Chapter-III

MATERIAL AND METHODS

The present project entitled “Genetic studies on yield and its components in vegetable pea (Pisum sativum L.)” was undertaken with a view to study the genetic architecture of some important quantitative and qualitative traits in respect of components of variance, combining ability variance and effects, heritability and genetic advance. The details of experimental material used and methods applied during the course of investigation are being described as follows.

Material:-

A set of ten varieties/lines of vegetable pea with diverse origin and wide phenotypic diversity were selected from the germplasm maintained at Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture Technology, Kalyanpur, Kanpur. The source and distinguishing features of the parental lines are given below in table 1.

Table-1: Source and characteristics of 10 parental varieties/ lines of vegetable pea

<table>
<thead>
<tr>
<th>Sl.No.</th>
<th>Varieties / Lines</th>
<th>Source</th>
<th>Characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>AZAD PEA-1 (AP-1)</td>
<td>Kalyanpur</td>
<td>Medium tall, high yielding, wrinkled seeded, medium in maturity, powdery mildew susceptible and wider adaptability</td>
</tr>
<tr>
<td>2.</td>
<td>Arkel</td>
<td></td>
<td>Table pea, dwarf, good yielder, wrinkled seeded, early maturity, yield 80-90 q/ha</td>
</tr>
<tr>
<td>3.</td>
<td>AZAD PEA-3 (AP-3)</td>
<td>Kalyanpur</td>
<td>Table pea, dwarf, good yielder, bold and wrinkled seeded, early in flowering, escape the powdery mildew disease with wider adaptability.</td>
</tr>
</tbody>
</table>
Table-1: Contd…

<table>
<thead>
<tr>
<th>Sl.No.</th>
<th>Varieties / Lines</th>
<th>Source</th>
<th>Characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>4.</td>
<td>AZAD PEA-4 (AP-4)</td>
<td>Kalyanpur</td>
<td>Medium in maturity, disease resistant, light green foliage, medium tall, branched, medium pod size, green pod, yield 100-110 q/ha.</td>
</tr>
<tr>
<td>5.</td>
<td>KS-156</td>
<td>Kalyanpur</td>
<td>Medium maturity, medium tall, green foliage, long poded, high yielder and disease susceptible.</td>
</tr>
<tr>
<td>6.</td>
<td>KS-175</td>
<td>Kalyanpur</td>
<td>Medium maturity, medium tall, green foliage, small poded, wrinkled seeded and disease susceptible.</td>
</tr>
<tr>
<td>7.</td>
<td>KS-150</td>
<td>Kalyanpur</td>
<td>Medium tall, high yielder, medium in maturity, round green seeded, powdery mildew susceptible, dark green foliage.</td>
</tr>
<tr>
<td>8.</td>
<td>E-6</td>
<td>Punjab</td>
<td>Extra early maturity, dwarf, medium pod size, round green seed, powdery mildew susceptible.</td>
</tr>
<tr>
<td>9.</td>
<td>PMR-20</td>
<td>Pant Nagar</td>
<td>Mid season, powdery mildew resistant, green pod yield 90 q/ha, yet to be released.</td>
</tr>
<tr>
<td>10.</td>
<td>PSM-3</td>
<td>Pant Nagar</td>
<td>Early maturity, powdery mildew resistant, green pod, yield 90-100 q/ha, yet to be released.</td>
</tr>
</tbody>
</table>

Experimental Condition:-

Experimental field is situated at Bundelkhand Research in Hamirpur. All the standard agronomical practices were applied during experimentation in Brahmanand Mahavidyalaya, Rath, Hamirpur.

Building up of material:-

The ten parents were planted in the experimental farm of Department of Genetics and Plant Breeding of Brahmanand Mahavidyalaya, Rath, Hamirpur.
during Rabi 2007 and the crosses were made in diallel design excluding reciprocals and F₀ or F₁ seeds from all the 45 crosses were procured.

**Experimental Design:**

The 45 F₁s along with their 10 parents were sown in November 2008 in a randomized block design with three replication for their performance in a single row length of 3.50 m maintaining row to row 50 cm and plant to plant spacing of 10 cm. Each replication comprised of 55 plots.

