Chapter-III

MATERIALS AND METHODS

A. MATERIALS

The material for the present investigation comprised of Ten diverse homozygous varieties/strains of green gram [Vigna radiata (L.) Wilczek] selected on the basis of morphological variability available for different characters in the germplasm lines maintained at Section of Economic Botanist (Legumes) of C.S. Azad University of Agriculture and Technology, Kanpur.

All possible crosses excluding reciprocals were made among the ten parents during.

SELECTION OF PARENTS

The basic material for present investigation comprised ten eco-geographically diverse mung bean cultivars. The sources, pedigree and salient features of the parental lines are given below (Table1).

Table 1: Salient features of strains/varieties used in 10 parents diallel cross in mung bean

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Variety/Strain</th>
<th>Source</th>
<th>Characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>K 851</td>
<td>CSA, Kanpur</td>
<td>Bold, shining seed, good yielder, 65 days maturity</td>
</tr>
<tr>
<td>2.</td>
<td>PDM 54</td>
<td>IIPR, Kalyanpur</td>
<td>Bold, good yielder, 65 days maturity</td>
</tr>
<tr>
<td>3.</td>
<td>HUM 2</td>
<td>Hissar</td>
<td>Medium Bold, resistant to mosaic, good yielder, 60 days maturity</td>
</tr>
<tr>
<td>4.</td>
<td>Pusa 9631</td>
<td>IARI</td>
<td>Bold, early 60 days, good yielder</td>
</tr>
<tr>
<td>5.</td>
<td>K 1310</td>
<td>Kanpur</td>
<td>Promising strain, high yielding, medium bold, 60 days</td>
</tr>
<tr>
<td>6.</td>
<td>K 1284</td>
<td>Kanpur</td>
<td>Promising strain, good yielder, bold, 60 days</td>
</tr>
<tr>
<td>7.</td>
<td>PDN 84-139</td>
<td>IIPR, Kalyanpur</td>
<td>Bold, very good yielder, 65 days</td>
</tr>
<tr>
<td>8.</td>
<td>PS 16</td>
<td>IARI</td>
<td>Bold, dull green, resistant, erect, resistant to high temp.</td>
</tr>
<tr>
<td>9.</td>
<td>T 44</td>
<td>Kanpur</td>
<td>Good yielder, widely adapted, dull green well suited for zaid &amp; kharif.</td>
</tr>
<tr>
<td>10.</td>
<td>K 92-140</td>
<td>Kanpur</td>
<td>High yielding strain, medium, bold, 60 days.</td>
</tr>
</tbody>
</table>
METHODS

(a) Plan of layout

A set of Ten parents and their 45 F₁s and 45 F₂s were grown during 1999-2000 in Randomized Complete Block Design with three Replication at Student's Instructional Farm, C.S. Azad University of Agriculture and Technology, Kanpur. The experimental material was sown during April, 2000. Normal cultural practices were followed for raising the good crop. The experimental plot was kept free of weeds. Incidence of mosaic was observed only in one or two plants in final trial. The Experimental plot was single row, 2.5 m long and 30 cm apart. The inter plant distance of 10 cm was maintained.

Ten randomly chosen plants from each treatment of three replications were marked to record the observations on 10 yield and quality traits.

(b) Procedure of recording observations

(i) Days to flower

Number of days from date of sowing to date of first flower opening was recorded as days to flower.

(ii) Days to maturity

Number of days from data of sowing to date of first pod ripening was recorded as days to maturity.

(iii) Plant height

The height of the plant was measured in centimeters from ground level to the tip of main shoot.
(iv) **Number of primary branches per plant**

Total numbers of primary branches per plant were counted at the time of maturity.

(v) **Number of clusters per plant**

Total numbers of clusters$^1$ were counted at the time of maturity.

(vi) **Number of pods per cluster**

Total numbers of pods per cluster were counted at maturity.

(vii) **Number of seeds per pod**

Five mature and effective pods were randomly taken from each plant, seeds were counted and average grain per pod was calculated.

(viii) **100-grain weight**

100-grains were taken randomly from individual plant yield and weighed in gram on a electronic balance.

