Chapter 3

MATERIALS AND METHODS

FOR the present study, ten diverse and elite lines/varieties of Okra (*Abelmoschus esculentus* (L.) Moench) were taken. These lines/varieties were obtained from the Vegetable Breeder, C. S. Azad University of Agriculture and Technology, (Kalyanpur) Kanpur. Their name, origin and salient features are presented in Table 3.1

3.1 Development of the Material

The ten parents lines/varieties were crossed in all possible combinations in summer season (*Zaid*) of 1999. Assuming the absence of extra nuclear inheritance, the reciprocal crosses were not attempted. Thus the cross combinations were 45, i.e., \( n(n - 1)/2 \) where \( n \) represents the number of parents. Large number of crosses were made to obtain sufficient F\(_1\) seeds in each case. During *Kharif* 1999, 30 seeds of each F\(_1\) were grown with the parents for producing the F\(_2\) seeds. Some F\(_1\) seeds were kept reserved to grow in the final experiment.

3.2 Preparation of Land and Fertilizer Application

The experimental plot at the Agriculture Farm of S. D. J. Post Graduate College, Chandeshwar, Azamgarh was homogeneous regarding soil fertility. Fertilizer was applied @ 60 kg N/ha, 40 kg P\(_2\)O\(_5\)/ha and 40 kg K\(_2\)O/ha. Whole amount of
Table 3.1: Parents used, their place of origin and salient features

<table>
<thead>
<tr>
<th>S.N.</th>
<th>Name of variety/line</th>
<th>Origin</th>
<th>Salient features</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>PS</td>
<td>I.A.R.I., New Delhi</td>
<td>Tall, branched, fruit long, good fruited, susceptible to yellow vein mosaic disease</td>
</tr>
<tr>
<td>2</td>
<td>KS410</td>
<td>C.S.A.U.A.T., Kalyanpur, Kanpur</td>
<td>Medium tall, branched, medium fruit length, heavy fruited, high yielding, resistant to yellow vein mosaic disease</td>
</tr>
<tr>
<td>3</td>
<td>PK</td>
<td>Agriculture Univ. Parbhani</td>
<td>Tall, branched, long fruit, large number of fruits, high yielding, resistant to yellow vein mosaic disease</td>
</tr>
<tr>
<td>4</td>
<td>KS401</td>
<td>C.S.A.U.A.T., Kalyanpur, Kanpur</td>
<td>Medium branched, medium fruited, medium fruit, medium yield, susceptible to yellow vein mosaic disease</td>
</tr>
<tr>
<td>5</td>
<td>KS427</td>
<td>C.S.A.U.A.T., Kalyanpur, Kanpur</td>
<td>Late flowering, medium tall, branched, medium fruit length, high fruited, susceptible to yellow vein mosaic disease</td>
</tr>
<tr>
<td>6</td>
<td>KS405</td>
<td>C.S.A.U.A.T., Kalyanpur, Kanpur</td>
<td>Tall, branched, long fruit, large number of fruits, high yielding, tolerant to yellow vein mosaic disease</td>
</tr>
<tr>
<td>7</td>
<td>KS404</td>
<td>C.S.A.U.A.T., Kalyanpur, Kanpur</td>
<td>Medium flowering, tall, branched, medium fruit, large number of fruits, high yielder, resistant to yellow vein mosaic disease</td>
</tr>
<tr>
<td>8</td>
<td>P7</td>
<td>Punjab Agricultural University, Ludhiana (Punjab)</td>
<td>Tall, branched, large fruit, medium yield, resistant to yellow vein mosaic disease</td>
</tr>
<tr>
<td>9</td>
<td>KS312</td>
<td>C.S.A.U.A.T., Kalyanpur, Kanpur</td>
<td>Dwarf, branched, medium fruit, heavy fruited, good yielder, tolerant to yellow vein mosaic disease</td>
</tr>
<tr>
<td>10</td>
<td>BO2</td>
<td>O.U.A.T., Bhubneshwar, Orissa</td>
<td>Medium, branched, medium fruit, medium fruited, medium in yield, resistant to yellow vein mosaic disease</td>
</tr>
</tbody>
</table>
phosphorus and potash were applied as basal dressing at the time of ploughing, while nitrogen (in the form of urea) was applied in 2 splits i.e., 1/2 as basal dressing and the rest as top dressing after one month of sowing.

