MATERIALS
AND
METHODS
3. MATERIAL AND METHODS

3.1 MATERIALS AND EXPERIMENT LAYOUT

Thirty seven genotypes of toria obtained from Indian Agriculture Research Institute, New Delhi, were used in the present investigation.

List of Genotypes used in Present Investigation

1. DT-1 20. IT-483
2. IT-479 21. IT-461
3. WB-132 22. T-9
4. WB-158 23. IT-463
5. IT-452 24. TWC-2
6. IT 462 25. IT-450
7. IT-455 26. IT-464
8. WB-138 27. TLK-15
9. WB-300 28. WB-172
10. IT-477 29. IT-456
11. IT-480 30. BHAWANI
12. IT-478 31. WB-127
13. IT-481 32. DT-3
14. TLK-115 33. DT-6
15. WB-116 34. IT-454
16. WB-176 35. IT-38
17. IT-484 36. M-27
18. WB—153 37. TS-29
19. PT-30

The experiment was conducted in two different years i.e. 1991-92 and 1992-93. During 1991-92 the experiment was conducted at one location with four micro-environments and during 1992-93 at two locations with four micro-environments at each location. Thus a total of twelve micro-environments were created
by using different doses of fertilizer and spacing at each location.

The details of these environments are given below:

<table>
<thead>
<tr>
<th>Year</th>
<th>Location</th>
<th>Fertilizer Level (Kg/Ha) N</th>
<th>P</th>
<th>K</th>
<th>Spacing (cm)</th>
<th>Environments</th>
</tr>
</thead>
<tbody>
<tr>
<td>1991-92</td>
<td>K.P.G. College</td>
<td>100</td>
<td>50</td>
<td>50</td>
<td>40x20</td>
<td>I</td>
</tr>
<tr>
<td></td>
<td>Simbhaoli</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>40x20</td>
<td>II</td>
</tr>
<tr>
<td></td>
<td></td>
<td>100</td>
<td>50</td>
<td>50</td>
<td>20x10</td>
<td>III</td>
</tr>
<tr>
<td></td>
<td></td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>20x10</td>
<td>IV</td>
</tr>
<tr>
<td>1992-93</td>
<td>K.P.G. College</td>
<td>100</td>
<td>50</td>
<td>50</td>
<td>40x20</td>
<td>V</td>
</tr>
<tr>
<td></td>
<td>Simbhaoli</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>20x10</td>
<td>VI</td>
</tr>
<tr>
<td></td>
<td></td>
<td>100</td>
<td>50</td>
<td>50</td>
<td>40x20</td>
<td>VII</td>
</tr>
<tr>
<td></td>
<td></td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>20x10</td>
<td>VIII</td>
</tr>
<tr>
<td>1992-93</td>
<td>G.B.P.U.A. &amp; T</td>
<td>100</td>
<td>50</td>
<td>50</td>
<td>40x20</td>
<td>IX</td>
</tr>
<tr>
<td></td>
<td>Panthagar</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>20x10</td>
<td>X</td>
</tr>
<tr>
<td></td>
<td>(Nainital)</td>
<td>100</td>
<td>50</td>
<td>50</td>
<td>40x20</td>
<td>XI</td>
</tr>
<tr>
<td></td>
<td></td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>20x10</td>
<td>XI</td>
</tr>
</tbody>
</table>

3.2 RECORDING OF DATA

The experiment was laid out in a randomized block design consisting of three replications in each environment. Data were recorded for the following characters by selecting five competitive plants for each genotype per treatment per replication.

(i) Days to Flowering

Days to flowering were recorded when 75% of the population represented in each line showed blooming condition.
(ii) **Days to Maturity:**

Days to maturity were recorded when 75% of the population matured.

(iii) **Plant Height (cm):**

Plant height was measured from soil surface to the top of plants at maturity.

(iv) **Number of Primary Branches per Plant:**

Number of primary branches per plant was recorded as branches arising from main shoot.

(v) **Number of Secondary Branches:**

Number of secondary branches was recorded as number of branches arising from primary branches.

(vi) **Siliqua per Plant:**

Number of siliqua per plant was recorded at maturity.

(vii) **Seeds per Siliqua:**

Number of seeds per siliqua was counted from five siliquae randomly selected for each genotype.

