Chapter-III

MATERIAL AND METHOD
MATERIAL AND METHODS

Materials:

The foundation materials of present investigation comprising of 10 parents of linseed (*Linum usitatissimum* L.) including Neelum, Shubhra, Sweta, LMH-62, DPL-21, J-23, RLC-6, Garima, KL-43 and LCK-88062 was taken from genetic stock maintained at All India Co-ordinated Research Project Centre, Mauranipur. The distinguishing features of these parents along with their parentage are given in table-1.

Methods:

(a) Experimental plan:

A set of 45 F₁ hybrids with reciprocal s were made during Rabi 1996-97 by using diallel cross techniques. In the year 1997-98 F₂ generation was raised and half of F₁ seed was kept reserved to conduct the trial.

Experiment consisting of 10 parents, each 45 F₁s and F₂s were grown during Rabi 1998-99 in a Randomized Complete Block Design with three replications at three different locations viz, Rath, Jabalpur and Kanpur. The sowing of the experiment was done on November 5, 1998 at Dairy Farm- B.N.P.G. college, Rath, November 6, 1998 at Crop Research Farm- Oil Seeds, Kanpur and November 8, 1998 at crop Research farm J.N.K.V.V, Jabalpur. The plot for non-segregating generations (parents and F₁s) and for segregating generations (F₂s) represented single row. Non-experimental rows were also planted to reduce the border effects. Rows were planted in 3m. of length spaced at 45 cm.
apart. Within the rows, seeds were sown at 10 cm apart in hill at each location. All the experiments were given equal dose of fertilizer @ 90 kg N₂, 30 Kg P₂O₅, 30 Kg K₂O per hectare at each location to raise a very good crop.

**OBSERVATIONS RECORDED:**

Data were recorded on 10 randomly selected plants in parents and F₁s and 20 in F₂s for following characters:

1. **Days to 50 per cent flowering:**

   The number of days for 50 percent of flowering was counted from the date of sowing in each parents/cross in each replication.

2. **Days to maturity:**

   Total number of days for physiological maturity was counted from the date of sowing.

3. **Plant height:**

   It was measured in centimeters from the ground level to the terminal shoot of the plant after maturity with the help of meter scale.

4. **Technical plant height (cm.):**

   It was measured in cm. from the base to the point from where branching starts.

5. **Number of tillers per plant:**

   Total number of tillers bearing capsules were counted to the base of the plant when it was to be matured.
6. **Number of branches per plant:**

   Total number of productive branches were counted before harvesting in sampled plants at the time of maturity.

7. **Number of capsules per plant:**

   Total number of capsules bearing seeds were counted in selected plants at the time of maturity and mean number were calculated as per plant.

8. **Number of seeds per capsule:**

   Seeds of ten randomly selected capsules were counted and average number were estimated.

9. **1000-seed weight:**

   Exact 1000-random seeds of each parents and crosses were counted from each replication and weighed in gram upto two decimal points with the help of electronic balance.

10. **Harvest Index:**

    The ratio of economic yield to the biological yield gives harvest index and the value is expressed in percentage (Donald, 1962), seed yield was divided by biological yield of plants and after multiplying by 100 it was measured as.

    \[ HI \% = \frac{\text{Seed yield (economic yield)}}{\text{Biological yield}} \times 100 \]

11. **Fibre yield per plant (g.)**:

    Single plant was harvested from ground level, threshed and the stalk was cut from first branching Bundles were prepared by tying 10 plants together and placed in retting
tank filled with water and left for 3 days Bundles were washed 8-10 times and then sun dried Each plant from the bundle was separated and beaten by Mugari on plain surface Wooden part of the stalk was discarded and the fibre was separated

12. Oil content %:

It was measured in percent with the help of Nuclear Magnetic Resonance (NMR) instrument as per methods suggested by Tiwari et al. (1974)

13. Seed yield per plant:

The seeds of each selected plants were bulked and weighed with the help of electronic balance in gram upto two decimal points then average weight were calculated

Statistical and Biometrical analysis:

The experimental data were computed by taking mean of each treatment in all the three replications location-wise and finally it was subjected to the following statistical and biometrical analysis

Analysis of variance:

The analysis of variance for the experiment was based on the model

\[ P_{ijk} = u + v_i + r_k + e_{ijk} \quad (i = 1, \ldots, t, \quad k = 1, \ldots, r) \]

Where,

- \( P_{ijk} \) = the phenotypes \( ijk^{th} \) observation
- \( u \) = the population mean
- \( v_i \) = the effect of \( i^{th} \) variety on \( j^{th} \) progeny
- \( r_k \) = the effect of \( k^{th} \) replication
- \( e_{ijk} \) = the error for \( e_{ijk}^{th} \) observations
Based on present model, the data obtained from 10 parents, diallel mating were first of all subjected location-wise for analysis to randomized complete block design analysis on the mean basis. The skeleton ANOVA is given as under:

**Skeleton of ANOVA for parents and F₁s**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>M.S.</th>
<th>F test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>(r-1)</td>
<td>Mr</td>
<td>$\text{Mr}/\text{Me}_2$ for r-1,(r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>Treatments</td>
<td>(t-1)</td>
<td>Mt</td>
<td>$\text{Mt}/\text{Me}_2$ for t-1, (r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>Parents (P)</td>
<td>(p-1)</td>
<td>Mp</td>
<td>$\text{Mp}/\text{Me}_2$ for p-1, (r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>F₁s</td>
<td>(F₁-1)</td>
<td>Mf₁</td>
<td>$\text{MF}_1/\text{Me}_2$ for F₁-1,(r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>Parents vs F₁s</td>
<td>1</td>
<td>Mh</td>
<td>$\text{Mh}/\text{Me}_2$ for 1, (r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (t-1)</td>
<td>Me₂</td>
<td></td>
</tr>
</tbody>
</table>

