

Genetic divergence in Brinjal (*Solanum melongena* L.)

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SUMMARY

Genetic divergence was studied using Mahalanobis D^2 statistic for fruit yield and fruit characters on fourteen brinjal genotypes. These genotypes were grouped into five different clusters irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. The highest inter cluster distance was observed between cluster I and II followed by cluster III and IV suggesting wide diversity among these groups. Considering cluster mean and the genetic distances the crossing between genotype of cluster I and II with IV were likely to recombine the gene for high fruit yield for tropical conditions like Chhattisgarh.

Key words : Brinjal, Divergence analysis, Cluster analysis.

Brinjal (*Solanum melongena* L.) is one of the most important and widely consumed vegetable crop in India, which can be grown throughout the year. India being the centre of diversity for this crop (Ganabus, 1964) provides a large amount of variation which promise a vast opportunity for its genetic improvement.

A good grasp of the nature and degree of genetic divergence is a prerequisite to choose the right type of parents for a purposeful hybridization programme. This crop having a greater genetic variation with regard to fruit yield and its components. The significance of genetic diversity in selection of parents for hybridization has been well recognized and for crop improvement, diverse parents offer substantial transgressive segregation and obtain heterotic F_1 's. Hence, looking to these facts genetic divergence analysis was worked out in Brinjal genotypes obtained from different parts of the country.

MATERIALS AND METHODS

Fourteen Brinjal genotypes collected from various parts of country were evaluated during 2004-2006 in randomized block design with three replication. Uniform recommended cultural practices were followed. The data on five randomly selected plants from each genotypes were recorded for fruit length (cm.), fruit girth (cm.), fruit weight (g) and fruit yield per plot (q/ha.). Multivariate analysis was done utilizing (Mahalanobis, 1936) D^2 statistics and genotypes were grouped into five different

clusters (Rao, 1952).

RESULTS AND DISCUSSION

Significant variation was found among the fourteen brinjal lines for all the attributes studied and all the genotypes were grouped into five clusters. Composition of different clusters are presented in Table 1. Among these, cluster IV and cluster V consisted of maximum number of genotypes followed by cluster III and I whereas, cluster II had only one genotype. The material under study included brinjal collections from various parts of country and clustering pattern of genotype indicates that geographical isolation has not contributed much to the genetic divergence. The observed genetic divergence, therefore seems to be possible due to differences in genotypes. These findings are in close agreement to earlier reports of (Doshi *et al.*, 1998; Mohanty and Prusti, 2000 and Sharma and Maurya, 2004) in brinjal.

The inter- and intra-cluster distances, which provided index of genetic diversity among and within the cluster,

Table 1: Clustering Pattern of fourteen Brinjal genotypes

Cluster number	Number of genotypes included	Name of genotypes	Place of origin
I	2	IGB-4, Local (c)	Chhattisgarh
II	1	IGB-69	Chhattisgarh
III	3	IGB-22, IGB-49, IGB-75	
IV	4	PB-61, ABR-02-03, JBR-02-11, JBR-03-16	Punjab, Anand (Gujrat), Jabalpur (M.P.)
V	4	PB-60, IGB-74, KS-224(c), DBR-8 (c)	Punjab, Chhattisgarh, Kalyanpur (U.P.), IARI (Delhi)

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