(ix) **Protein content (%)**

The protein content (%) in grain flour of each treatment was estimated by Biuret method.

The method involves the oxidation of the sample with sulphuric acid and a catalyst. Carbon and hydrogen are oxidized to CO$_2$ and H$_2$O and reduced form of nitrogen (such as $–$ NH$_2$ or $=$ NH) are retained in the digest as ammonium ions. The digest may be made alkaline and the ammonia distilled off collected and titrated.
**Grain yield per plant**

All the pods of a plant were hand threshed and yield was recorded in gram on an electronic balance.

Mung protein content -------- of nitrogen.

**STATISTICAL AND BIOMETRICAL PROCEDURES**

The experimental data was compiled by taking the mean of each treatment for all the three replications, separately. Then it was subjected to the following statistical and biometrical analyses.

1. Analysis of variance
2. Diallel analysis
   (a) Graphical analysis
   (b) Variance Component analysis
   (c) Combining Ability analysis
   (d) Degree of Dominance
3. Estimation of Heterosis and Inbreeding Depression.
4. Estimation of Selection Parameters
   (a) Heritability
   (b) Genetic Advance
   (c) Correlation Coefficient

The outlines of the methodology used in the above analyses are given below:

**1. Analysis of variance**

Analysis of variance (ANOVA) for the experimental design was based on the model:

\[ P_{ijk} = \mu + V_{ij} + r_k + e_{ijk} \quad (ij = 1 \ldots t; \, k = 1 \ldots r) \quad i = j \]
Where,

\[ P_{ijk} = \text{the phenotype of } ijk^{th} \text{ observation} \]
\[ \mu = \text{the population mean} \]
\[ V_{ij} = \text{the effect of the } i^{th} \text{ variety at } j^{th} \text{ progeny} \]
\[ r_k = \text{the effect of the } k^{th} \text{ replication} \]
\[ e_{ijk} = \text{the error of the } eijk^{th} \text{ observation} \]

'ANOVA' for design of experiment was done for partitioning the variance into treatments and replications according to procedure given by Panse and Sukhatme (1967) as given below:

### Skeleton of ANOVA for the experiment

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>Degree of Freedom (d.f.)</th>
<th>Mean Squares</th>
<th>'F' values</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>(r-1)</td>
<td>Mr</td>
<td>Mr/Me</td>
</tr>
<tr>
<td>Treatment</td>
<td>(t-1)</td>
<td>Mt</td>
<td>Mt/Me</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (t-1)</td>
<td>Me</td>
<td></td>
</tr>
</tbody>
</table>

Since the experiment consisted of parents, \( F_1s \) and \( F_2s \), the ANOVA was prepared separately involving parents + \( F_1s \), and parents + \( F_1s + F_2s \) to test the variability among treatments and heterosis inbreeding depression as follows:

### Skeleton of ANOVA for parents and \( F_1s \)

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>Degree of Freedom (d.f.)</th>
<th>Mean Squares</th>
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<tr>
<td>Treatment</td>
<td>(t-1)</td>
<td>Mt</td>
<td>Mt/Me</td>
</tr>
<tr>
<td>Parents (P)</td>
<td>(P-1)</td>
<td>Mp</td>
<td>Mp/Me</td>
</tr>
<tr>
<td>( F_1s )</td>
<td>(F1-1)</td>
<td>MF1</td>
<td>MF1/Me</td>
</tr>
<tr>
<td>P Vs F1s</td>
<td>1</td>
<td>MpF1</td>
<td>MpF1/Me</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (t-1)</td>
<td>Me</td>
<td></td>
</tr>
</tbody>
</table>
Skeleton of combined ANOVA for (Parents + F₁s + F₂s)

<table>
<thead>
<tr>
<th>Source of Variation</th>
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<tr>
<td>Treatment</td>
<td>(t-1)</td>
<td>Mt</td>
<td>Mt/Me</td>
</tr>
<tr>
<td>Parents (P)</td>
<td>(P-1)</td>
<td>Mp</td>
<td>Mp/Me</td>
</tr>
<tr>
<td>F₁s</td>
<td>(F₁-1)</td>
<td>MF₁</td>
<td>MF₁/Me</td>
</tr>
<tr>
<td>P Vs F₁s</td>
<td>1</td>
<td>MpF₁</td>
<td>MpF₁/Me</td>
</tr>
<tr>
<td>F₂s</td>
<td>(F₂-1)</td>
<td>MF₂</td>
<td>MF₂/Me</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (t-1)</td>
<td>Me</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>(rt-1)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Skeleton of ANOVA for F₁s and F₂s

