Chapter III

MATERIALS AND METHODS

The present investigations were conducted at the Vegetable Research Station, Himachal Pradesh University, Solan, during four crop seasons, from 1972 to 1975. The geographical location of the site is as follows:

\[
\begin{align*}
\text{Altitude} & \quad 1500 \text{ m a.s.l.} \\
\text{Latitude} & \quad 30^\circ 51' \text{ N} \\
\text{Longitude} & \quad 70^\circ 11' \text{ E}
\end{align*}
\]

Environmental Conditions

The Vegetable Research Station, Solan, falls in mid-hill zone of Himachal Pradesh and is characterized by sub-temperate climate with high rainfall (60-100 cm) during summer months. There are early showers in the second fortnight of May, but regular monsoons start by the middle of June. High temperatures coupled with high humidity right from June to end of September, are highly congenial for the appearance and spread of fruit rot diseases in Capsicum spp. The meteorological data pertaining to the period of studies, is presented in Appendix I.
Materials

Forty genotypes of Capsicum annuum L. including hot and sweet types were grown in 1972 for evaluating against Phytophthora capsici and also scoring for other economic characters. Of the 40 genotypes, ten varieties were selected on the basis of resistance or susceptibility to P. capsici; green matured fruit colour, shape, and green fruit yield. Ten plants in each selected variety were inbred for further use in the hybridization programme. The important characteristics of these are given below:

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Variety</th>
<th>Source</th>
<th>Important characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Waxy Globe</td>
<td>Vegetable Botanist, Botanist, Himachal Pradesh, Solan.</td>
<td>Plants dwarf and compact; leaves small sized, narrow and green; flowers borne singly having white corolla and purplish anthers; fruits round very small, green creamy coloured with dark purple spots when immature and red at maturity; very pungent and resistant to fruit rot disease.</td>
</tr>
<tr>
<td>2.</td>
<td>Chinese Giant</td>
<td>P.Pooha and Sona, Poona.</td>
<td>Plants medium tall with non bushy appearance; plants green with large leaves; flowers borne singly with dirty white corolla and bluish purple anthers. Fruits thick fleshed large in size, green when immature and red when ripe; fruits pendent with 4 to 7 deep furrows from base to tip leading to the formation of knobs at the tip; sweet bell pepper variety highly susceptible to fruit rot.</td>
</tr>
</tbody>
</table>
3. California Wonder  Takii and Co.  Japan
Plants resemble in appearance and bearing habit to Chinese Giant. Fruits oblong and have three locules leading to the formation of three knobs at the tip; sweet bell pepper variety and highly susceptible to disease.

4. Osh Kosh  P. Poche and Sons, Poona.
Plants medium in height with open appearance; leaves large sized and green; flowers borne singly at nodes and are mostly erect but fruits become pendent with the increase in size and weight; fruit bulged and appear to have two locules, green when young and yellow at maturity; sweet bell pepper highly susceptible to P. capsici.

5. Volo Wonder  Asgrow  U.S.A.
The plant habit resembles Chinese Giant resistant to tobacco virus mosaic; fruits large, dark green when immature and red at maturity; sweet bell pepper, highly susceptible to fruit rot disease.

Plants medium tall and non-bushy; leaves medium in size with purplish tinge at petiole and leaf ribs; fruits thick at neck and elongated, light yellow when young and red at maturity; sweet salad and pickle pepper and highly susceptible to fruit rot.
<table>
<thead>
<tr>
<th>No.</th>
<th>Variety</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>7.</td>
<td>Hungarian Wax</td>
<td>Plants medium tall, non bushy; leaves large sized, green; fruits borne singly, pendent tapering slightly curved, flattened near the stem-end, light yellow at the green maturity stage and red at maturity; mild in pungency; a pickle variety susceptible to P. capsici.</td>
</tr>
<tr>
<td>8.</td>
<td>African Black</td>
<td>Plants medium in height, non bushy dark purple in appearance; leaves medium sized, dark coloured; flowers long pedicellate, singly at each node, corolla tips dark purple with anthers, style, stigmas pigmented; fruits medium sized; pendent, oblong, dark when immature and dark red at maturity; a pungent chilli, suffers moderate attack of P. capsici.</td>
</tr>
<tr>
<td>9.</td>
<td>Solan Yellow</td>
<td>Plants medium in height, bushy, leaves small, narrow, green; flowers long pedicellate, possess white corolla, green style and stigmas; fruits erect, small, oblong, blunt at the tip, green at young stage and yellow at maturity; pungent chilli, shows resistance to P. capsici.</td>
</tr>
<tr>
<td>10.</td>
<td>Hot Portugal</td>
<td>Plants tall, non bushy; leaves narrow and long; fruits pendent, long, thin, tapering, corrugated at the base and pointed at apex green at immature stage and red at maturity; pungent chilli, imparts red colour to culinary preparations and suitable for pickle preparation, susceptible to fruit rot disease.</td>
</tr>
</tbody>
</table>
Forty-five possible crosses among the ten parents (Diallal) were obtained during Kharif 1973 and these were advanced to $F_2$ in 1974 by covering the whole plant with muslin cloth bags for selfing them.