3.3 Experimental Design

The final experiment was done during *Kharif* 2000. The experimental material consisted of 10 parents, 45 F₁s and 45 F₂s, making a total entry of 100. The seeds were sown on 2nd July 2000 in a randomized complete block design using 3 replications. Parents and F₁s were grown in single rows, while F₂s were grown in 5 rows with 10 plants in each row. The rows were 5 meter long and placed 50cm apart. The plant to plant spacing was maintained at 50cm.

3.4 Observations Recorded

The observations were recorded on randomly selected five plants in each parent and F₁ and 30 plants in case of each F₂ population in each replication. The data was recorded on the following characters.

1. **Days to flowering**: Number of days from date of sowing to the opening of first flower were recorded.

2. **Plant height (cm)**: The height of plant was measured from the base to the top at the time of final harvesting.

3. **First fruiting node (cm)**: The height of the first fruiting node was measured from the base of the plant to the node at which first flower opened.

4. **Number of branches per main shoot**: Number of fruit bearing branches were counted at the time of final picking.

5. **Number of nodes per main shoot**: The number of nodes were counted from the base to the top at the time of final picking.
6. **Petiole length (cm):** It was measured from leaf base to the beginning of the lamina.

7. **Number of ribs per fruit:** The number of ribs in five fruits were counted and the average was worked out.

8. **Fruit length (cm):** The length of the fruit was measured from the base to the tip of the fruit.

9. **Width of fruit (cm):** The width of the fruit was measured at the middle of the fruit with the help of vernier callipers.

10. **Number of fruits per plant:** The total number of fruits picked from each plant was calculated by adding all the picking from that plant.

11. **Fruit yield per plant (g):** The marketable fruits were harvested twice a week from each plant and weighed in grams on a physical balance. The total weight of fruits from a plant was calculated by adding the weight of fruits of each picking from that particular plant.

### 3.5 Statistical Methods

The experimental data were analysed following suitable statistical and biometrical models. Following analyses were done:

1. Analysis of variance.

2. Diallel analysis:
   
   (i) Variance components analysis.

   (ii) Combining ability analysis.

3. Heterosis and inbreeding depression.

5. Associations and path coefficient analysis.

3.5.1 Analysis of variance for experimental design

Outlines of the methodology used in the above analyses are given as under:

Analysis of variance

The analyses of variance was based on the model:

\[ P_{ijk} = u + v_{ij} + r_k + e_{ijk} \quad (i,j = 1...t; \ k = 1...b; \ i \neq j) \]

where,

- \( P_{ijk} \) = the phenotype of \( ijk \)th observation
- \( u \) = the population mean
- \( v_{ij} \) = the effect of \( i \)th variety at \( j \)th progeny
- \( r_k \) = the effect of \( k \)th replication
- \( e_{ijk} \) = the error for \( ijk \)th observation

Skeleton of combined ANOVA for parents, \( F_1 \)s and \( F_2 \)s.

<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 = 2 )</td>
<td>( M_r )</td>
<td>( M_r/M_{e1} ) for ( r - 1 ), ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>Treatments</td>
<td>( t - 1 = 99 )</td>
<td>( M_t )</td>
<td>( M_t/M_{e1} ) for ( t - 1 ), ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>Parents</td>
<td>( p - 1 = 9 )</td>
<td>( M_p )</td>
<td>( M_p/M_{e1} ) for ( p - 1 ), ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>( F_1 )s</td>
<td>( f_1 - 1 = 44 )</td>
<td>( M_{f1} )</td>
<td>( M_{f1}/M_{e1} ) for ( f_1 - 1 ), ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>( F_2 )s</td>
<td>( f_2 - 1 = 44 )</td>
<td>( M_{f2} )</td>
<td>( M_{f2}/M_{e1} ) for ( f_2 - 1 ), ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>Parents vs. ( F_1 )s</td>
<td>1</td>
<td>( M_{pf1} )</td>
<td>( M_{pf1}/M_{e1} ) for 1 and ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>Parents vs. ( F_2 )s</td>
<td>1</td>
<td>( M_{pf2} )</td>
<td>( M_{pf2}/M_{e1} ) for 1 and ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>Error</td>
<td>( (r - 1)(t - 1) )</td>
<td>198</td>
<td>( M_{e1} )</td>
</tr>
</tbody>
</table>