**Skeleton of ANOVA for parents and F₂s**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>M.S.</th>
<th>'F' test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>(r-1)</td>
<td>Mr</td>
<td>$\text{Mr}/\text{Me}_2$ for 1, (r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>Parents</td>
<td>(p-1)</td>
<td>Mp</td>
<td>$\text{Mp}/\text{Me}_2$ for p-1, (r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>F₂s</td>
<td>(F₂-1)</td>
<td>Mf₂</td>
<td>$\text{Mf}_2/\text{Me}_2$ for F₂-1,(r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>Parents Vs F₂</td>
<td>1</td>
<td>Mh</td>
<td>$\text{Mh}/\text{Me}_2$ for 1, (r-1) (t-1) d.f.</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (t-1)</td>
<td>Me₂</td>
<td></td>
</tr>
</tbody>
</table>
Skeleton of pooled ANOVA:

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>d.f.</th>
<th>S.S.</th>
<th>M.S.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotypes</td>
<td>(v-1)</td>
<td>((1/nr) \sum y^2, -(y^2/vrn))</td>
<td>(M_1)</td>
</tr>
<tr>
<td>Locations</td>
<td>(n-1)</td>
<td>((1-vr) \sum y^2_j - (y^2/vrn))</td>
<td>(M_2)</td>
</tr>
<tr>
<td>Replication within location</td>
<td>n(n-1)</td>
<td>(\Sigma [1/v \sum (y^2_j, k-y^j/vr)])</td>
<td>(M_3)</td>
</tr>
<tr>
<td>Genotypes \times locations</td>
<td>(v-1)</td>
<td>((1/r) \sum y^2_{yk} - y^2/\text{vn})</td>
<td>(M_4)</td>
</tr>
<tr>
<td>Error</td>
<td>n(n-1)(v-1)</td>
<td>Pooled over environments</td>
<td>(M_5)</td>
</tr>
</tbody>
</table>

Where,

\(v, n\) and \(r\) stand for the number of genotypes, environments and replications, respectively.

Diallel Analysis:

Testing the validity of the hypothesis:

To test the validity of the hypothesis i.e., the assumptions regarding the diallel analysis as proposed by Hayman (1954), like (i) diploid segregation (ii) no maternal effect (iii) no linkage (iv) no multiple allelism (v) independent action of non-allelic genes and (vi) homozygosity of parents, the \(t^2\) test was applied as suggested by Hayman (1954 a):

\[
t^2 = \frac{(n-2)/4}{\frac{\text{var} (\text{Vr-var Wr})^2}{\text{Var Vr} \times \text{Var Wr}} - (\text{Cov}^2 \text{Vr,Wr})}
\]

which is an F test with 4 and \((n-2)\) degree of freedom.

A significant value of \(t^2\) would indicate the non-uniformity of Wr, Vr, and thus, invalidates the hypothesis.
postulated. The failure of hypothesis is also indicated by non-significant regression co-efficient.

\[
b = \frac{\text{Cov}(W_r,V_r)}{\text{Var } V_r}
\]

Where, \(\text{Cov}(W_r,V_r) = \frac{\{\sum V_r W_r - \sum V_r \sum W_r\}/n - 1}{N}\)

and \(\text{Var } V_r = \frac{\{\sum V_r^2 - (\sum V_r)^2/n\}/n - 1}{n - 1}\)

The standard error of regression coefficient (b) was calculated as

\[
\text{SE} (b) = \frac{\text{Var } W_r - b \text{ Cov } W_r V_r}{\text{Var } V_r (n-2)^{\frac{1}{2}}}
\]

Where, \(n = \text{number of parents}\)

Now the significance of difference of ‘b’ from zero and unity was tested by using ‘t’ value of b/o \(\text{SE} (b)\) and \((1-b)/\text{SE} (b)\) with \((n-2)\) degree of freedom.

1. Variance components analysis:

The components of variance in diallel cross were computed by the equation as given by Hayman (1954 a).

**Expectation for F₁ diallel are**:

\[
\begin{align*}
V_p &= \hat{D} + \hat{E} \\
V_r &= (\frac{1}{4}) \hat{D} + (\frac{1}{4}) \hat{H}_1 - (\frac{1}{4}) \hat{F} - (\frac{n+1}{2n}) \hat{E} \\
W_r &= (\frac{1}{2}) \hat{D} - (\frac{1}{4}) \hat{F} + (\frac{1}{2} n) \hat{E} \\
V_m &= (\frac{1}{4}) \hat{D} + (\frac{1}{4}) \hat{H}_1 - (\frac{1}{4}) \hat{H}_2 - (\frac{1}{4}) \hat{F} + (\frac{1}{2} n) \hat{E}
\end{align*}
\]
Expectations for $F_2$ diallel are -

