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Diversity studies in brinjal (Solanum melongena L.)

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ABSTRACT

Twenty four genotypes of brinjal were studied for genetic diversity. Cluster I had three genotypes, cluster II had fourteen genotypes, cluster III had two genotypes and cluster IV had five genotypes. The maximum inter cluster distance was observed between cluster II and cluster IV (43.45), while minimum was recorded between cluster I and III (24.39). Considering cluster means and the genetic distances, the genotypes of cluster IV with the genotypes of cluster III were likely to recombine the genes for high yield. The contribution of characters towards genetic divergence was noticed more in fruit yield per plant

Key words: Brinjal, Genetic diversity, D² Analysis, Clustering.

Brinjal (*Solanum melongena* L.) is the most popular and widely cultivated vegetable crop grown in India due to its high productivity, round the year availability, better transport qualities and good storability. The crop is extremely variable in India and Vavilov for this reason regarded the crop to be of Indian origin. This was substantiated by the presence of wild S. melongena in India which is a perennial herb or shrub with better fruits. Any plant breeding programme needs clear understanding of existing genetic divergence in available population. A knowledge on genetic diversity, its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. Mahalanobis D² techniques appears to be a fruitful approach which is based on multivariate analysis and serves to be a good index of genetic diversity. The present study was planned to generate information on genetic diversity present in twenty four diverse genotypes of brinjal so as to help the breeder in selecting promising and genetically diverse parents for bringing the desired improvement.

MATERIALS AND METHODS

This experiment was carried out at Pandit Jawaharlal Nehru College of Agriculture and Research Institute Karaikal, U.T. of Puducherry, during 2005-2006. The materials for the study consisted of twenty four genotypes of brinjal collected from various SAU's and local areas. The experiment was conducted in randomized block design with two replications. Each plot consisted of five rows with spacing of 60 cm x 60 cm. Five plants were chosen at random from each plot for recording the observations

on twelve economic traits *viz.*, plant height, number of primary branches per plant, days taken to first flowering, fruit length, fruit girth, number of fruits per plant, fruit weight, fruit yield per plant, days taken to first harvest, total number of harvest, ascorbic acid and total phenols. Plot means were subjected to analysis of variance and then multivariate analysis by Mahalanobis D² statistic (Mahalanobis, 1936). On the basis of magnitude of D² values the cultivars were grouped into different clusters following Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance showed highly significant differences among genotypes for all the traits under study. The genotypes were grouped into four clusters based on the D² values (Table 1). Cluster II had the maximum number of fourteen genotypes. The remaining ten genotypes were distributed in three clusters of which, five genotypes were in cluster IV, three genotypes in cluster I and two genotypes in cluster III. The grouping pattern of genotypes was observed to be random indicating that geographical diversity and genetic divergence were unrelated. Further, it was observed that genotypes belonging to the same origin not only appeared in the same cluster but many of them also distributed in different clusters, which may be due to preferential selection of idiotypes suitable for various vegetable purposes. These findings clearly demonstrated that there was no parallelism between the geographic origin and genetic diversity in brinjal as reported by Yadav et al. (1996). Therefore, the selection of genotypes for hybridization should be based