**Experimental Plantings**

The *Capsicum* collections were planted in the main season, i.e. on 10th June, 1972, for effective screening for disease and other characters. However, for attempting crosses to raise $F_1$ seed, it was grown as an early crop and plantings done on 20th March, 1973. In 1974, parents and $F_1$ generation were raised in monsoon season (planted on 6th June, 1974) for recording of data and advancing it to $F_2$ generation. In 1975, the plantings were again done in the main season i.e. 10th June, 1975, for scoring the parents and $F_2$ generation.

Standard cultural practices were followed during the growth periods of the crop.

**Experimental Design**

Ten parents and 45 $F_1$'s in 1974 ($F_1$ set) and the same number of entries in 1975 viz. 10 parents and 45 $F_2$'s ($F_2$ set), were grown in a randomised block design with four replications. Forty plants each of the parents and $F_1$ and 200 of the $F_2$ were planted in each block. Two guard rows of Chinese Giant, a highly susceptible variety
of bell pepper to *P. capsici*, were planted after every block, to ensure maximum disease infection.

**Observational Procedures**

Observations on various characters were recorded on 10 randomly selected plants in each plot. These plants were labelled for easy identification at the time of scoring data.

1. **Yield per plant** : The pickings of the matured green fruits were done thrice during the crop season and individual plant yields recorded in grams. Only the yield of healthy and marketable fruits was taken into account.

2. **Plant height** : Height of the plant was measured in centimetres at the time of physiological maturity of the crop. It was recorded from the soil line to the highest tip of the plant.

3. **Fruit breadth** : Fruit diameter was measured with the help of vernier caliper of the three well developed fruits on the ten randomly selected plants. The measurements were made from peduncle end, middle and near apex, of each fruit and average of the three readings was taken as diameter of the fruit.

4. **Fruit length** : The results used for recording the breadth were also measured for fruit length. It was taken from the point of contact of the fruit with the peduncle,
to the tips of the fruit. In curved fruits, the length was measured with the help of thread.

5. **Number of branches**: In Capsicum spp. the plants branch dichotomously and as such there is no main or central stem. Only well developed, main branches were counted.

6. **Number of fruits per plant**: During all the three pickings, the number of healthy fruits was counted on the tagged plants.

7. **Leaf area**: The length and breadth of the third leaf on the first branch of labelled plants were recorded in centimetres. The actual leaf area was obtained by multiplying the product of length and breadth with a common factor of 0.57. The common factor was obtained by recording the apparent leaf area (the product of the length and breadth) on 50 leaves each of the 10 parental lines and also measuring the actual area of these leaves by glass-slab method as suggested by Saini (1948). A highly significant correlation ($r = 0.99$) existed between the apparent and actual leaf area and thus the common factor was calculated.

8. **Number of seeds per fruit**: One healthy mature and well developed fruit per plant was selected and the seeds counted.

9. **Ascorbic acid**: The ascorbic acid content was estimated by titrimetric method as described by Horwitz (1960), wh
the fruits were in green marketable stage. One well
developed fruit each from labelled plants was harvested;
all the 10 fruits of a genotype in each block were chopped
together in a semi-dark room and 20 grams of representative
sample taken. Aliquots were prepared by macerating the
sample in the presence of metaphosphoric acid solution
and titrating it with 2,6-dichloroindophenol. The ascorbic
acid content of the aliquots was then found out by using
the formula \( V \times S \times D \) mg ascorbic acid per unit of the
sample, where \( V \) was ml of the dye used for titration, \( S \) was
the standardization value of the dye expressed in mg and
\( D \) was the dilution factor. The ascorbic acid content per
100 grams of the material was calculated by multiplying
with a common factor of 5.