<table>
<thead>
<tr>
<th>Source of Variation</th>
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<th>Mean Squares</th>
<th>‘F’ values</th>
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<td>Treatment</td>
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<td>F₁s</td>
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<td>MF₁</td>
<td>MF₁/Me</td>
</tr>
<tr>
<td>F₂s</td>
<td>(F₂-1)</td>
<td>MF₂</td>
<td>MF₂/Me</td>
</tr>
<tr>
<td>F₁ Vs F₂</td>
<td>1</td>
<td>MF₁F₂</td>
<td>MpF₁/Me</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (t-1)</td>
<td>Me</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>(rt-1)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Where,

\[ r = \text{number of replications} \]
\[ t = \text{total number of treatments} \]
\[ P = \text{number of parents} \]
\[ F₁ = \text{number of F₁ hybrids} \]
\[ F₂ = \text{number of F₂ progenies} \]

2. Diallel Analysis

(a) Graphical Analysis

The graphical analysis was based on the variance and covariance values following the procedures given by Jinks and Hayman (1953) and later on elaborated by Jinks (1954, 56) and Hayman (1954a, b; 1957) and Aksel and Johnson (1963).

The variances and covariances were calculated from the following statistics:
Where,

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

\[ \text{C.F.} = \text{correction factor} \]

\[ \text{Vr} = \text{Variance of each array} \]

\[ = \frac{1}{n-1} \left( \text{Sum of squares of crosses involving a particular parent} - \text{C.F.} \right) \]

Where,

\[ \left( \text{Sum of all 'n' crosses involving a particular line} \right)^2 \]

\[ = \frac{1}{\text{Number of crosses (Vr)}} \]

\[ \text{Mean variance of the arrays (Vr)} = V_{r1}L_1 \]

\[ = \frac{1}{n} \left( \Sigma V_{ri} \right) \]

\[ \text{The variance of the mean of arrays (Vm)} = V_{g1}L_1 \]

\[ = \frac{1}{(n-1)} \left[ \text{Mean of the crosses involving first parent}^2 + \ldots + \text{Mean of the crosses involving n parents}^2 \right] - \frac{(\text{Grand mean})^2}{n} \]
Covariance between parents and their offspring = \( W \)

\[ W = \frac{1}{n-1} \left( \sum_{i=1}^{n} (P_i \times P_j) - \frac{1}{n} (\sum_{i=1}^{n} P_i) \times (\sum_{j=1}^{n} P_j) \right) \]

\[ W = \frac{1}{n-1} \left( \sum_{i=1}^{n} (P_i \times P_j) - \frac{1}{n} \left( \sum_{i=1}^{n} P_i \right)^2 \right) \]

The expected environmental component of variation, \( E \), is calculated as with ungrouped randomization as suggested by Aksel and Johnson (1963).

\[ E = \frac{\text{Replication SS} + \text{Error SS}}{\text{Number of replications} - 1} \]

To test the validity of the hypothesis, the analysis of diallel cross is based on seven assumptions proposed by Hayman (1954), viz., (i) Normal diploid segregation (ii) lack of maternal effects (iii) absence of multiple alleles (iv) absence of linkage (v)
absence of epistasis (vi) homozygosity of parents and (vii) random mating. The following tests were made as per procedure described by Hayman (1954a, b).

(a) Uniformity test of \((W_r, V_r)\) using \(t^2\) test at 4 and \((n-2)\) degree of freedom:

\[
t^2 = \frac{(n-2)}{4} \times \left( \frac{(Var. V_r - Var. W_r)^2}{(Var. V_r \times Var. W_r) - CoV^2(W_r, W_r)} \right)
\]

Which is an \(F\) with 4 and \((n-2)\) degrees of freedom. A significant value of \(t^2\) would indicate the non-uniformity of \(W_r, V_r\) and thus invalidates the hypothesis postulated.