where,

- \( r \) = number of replications.
- \( t \) = total number of treatments.
\[ p = \text{number of parents.} \]

\[ f_1 = \text{number of F}_1 \text{ hybrids.} \]

\[ f_2 = \text{number of F}_2 \text{ progenies.} \]

Skeleton of ANOVA for parents, F\textsubscript{1}s and F\textsubscript{2}s separately.

<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>( M_r )</td>
<td>( M_r/M_{e2} ) for ( r - 1 ), ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>Treatments</td>
<td>( t - 1 )</td>
<td>( M_t )</td>
<td>( M_t/M_{e2} ) for ( t - 1 ), ( (r - 1)(t - 1) ) d.f.</td>
</tr>
<tr>
<td>Error</td>
<td>((r - 1)(t - 1))</td>
<td>( M_{e2} )</td>
<td>( = 108 )</td>
</tr>
</tbody>
</table>

where d.f. for parents = 9, for F\textsubscript{1}s = 44, for F\textsubscript{2}s = 44, for parents + F\textsubscript{1}s + F\textsubscript{2}s = 99.

### 3.5.2 Diallel analysis

The component analysis of the diallel crosses were carried out by the methods of Hayman (1954). The analyses are based on the following assumptions: (i) homozygosity of the parents, (ii) diploid segregation, (iii) no reciprocal differences, (iv) no genotype × environment interaction, (v) no epistatis, (vi) no multiple alleles, and (vii) no linkage.

**Testing the validity of the hypothesis**

The uniformity of \((W_r - V_r)\) would indicate the validity of hypothesis as postulated by Hayman (1954) with ungrouped randomization which may be calculated by the following formula.

\[
t^2 = \frac{n - 2}{4} \times \frac{(\text{Var.} V_r - \text{Var.} W_r)^2}{(\text{Var.} V_r \times \text{Var.} W_r) - \text{Cov.}^2(\text{V}_r, \text{W}_r)}
\]
3.5.2.1 Estimation of the components of genetic variances in $F_1$

Hayman (1954a) derived the expectations for the statistics calculated from $F_1$ diallel table and the expected values of the components of variations using least-square techniques. It was demonstrated that:

$$\hat{D} = V_{OLD} - \hat{E}$$
$$\hat{F} = 2V_{OLD} - 4W_{OLD1} - 2(n - 2)\hat{E}/n$$
$$\hat{H}_1 = V_{OLD} - 4W_{OLD1} + 4V_{1L1} - (3n - 2)\hat{E}/n$$
$$\hat{H}_2 = 4V_{1L1} - 4V_{OLD} - 2\hat{E}$$
$$\hat{h}^2 = 4(M_{L1} - M_{LO})^2 - 4(n - 1)\hat{E}/n^2$$
$$\hat{F}_r = 2(V_{OLD} - W_{0OLS} + V_{1L1} - W_r - V_r) - 2(n - 2)\hat{E}/n$$

where,

$\hat{D}$ = Component of variation due to additive effects of genes.
$\hat{E}$ = The expected environmental component of variation.
$\hat{F}$ = The means of $F_r$ over all arrays.
$\hat{H}_1$ = Component of variation due to dominance effects of genes.
$\hat{H}_2$ = $\hat{H}_1[1 - (u - v)^2]$,

where $u$ = proportion of the positive genes
and $v$ = proportion of the negative genes in the parents.

$\hat{h}^2$ = Dominance effects
(as the algebraic sum over all loci in the heterozygous phase in all crosses).

$\hat{F}_r$ = Covariation of additive and dominance effects in a single array.

$V_{OLD}$ = Variance of the parents.

$V_{1L1}$ = Mean variance of the arrays.