10. Vitamin A content: The vitamin A content was
estimated by developing columns as suggested by Booth (1957).

One gram of fresh sample from the same material
used for ascorbic acid studies was drawn and ground finely
with pestle and mortar under the solvent light petroleum
ether and acetone in 1:1 ratio saturated with quinol. The
coloured solution was then decanted in a separatory funnel
containing water. 15-20 ml of solvent was used for each
sample. The acetone was removed from the extract by
repeated washings with water. Thus all the carotenoids and
chlorophylls were concentrated in the light petroleum layer.
Columns of alumina - sodium sulphate mixture (1:1) of 2 cm diameter and 4 cm high, were prepared. The alumina as well as sodium sulphate were activated at 150°C for 12 hours before use. The solution of pigments was passed through these columns; the pigments were adsorbed on the alumina mixture and the filtrate was colourless. When 3 per cent acetone in light petroleum was drawn through the column, a narrow orange band of δ-carotene separated and passed down the column, leaving other carotenoids and chlorophylls still adsorbed. The elute was collected in 50 ml volumetric flask and its volume raised to the mark with 3 per cent acetone in light petroleum. The absorption of the elute was observed at 450 nm with the properly calibrated spectrophotometer and vitamin A content per 100 grams of the material worked out as under:

\[ C = \frac{(A \times 100)}{(196 \times L \times W)}, \]

where \( C \) = δ-carotene mg/100 g of material
\( A \) = Absorption value
\( L \) = Cell length in cm
\( W \) = Grams sample/ml final dilution.

δ-carotene was multiplied by 1667 to give international units of vitamin A per 100 grams of material.

11. Capsaicin content: Capsaicin content was determined by colorimetric method developed by Casado, Horvath and Nagy (1960) and modified by Quaglietti (1971).
Ten mg of capsaicin was dissolved in 100 ml of sodium hydroxide N/10 solution. From the above solution 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 4.0, 4.5 and 5.0 ml were taken and volume raised to 5 ml with sodium hydroxide N/10. To each one of these solutions, 3.0 ml of 3.0 per cent phosphomolybdic acid solution (3 g/100 ml of distilled water) was added. These were kept for rest for one hour and compared the tubes in transmitted light at 650 nm. The standard graph was drawn, with different concentrations as base and optical density taken on Y axis.

Peppers from the labelled plants were chopped and then dried in a forced air oven at 75.0°C for four hours, followed by 65.0°C for eight hours. One gram of representative sample for each plot was taken for the estimation of capsaicin content. The sample was dissolved in 20 ml of acetone and allowed to macerate for 2 to 3 hours with occasional shakings, 5 ml of acetone extract was taken and heated to dryness on a water bath; then to this added 5 ml of NaOH N/10 and also 3 ml of 3 per cent phosphomolybdic acid solution. After resting for one hour, the solutions were compared at spectrophotometer in transmitted light at 650 nm wave length.

The content of capsaicin present in different samples was obtained from the standard graph and converted into percentage.
Statistical Analysis

The mean values of 10 plants per progeny in each replication were subjected to randomized complete block analysis. The data were analysed in two sets i.e. 10 parents + 45 $F_1$'s and 10 parents + 45 $F_2$'s. The analysis of variance table was set up as under:

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>Mean sum of squares</th>
<th>Variance ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blocks</td>
<td>b-1</td>
<td>$M_b$</td>
<td>$M_b/M_e$</td>
</tr>
<tr>
<td>Progenies</td>
<td>p-1</td>
<td>$M_p$</td>
<td>$M_p/M_e$</td>
</tr>
<tr>
<td>Error</td>
<td>$(b-1)(p-1)$</td>
<td>$M_e$</td>
<td>$M_e$</td>
</tr>
<tr>
<td>Total</td>
<td>$b(p-1)$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Where

- $b$ = Number of blocks
- $p$ = Number of progenies
- $M_p$ = Progeny mean square
- $M_b$ = Block mean square
- $M_e$ = Error mean square

If the F test was found significant, critical differences were calculated to find the superiority of one entry over the other.