(b) Another way of testing the hypothesis is through the regression coefficient. Here we calculate the regression of covariance on the variance. The failure of hypothesis is also indicated by non-significant regression coefficient \((b)\) using the formula:

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

Where,

\[
Cov (W_r, V_r) = \frac{\sum V_r W_r - \sum V_r \sum W_r/n}{(n-1)}
\]

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

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

\[
SE (b) = \left[ \left( Var. W_r - b \times Cov. W_r V_r \right) \times Var. V_r (n-2) \right]^{0.5}
\]

Where,

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

Now the significance of \(b\) from zero and unity was tested by suing 't' value with \((n-2)\) degree of freedom:
\[ \text{Ho: } b = 0 \]
\[ = (b-0)/\text{SE}(b) \]

\[ \text{Ho: } b = 1 \]
\[ = (1-b)/\text{SE}(b) \]

These pairs of \((W_r, Y_r)\) values represent the parental array points along the regression line in the geometric presentation of the diallel data. The linear regression of \(W_r\) and \(V_r\) was tested for significance \((b+0)\) and for deviation from unity \((b+1)\) against table value of “t” for \((n-2)\) degrees of freedom.

In the absence of non-allelic interaction, \(W_r\) is related to \(V_r\) by straight regression line of unit slope.

**\(W_r, V_r\) Graph**

The relationship of \(W_r\) with \(V_r\) provides some useful information regarding parents. The \(W_r\) values are plotted against the corresponding value of \(V_r\). The limiting parabola was plotted by obtaining \(W_{ri}\) values from the following relationship.

\[ W_{ri} = (V_{ri} \times \text{VoLo})^{0.5} \]

Where, \(V_{ri}\) is the variance of \(i^{th}\) array and \(\text{VoLo}\) is the variance of parents.

For drawing regression line, we require \(W_{re}i\) values, which were calculated as follows:

\[ W_{re}i = W_r - b \times V_r + b \times V_{ri} \]

Where,

\[ W_r = \text{Mean of } W_r \text{ for all the arrays} \]

\[ V_r = \text{Mean of } V_r \text{ for all the arrays} \]
\[ W_{rei} = \text{Expected value of } W_r \text{ corresponding to } V_r \]

By plotting these values, a straight line was obtained. This would be a regression line.

The point of interception of the regression line with \( W_r \) ordinate, i.e., \( \partial \) was obtained by following equation:

\[ \partial = W_r - bV_r \]

(b) Variance component analysis

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

**Expectations for \( F_1 \) diallel:**

\[ V_p = V_{0Lo} = D + E \]

\[ V_r = V_{1L_1} = (1/4) D + (1/4) H_1 - (1/4) F + [(n+1)]/2n]E \]

\[ W_r = W_{0Lo1} = (1/2) D - (1/4) F + (1/n) E \]

\[ V_m = V_{0L_1} = (1/4) D + (1/4) H_1 - (1/4) H_2 - (1/4) F + (1/2 n) E \]

Where,

\[ D = \text{Components of variation due to additive effect of genes} \]

\[ H_1 = \text{Components of variation due to dominance effect of genes} \]

\[ H_2 = H_1 [1 - (4-V)^2] \]

Where,

\[ u = \text{Proportion of positive genes in the parents} \]
\[ h^2 = \text{Dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses)} \]

\[ V = \text{Proportion of negative genes in parents} \]

\[ F = \text{The mean of "Fr" over the arrays,} \]

Where,

Fr is the covariance of additive and dominance effects in a single array.

\[ E = \text{The expected environmental component of variation.} \]

**Estimation of components of variation**

The estimates of these components of genetic variation were determined by using the following equations:

\[ D = VoLo - E \]

\[ H_1 = VoLo - 4WoLo1 - 4V_1L_1 - \frac{(3n-2)}{n} E \]

\[ H_2 = 4V_1L_1 - 4VoL_1 - 2E \]

\[ h^2 = 4(ML_1 - MLo)^2 - \frac{2(n-2)}{n} E \]

\[ Fr = 2(VoLo - WoLo1 + V_1L_1 - Wr - Vr) - \frac{2(n-2)}{n} E \]