Jinks (1956) and Hayman (1958) gave the expectations for $F_2$ diallel crosses. The expected statistics for $F$ generation are the same as that of $F_1$, except that the contributing of $h^2$, is halved by one generation of inbreeding. Hence, the coefficient of $H_1$ and $H_2$ are half of those of $F$ statistics, while the coefficient of $F$ is halved being second an first degree statistics of $h^2$, receptively (Jinks, 1956; Haymar 1958, Mather and Jinks 1971). These expectations are as follows

\[
\begin{align*}
V_p &= \hat{D} + \hat{E} \\
V_r &= (1/4) \hat{D} + (1/16) \hat{H}_1 - (1/8) \hat{F} + \{(n+1)/2n\}\hat{E} \\
W_r &= (1/2) \hat{D} - (1/8) \hat{F} + (1/n) \hat{E} \\
V_m &= (1/4) \hat{D} + (1/16) \hat{H}_1 - (1/16) \hat{H}_2 - (1/8) \hat{F} \\
& \quad (1/2n)\hat{E}
\end{align*}
\]

Where,

\[
\begin{align*}
\hat{D} &= \text{components of variation due to additive effect of genes} \\
&= V_0 L_0 - \hat{E} \\
\hat{H}_1 &= \text{Components of variation due to dominant effects of genes} \\
&= V_0 L_0 - W_0 L_0 -(3n-2) \hat{E}/n \\
\hat{H}_2 &= \hat{H}_1 \left\{1-(u-v)^2 \right\} - 4 V_1 L_1 - 4 V_o L_o - 2\hat{E}
\end{align*}
\]
Where,

\[ u = \text{proportion of positive genes in the parents} \]

\[ v = \text{proportion of negative genes in the parents} \]

\[ F = \text{mean of Fr over arrays} \]

\[ F_1 = 2 (V_0 L_0 - W_0 L_0 + V_1 L_1 W_1 - V_1 L_1 V_1 W_1) - 2 (n-2) E / n \]

\[ \hat{h}^2 = \text{dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses)} \]

\[ = 4 (M_{LI} - M_{LO})^2 - 4 (n-1) E / n^2 \]

\[ \hat{E} = \text{the expected environmental component of variation} \]

\[ = (\text{Error SS} + \text{Replication SS} / d.f.) / \text{number of replication} \]

In order to estimate the accuracy of the components (\( \hat{D}, \hat{F}, \hat{H}_1, \hat{H}_2, \hat{h}^2 \) and \( \hat{E} \)) of variance, the term of main diagonal of the matrix given by Hayman (1954) with common multipliers \( s^2/n^5 \) was used.

Where,

\[ S^2, = \frac{1}{2} \text{Var, (wr-vr). The formula being:} \]

\[ \text{SE} (\hat{D}) = \pm\{ S^2 (n^5 + n^4) / n^5 \}^{0.5} \]

\[ \text{SE} (\hat{F}) = \pm\{ S^2 (4n^5 + 20n^4 - 16n^3 + 16n^2) / n^5 \}^{0.5} \]

\[ \text{SE} (\hat{H}_1) = \pm\{ S^2 (n^5 + 41n^4 - 12n^3 + 4n^2) / n^5 \}^{0.5} \]

\[ \text{SE}(\hat{H}_2) = \pm\{ S^2 (36n^4) / n^5 \}^{0.5} \]
\[ SE (\hat{h}^2) = \pm \sqrt{\frac{S^2 (16n^4 + 16n^2 - 32n + 16)}{n^5}} \]
\[ SE (\hat{\mu}) = \pm \sqrt{\frac{S^2 (n^4 / n^5)}{n^5}} \]

After testing the significance of the components of variation, the mean degree of dominance was calculated as \((\hat{H}_1 / \hat{D})^{0.5}\) in \(F_1\) and \((0.25 (\hat{H}_1 / \hat{D}))^{0.5}\) in \(F_2\) generation. The proportion of genes with positive and negative effects were calculated as \(\hat{h}_2 / 4\hat{H}_1\), the proportion of dominant and recessive genes in parents as \(\frac{(4\hat{D}\hat{H}_1)^{0.5} + \hat{\mu}}{[(4\hat{D}\hat{H}_1)^{0.05} - \hat{\mu}] / [0.25 (4\hat{D}\hat{H}_1)^{0.5} - 0.5\hat{\mu}]}\) in \(F_1\) and \(0.25 (4\hat{D}\hat{H}_1)^{0.5} - 0.5\hat{\mu}\) in \(F_2\) generation, the number of gene groups which control the character and exhibit dominance as \(\hat{h}_2 / \hat{H}_2\), and coefficient of correlation between the parental order of dominance \((W_r + V_r)\) and parental measurement \((Y_r)\) as \(r\).

**Combining ability analysis:**

The combining ability analysis was worked out by the procedure suggested by Griffing’s (1956 b) Method 2, Model I. The mathematical model for combining ability analysis is assumed to be

\[ X_{ijkl} = u + g_i + g_j + S_{ij} + 1/bc e_{ijkl} \]

\[ i, j = 1, 2, 3, \ldots, n, \]

\[ k = 1, 2, 3, \ldots, b, \]

\[ l = 1, 2, 3, \ldots, c, \]

Where, \(u\) = population mean

\(g_i\) = general combining ability (gca) of \(i^{th}\) parent.