(viii) **Length of Siliqua (cm):**

Length of siliqua was measured using five siliquae taken at maturity.

(ix) **1000-Seed Weight (g):**

1000-seed weight was recorded by weighing 1000-seeds for each genotype.
(x) **Seed Yield per Plant (g):**

Seed yield per plant was recorded by using seed yield of five randomly selected plants.

(xi) **Total Biological Yield (g):**

Total biological yield was measured in (g) by taking weight of whole plant including stem, leaves and seeds.

(xii) **Harvest Index:**

Harvest index was calculated for each genotype using the formula—

\[
\frac{\text{Seed yield per plant}}{\text{Biological yield per plant}} \times 100
\]

3.3 **STATISTICAL ANALYSIS**

The analysis of variance was done on the basis of mean of the observations per replication and the following parameters were worked out:

3.3.1 **Variability, Heritability and Genetic Advance**

Means for all the characters were subjected for analysis of variance and covariance as given by Panse and Sukhatme (1967). The genetic parameters were calculated as:

\[
\hat{h}_q^2 = \frac{\text{MS}_g - \text{MS}_e}{r}
\]

Where,

\[
\text{MS}_e = \text{Mean squares due to treatment}
\]
\[ MS_e = \text{Mean squares due to error} \]

\[ r = \text{Number of replications} \]

And,

\[ \hat{\sigma}^2 = \hat{\sigma}^2_a + \hat{\sigma}^2_p + \hat{\sigma}^2_e \]

Where,

\[ \hat{\sigma}^2_a = \text{estimates of phenotypic variance} \]

\[ \hat{\sigma}^2_p = \text{estimates of genotypic variance} \]

And, \[ \hat{\sigma}^2_e = \text{estimates of error variance} \]

Phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were calculated using the formula as suggested by Burton (1952).

\[ PCV = \frac{\sqrt{\hat{\sigma}^2}}{X} \times 100 \]

\[ GCV = \frac{\sqrt{\hat{\sigma}^2}}{X} \times 100 \]

Where,

\[ X = \text{is the mean of the character.} \]

Heritability \( h^2 \) in broad sense was calculated according to Burton (1952).

\[ h^2 = \frac{\hat{\sigma}^2_p}{\hat{\sigma}^2_e} \]
The customary symbol $h^2$ stands for the heritability itself and not for its square. The symbol derives from Wright's (1921) terminology, where $h^2$ stands for the corresponding ratio of standard deviation; Falconer (1981).

The expected genetic advance at 5% intensity of selection differential was calculated for each character following the formula suggested by Johnson et al. (1955),

$$G.A. = K \hat{h}$$

Where,

$K =$ constant i.e. value of selection intensity e.g. 2.06 at 5% selection intensity (Lush, 1949).

3.3.2 Character Association Analysis

The genotypic phenotypic correlation coefficients were estimated following Al-Jibouri et al. (1958) as given below:

$$\text{Genotypic correlation coefficient (rg)} = \frac{\text{CoV}_{(g)i}.X.Y}{\sqrt{\text{Var}_{(g)i}.X.\text{Var}_{(g)i}.Y}}$$

Where,

$\text{CoV}_{(g)i}.X.Y.$ = genotypic covariance of $X$ and $Y$ character
$\text{Var}_{(g)i}.X$ and $\text{Var}_{(g)i}.Y.$ = Genotypic variance of $X$ and $Y$ characters respectively.

$$\text{Phenotypic correlation coefficient (rf)} = \frac{\text{Cov}_{(f)i}.X.Y}{\sqrt{\text{Var}_{(f)i}.X.\text{Var}_{(f)i}.Y}}$$

Where.
Cov_{xy} = Phenotypic covariance of X and Y character
Var_{x} X and Var_{y} Y = Genotypic variance of X and Y characters respectively. The significance of correlation coefficients were
however, tested against r value from r table of Fisher and Yates
(1949) for (n-2) degrees of freedom at P=0.05 and P=0.01 levels of
significance, respectively.