**Standard error of estimates**

In order to estimate the accuracy of the above components of variance, the terms of main diagonal of the matrix given by Hayman (1954a) with common multipliers \((S^2/n^5)\) was used:

\[ S^2 = \frac{1}{2} \left[ \text{Var.} (Wr - Vr) \right] \]
The formula being:

\[
\begin{align*}
\text{SE (D)} & = \pm \left[ S^2 \left( \frac{n^5 + n^4}{n^5} \right) \right]^{0.5} \\
\text{SE (H)} & = \pm \left[ S^2 \left( \frac{n^5 + 41n^4 - 12n^3 + 4n^2}{n^5} \right) \right]^{0.5} \\
\text{SE (F)} & = \pm \left[ S^2 \left( \frac{36n^4}{n^5} \right) \right]^{0.5} \\
\text{SE (E)} & = \pm \left[ S^2 \left( \frac{n^4}{n^5} \right) \right]^{0.5} \\
\text{SE (F)} & = \pm \left[ S^2 \left( \frac{4n^5 + 20n^4 - 16n^3 + 16n^2}{n^5} \right) \right]^{0.5}
\end{align*}
\]

If the value of the parameter divided by its standard error exceeds 1.96, than it is significant.

**Other related parameters**

(a) Mean degree of dominance = \( \left( \frac{H}{D} \right)^{0.5} \)

(b) Proportion of genes with positive and negative effects in the parents = \( \frac{H}{4H_1} \)

It measures average value of \( uv \) over all loci and less than its maximum value, 0.25 which happens when \( u = v = 0.5 \) at all loci.

(c) Proportion of dominant and recessive genes in the parents \( KD/KR = \left( \frac{(4DH_1)^{0.5} + F}{(4DH_1)^{0.5} - F} \right) \)

(d) The coefficient of correlation (r) between the parental order of dominance (\( W_r + V_r \)) and parental measurement (\( Y_r \)).

**Expectations for F2 diallel**

Jinks (1956) and Hayman (1958) gave expectation for F2 diallel crosses. The expected statistics for F2 generation are of the same from as those of F1 except that contribution of “h” is halved by are generation of inbreeding. Hence, the coefficients of
H₁ and H₂ are ¼ of those of the F₁ statistics, while the coefficients of F is halved, being second and first degree statistics in h, respectively (Jinks, 1956; Hayman, 1958 and Mather and Jinks, 1971). These expectations are as follows:

\[ \begin{align*}
V_p &= V_\nu Lo = D + E \\
V_r &= V_1L_2 = (1/4) D + (1/16) H_1 - (1/8) F + E_2 \\
W_r &= W_oLo2 = (1/2) D - (1/8) F + (1/n) E_2 \\
V_m &= V_\nu L_2 = (1/4) D + (1/16) H_1 - (1/16) H_2 - (1/8) - F + (1/n) E_2
\end{align*} \]

Where,

\[ E_2 = VE/r = Me of F_2 \]

**Estimation of components of variation**

\[ \begin{align*}
D &= V_\nu Lo - E \\
H_1 &= 16 V_1L_2 - 16 W_oLo2 + 4 V_\nu Lo - 4 (5n-4) \frac{E_2}{n} \\
H_2 &= 16 V_1L_2 - 16 V_oL_2 - 16 (n-1) \frac{E_2}{n} \\
h^2 &= 4 (ML_2 - ML_o)^2 - 16 (n-1) \frac{E_2}{n} \\
F &= 4 V_\nu Lo - 8 W_oLo2 - 4 \frac{E_2}{n}
\end{align*} \]

**Standard error of estimates**

SE to test the significance of components given above are calculated as follows:

\[ \begin{align*}
SE (D) &= \pm [S^2 (n^5+n^4)/N5]^{0.5} \\
SE (H_1) &= \pm [S^2 (16n^5+656n^4-192n^3+64n^2)/n5]^{0.5}
\end{align*} \]
SE(H₂) = ± [S²(576n⁴/n⁵)⁰.⁵]
SE(h²) = ± [S²(256n⁴+256n²-512n+256)/n⁵]⁰.⁵
SE(F) = ± [S²(16n⁵+80n⁴-64n³+6n²)/n⁵]⁰.⁵
SE(E₂) = ± [S²(n⁴/n⁵)]⁰.⁵