\(g_j\) = gca of \(j^{th}\) parent.
\[ S_{ij} = \text{specific combining ability of the cross between } i^{th} \]
\[ J^{th} \text{ parent such that } S_{ij} = S_{ji} \]

\[ E_{ijk} = \text{environmental effect associated with the } ijk^{th} \]
\[ \text{individual observation of } i^{th} \text{ individual in } k^{th} \text{ block with } i^{th} \text{ as } \]
\[ \text{female parent and } j^{th} \text{ as male parent} \]

The usual restrictions, such as \( g_{i} = 0 \) and \( s_{j} = 0 \), (for each \( i \)) are imposed.

The analysis of variance table for combining ability is as follows

**ANOVA for combining ability:**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.F.</th>
<th>S.S</th>
<th>M.S.</th>
<th>‘F’ test</th>
</tr>
</thead>
<tbody>
<tr>
<td>GCA</td>
<td>( n-1 )</td>
<td>( S_{g} )</td>
<td>( M_{g} )</td>
<td>( M_{g}/M_{e}, \text{for } n-1, \text{ m.d.F.} )</td>
</tr>
<tr>
<td>SCA</td>
<td>( n(n-1)/2 )</td>
<td>( S_{s} )</td>
<td>( M_{s} )</td>
<td>( M_{s}/M_{e}, \text{for } n(n-1)/2, \text{ m.d.f.} )</td>
</tr>
<tr>
<td>Error</td>
<td>( m )</td>
<td>( M_{e} )</td>
<td>( M_{e} )</td>
<td></td>
</tr>
</tbody>
</table>

Where,

\[ S_{g} = 1/n + 2 \left\{ \frac{1}{n} \sum (x_{1} + x_{2})^2 - (4/n) \right\} x^2. \]

\[ S_{p} = \frac{1}{n} \sum x_{i}^2 - 1/n+2 \sum (x_{1} + x_{2})^2 + \left\{ \frac{2}{(n+1) (n+2)} \right\} x^2 \]

\[ M_{e} = \frac{M_{e}}{r} \]
Where

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

\[ M_{c'} = \text{Error M.S obtained from main ANOVA} \]

\[ S_g = \text{sum of squares (S S) due to g.c.a.} \]

\[ S_s = \text{sum of squares due to s.c.a.} \]

\[ n = \text{number of parents.} \]

\[ x_i = \text{total of the array involving } i^{\text{th}} \text{ as a female} \]

\[ x = \text{grand total} \]

\[ x_{ii} = \text{value of } i^{\text{th}} \text{ parent of the array} \]

\[ x_{ij} = \text{value of the cross, with } i^{\text{th}} \text{ as a female parent and } j^{\text{th}} \text{ as a male parent} \]

The component of variances were estimated (Singh, 1979) as under:

\[ \text{gca expected m.s} = \hat{\sigma}^2 + \frac{1}{(n-1)} \sum \hat{g}_i^2 \text{ or } \sigma^2 \text{ gca} = \frac{(Mg-Me)}{n+2} \]

\[ \text{sca expected m.s} = \hat{\sigma}^2 + \frac{2}{n(n-1)} \hat{g}_j^2 \text{ or } \sigma^2 \text{ sca} = \frac{(Ms-Me)}{n+2} \]

where,

\[ Mg = Mss \text{ gca, Ms = Mss sca and Me = Mss error obtained from combining ability analysis and } n = \text{number of parents.} \]

The general predictability ratio (GPR) was computed as:

\[ \text{GPR} = \frac{2\hat{\sigma}^2 \text{ gca} \cdot 2\hat{\sigma}^2 \text{ gca} + \hat{\sigma}^2 \text{ sca}}{} \]
Estimates of various effects:

The various effects were estimated as follows.

\[
gca \text{ effect on } i^{th} \text{ parent } = \hat{g}_i = \frac{1}{n+2} \{(\sum x_i + x_{ij}) - (2/n) x\ldots\}
\]

\[
sca \text{ effect on } j^{th} \text{ cross } = \hat{s}_{ij} = x_{ij} - 1/(n+2) \{x_i - x_{ii} x_{ij} + x_{jj}\} + 2x/(n+1) (n+2) x \ldots
\]

Where, \(\hat{g}_i\) and \(\hat{s}_{ij}\) are the estimates of the general and specific combining ability effects respectively, and \(n, x_i, x_{ii}, x_{ij}\ldots\) and \(x_{ij}\) are the same as explained earlier, \(x_j = \text{ total of the arrays involving } j^{th} \text{ parent as a male and } x_{ij} = \text{ the value of } j^{th} \text{ parent of the array}\).

Estimation of standard errors:

\[
\text{SE} (\hat{g}_i) = \left(\frac{(n-1) \sigma^2e}{n(n+2)}\right)^{0.5}
\]

\[
\text{SE} (\hat{s}_{ij}) = \left(\frac{(n^2+n+2) \sigma^2e}{(n+1)(n+2)}\right)^{0.5}
\]

\[
\text{SE}(\hat{s}_{ij}) = \left(\frac{2(n-1) \sigma^2e}{(n+1)(n+2)}\right)^{0.5}
\]

\[
\text{SE}(\hat{g}_i - \hat{s}_{ij}) = \left(\frac{2\sigma^2e}{(n+2)}\right)^{0.5}
\]

\[
\text{SE}(\hat{s}_{ij} - \hat{s}_{ik}) = \left(\frac{2(n-2) \sigma^2e}{(n+2)}\right)^{0.5}
\]

\[
\text{SE}(\hat{s}_{ij} - \hat{s}_{kl}) = \left(\frac{2n \sigma^2e}{(n+2)}\right)^{0.5}
\]

Where,

\(\sigma^2e = Me^2/r\), taken as error M S. from the combining ability analysis.