Diallel tables were compiled separately for the characters for which the progenies significantly differed. Diallel tables were analysed for general and specific
combining ability, variance components and graphic analysis.

**Estimation of heterosis**: Heterotic effects of \( F_1 \) and \( F_2 \) generations were calculated over the mid parent and the higher parent and were expressed as percentage increase or decrease in the mean values. Heterosis over mid parent

\[
\text{Heterosis over mid parent} = \frac{\bar{H} - \bar{M.P.}}{\bar{M.P.}} \times 100
\]

Heterosis over better parent

\[
\text{Heterosis over better parent} = \frac{\bar{H} - \bar{B.P.}}{\bar{B.P.}} \times 100
\]

where \( \bar{H} \) refers to means of \( F_1 \) or \( F_2 \), in which heterosis was calculated, \( \bar{M.P.} \) to mean value of 2 parents of that particular \( F_1 \) or \( F_2 \), and \( \bar{B.P.} \) to mean value of the better parent of that particular \( F_1 \) or \( F_2 \).

**Combining ability analysis**: The estimates of variance for general and specific combining ability and their effects were computed by method 2 (parents plus one set of crosses, but no reciprocals) and Model I (fixed effect model) as given by Griffing (1956 b).

Model I assumes that variety and block effects are constant and environment effect is variable and the experimental material constitutes the population about which the inferences are to be made. It compares combining ability of the parents, when these themselves are used as
tasters. Errors are independently distributed with the mean as zero and variance $s_e$. On Method 2 Model I, the mathematical model was:

$$P_{ijk} = m + g_{ii} + g_{jj} + s_{ij} + b_k + e_{ijk}$$

Where

- $P_{ijk}$ = Phenotype of $ijk$th observation
- $m$ = Population mean
- $g_{ii}$ = general combining ability of the $i$th parent
- $g_{jj}$ = general combining ability of the $j$th parent
- $s_{ij}$ = specific combining ability of the cross involving $i$th as the female and $j$th as the male parent such that $s_{ij} = s_{ji}$
- $b_k$ = block effect
- $e_{ijk}$ = error term associated with $ijk$th observation

The restrictions imposed on this model were:

$$\sum g_{ii} = 0 \quad \text{and} \quad \sum s_{ij} + s_{ji} = 0 \quad (\text{for each } i)$$

### Analysis of variance table for combining ability

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>S.S.</th>
<th>M.S.</th>
<th>Expected mean square</th>
</tr>
</thead>
<tbody>
<tr>
<td>General combining ability</td>
<td>$(p-1)$</td>
<td>$g_p$</td>
<td>$g_p$</td>
<td>$\sigma^2 + \frac{1}{p+2} \sum g_{ii}^2$</td>
</tr>
<tr>
<td>Specific combining ability</td>
<td>$\frac{a(p-1)}{2}$</td>
<td>$s_{a}$</td>
<td>$s_{a}$</td>
<td>$\sigma^2 + \frac{1}{p(p-1)} \sum s_{ij}^2$</td>
</tr>
<tr>
<td>Error</td>
<td>$(b-1)(p-1)$</td>
<td>$e_{b}$</td>
<td>$e_{b}$</td>
<td>$\sigma^2$</td>
</tr>
</tbody>
</table>
Where

\[
\begin{align*}
S_g &= \frac{1}{p+2} \left[ \sum_i (x_{1i} + x_{i1})^2 - \frac{4}{p} \bar{x}_i^2 \right] \\
S_r &= \sum_{i,j} x_{ij}^2 - \frac{1}{p+2} \sum_i (x_{1i} + x_{i1})^2 - \frac{2}{(p+1)(p+2)} \bar{x}_i^2 \\
\end{align*}
\]

- error mean square/number of replications
- \( p \) = number of parents
- \( x_{1i} \) = total of the array of \( i \)th parent
- \( x_{i1} \) = value of \( i \)th parent
- \( x_{..} \) = grand total of \( \frac{1}{p}(p-1) \) progenies and \( p \) parental values, and
- \( x_{ij} \) = progeny mean value in the diallel table

Combining ability estimates and their standard errors:

General combining ability effect of \( i \)th parent:

\[
g_i = \frac{1}{(p+2)} (x_{1i} + x_{i1} - \frac{2}{p} x_{..}) \quad \text{and}
\]