Where,

n = Number of parents and S² = (1/2) Var. (Wr - Vr)

The significance is tested by 't' value at (n-2) degrees of freedom.

t = \frac{Parameter}{SE of parameter}

Proportion of the related genetic components

(a) Degree of dominance: The mean degree of dominance in F₂ is [1/4 (H₁/D₁)]⁰.⁵ following Verhalen et al. (1971).

\[ \text{If } [1/4 (H₁/D₁)]^{0.5} = 1 \text{ (Complete dominance)} \]
\[ > 1 \text{ (Over dominance)} \]
\[ < 1 \text{ (Partial dominance)} \]

(b) Proportion of genes with positive and negative effects in the parents when u and v are symmetrically distributed, i.e, u = v = 0.5. The formula is same as F₁.

(c) Proportion of dominant and recessive genes in the parents:

\[ KD/KR = [(4DH₁)^{0.5} + (1/2) F]/[(4DH₁)^{0.5} - (1/2) F] \]

(d) Number of groups of genes which control the character and exhibit dominance:

\[ h²/H₂ \text{ is the same as } F₁. \]
(c) Combining ability analysis

The combining ability analysis was worked out by the procedure suggested by Griffing’s (1956 b) Method 2 Model 1. The mathematical model for the combining ability analysis is assumed to be:

\[ X_{ijKL} = \mu + g_i + g_j + S_{ij} + \frac{1}{bc} \sum_{k} \sum_{l} e_{ijkl} \]

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

\[ K = 1, 2, \ldots, b \]

\[ L = 1, 2, \ldots, c \]

Where,

\[ X_{ijKL} = \text{The mean of } iJ^{th} \text{ genotype over } K \text{ and } L \]

\[ \mu = \text{The population means} \]

\[ g_i = \text{the general combining ability (gca) effect of } i^{th} \text{ parent.} \]

\[ g_j = \text{The gca effect of } j^{th} \text{ parent} \]

\[ S_{ij} = \text{The interaction, i.e. the specific combining ability (sca) for the cross between } i^{th} \text{ and } j^{th} \text{ parents such that } S_{ij} = S_{ji} \]

\[ e_{ijkl} = \text{The environmental effects associated with the } ijKL^{th} \text{ individual observation on } i^{th} \text{ individual in } K^{th} \text{ block with } i^{th} \text{ as female parent and } j^{th} \text{ as male parent, i.e. the mean error effect. The usual restriction such as} \]

\[ \sum_{i} g_i = 0, \text{ and } \sum_{j} S_{ij} + S_{ii} = 0 \text{ (for each } i) \text{ are imposed.} \]

The analysis of variance table for combining ability is as follows:
## ANOVA for combining ability

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Degrees of freedom</th>
<th>Sum of Squares</th>
<th>Mean Squares</th>
<th>Expectation</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>$\sigma^2e + \sigma^2s \frac{(n-2)}{n} \sigma^2g$</td>
<td>$M_g/Me$</td>
</tr>
<tr>
<td>sca</td>
<td>$n(n-1)^2$</td>
<td>$S_s$</td>
<td>$M_s$</td>
<td>$\sigma^2e + \sigma^2s$</td>
<td>$M_s/Me$</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1) (t-1)</td>
<td>$S_e$</td>
<td>$M_e$</td>
<td>$\sigma^2e$</td>
<td></td>
</tr>
</tbody>
</table>

