

Genetic divergence in tomato (*Lycopersicon esculentum* Mill.)

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ABSTRACT

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Sixty-seven tomato genotypes of different geographical origin were assessed to know the value and magnitude of genetic divergence using Mahalanobis D^2 statistics. A wide genetic diversity was observed among the genotypes and was grouped into seven clusters. The clustering pattern indicated that the geographic diversity need not necessarily be related to genetic diversity. The maximum inter cluster distance was observed between cluster V and VI ($D^2=243.700$), closely followed by cluster III and V ($D^2=239.740$), cluster IV and V ($D^2=222.521$), cluster IV and VII ($D^2=211.82$), cluster VI and VII ($D^2=209.086$) and cluster V and VII ($D^2=207.860$). The cluster II revealed the least distance relationship with the cluster III ($D^2=86.717$). Therefore, selection of divergent parents based on these cluster distance is recommended for getting good hybrids or segregants in tomato.

Key words : Genetic divergence, D^2 analysis, Clustering pattern and Tomato

Tomato is one of the most popular, widely grown and versatile vegetables grown in the world. Tomato can be consumed either in the form of fresh as salads, after cooking and utilized in the preparation of range of processed products such as puree, paste, ketchup, sauce, soup, pickles, chutney and canned whole fruits. Now a day's cultivation of commercial F_1 hybrids are very common to achieve higher productivity, uniformity and good quality fruits and selection of newer parents for higher heterosis is thus a continuous process. Generally diverse parents are expected to give high hybrid vigour (Harrington, 1940). Mahalanobis D^2 multivariate analysis (Mahalanobis, 1936) is one of the valuable tool for obtaining quantitative estimates of genetic divergence between biological populations. Further grouping of the genotypes based on Tochers method will be more useful in choosing suitable parents for heterosis breeding. Therefore, an attempt was made in the present investigation to examine the nature and magnitude of genetic divergence in tomato genotypes.

MATERIALS AND METHODS

Sixty-seven genotypes collected from different sources were evaluated during 2002-2003 in the Department of Olericulture, Kittur Rani Channamma, College of Horticulture, Arabhavi. The crop was grown in a randomized block design with three replications at spacing of 75 x 60 cm. Five randomly chosen plants in each replication of each genotype were labelled and used for recording the observations. The data were subjected to multivariate analysis. The original mean values were transformed to normalize variables and all possible D^2 values were calculated. The grouping of the genotypes

was done by using Tochers method as described by Rao (1952). The criterion used in clustering by this method is that genotypes belonging to the same cluster should show a smaller D^2 value than those belonging to different clusters.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters under study. After computing D^2 values for all the possible pairs, sixty-seven genotypes were grouped into seven clusters, which indicated a large genetic diversity (Table 1). The cluster I was the largest with 44 genotypes followed by cluster II with 11 cluster IV with 7 and cluster III with 2 genotypes. The clusters V, VI and VII included only one genotype each. Genotypes from different geographical regions were grouped in the same cluster indicating no relationship between geographic distribution and genetic divergence. Present result supported the findings of Dharmatti *et al.* (2001) and Parthasarathy and Aswath (2002). Intra-cluster distance (Table 2) revealed that, cluster IV with 7 numbers of genotypes showed maximum intra-cluster diversity ($D^2=68.998$) followed by cluster I ($D^2=61.060$) with 44 genotypes, cluster II ($D^2=57.351$) with 11 genotypes and cluster III ($D^2=23.327$) with 2 genotypes. The clusters V, VI and VII had no intra-cluster distance ($D^2=0.000$) as they possessed single genotype in each. Based on distance between clusters, *i.e.*, inter-cluster distance, the maximum divergence was observed between cluster V and VI ($D^2=243.700$), closely followed by cluster III and V ($D^2=239.740$), cluster IV and V ($D^2=222.521$), cluster IV and VII ($D^2=211.820$), cluster VI and VII ($D^2=209.086$) and cluster V and VII