$V_r$ = Variance of the $r^{th}$ array.

$W_r$ = The covariance between parents and their offsprings in the $r^{th}$ array.
\( W_{OL1} \) = The mean covariance between parents and arrays.

\( V_{OL1} \) = The variance of the mean of arrays.

\((M_{L1} - M_{LO})\)

= The difference between the mean of parents and the mean of their \( n^2 \) progenies.

### Standard errors of estimates

As suggested by Hayman (1954), to calculate the standard errors of these components, first of all common multiplier or variance \( (S^2) \) is calculated by using the formula:

\[
S^2 = \frac{1}{2} \left[ \text{Var}(W_r - V_r) \right]
\]

\[
= \frac{1}{2} \left[ \frac{1}{n - 1} \sum (W_{ri} - V_{ri})^2 - \frac{1}{n} \sum (W_{ri} - V_{ri})^2 \right]
\]

and then,

\[
\text{S.E.} \hat{D} = \sqrt{\frac{S^2(n^5 + n^4)}{n^5}}
\]

\[
\text{S.E.} \hat{F} = \sqrt{\frac{S^2(4n^5 + 20n^4 - 16n^3 + 16n^2)}{n^5}}
\]

\[
\text{S.E.} \hat{H}_1 = \sqrt{\frac{S^2(n^5 + 41n^4 - 12n^3 + 4n^2)}{n^5}}
\]

\[
\text{S.E.} \hat{H}_2 = \sqrt{\frac{S^2(36n^4)}{n^5}}
\]

\[
\text{S.E.} \hat{h}^2 = \sqrt{\frac{S^2(16n^4 + 16n^2 - 32n + 16)}{n^5}}
\]

\[
\text{S.E.} \hat{E} = \sqrt{\frac{S^2(n^4)}{n^5}}
\]

where \( n = 10 \) is the number of parents.

#### 3.5.2.2 Estimation of components of variation of \( F_2 \) generation

Analysis for \( F_2 \) generation is done on the basis of different formulae, suggested by Jinks (1956), Hayman (1958) and Mather and Jinks (1971). Analysis of \( F_2 \) generation is of the same form as for \( F_1 \) generation, except the contribution of
'h' is halved by one generation of inbreeding, with the result that coefficients of $H_1$ and $H_2$ are $1/4$ of that of $F_1$, while coefficient of $F$ is halved. The various formulae used are given as under:

$$
\bar{V}_r = V_1L_2 = (1/4)\bar{D} + (1/16)\bar{H}_1 - (1/8)\bar{F} + \bar{E}_2
$$

$$
\bar{W}_r = W_{oLo} = (1/2)\bar{D} + -(1/8)\bar{F} + (1/n)\bar{E}_2
$$

$$
V_m = V_{oLo} = (1/4)\bar{D} + (1/16)\bar{H}_1 - (1/16)\bar{H}_2 - (1/8)\bar{F} + (1/n)\bar{E}_2
$$

$$
V_p = V_{oLo} = \bar{D} + \bar{E}
$$

where,

$$
\bar{E}_2 = V E/r = M_r' \text{ of } F_2
$$

$$
n = \text{number of parents}
$$

The various genetic components were obtained following the formulae given by Singh and Chaudhary (1985):

$$
\bar{D} = V_{oLo} - \bar{E}
$$

$$
\bar{H}_1 = 16V_{1L_2} - 16W_{oLo} + 4V_{oLo} - 4(5n-4)/n\bar{E}_2
$$

$$
\bar{H}_2 = 16V_{1L_2} - 16V_{oLo} - 16(n-1)/n\bar{E}_2
$$

$$
\bar{h}^2 = (4M_{L_2} - 4M_{Lo})^2 - 16(n-1)/n\bar{E}
$$

$$
\bar{F} = 4V_{oLo} - 8W_{oLo} - 4(n-2)/n\bar{E}
$$

Standard error of various components

$$
\text{S.E.}\bar{D} = \sqrt{S^2(n^5 + n^4)/n^5}
$$

$$
\text{S.E.}\bar{H}_1 = \sqrt{S^2(16n^5 + 656n^4 - 192n^3 + 64n^2)/n^5}
$$

$$
\text{S.E.}\bar{H}_2 = \sqrt{S^2(576n^4)/n^5}
$$

$$
\text{S.E.}\bar{h}^2 = \sqrt{S^2(256n^2 + 512n + 256)/n^5}
$$
S.E. $F = \sqrt{S^2(16n^5 + 80n^4 - 64n^3 + 64n^2)/n^5}$