Specific combining ability effect of \( ij \)th cross:

\[
s_{ij} = x_{1ij} - \frac{1}{(p+2)} (x_{1i} + x_{i1} + x_{1j} + x_{ij}) + \frac{2}{(p+1)(p+2)} x_{..}
\]

To test the significance of general and specific combining ability estimates, different standard errors were calculated as under:

\[
\text{S.E. for g.c.a. effects} = \sqrt{\frac{S_r}{p(p+2)}}
\]

\[
\text{S.E. for s.c.a. effects} = \sqrt{\frac{S_r}{(p+1)(p+2)}}
\]
S.E. for difference between two g.c.e. effects

\[ (g_i - g_j) = \sqrt{\frac{2 m}{p+2}} \]

S.E. for difference between two s.c.e. effects in different arrays

\[ (S_{ij} - S_{jk}) = \sqrt{\frac{2 m}{p+2}} \]

Critical differences were estimated by multiplying the corresponding S.E. of difference with the table value of 't' at error degrees of freedom.

**Geometric or graphic analysis**: The graphic analysis was based on the variance-covariance matrix, following the methodology given by Jinks and Hayman (1953), Hayman (1954, 1956) and Jinks (1954, 1955). Data were set in diallel table and following second degree statistics computed from it:

- \( W_r \) = Variance of all offsprings in each parental array, when an array consisted of parental mean and mean values of all the crosses involving that parent.

- \( W_r \) = Covariance of the offspring in each parental array with the non-recurrent parent.

- \( W_p \) = Variance of parents.

- \( W_m \) = Variance of array means.
- 36 -

The limits of the VR, WR graph were set by a parabola with the equation VR = VP x VR. The slope of the regression line (b) and the Y - intercept (a) were obtained from the relationship

\[ VR = a + b VR \] or say
\[ a = VR - b VR \]

\[ b = \frac{Cov VR, WR}{Var VR} \]

The standard error of 'b' was obtained from the formula:

\[ Sb = \left[ \frac{\sum(v-\bar{v})^2 - b \sum(x-\bar{x})(y-\bar{y})}{(n-2)(x-\bar{x})^2} \right]^{1/2} \]

Where,

- \( x = VR \), and
- \( y = WR \)

The significance of difference of 'b' from zero and from unity was tested by using 't' value of \((b-0)/Sb\) and \((1-b)/Sb\) with \((n-2)\) degrees of freedom.

The assumptions of this analysis are:-

1. Diploid segregation
2. Independent action of non-allelic genes
3. Homozygous parents
4. Genes independently distributed between the parents
5. No maternal effects
6. No multiple allelism
Plotting of the graphs: \( V_r, W_r \) graph was plotted by taking \( V_r \) along the \( x \)-axis and \( W_r \) along the \( y \)-axis. Since \( V_r \) value is always positive while \( W_r \) can be positive or negative, \( V_r W_r \) is only a two quarter graph.

Estimation of components of genetic variation: Hayman (1954, 1955) gave the following expectations for the statistics calculated from a diallel table:

\[
\begin{align*}
F_1
V_{OLO} & = (V_p) = D + \bar{e} \\
W_{OLOI} & = (\bar{V}_r) = 1/2D - 1/4F + \bar{e}/n \\
V_{ILI} & = (\bar{V}_r) = 1/4D - 1/4F + 1/4H_1 + n+1/2nE \\
V_{OLI} & = (V_m) = 1/4D - 1/4 F + 1/4H_1 - 1/4H_2 + \bar{e}/2n \\

F_2
V_{OLO} & = (V_p) = D + \bar{e} \\
W_{OLOI} & = (\bar{V}_r) = 1/2D - 1/8F + \bar{e}/nE \\
V_{ILI} & = (\bar{V}_r) = 1/4D - 1/8F + 1/16H_1 + n+1/2n E \\
V_{OLI} & = (V_m) = 1/4D - 1/8F + 1/16H_1 - 1/16H_2 + 1/2nE \\
\end{align*}
\]

The expected values of the components of variation obtained by the least squares are as follows:

\[
\begin{align*}
D & = V_{OLO} - \bar{e} \\
F & = 2V_{OLO} - 4W_{OLOI} - 2(n-2) \bar{e}/n \\
\end{align*}
\]
\[ H_1 = V_{OLO} - 4V_{OLO} + 4V_{ILI} - (3n-2)E/n \]
\[ H_2 = 4V_{ILI} - 4V_{OLI} - 2E \]