Diallel Cross analysis for combining ability over environments.

Pooled analysis for combining ability for Method 2 was carried out on lines suggested by Singh (1973 & 1979). The mathematical model for estimating the parameter is based on:

\[
x_{ijk} = \hat{u} + \hat{g}_i + \hat{g}_j + \hat{s}_{ij} + 1_k + (\hat{g}_i)_{ik} + (\hat{g}_j)_{jk} + (\hat{s}_{ij})_{yk} + f_{ijk}
\]
Least Square estimates of effects for $g_i$ and $S_j$ were estimated as follows:

\[ g_i = \frac{[x_i + x_{ii} - (2/n) x]}{(n-2) 1} \]

\[ s_{ij} = \frac{(x_{ij}/1) - (x_i + x_{ii} + x_j + x_{jj})}{(n+2) 1} + 2x \ldots (n+1) (n+2) 1 \]

Sum of squares were worked out as under:

\[
ss(g) = \frac{s (x_i + u)^2}{(n+2) 1} - \frac{4x^2}{n (n+2) 1}
\]

\[
ss(s) = \frac{s s_j x_{ii}^2}{1} + \frac{s (x_i + x_{ii})^2}{(n+2) 1} + \frac{(n+1) (n+2) 1}{2x^2}
\]

\[
ss(i) = \frac{2s x_k}{n (n+1)} - \frac{2x^2}{n (n+1) 1}
\]

\[
ss(g_{ij}) = \frac{ss (x_i k + x_{ijk})^2}{k (n+2)} - \frac{4s x^2 k}{n (n+2) 1}
\]

\[
ss(s_{ij}) = \frac{s s_{ji} x^2_{ijk}}{k (n+2) 1} - \frac{ss (x_i k + x_{ijk})^2}{n+2}
\]

\[
= \frac{2s x^2 k}{(n+1) (n+2)} - \frac{S_{i} S_{j}}{1} + \frac{S (x_i^2 + x_j^2)^2}{(n+2) 1} + \frac{2x^2}{(n+1) (n+2) 1}
\]
The skeleton of ANOVA along with expectations of mean squares for the random effects – Model II is given as below:

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>d.f.</th>
<th>S.S.</th>
<th>M.S.</th>
<th>Expectations of mean squares</th>
</tr>
</thead>
<tbody>
<tr>
<td>General combining</td>
<td>(n-1)</td>
<td>ss(g)</td>
<td>Ag</td>
<td>$\sigma^2 e + \sigma^2 s_l + (n+2) \sigma^2 g_l +$</td>
</tr>
<tr>
<td>Ability (GCA)</td>
<td></td>
<td></td>
<td></td>
<td>$\sigma^2 s_l + 10^2 s + (n+2) \times 10^2 s$</td>
</tr>
<tr>
<td>Specific combining</td>
<td>n(n-1)/2</td>
<td>ss(s)</td>
<td>As</td>
<td>$\sigma^2 e + \sigma^2 s_l + 1 \sigma^2 s$</td>
</tr>
<tr>
<td>Ability (SCA)</td>
<td></td>
<td></td>
<td></td>
<td>$\sigma^2 e + \sigma^2 s_l$</td>
</tr>
<tr>
<td>Environment (L)</td>
<td>(l-1)</td>
<td>ss(l)</td>
<td>Al</td>
<td>$\sigma^2 e + \sigma^2 s_l (n+1) \sigma^2 g_l +$</td>
</tr>
<tr>
<td>GCA x L</td>
<td>(n-1)</td>
<td>ss(gl)</td>
<td>Agl</td>
<td>$\sigma^2 e + \sigma^2 s_l (n+1) \sigma^2 g_l + (n+1)/2 \sigma^2 L$</td>
</tr>
<tr>
<td>SCA x L</td>
<td>n(n-1)(l-1)/2</td>
<td>ss(sl)</td>
<td>Asl</td>
<td>$\sigma^2 e + \sigma^2 s_l$</td>
</tr>
<tr>
<td>Error</td>
<td>1 (b-1)</td>
<td>m</td>
<td>Ae</td>
<td>$\sigma^2 e$</td>
</tr>
</tbody>
</table>

$E (A_1) = \sigma^2 e + [i_s] \sigma^2 s_l + [(g_l)] \sigma^2 g_l + [(11) \sigma^2 1]$

$E(A_{gl}) = \sigma^2 e + (g_s) \sigma^2 s_l + [g_g] \sigma^2 g_l$

$E(A_{sl}) = \sigma^2 e + [s_s] \sigma^2 s_l$

$S(A_e) = \sigma^2 e$

Where, $[(i_s)]$, $[(g_l)]$ and $[(11)]$ are the coefficients of $\sigma^2 s_l, \sigma^2 g_l$ and $\sigma^2 e$ in $E (A_1)$

Values of (xa) $= g_s = 1$, $g_g = n+2$, $ss = 1$

Values of (la) $= i_s=1, lg= 2(n+1)$, $l1 = n$, $(n+1)/2$
The estimates of \( \sigma^2_x \) could be expressed as linear functions of \( AY \) [(xa)] and [(la)]. The estimate of \( \sigma^2_x \) could however, be given in simple form for method 2.