S.E. $E_2 = \sqrt{S^2(n^4)/n^5}$

where,

$$S^2 = \frac{1}{2} \text{Var.}(W_r - V_r)$$

$n = \text{number of parents}$

**Test of significance of components of variation**

The significance of various statistics was tested by 't' ($n - 2$) degree of freedom (Singh and Chaudhary, 1985), where $n$ is the number of parents, and

$$t = \frac{\text{Parameter}}{\text{S.E. of parameter}}$$

**3.5.2.3 Other Statistics**

The different proportion of the genetic parameter was also worked out as follows:

(a) (i) Mean degree of dominance ($F_1$) = ($\widehat{H}_1/\widehat{D}$)$^{1/2}$

(ii) Mean degree of dominance ($F_2$) = $[1/4(\widehat{H}_1/\widehat{D})]^{1/2}$

If it is

- 0, no dominance
- 1, complete dominance
- > 1, over-dominance
- < 1, partial dominance

(b) Proportion of genes with positive and negative effects in the parents

$$= \frac{\widehat{H}_2}{4\widehat{H}_1}$$

It denotes the mean product of $u_i$ and $v_i$ averaged over all parents of a diallel set of crosses.

when $\widehat{H}_2/4\widehat{H}_1 \approx 0.25$, it denotes symmetrical gene distribution.
when $\frac{H_2}{4H_1} >$ or $< 0.25$, it denotes asymmetrical gene distribution.

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

(i) in $F_1$, it is $= \frac{(4DH_i)(1/2)F}{(4DH_i)(1/2)F}$

(ii) in $F_2$, it is $= \frac{[1/4(4DH_i)(1/2)F]}{[1/4(4DH_i)(1/2)F]}$

If the ratios are

$= 1$, equality of dominant and recessive genes

$> 1$, excess of dominant genes

$< 1$, excess of recessive genes

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

$$z = \frac{h^2}{H_2}$$

It is an approximate measure of sets of genes exhibiting dominance.

3.5.3 Combining ability analysis

The combining ability analysis was carried out by the procedure given by Griffing (1956 b) Method 2, Model I. The mathematical model for the combining ability in Model I is assumed to be:

$$X_{ij} = u + g_i + g_j + s_{ij} + 1/b \sum_k e_{ijk}$$

where,

$i, j = 1, ..., P$ (number of parents)

$k = 1, ..., b$ (number of replications)

$u$ = population mean

$g_i$ = general combining ability effect of $i^{th}$ parent

$g_j$ = general combining ability effect of $j^{th}$ parent

$s_{ij}$ = specific combining ability effect of $ij^{th}$ combination such that $s_{ij} = s_{ji}$

$e_{ijk}$ = the environmental effect pertaining to $ijk^{th}$ observation
The restrictions imposed to this model are:
\[ \sum_i g_i = 0, \text{ and } \sum_j s_{ij} + s_{ii} = 0 \text{ (for each } i). \]

### 3.5.3.1 Estimation of the combining ability variances

General and specific combining ability variances are estimated by the following formulae:

\[
S_g = \frac{1}{p+2} (X_{i*i} + X_{i*})^2 - \frac{4}{p} X_{..}^2
\]
\[
S_s = \sum X_{ij}^2 - \frac{1}{p+2} \sum_i (X_{i*i} + X_{ii})^2 + \frac{2}{(p+1)(p+2)} X_{..}^2
\]

where,

\( S_g \) = the sum of squares due to gca.
\( S_s \) = the sum of squares due to sca.
\( p \) = number of parents.
\( X_{ii} \) = mean value of the \( i \)th parent.
\( X_{i*} \) = total of array of \( i \)th parent.
\( X_{..} \) = Grand total of \( p(p - 1)/2 \) progenies and \( p \) parental values.
\( X_{ij} \) = The progeny mean value in the diallel table.