3.3.3 Path Coefficient Analysis

The path coefficient analysis was done following Wright
(1921). The path coefficient was calculated by solving the following
set of simultaneous equations abbreviated by Doolittle technique
as described by Goulden (1959).

\[ P_{y1} + P_{y2}r_{12} + \ldots + P_{yp}r_{1p} = r_{y1} \]
\[ P_{y1}r_{12} + P_{y2}r_{13} + \ldots + P_{yp}r_{2p} = r_{y2} \]
\[ P_{y1}r_{1n} + P_{y2}r_{2n} + \ldots + P_{yn} = r_{yn} \]

Where,

\[ P_{y1}, P_{y2}, \ldots, P_{yn} \] are the direct path effects of 1, 2, \ldots, \( n \) variables.

Where,

\[ X_{ij} \] and \( X_{i} \) are the performance of \( i^{th} \) and \( i^{th} \) genotypes, respectively in the \( j^{th} \) environment; \( X_{i} \) and \( X_{i} \) are the mean of the \( i^{th} \) and \( i^{th} \) genotypes, respectively, over environments. \( S_{i} \) and \( S_{i} \) are the standard deviation of the \( i^{th} \) and \( i^{th} \) genotypes, respectively, over environments.
Group constellations were formed following Tcher's method (Rao, 1952). The criterion of grouping was that any two populations belonging to the same cluster should at least on the average show smaller $d^2_s$ (A) ii than those belonging to different clusters. One can possibly start with two close associated treatments with repeat to the response to environmental variation and find a third treatment that has the smallest average $d^2_s$ (A) ii from the first two. Similarly the fourth was chosen to have the smallest $d^2_s$ (A) ii from the first three and so on.

On an average $d^2_s$ (A) ii shows smaller values than those belonging to different clusters. One can possibly start with $r_{12}, r_{13}, r_{14}-----r_{1n-1}$ are the possible correlation coefficients between various independent variables and $r_{y1}, r_{y2}-------r_{yn}$ are the correlations of independent variables with the dependent variable.

The indirect effect of $i^{th}$ variable via $j^{th}$ variable was worked out as $P_{xy} \times r_{ij}$ the residual effect was also calculated as under:

$$P_{vw} - 1 - (P_{x1}^2 + 2P_{x1}P_{x2}r_{12} + 2P_{x1}P_{y2}r_{13} + \cdots P_{xj}^2 + 2P_{xj}P_{yj}r_{j2} + \cdots P_{xn}^2)$$

Residual effect $= \sqrt{P_{vw}}$

3.3.4 $D^2$ Analysis

Standardised distance was estimated and utilised for clustering of genotypes as suggested by Singh (1988). Standardized distance ($d^2_s$ (A) ii) as suggested by Fox and
Rosielle (1963) was employed to determine the degree of divergence of genetic response among pairs of genotypes as described below:

$$\text{Standardized distance} = \sum_{i=1}^{n} \left[ \frac{X_{ij} - X_{i.}}{S_{i.}} - \frac{X_{i.} - \bar{X}}{S_{i.}} \right]^2.$$  

Two close associated treatments with repeat to their response to environmental variation and find a third treatment that has smallest average $d_{ij}^2$ (A) ii from the first two. Similarly the fourth was chosen to have the smallest average $d_{ij}^2$ (A) ii from the first three or so.

3.3.5 Stability Analysis

Eberhart and Russell (1966) gave the following model for estimating the phenotypic stability:

$$y_{ij} = \mu + \beta_i \cdot t_i + \sigma_i^2 \quad (i = 1, 2, \ldots, t \text{ and } j = 1, 2, \ldots, s)$$

Where,

- $y_{ij}$: Performance of $i^{th}$ variety in $j^{th}$ environments
- $\mu$: Mean of all the varieties over all environments
- $\beta$: The regression coefficient of the $i^{th}$ variety one the environmental index which measure the response of this variety to varying environments.
- $I$ : the environmental index which is defined as the deviation of the mean of all the varieties at a given location from the overall mean.
And \( \sigma_i^2 \) = the deviation from regression of the \( i^{th} \) variety at \( j^{th} \) environment.

\[
\sigma_i^2 = \frac{\sum y_i \cdot t}{\sum y_i \cdot t s - \left( \sum y_i \right)^2 / \sum t}
\]

The two parameters of stability (\( b_i \) and \( S_i^2 \)) used in this model were computed as below:

(i) Regression coefficient (\( b_i \)) = \[
\frac{\sum y_i}{\sum t}
\]