The estimates were,

\[
\begin{align*}
\sigma^2_g &= (A_{sl} - A_{gl} - A_s + A_g) / [gg] 1 \\
\sigma^2_s &= (A_s - A_{sl}) / [ss] 1 \\
\sigma^2_i &= [(w-t) A_e - (w-q) A_{si} - qa_{gl} + tA_1] / (11) t \\
\sigma^2_{gl} &= (A_{gl} - A_{si}) / [gg] \\
\sigma^2_{si} &= (A_{si} - A_s) / [ss] \\
\sigma^2_e &= A_e
\end{align*}
\]

Where,

\[
W = [1s] [gg]; \quad t = [ss] [gg]; \quad q = [ss] [1g]
\]

Procedure for testing \( \sigma^2_x = 0 \)

The Variances were calculated as follows.

\[
\begin{align*}
\text{Var} (g_i) &= [(n-1) / n (n+2) 1] \sigma^2 \\
\text{Var} (g_i - g_j) &= [2/(n+2)1] \sigma^2 \quad (i = j) \\
\text{Var} (s_{ij}) &= [(n^2+n-2) / (n+1) (n+2) 1] \sigma^2 \quad (i = j) \\
\text{Var} (s_{ij} - s_{ik}) &= [2(n+1) / (n+2) 1] \sigma^2 \quad (i = j) j, k; (j = k)
\end{align*}
\]

Expectations of mean squares in terms of coefficients of variance components in the expectations of mean squares for single environment.

The procedure of estimates could be simplified by using the expectations of mean squares for a single environment. We could express the expectations of mean squares as:

\[
E (B_g) = \sigma^2 + [gs] \sigma^2_s + [gg] \sigma^2_g
\]
\[
E(B_x) = \sigma^2 + \begin{bmatrix} ss \end{bmatrix} \sigma^2_{s} \\
E(B_x) = \sigma^2 + \begin{bmatrix} rr \end{bmatrix} \sigma^2_{r}
\]

Where, \( B \) is the observed mean square due to \( x \) and \( xa \), the coefficient of \( \sigma^2 \) in the expectation of \( B_x \) taking into account the appropriate experimental method under consideration.

It could not be shown that the expectations of the mean squares for the case of 1 environment could be expressed in terms of \( (xa) \) as

\[
E(A_g) = \sigma^2 + \begin{bmatrix} gs \end{bmatrix} \sigma^2_{gs} + \begin{bmatrix} gg \end{bmatrix} \sigma^2_{gg} + \begin{bmatrix} gs \end{bmatrix} \sigma^2_{as} + \begin{bmatrix} gg \end{bmatrix} \sigma^2_{gg} \begin{bmatrix} 1 \end{bmatrix} \sigma^2_{g}
\]

\[
E(A_a) = \sigma^2 + \begin{bmatrix} ss \end{bmatrix} \sigma^2_{ss} + \begin{bmatrix} (ss) \end{bmatrix} \begin{bmatrix} 1 \end{bmatrix} \sigma^2_{s}
\]

The following \( F \)-values were calculated as,

(i) To test \( \sigma^2_{g} = 0 \)

\[
F(p-1), \frac{1}{g} = \frac{(A_g/A_g^*)}{(A_g = A_{gs} + A_s)^2}
\]

Where,

\[
A^*g = \frac{df(s) A^2_{gl} + (p-1) A^2_{as} + (p-1) (1-1) As}{df(s) A^2_{gl} + (p-1) A^2_{as} + (p-1) (1-1) As}
\]

(ii) To test \( \sigma^2_{s} = 0 \)

\[
F[df(s), (1-1)df(s)]As/Asl
\]

(iii) To test \( \sigma^2_{s} = 0 \)

\[
F(1-1), \frac{1}{s} = (A_s/A_s^*)
\]

where,

\[
A_s^* = (t-w) A_e - (q-w) A_{sl} + qa_{gl}/t
\]

\[
[(t-w)A_e-(q-w)A_{sl}+qa_{gl}]^2 (v-1)(b-1)(p-1) (1-1) df (s)
\]

\[
f_1 = \frac{(p-1) (1-1) df (s) (t-w)^2 A_e + 1(v-1)(b-1)(p-1)(q-w)^2 A_{sl} + df (s)q^2 A_{gl}}{(p-1) (1-1) df (s) (t-w)^2 A_e + 1(v-1)(b-1)(p-1)(q-w)^2 A_{sl} + df (s)q^2 A_{gl}}
\]
(iv) To test \( \sigma^2_{gl} = 0 \)

\[ F[(p-1)(1-1), df(s) (1-1)] = A_{gl} / A_{sl} \]

(v) To test \( \sigma^2_{sl} = 0 \)

\[ F[df(s) (1-1), 1 (v-1) (b-1)] = A_{sl} / A_e \]

**ESTIMATION OF HETEROSIS AND INBREEDING DEPRESSION**

**Heterosis:**

The magnitude of heterosis was estimated with the help of the following formula

\[
\text{Heterosis (\% over S P)} = \frac{\overline{F}_1 - \overline{SP}}{\overline{SP}} \times 100
\]

\[
\text{Heterosis\% over M.P} = \frac{\overline{F}_1 - \overline{M.P.}}{\overline{M.P.}} \times 100
\]

Where,

\( \overline{F}_1 = \) mean of the \( F_1 \)