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

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>Sum of squares</th>
<th>Mean sum of squares</th>
<th>'F' Test</th>
</tr>
</thead>
<tbody>
<tr>
<td>General combining ability</td>
<td>( p - 1 )</td>
<td>( S_g )</td>
<td>( M_g )</td>
<td>( M_g/M'_c ) for ( p - 1 ), m.d.f.</td>
</tr>
<tr>
<td>Specific combining ability</td>
<td>( \frac{1}{2}p(p - 1) )</td>
<td>( S_s )</td>
<td>( M_s )</td>
<td>( M_s/M'_c ) for ( \frac{1}{2}p(p - 1) ), m.d.f.</td>
</tr>
<tr>
<td>Error</td>
<td>( m )</td>
<td>( S_e )</td>
<td>( M'_e )</td>
<td></td>
</tr>
</tbody>
</table>

where, \( p \) = number of parents, \( S_e \) is obtained by deduction, \( M_g \), \( M_s \) and \( M'_c \) are the mean sum of squares (variances) due to gca, sca and error, respectively.
The mean sum of squares for gca and sea are obtained by dividing $S_{gf}$ and $S_s$ with the respective degrees of freedom. $M'_e$ was obtained by dividing error mean squares from the general analysis with number of replications:

$$M'_e = M_e / r$$

For 'F' test, each mean sum of square was tested against $M'_e$ at $n_1$ and $n_2$ degrees of freedom.

### 3.5.3.2 Estimation of gca and sca effects

These effects were obtained as follows:

**General combining ability (gca) of $i^{th}$ parent**

$$\hat{g}_i = \frac{1}{p + 2} (X_{i.} + X_{ii} - \frac{2}{p} X_{..})$$

**Specific combining ability (sca) of $ij^{th}$ cross**

$$\hat{S}_{ij} = X_{ij} - \frac{1}{p + 2} (X_{i.} + X_{ii} + X_{..} + X_{jj} + \frac{2}{(p + 1)(p + 2)} X_{..})$$

### Standard error of the estimates

Standard error of an estimate was calculated as the square root of the variance of the estimate. The variances of the various estimates were calculated as follows:

- Variance ($\hat{g}_i$) = $\frac{p-1}{p(p+3)} \sigma^2_e$
- Variance ($\hat{S}_{ij}$) = $\frac{p^2 + p + 2}{(p+1)(p+2)} \sigma^2_e$, where $i \neq j$
- Variance ($\hat{g}_i - \hat{g}_j$) = $\frac{p}{p+2} \sigma^2_e$, where $i \neq j$
- Variance ($\hat{S}_{ij} - \hat{S}_{ik}$) = $\frac{2(p+1)}{p+2} \sigma^2_e$
- Variance ($\hat{S}_{ij} - \hat{S}_{kl}$) = $\frac{2p}{p+2} \sigma^2_e$
where, \( \sigma^2 = M'_e \), taken as error m.s.s. from the combining ability analysis, and \( g_i \) and \( s_{ij} \) are the estimates of general and specific combining ability effects, respectively.

### 3.5.3.3 Test of the significance of gca and sca effects

Each gca and sca value was tested against zero for its significance by 't' test.

\[
t = \frac{\hat{g}_i - \bar{g}}{S.E.(\hat{g}_i)} \text{, and}
\]
\[
t = \frac{\hat{s}_{ij} - \bar{s}}{S.E.(\hat{s}_{ij})}
\]

The t value obtained was tested at error degree of freedom at 5% and 1% probability levels.

### 3.5.4 Heterosis and inbreeding depression

#### 3.5.4.1 Estimation of heterosis

Heterosis was calculated over superior or better parent (over-dominance) and over PK (economic heterosis) as follows:

Heterosis over superior parent (S.P.) = \( \bar{F}_1 - \bar{S}.P. \)

Heterosis over standard variety (S.V.) = \( \bar{F}_1 - \bar{S}.V. \)

where,

\( \bar{F}_1 \) = Mean value of the F1 generation.