Where,

$$S_g = (S.S. \text{ due to g.c.a.}) = \frac{1}{n+2} \left[ \Sigma (y_i + y_{ii})^2 - \frac{4}{n} y^2 \right]$$

$$S_s \text{ (S.S. due to s.c.a.)} = \left[ \Sigma y_{ij}^2 - \frac{1}{n+2} \Sigma (y_i + y_{ij})^2 + \frac{2}{(n+1)(n+2)} y^2 \right]$$

$$Me_2 = Me_2/r \text{ for } F_1$$

$$Me_3 = Me_3/r \text{ for } F_2$$

$$\sigma^2g = \frac{1}{n+2} (Mg-Me)$$

$$\sigma^2s = Ms - Me$$

$$\sigma^2e = Me$$

Where,

$$r = \text{Number of replications}$$

$$S_g = \text{The sum of squares due to gca}$$

$$S_s = \text{The sum of squares due to sca}$$

$$M_g = \text{The mean of squares gca}$$

$$M_s = \text{The mean of squares sca}$$

$$M_e = \text{The error of M.S. obtained from main ANOVA}$$

$$n = \text{Number of parents}$$
\[ y_i = \text{Total of the array involving } i^{th} \text{ as a female parent} \]

\[ y_{ii} = \text{Value of the } i^{th} \text{ parent of the array} \]

\[ Y = \text{The grand total} \]

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

**Estimation of various effects**

The various effects were estimated as follows:

(i) **Estimation of gca effect**

\[ gca \text{ effect of } i^{th} \text{ parent} \]

\[ g_i = \frac{1}{n+2}[y_i + y_{ii}] - \frac{2}{n} Y \ldots \]

(ii) **Estimation of sca effect**

\[ sca \text{ effect of } ij^{th} \text{ cross} \]

\[ S_{ij} = y_{ij} - \left[ \frac{1}{(n+2)(y_i + y_j + y_{jj})} + \frac{2}{(n+1)(n+2)} Y \right] \ldots \]

Where,

\[ G_i \text{ and } S_{ij} \text{ are the estimates of the general and specific combining ability effects, respectively, and } n, y_i, y_{ii} \text{ and } y_{ij} \text{ are the same as explained earlier, } y_{jj} = \text{the value of the } j^{th} \text{ parent of the array.} \]

(iii) **Estimation of standard errors**

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

\[ \text{SE (}S_{ii}\text{)} = \left[\frac{(n^2+n+2) \sigma^2}{(n+1)(n+2)}\right]^{0.5} \]
\[
\begin{align*}
\text{SE (gi-gj)} & = \left[\frac{2 \sigma^2_e}{(n+2)}\right]^{0.5} \\
\text{SE (Sij)} & = \left[\frac{2(n-1) \sigma^2_e}{(n+1)(n+2)}\right]^{0.5} \\
\text{SE (Sii-Sij)} & = \left[\frac{2(n-2) \sigma^2_e}{(n+2)}\right]^{0.5} \\
\text{SE (Sij-Sik)} & = \left[\frac{2(n+1) \sigma^2_e}{(n+2)}\right]^{0.5} \\
\text{SE (Sij-SKL)} & = \left[\frac{2n \sigma^2_e}{(n+2)}\right]^{0.5}
\end{align*}
\]

Where,

\[
\sigma^2_e = \frac{Me}{r}, \text{ taken as error M.S. from the combining ability analysis,}
\]

critical differences were calculated by multiplying the corresponding standard error with table value of ‘t’ at error degree of freedom.

(d) Degree of dominance

Average degree of dominance was calculated following Kempthorne and Curnow (1961).

Average degree of dominance = \((\sigma^2_s/\sigma^2_g)^{0.5}\)

(e) Predictability ratio

Predictability ratio was calculated as suggested by Baker (1978).

Predictability ratio = \(\frac{2\sigma^2_g}{2\sigma^2_g + \sigma^2_s}\)

3. ESTIMATION OF HETEROESIS AND INBREEDING DEPRESSION

(i) Heterosis

The nature and magnitude of heterosis in F_1 over better parent and Economic parent was estimated with the help of following formula:
(a) Heterosis over better parent (%) = \( \frac{F_1 - BP}{BP} \times 100 \)

(b) Heterosis over standard variety (%) = \( \frac{F_1 - SV}{SV} \times 100 \)

Where,

\[ F_1 = \text{Mean of } F_1 \]
\[ BP = \text{Mean of the better parent} \]
\[ SV = \text{Mean of standard variety} \]

Test of significance

Significance of heterosis over better parent and economic parent was tested by using simple 't' test.