Where,

\( V_{OLO} \) = Variance of the parents (\( \hat{V}_p \))
\( V_{OLO} \) = the mean covariance between the parents and the arrays (\( \hat{V}_r \))
\( V_{ILI} \) = the mean variance of the arrays (\( \hat{V}_r \))
\( V_{OLI} \) = the variance of the means of the arrays (\( \hat{V}_m \))
\( E \) = the expected environmental components of variance which is the same as the observed one
\( D \) = component of variation due to additive effects of genes
\( H_1 \) = component of variation due to dominance effects of genes
\( F \) = the mean of the Fr (the covariation of additive and dominance effects in a single array) over the arrays.
\( H_2 \) = \( H_1 (1 - (u-v)^2) \) where \( u = \) proportion of positive genes in the parents, \( v = \) proportion of negative genes in the parents (or of the genes with positive/negative effects), and \( u + v = 1 \)

In order to estimate the accuracy of these genetic components of variation, listed above, the equation used is \( 1/2 \text{Var}(u_r, v_r) = s^2 \), and the terms of the main diagonal of covariance matrix given by Hayman (1954), as corresponding
multipliers. The following formulae were used in computing the standard errors:

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

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

\[
\text{S.E. of } H_1 = \sqrt{\frac{a^2(n^5 + 4n^4 - 12n^3 + 4n^2)}{n^5}}
\]

\[
\text{S.E. of } H_2 = \sqrt{\frac{a^2(3n^4)}{n^5}}
\]

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

After testing the significance of components of D, H₁, H₂ and F, the following estimates were calculated:

\[
\text{Dominance ratio } = \sqrt{\frac{H_1}{D}}
\]

The proportion of dominant and recessive genes in parents \((K_D/K_R) = (4D H_1)^{1/2} + F/(4D H_1)^{1/2} - F\)

The mean value of \(u, v\) over all loci = \(1/4 H_2/H_1\) when \(u\) refers to the frequency of dominant alleles and \(v\) to recessive alleles.

\[
\text{Heritability (broad sense) } = \frac{1/2 D + 1/4 H_1}{\sqrt{2D + \sqrt{4H_1} + 1}}
\]

\[
\text{Heritability (narrow sense) } = \frac{1/2 D}{\sqrt{2D + \sqrt{4H_1} + 1}}
\]
Where,

\[ D = \text{additive variance} \]
\[ H_1 = \text{dominance variance} \]

**Standard deviation graph**: The standardized deviation graphs were drawn according to Johnson and Aksel (1959). The standardized deviation of \( Y_r \), the parental measurement and \( (U_r+V_r) \) the order of dominance of the parents were computed by the formula \((x_i - \bar{x})/s\), where \( x_i \) is the value of the individual parent, \( \bar{x} \) is the mean of the parent and \( s \), the standard deviation. The values of the \( Y_r \) were taken on the \( x \)-axis and those of \( (U_r+V_r) \) on the \( y \)-axis.

**Correlation studies**: The genotypic and phenotypic correlations were calculated from the variance and covariance components according to the method given by Fisher (1954) and Aljibouri, Miller and Robinson (1958). The formulae applied in the analysis:

**Phenotypic correlation** \((r_{xy(p)})\):

\[
\frac{\text{Cov} \ xy(p)}{\sqrt{\delta^2 x(p) \times \delta^2 y(p)}}
\]

When,

\[ \text{Cov} \ xy(p) = \text{covariance of characters } x \text{ and } y \]
\[ \delta^2 x(p) = \text{variance of character } x \]
\[ \delta^2 y(p) = \text{variance of character } y \]
Genotypic correlation ($r_{xy}(g)$):

\[
\frac{\text{Cov } x y(g)}{\sqrt{\sigma^2_x(g) \times \sigma^2_y(g)}}
\]

When, \( \text{Cov } x y(g) \) = Genotypic covariance of characters \( x \) and \( y \)

\( \sigma^2_x(g) \) = Genotypic variance for the character \( x \)

\( \sigma^2_y(g) \) = Genotypic variance for the character \( y \)

The levels of significance of \( r_{xy}(p) \) and \( r_{xy}(g) \)
at \( p = 2 \) degrees of freedom, were tested.