GENETIC DIVERGENCE FOR FRUIT CHARACTERS IN TOMATO
(LYCOPERSICON ESCULENTUM MILLER)

Nandan Mehta and B. S. Asati*
Department of Horticulture,
Indira Gandhi Krishi Vishwavidyalaya, Raipur-492006 (CG), India

ABSTRACT

Genetic divergence analysis using Mahalonabis D2 statistic was carried out in twenty two
tomato determinate genotypes. These genotypes were grouped into six clusters based on sixteen
important fruit characteristics. The cluster-I was the largest containing seven genotypes followed by
cluster-III with six genotypes. The diversity among the cultivars was measured by inter-cluster
distance. The higher order of divergence was recorded between cluster II and V which was adequate
for improvement of tomato by hybridization and selection. The genotypes included from the diverse
cluster can be used as promising parents for hybridization, programme to obtain high heterotic
response and thus better segregants in tomato for industrial purpose.

The important vegetable crop tomato
(Lycopersicon esculentum Mill) is rightly known
as industrial crop because of its outstanding
processing qualities. The genetic improvement
of tomato mainly depends upon the amount of
genetic variability present in the population for
different fruit characters. The information on the
nature and degree of genetic divergence for fruit
characters would help in choosing the right parent
for the development of variety with improved
processing quality of tomato, which can be
exploited in the processing industries. Keeping
these in view, the present investigation was carried
out to know the nature and magnitude of
important fruit traits towards genetic diversity in
available tomato genotypes.

The experiment material consisting of
twenty-two genotypes of tomato (Table 1). These
were grown in a randomized complete block
design with four replications at Horticultural Farm
of Indira Gandhi Agricultural University, Raipur
during rabi 2005-06. Each plot consisted of seven
rows of 4.2 meter length and spaced 60 cm and
50 cm row-to-row and plant to plant,
respectively. All the recommended package of
practices were followed to raise the healthy crop.
Data were recorded on ten randomly taken
competitive plants from each plot for the
characters viz., plant height (cm), number of
primary branches, fruit weight (g), fruit volume
(cc), fruit diameter (cm), fruit length (cm), number
of fruits per cluster, pericarp thickness (cm),
number of locules per fruit, specific gravity, juice
percent (%), total soluble solids (%), acidity (%),
ph and fruit yield per plant (kg). Replication wise
data for each character were subjected to analysis
of variances and covariances. Multivariate
analysis was done utilizing Mahalonabis D2
statistic and genotypes were grouped into six
different clusters following Tocher’s methods, as
described by Rao (1952).

The analysis of variances for each
individual character showed highly significant
differences among the genotypes for all the
sixteen characters. Twenty two genotypes were
grouped in to six clusters (Table-1). Cluster I was
the largest and consisted of seven genotypes
followed by cluster III with six genotypes. Cluster
IV and cluster V each had three genotypes where
as, cluster II and VI had two and one genotype,
respectively. The random distribution of genotype
was evident from cluster I having maximum
genotype with different distribution. The grouping
pattern did not show any relationship between
 genetic divergence and geographic diversity,
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Murty and Arunachalam (1966) reported that
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The inter cluster D2 values ranged from
3.65 to 7.01 (Table 2). The minimum inter cluster
TABLE 1. Composition of clusters in tomato.

<table>
<thead>
<tr>
<th>Cluster number</th>
<th>Number of genotypes</th>
<th>Genotypes</th>
<th>Source</th>
</tr>
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<tr>
<td>I</td>
<td>7</td>
<td>VLT-13</td>
<td>VPKAS, Almora</td>
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<td></td>
<td></td>
<td>VLT-20</td>
<td>VPKAS, Almora</td>
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<td></td>
<td></td>
<td>DT-39</td>
<td>IARI, New Delhi</td>
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<td></td>
<td></td>
<td>DVRT-1</td>
<td>IIVR, Varanasi</td>
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<tr>
<td></td>
<td></td>
<td>CHRT-4</td>
<td>BAU, Ranchi</td>
</tr>
<tr>
<td>I</td>
<td>2</td>
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<tr>
<td></td>
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<td>NDT-74</td>
<td>NDUAT, Faizabad</td>
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<tr>
<td>I</td>
<td>6</td>
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<td>GNU, S.K. Nagar, Anand</td>
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<tr>
<td></td>
<td></td>
<td>ATL-16</td>
<td>GNU, S.K. Nagar, Anand</td>
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<td>CHRT-1</td>
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<tr>
<td></td>
<td></td>
<td>NDT-4</td>
<td>NDUAT, Paizabad</td>
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<tr>
<td>IV</td>
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<td>NDT-3</td>
<td>NDUAT, Paizabad</td>
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<td>IIVR, Varanasi</td>
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<td>SEL-7</td>
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<tr>
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</table>

D² value (3.65) was observed between cluster I and III indicating the close relationship among the genotypes. Maximum inter cluster value was observed between cluster II and V (7.01), which indicated that the genotypes included in these cluster had maximum divergence. Hence, intermating between genotypes included in these cluster may give high heterotic response and thus better segregants. There was a wide range of variation in the mean values for most of the fruit characters under study. The maximum and minimum values for characters fruit weight (g) 97.50 (II) and 38.06 (V); number of flowers per cluster 6.13 (III) and 4.65 (II); number of primary branches 7.20 (II) and 4.93 (V) respectively were observed. This indicated that while planning hybridization genotypes from diverse clusters II and V should be included as parents for desirable fruit characters to get heterotic hybrids that would be exploited in processing industries and getting better segregants for these fruit traits in tomato. These findings are in accordance with the findings of Peter and Rai (1976) and Godekar et al. (1992) in tomato.

REFERENCES