Where,

\[ SE = (2 Me/r)^{0.5} \]

SE is standard error of the difference of the treatment mean to be compared, and is equal to

Where,

\[ Me = \text{Error mean squares obtained from } F_1 \text{s.} \]
\[ r = \text{Number of replications} \]
\[ t = \text{Tabular value of 't' at 5% and 1% level of significance for the degree of freedom of error mean squares:} \]
\[ CD = SE \times 't' \text{ ('t' value at 5% and 1%)} \]

't' value (BP) = \( \frac{F_1 - BP}{SE} \)
(ii) Inbreeding depression

The coefficient of inbreeding depression was calculated by the following formula:

\[
\text{Inbreeding Depression} = \frac{F_1 - F_2}{F_1} \times 100
\]

Where,

\[F_1 = \text{mean of the } F_1 \text{ generation}\]
\[F_2 = \text{mean of the } F_2 \text{ generation}\]

Test of significance

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

Where,

\[\text{Me} = \text{Error variance obtained from } F_1 \text{ and } F_2 \text{ combination.}\]
\[r = \text{Number of replications.}\]

4. ESTIMATION OF SELECTION PARAMETERS

The selection parameters, (Heritability, Genetic advance, Correlations and Path analysis) were calculated to analyse the suitability of direct and indirect selection parameters.

(a) Heritability

Coefficient of heritability (in narrow sense) in F₁ generation was calculated by the formula proposed by Crumpacker and Allard (1962).

\[
\text{Heritability (} h^2 \text{)} = \frac{\frac{1}{4} D}{\frac{1}{4} D + \frac{1}{4} H_1 - \frac{1}{4} F + E} \times 100
\]
Heritability in F2 generation was calculated according to the methodology proposed by Verhalen and Murray (1969).

\[
\text{Heritability (} h^2 \text{)} \quad = \quad \frac{\frac{1}{4} D}{\frac{1}{4} D + \frac{1}{16} H_1 - \frac{1}{8} F + E} \times 100
\]

Where,

\[
h = \quad \text{Estimates of heritability coefficient and D, H}_1, \text{ F and E are the same as explained earlier.}
\]

(b) Genetic advance

The genetic advance was calculated by the formula given by Robinson et al. (1949) as:

\[
\text{Genetic advance} \quad = \quad (\sigma \text{ phj} \times k) \times (h^2)
\]

and Genetic advance in percentage over mean of the character was estimated as:

\[
\text{G.A. (} \% \text{)} \quad = \quad \frac{\sigma \text{ phj} \times k \times h^2}{X} \times 100
\]

Where,

\[
\text{G.A. (} \% \text{)} \quad = \quad \text{Estimate of genetic advance}
\]

\[
K \quad = \quad \text{Selection differential at 5% selection intensity (K=2.06)}
\]

\[
h^2 \quad = \quad \text{Heritability coefficient in narrow sense}
\]

\[
\sigma \text{ ph} \quad = \quad \text{Phenotypic standard deviation}
\]

\[
X \quad = \quad \text{Mean value of the character concerned}
\]

(c) Correlation coefficient

The following formulae were used for calculating the phenotypic and genotypic coefficients of correlations as suggested by AL-Jibouri et al. (1958).
(a) Correlation between characters \( X \) and \( y \) at phenotypic level.

\[
    r_{pxy} = \frac{\text{Cov. } Xy (p)}{\sqrt{\text{Var. } x (p) \cdot \text{Var. } y (p)}},
\]

(b) Correlation between characters \( x \) and \( y \) at genotypic level

\[
    r_{gry} = \frac{\text{Cov. } Xy (g)}{\sqrt{\text{Var. } x (g) \cdot \text{Var. } y (g)}},
\]

Where,

\( r_{xy} \) = Correlation coefficient between character \( x \) and \( y \).
\( \text{Cov.} \ xy \) = Co-variance between characters \( x \) and \( y \)
\( \text{Var. } x \) = Variance of character \( x \).
\( \text{Var. } y \) = Variance of character \( y \).

**Test of significance of correlation coefficients**

Phenotypic correlation coefficient (\( rp \)) were tested against the table value of correlation coefficient (Fisher and Yates, 1938) at \( n-2 \) degrees of freedom at 5 and 1 percent level of probability.

Where,

\( n \) = number of treatments in the population concerned.