Where,

\( \sum y_i \) is the sum of the product and

\( \sum t \) is the sum of squares (environment Index)

(ii) Mean deviation from regression (\( S_i^2 \))

\[
S_i^2 = \frac{\sum \sigma_i^2}{s^2}
\]

Where,

\[
\sum \sigma_i^2 = \left( \sum y_i \right)^2 / t - \left( \sum y_i \right)^2 / \sum t
\]

And, \( S^2 e / r \) = estimate of pooled error

\( S^2 e \) = error mean square

\( r \) = number of replications

The detailed analysis of variance for the estimation of stability parameters are given below in Table-2.
<table>
<thead>
<tr>
<th>Source of variance</th>
<th>D.F.</th>
<th>S.S.</th>
<th>M.S.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Varieties (v)</td>
<td>V</td>
<td>[\frac{1}{n} \sum_{i=1}^{n} y_i^2 - \text{C.F.}]</td>
<td>MS_1</td>
</tr>
<tr>
<td>Environments (E)</td>
<td>(V-1)(n-1)</td>
<td>[V(n-1) \sum_{i=1}^{n} y_{ij}^2 / n]</td>
<td>MS_2</td>
</tr>
<tr>
<td>V x E (linear)</td>
<td>(V-1)</td>
<td>[1 / \sqrt{\frac{\sum y_i^2}{\sum I_i^2}}]</td>
<td>MS_3</td>
</tr>
<tr>
<td>V x E (linear)</td>
<td>(V-1)</td>
<td>[\frac{\sum y_i^2}{\sum I_i^2} / \sum I_i^2]</td>
<td>SS = Environment (linear)</td>
</tr>
<tr>
<td>Pooled deviation</td>
<td>V(n-2)</td>
<td>[\sum_{i=1}^{n} \sum_{j=1}^{v} y_{ij}^2 - \frac{(\sum y_i^2)^2}{n}]</td>
<td>MS_5</td>
</tr>
<tr>
<td>Variety (i)</td>
<td>(n-2)</td>
<td>[\frac{\sum y_i^2 - \frac{y_{ii}^2}{n}}{n} \frac{\left(\sum y_i^2\right)^2}{\sum I_i^2}]</td>
<td></td>
</tr>
<tr>
<td>Variety (v)</td>
<td>(n-2)</td>
<td>[\frac{\sum y_{ij}^2 - \frac{y_{ii}^2}{n}}{n} \frac{\left(\sum y_i^2\right)^2}{\sum I_i^2}]</td>
<td>[\sum \sum_{i=1}^{v} \sigma_i^2]</td>
</tr>
<tr>
<td>Pooled error</td>
<td>(n-1)(V-1)</td>
<td>[\sum_{i=1}^{v} \sum_{j=1}^{n} y_{ij}^2 / n]</td>
<td>MS_6</td>
</tr>
<tr>
<td>Total</td>
<td>(n-1)(V-1)</td>
<td>[\sum_{i=1}^{n} \sum_{j=1}^{v} y_{ij}^2 / n]</td>
<td>C.F.</td>
</tr>
</tbody>
</table>

Where,

\[V = \text{number of variety, } n = \text{number of environments and}\]

\[\sum \sigma_i^2 = \sum \left(\sum y_{ij}^2 - \frac{y_{ii}^2}{n}\right) \frac{\left(\sum y_i^2\right)^2}{\sum I_i^2}\]

\[\sum y_{ij}^2 - \frac{y_{ii}^2}{n} = \text{Variance due to dependent variable and}\]
\[(\sum y_{ij})^2 / \sum l_j^2 = \text{Variance due to regression}\]

The test of significance of different stability parameters are given below:

(i) The significance of difference among variety means was tested using the F test,
    \[F \approx \frac{\text{M.S.}_1}{\text{M.S.}_4}\]

(ii) Variety x environment interaction was tested using the F test,
    \[F \approx \frac{\text{M.S.}_2}{\text{M.S.}_5}\]

(iii) The genetic difference among varieties for their regression the environmental index was tested using the F test,
    \[F \approx \frac{\text{M.S.}_2}{\text{M.S.}_4}\]

(iv) Deviation from regression for each variety was tested using the F test,
    \[F \approx \frac{(\sum \sigma_i^2 / n - 2)}{\text{M.S.}_5}\]
RESULTS