\( \bar{S}.P. \) = Mean value of the superior parent.

\( \bar{S}.V. \) = Mean value of the standard variety.

Percentage heterosis over the superior parent and over the standard variety was calculated as given below:
Percent heterosis over better or superior parent (S.P.) = \( \frac{F_1 - S.P.}{S.P.} \times 100 \)

Percent heterosis over standard variety (S.V.) = \( \frac{F_1 - S.V.}{S.V.} \times 100 \)

**Test of significance of heterosis**

The test of the significance of heterosis was done by the 't' test as given below:

\[
t = \frac{F_1 - S.P.}{\text{S.E. of heterosis over superior parent}}
\]

\[
t = \frac{F_1 - S.V.}{\text{S.E. of heterosis over standard variety}}
\]

where,

\[
\text{S.E. of heterosis over superior parent and standard variety} = \sqrt{S_1^2(1/r + 1/r)}
\]

\( S_1^2 \) = Error variance obtained by using parents and \( F_1 \)s together

\( r \) = number of replications

The calculated t value was compared with table of t at error d.f. (108 d.f.) at P=0.05 and P=0.01. The difference of the two estimates was tested against C.D.

\[
\text{C.D.} = \text{S.E. of diff.} \times t\text{ 5% error d.f.}
\]

Here, S.E. difference will be = \( \sqrt{\frac{\sigma_e^2}{r}} \times \frac{3}{2} \)

where,

\( \sigma_e^2 \) = Error variance obtained by using parents and \( F_1 \)s

\( r \) = number of replications

**3.5.4.2 Estimation of inbreeding depression (I.D.)**

The inbreeding depression was calculated as follows:

Inbreeding depression = \( F_2 - F_1 = \) reduction in \( F_2 \) from \( F_1 \).
Per cent inbreeding depression (I.D.) = \( \frac{F_1 - F_2}{F_1} \times 100 \)

where,

\( F_1 \) = Mean value of the F_1 generation.
\( F_2 \) = Mean value of the F_2 generation.

Standard error of inbreeding depression was calculated as
\[ \text{S.E.}(i) = \sqrt{S^2_2 (\frac{1}{r} + \frac{1}{10r})} \]

where,

\( S^2_2 \) = Error variance obtained by using parents, F_1s and F_2s together.

Significance of inbreeding depression (I.D.) was tested by t test.

\[ t = \frac{F_1 - F_2}{\text{S.E.}(i)} \]

The t values were compared at error d.f. (198 d.f.) at P=0.05 and P=0.01. The difference of two estimates was tested against C.D. where C.D. = S.E. diff \( \times t \) for 5% at error d.f.

**3.5.5 Variability**

The genotypic and phenotypic variances were obtained from analysis of variances and genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated with the help of the following formulae:

\[
\text{GCV} = \frac{\sqrt{\sigma^2_g}}{\overline{X}} \times 100
\]
\[
\text{PCV} = \frac{\sqrt{\sigma^2_p}}{\overline{X}} \times 100
\]

where,

\( \sigma^2_g \) = genotypic variance = \( \frac{\text{M.S. Treatment} - \text{M.S. Error}}{\text{No. of replication}} \)
\( \sigma^2_p \) = phenotypic variance = \( \sigma^2_g + \sigma^2_e \) (\( \sigma^2_e \) = error variance)
\( \overline{X} \) = General mean of the character
3.5.6 Heritability and genetic advance

3.5.6.1 Heritability

Heritability in narrow sense was estimated according to Crumpacker and Allard (1962) in $F_1$ as follows:

$$h^2_{(ns)} = \frac{1}{4S}/(1/4S + 1/4T - 1/4H - E)$$

$h^2$ = Estimate of heritability coefficient,

and $D$, $H_1$, $H_2$, $F$ and $E$ are the same as explained earlier.

In $F_2$ it was calculated following the formula given by Verhabri and Murray (1969) as given below:

Heritability = $(1/4D)/(1/4D + 1/4H_1 - 1/8F + E)$

3.5.6.2 Genetic advance

In the present investigation heritability in narrow sense was used for estimating genetic advance. The genetic advance was calculated by the formula given by Robinson et al. (1951).

$$G.A. = i . h^2 \sigma_{ph}$$

where,

G.A. = Estimate of genetic advance

i. = selection differential at a particular selection intensity,

i.e., 2.06 at 5 per cent selection intensity given by Lush (1945).