\( \overline{SP} = \) mean of the superior parent

\( \overline{M.P} = \) Mean of the mid parent

**Test of significant:**

Significance of heterosis over economic parents was tested as

\[
\text{SE} = \left(2Me^2/r\right)^{0.5}
\]
Where

\[ Me_2 = \text{Error variance obtained from parents and } F_1 \text{ combination} \]

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

\[ CD = \text{SE} \times t \text{ ('t' value at 5% and 1%)} \]

**Inbreeding Depression:**

The coefficient of inbreeding depression was calculated by the following formula

\[
\text{Inbreeding depression (\%)} = \frac{\overline{F}_1 - \overline{F}_2}{\overline{F}_1} \times 100
\]

Where, \( \overline{F}_1 = \text{mean of } F_1 \text{ generation} \)

\( \overline{F}_2 = \text{mean of } F_2 \text{ generation} \)

**Test of significance:**

The significance of estimate was tested as

\[ \text{SE (inbreeding depression)} = (2Me_3/r)^{0.5} \]

Where,

\[ Me_3 = \text{Error variance obtained from } F_1s + F_2s \text{ combination} \]

\[ r = \text{number of replications.} \]

**Stability Analysis:**

The statistical technique proposed by Eberhart and Russell (1966) was utilized to estimate stability
parameters and genotype x environment interaction for different genotypes with respect to different characters.

Eberhart and Russell (1966) suggested three parameters to measure stability of cultivars. These are (i) mean ($v$), (ii) regression of individual mean performance of environmental index ($b_i$) and (iii) deviation from regression ($s^{2}_{d_i}$). These parameters are defined in the following model:

Where,

\[
Y_{ij} = u_i + b_i I_j + \sigma_{ij}
\]

\[
Y_{ij} = \text{mean performance of } i^{th} \text{ genotypes in } j^{th} \text{ environment} \quad (i = 1, 2, 3----v; \; j = 1, 2, 3----n)
\]

\[
v = \text{number of genotypes}
\]

\[
n = \text{number of environments}
\]

\[
u = \text{mean performance of } i^{th} \text{ genotypes over all the environment}
\]

\[
b_i = \text{regression coefficient of } i^{th} \text{ individual mean performance on environmental index, } I_j
\]

\[
I_j = \text{ } j^{th} \text{ environmental index, and}
\]

\[
\sigma_{ij} = \text{deviation from regression of the } k^{th} \text{ genotype at } j^{th} \text{ environment},
\]
The environmental index for \( j \)th environment, \( i=j \) is obtained as

\[
l_j = \frac{\sum_{j=1}^{n} Y_{ij}}{v} - \sum_{i=1}^{n} \frac{\sum_{j=1}^{n} Y_{ij}}{v} n
\]

where,

\[
\sum_{j=1}^{n} l_j = 0
\]

The first stability parameter regression coefficient \( (b_i) \) was estimated using following formula:

\[
b_i = \left[ \left( \sum_{i=1}^{n} Y_{ij} I_j \right) / \left( \sum_{j=1}^{n} I_j^2 \right) \right]
\]

The second stability parameter \( (s^2_{di}) \) was estimated using the following formula:

\[
s^2_{di} = \left( \frac{1}{n-2} \right) \sum_{j=1}^{n} \sigma^2_{y}- \text{ pooled error}
\]

where,

\[
\sum_{j=1}^{n} \sigma^2_{y} = \left( \sum_{j=1}^{n} y_{ij}^2 - \frac{1}{n} \left( \sum_{j=1}^{n} y_{ij} \right)^2 \right) - \frac{1}{n} \left( \sum_{j=1}^{n} Y_{ij} I_j \right)^2
\]

The average of error mean squares over all the environments was taken as the estimate of pooled error.

The detailed analysis of variance for the estimation of stability parameters and their tests of significance are given as follows.
### Analysis of variance for estimation of stability parameters:

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f</th>
<th>s.s</th>
<th>M.S.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>(nv-1)</td>
<td>[ \sum_{i=1}^{n} \sum_{j=1}^{n} Y_{ij}^2 - CF = TSS ]</td>
<td></td>
</tr>
<tr>
<td>Genotypes (G)</td>
<td>(v-1)</td>
<td>[ \frac{1}{n} \sum_{i=1}^{n} Y_{i.}^2 - CF = GSS ]</td>
<td>MS_1</td>
</tr>
<tr>
<td>Environment (E)</td>
<td>n \ 1</td>
<td>[ \frac{1}{v} \sum_{j=1}^{v} Y_{.j}^2 - CF = ESS ]</td>
<td></td>
</tr>
<tr>
<td>E x G</td>
<td>(n-1)</td>
<td>TSS - (GSS + ESS)</td>
<td>MS_2</td>
</tr>
<tr>
<td>E + (G x E)</td>
<td>v \ (n-1)</td>
<td>[ \sum_{i=1}^{v} \sum_{j=1}^{n} Y_{ij}^2 - \frac{1}{n} \sum_{i=1}^{v} Y_{i.}^2 ]</td>
<td></td>
</tr>
<tr>
<td>E (Linear)</td>
<td>1</td>
<td>[ \frac{1}{v} \sum_{j=1}^{v} Y_{.j}^2 / \sum_{j=1}^{v} I_{j}^2 ]</td>
<td></td>
</tr>
<tr>
<td>G x E (Linear)</td>
<td>v \ -1</td>
<td>[ \sum_{i=1}^{n} \sum_{j=1}^{v} Y_{ij}^2 / \sum_{j=1}^{v} I_{j}^2 - E (Linear) ]</td>
<td>MS_3</td>
</tr>
<tr>
<td>Pool deviation</td>
<td>v((n-2))</td>
<td>[ \sum_{i=1}^{v} \sum_{j=1}^{n} \sigma_{ij}^2 ]</td>
<td>MS_4</td>
</tr>
<tr>
<td>Genotype</td>
<td>v \ (n-2)</td>
<td>[ \sum_{i=1}^{n} Y_{ij} - (1/n)Y_{i.}^2 { \sum_{i=1}^{n} Y_{ij}^2 / \sum_{i=1}^{n} I_{j}^2 } ]</td>
<td></td>
</tr>
<tr>
<td>Genotype</td>
<td>v \ (n-2)</td>
<td>[ \sum_{j=1}^{v} Y_{ij}^2 - (1/v) Y_{.j}^2 { \sum_{j=1}^{v} Y_{ij}^2 / \sum_{j=1}^{v} I_{j}^2 } ]</td>
<td></td>
</tr>
<tr>
<td>Pooled error</td>
<td>n(1-1)</td>
<td>[ \sum_{i=1}^{n} \sum_{j=1}^{v} \sigma_{ij}^2 = TSS - Grand SS (GxE) ]</td>
<td>MS_5</td>
</tr>
</tbody>
</table>
where,

\[ v = \text{number of genotypes} \]

\[ n = \text{number of environment} \]

\[ \sigma^2_e = \text{estimates of error mean square at each location (environment)} \]

following test of significance were applied.

(i) The test of significance of differences among the mean performance of genotypes was calculated using the 'F' test

\[ F = \frac{\text{MS}_1}{\text{MS}_4} \]

(ii) The test of significance of difference among genotypes in respect of mean was calculated using the 't' test.

\[ t = \frac{(u_i - \bar{u})}{\text{SE}(x)} \]

\[ \text{SE}(x) = \sqrt{\frac{\text{Pooled deviation MS}}{\text{Number of environments}-1}} \]

\( u_i \) = mean performance of 1\textsuperscript{st} genotype over all the environments, and

\( u \) = grand mean

(iii) Genotype x environment interaction was tested using the 'F' test

\[ F = \frac{\text{MS}_2}{\text{MS}_4} \]
(iv) The genotypic differences among genotypes for their regression on the environmental index were tested using the 'F' test

\[ F = \frac{MS_3}{MS_4} \]

(v) The deviation of b, value from unity was tested using the 't' test

\[ t = \frac{(b_i - 1)}{SE(b)} \text{ at } v(n-2) \text{ d.f} \]

where,

\[ SE(b) = \sqrt{\frac{\text{Pooled deviation MS}}{\sum_{j=1}^{n} I_j^2}} \]

(vi) Deviation from regression for each genotype was tested using the 'F' test.

\[ F = \frac{1/(n-1) \sum_{j=1}^{n} \sigma_{yj}^2/MS_5}{MS_5} \]

**Estimation of Selection Parameters:**

(i) **Heritability**

(i) Heritability (narrow sense) in F₁ generation was calculated by the formula given by Crumpacker and Allard (1962) as given below

\[ h^2 = \frac{(1/4)D_1}{(1/4)D_1 + (1/4)H_1 - (1/4)F + E} \]

Heritability, in F₂ generation was calculated according to the formula proposed by Varhalen and Murray (1969) as given below
\[ h^2 = \frac{1}{16} D + \left( \frac{1}{16} D + \frac{1}{16} H + \frac{1}{16} F \right) - \frac{1}{8} E \]

Where,

\[ h^2 = \text{estimate of heritability coefficient and } \hat{D}, \hat{H}, \hat{F}, \text{ and } \hat{E} \text{ are the same as explained earlier} \]

Heritability (in per cent) = heritability coefficient \( \times \) 100

Heritability estimates in percent over locations, based on different genetic values obtained from pooled analysis of combining ability (Singh, 1973 and 1979), was computed as under

\[ h^2 (\%) \text{ in } F_1 = \left[ \frac{2\sigma^2_g}{2\sigma^2_g + \sigma^2_s + \sigma^2_{gt} + \sigma^2_{st} + \sigma^2_e} \right] \times 100 \]

\[ h^2 (\%) \text{ in } F_2 = \left[ \frac{2\sigma^2_g}{2\sigma^2_g + \frac{1}{2}\sigma^2_s + \sigma^2_{gt} + \sigma^2_{st} + \sigma^2_e} \right] \times 100 \]

**Genetic advance:**

The genetic advance was worked out by the formula proposed by Robinson *et al* (1949) as-

\[ GA = \left( k \right) \left( h^2 \right) \left( \bar{\sigma}^2_{ph} \right) \]

And genetic advance over mean of the character

\[ GA (\%) = \left( \frac{GA}{\bar{x}} \right) \times 100 \]

Where,

GA = estimate of genetic advance

k = selection differential at 5% selection intensity, i.e. 2.06

\[ \bar{\sigma}^2_{ph} = \text{phenotypic standard deviate} \]

\[ h^2 = \text{estimate of heritability coefficient} \]

\[ \bar{x} = \text{mean of the character concerned} \]