.014	(1.307)			
11.	2.880	2.249	2.350	3.154	2.529	1.443	2.150	5.037	3.312	1.654	(1.078)		
12.	2.487	2.376	2.902	3.011	1.865	3.562	2.102	4.883	3.160	3.333	2.683	(1.193)	
13.	12.409	12.409	12.303	12.465	12.353	12.302	12.398	13.137	12.876	12.469	12.347	12.000	(0.000)

(Values in parenthesis are intra cluster distance)

and maturity types. The maximum number of pods with mean value of 44 per plant were obtained in cluster 13 which is a single entry cluster with accession ShU-9641 collected from Shergarh in district Bareilly. This cluster also had maximum number of seeds per pod. The entry was typically distinct and exclusive. This cluster was in maximum diverse end (Fig. 1).

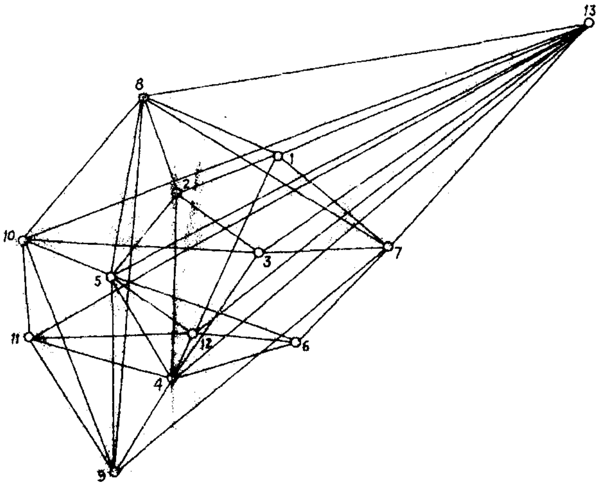

Fig. 1. Cluster diagram showing relative inter cluster distances among uridbean germplasm

Table 4. Identified genetic donors for various characters in uridbean germplasm

	Character	Entry Name
1.	Plant height (cm)	ShU 9511, ShU 9512, ShU 9537, ShU 9539, ShU 9606
2.	Days to 50% flowering	ShU 9636, ShU 9603, ShU 96104
3.	Days to maturity	ShU 9636, ShU 9603, ShU 96104
4.	Pods/Plant	ShU 9636, ShU 9603, ShU 96104
5.	Pod Length (cm)	ShU 96104, ShU 9603, ShU 9634
6.	Seed/Pod	ShU 9641
7.	100 Seed Weight (g)	ShU 9536, ShU 9603, ShU 96104

The presentation in the Fig. 2 allowed convenient selection of superior clusters for different traits and their accessions within these clusters. The promising accessions identified as genetic donors have been given in Table 4, which can be utilized in breeding programmes.

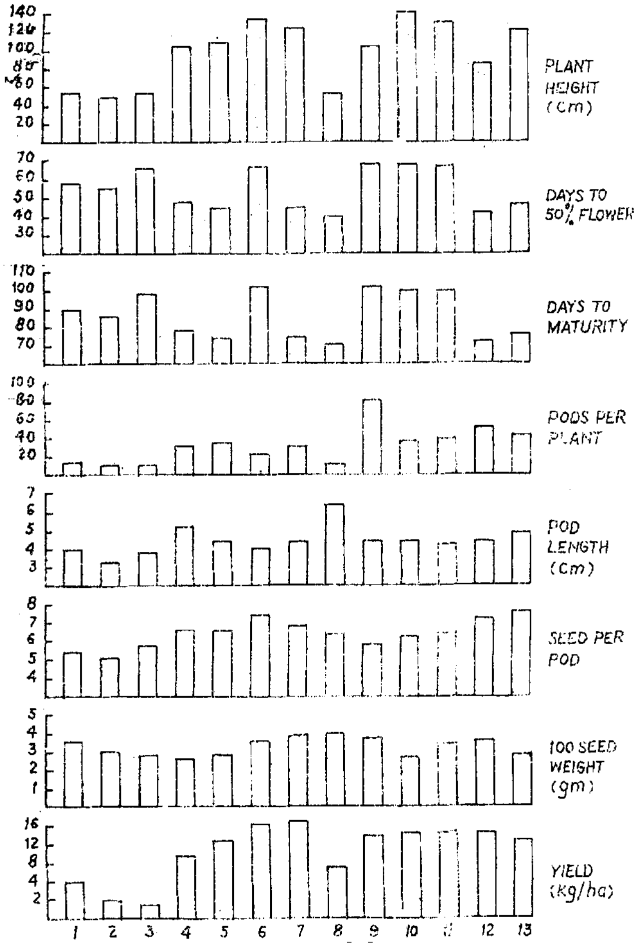

Fig. 2. Cluster means of different characters in uridbean germplasm

ACKNOWLEDGEMENT

The authors are highly thankful to U.P. Council of Agricultural Research (UPCAR) for providing finance to conduct this work.

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