$\sigma_{ph}$ = Phenotypic standard deviation

$h^2$ = Estimate of heritability coefficient
Genetic advance in per cent of mean (Genetic gain) was calculated by the formula

\[
\text{Genetic gain (\%)} = \frac{\text{G.A.}}{\bar{X}} \times 100
\]

where,

\(\bar{X}\) = Mean of the population for a particular character under study.

### 3.5.7 Estimation of genetic associations and path coefficients

#### 3.5.7.1 Correlation coefficients

The following formulae were used for calculating the phenotypic and genotypic coefficients of correlations:

- **Phenotypic Correlation Coefficient** (\(\gamma^p\))
  \[
  \text{Phenotypic Correlation Coefficient (} \gamma^p \text{) } = \frac{\text{Cov}.^p_{xy}}{\sqrt{(\sigma^p_x)(\sigma^p_y)}}
  \]

- **Genotypic Correlation Coefficient** (\(\gamma^g\))
  \[
  \text{Genotypic Correlation Coefficient (} \gamma^g \text{) } = \frac{\text{Cov}.^g_{xy}}{\sqrt{(\sigma^g_x)(\sigma^g_y)}}
  \]

where,

- \(\text{Cov}.^p_{xy}\) = phenotypic covariance of \(x\) and \(y\).
- \(\text{Cov}.^g_{xy}\) = genotypic covariance of \(x\) and \(y\).
- \(\sigma^2_p\) = phenotypic variance of \(x\) or \(y\).
- \(\sigma^2_g\) = genotypic variance of \(x\) or \(y\).

The covariances were obtained as:

- Error Covariance (\(\text{Cov}.^e_{xy}\)) = \(\text{MSP}_e\).
- Genotypic covariance (\(\text{Cov}.^g_{xy}\)) = \((\text{MSP}_g - \text{MSP}_e)/r\)
- Phenotypic covariance (\(\text{Cov}.^p_{xy}\)) = \(\text{Cov}.^g_{xy} + \text{Cov}.^e_{xy}\)
where,

\[ MSP_t = \text{Mean sum of products (treatment)} \]
\[ MSP_e = \text{Mean sum of products (error)} \]
\[ r = \text{Number of replications} \]

**Significance of correlation coefficients**

The significance of correlation coefficients was tested against 'r' values from 'r' table of Fisher and Yates (1938) at P=0.05 and P=0.01 levels for \((n - 2)\) degrees of freedom, where \(n\) is the number of paired observations.

**3.5.7.2 Path coefficient analysis**

The path coefficient analysis was done following Dewey and LU (1959) for ten characters, keeping fruit yield as the dependent character. The procedure as detailed by Singh and Chaudhary (1985) was followed. The formula is given below:

\[ \sum_{j=1}^{n-1} r_{ij} P_j N = r_i N \quad i = 1, \ldots, (n - 1) \]

where,

\(N\) = characters taken as the effect
\(i\) = column index
\(r\) = row index
\(n\) = characters taken as the causes
\(P\) = path coefficient
Direct effects were calculated by solving the equations:

\[ \sum_{j=1}^{10} r_{ij} P_j = r_{iy} \]

for \( i = 1, \ldots, 10 \) and \( y = 11 \). Here

\( r = \) correlation coefficient between fruit yield and the independent character

\( P = \) direct effect of different characters, viz., 1, 2, 3 etc.

Indirect effect was calculated as:

\[ r_{ij} \times P_{ij} \]

where \( i = 1, \ldots, n \)

\( j = 1, \ldots, n \)

\( P_{ij} = P_{1y}, P_{2y}, \ldots, P_{ny} \)

Residual effect was calculated by the following formula (Singh and Chaudhary 1985):

\[ 1 = P^2 R_{11} + \sum_{i=1}^{10} P_i r_{iy} \]

where \( y = 11 \).