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Short Communication

CLASSIFICATION OF GERMPLASM IN URID BEAN (*VIGNA MUNGO* (L.) HEPPER)

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India being an important centre of diversity for urid bean, a thrust for germplasm evaluation and exploitation is an urgent requirement. Evaluation of germplasm will provides potential value as a breeding material. Quite often in a germplasm collection, many of the accessions are duplicates and to find unique types for various characters, it becomes difficult unless germplasm is characterised and classified. The ordination techniques like principal component analysis follwed by cluster analysis was found to be a useful tool for getting multicorrelated variables into an other set of uncorrelated variables from which few or all can be utilized for classification of genotypes into homogenous groups or clusters in a geometric space. In this, the between cluster diversity will be maximum and thus the representative types from diverse clusters can be earmarked for different breeding objectives. In view of the above the present studies were taken up with 216 genotypes of uridbean to characterise and classify the set of collection.

The experimental material comprised of 216 germplasm accession obtained from Pulse Breeding Project at Pantnagar. The sowing was done in kharif 1990 at Crop Research Centre, Pantnagar, India (29.5°N La, 29.3°E Lo, 234 m al). All the germplasm accessions were evaluated in an augmented design with three intermittent checks namely Pant U-19, Pant U-30 and Pant U-35 after every 10th row. Each plot consisted of single row of 4 m length with 30 cm. row to row and 10 cm plant to plant spacings. Observations on 27 descriptors were taken as per descriptor list of IPGRI for *Vigna* sp., Among them five quantitative characters (pod length, plant height, 1000 seed weight, pods per plant and yield per plant) are the subject of this paper.

The data obtained for the said 5 variables was analysed for variance and to obtain adjusted means by using methods described by Federer (1956) and elaborated by Federer and Raghavrao (1975) and Peterson (1985). This analysis gave adjusted values of genotypic means in the form of multivariate matrix on which principal component analysis as given by Hotelling (1933) and Mardia (1971) was applied. For a matrix of r non zero eizen values the r number of principal components were extracted, where r = 5 in the present study. These extracted principal components scores obtained from original variables were utilized for Non- hierarchical Eucludian cluster analysis (Beale, 1969; Spark, 1973). The different genotypes were assigned to different clusters on the assumption that the Eucludian distance "D" separating "n" points in a "p" dimensional space are proportional to the dissimilarities between the objects and no object can belong simultaneously to two clusters. For determining the appropriate number of clusters, F-test was applied.

The classificatory analysis gave five principal components. The *eigenvector* and roots are associated with latent roots of observed variables with maximum value 1.90 obtained for eigen vector 1 and 1.25, 0.92, 0.63 and 0.28 for corresponding second to fifth vectors, the maximum variation (%) 38.15 was explained by first vector and 25.09, 18,47, 12.62, and 5.64 by other four vectors, respectively. The obtained five components were utilized for clustering genotypes.

These clusters were arranged in a geometrical space with different inter cluster distances as depicted in Fig.1. The intra cluster distances ranged from

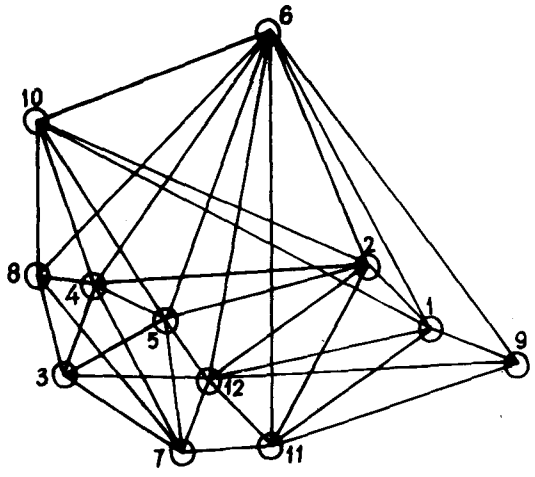

Fig. 1. Cluster diagram showing relative inter cluster distances among germplasm lines

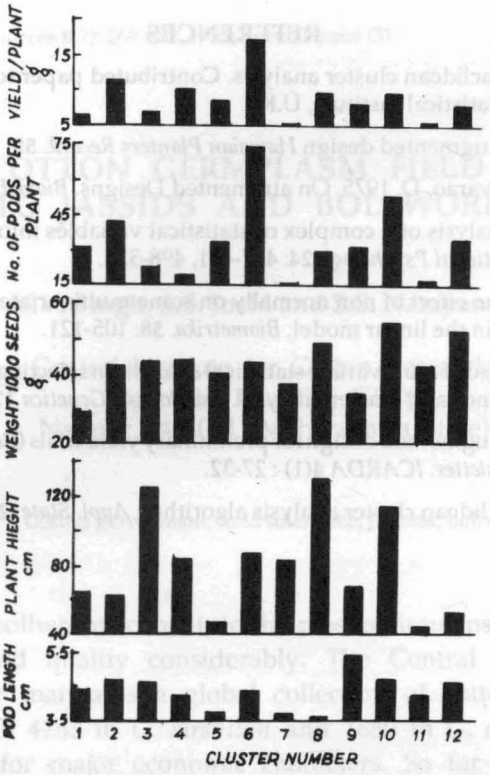

Fig. 2. Cluster mean for different characters

1.2 to 2.63. It was maximum in cluster 6 and minimum in cluster 7. The maximum intercluster distance (4.62) was found between cluster 6 and 11 followed by 6 and 9 (4.51). The minimum distance was observed between cluster 11 and 12 (1.65). The observed distances are indicative of diversity in genotypes as well as their linkage with respect to one another. Although, the diversity studies by utilizing cluster analysis are not reported in urid bean but in other crops like wheat Martinov (1983) showed that cluster analysis allowed genetically related varieties to group together. The clusters having superior genotypes with highest grain yield per plant and pods per plant fell into cluster number 6 while bold seeded genotypes converged to cluster number 10. For longest and shortest plant height genotypes gathered into cluster 9 and 11.

The studies allowed convenient selection of superior clusters for different traits, in the germplasm for distant hybridisation. The procedure also provided a basis for evaluating the role of pedigree in observed association between phenotypic characters.

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