**Observations recorded:**

Observations were recorded on ten randomly selected plants from both parents and F₁s from each replication. The selected plants were labeled properly before flowering for recording the observations. The data on the following characters were recorded.

1. **Days to flowering:**

   Days to flowering was considered as number of days from sowing to the opening of first flower in each randomly selected plant.

2. **Days to maturity:**

   Days to maturity was recorded as the number of days from the date of sowing to the maturity of first pod (edible pod for marketing) in ten selected plants.

3. **Plant length:**

   The plant length was recorded at the time of final harvest from base of the plant to the tip by meter scale in cm.
4. Number of pods per plant:-

Number of edible pods per plant harvested at each picking were recorded and added together after final harvesting of pods which was recorded as number of pods per plant in selected plants.

5. Pod length:-

Ten edible pods were selected from parents and F₁s of equal age and was measured in cm from their stalk junction to the tip of pod and average was calibrated.

6. Pod width:-

The width of pod was recorded in cm with the help of vernier calipers. The average of 10 pods of parents and F₁’s were recorded.

7. Number of seeds per pod:-

The number of developed ovules was counted in 10 edible pod in parents and F₁’s both and average was worked out.

8. Length of first fruiting inter node:-

It was recorded as distance in cm from the base to the node at which first pod formed.

9. Number of first fruiting node:-

It was recorded as number from the very first node from the base to the node at which first pod formed.

10. 100 grain weight

100 grain seed farm each plant were counted and weighted in grams.
11. Green pod yield per plant:-

Green pod yield per plant was recorded at each picking from tagged plants and were added together after final harvest of pods to get green pod yield per plant (g).

12. Yield per plant

The total seed collected separately from each selected plant and its weight was recorded in gram.

METHODS:-

Statistical and biometrical techniques:-

The experimental data were computed by taking the mean of each treatment over three replication and subjected to the following statistical and biometrical computations.

1) Analysis of variance.

2) Diallel analysis.
   a) Genetic component analysis.
   b) Graphical analysis.
   c) Combining ability analysis.
   d) Degree of dominance.

3) Estimation of heterosis.

4) Selection parameters.
   a) Variability.
   b) Heritability.
   c) Genetic advance.
(1) Analysis of variance:-

The analysis of variance (ANOVA) for the experimental design was based on the following model.

\[ P_{ijk} = \mu + v_{ij} + r_k + e_{ijk}. \]

\[ (ij = 1,2,3\ldots\ldots t) \]

\[ (k = 1,2,3\ldots\ldots r) \]

Where,

- \( P_{ijk} \) = The phenotype of ijk\( ^{th} \) observation.
- \( \mu \) = The population mean.
- \( v_{ij} \) = The effect of ij\( ^{th} \) progeny.
- \( r_k \) = The effect of k\( ^{th} \) replication.
- \( e_{ijk} \) = The error for ijk\( ^{th} \) observation.

The analysis of variance (ANOVA) of the experimental design was done by partitioning the treatment variance into their components, namely variance due to parents, \( F_1 \)\( s \) and the Parents vs \( F_1 \)\( s \) in the following ways.

**ANOVA Table**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>M.S.S.</th>
<th>‘F’ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</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>Parents</td>
<td>(p-1)</td>
<td>Mp</td>
<td>Mp/Me</td>
</tr>
<tr>
<td>( F_1 )( s )</td>
<td>f( _1 )-1</td>
<td>Mf( _1 )</td>
<td>Mf( _1 )/Me</td>
</tr>
<tr>
<td>Pvs ( F_1 )( s )</td>
<td>1</td>
<td>Mp( _f_1 )</td>
<td>Mp( _f_1 )/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,

\[ r = \text{Number of replications.} \]
\[ t = \text{Number of treatments.} \]
\[ p = \text{Number of parents.} \]
\[ F_1 = \text{Number of } F_1 \text{ crosses.} \]

2) Diallel analysis:

(A) Analytical approach:

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

Expectations for \( F_1 \) diallel are

\[
\begin{align*}
V_p &= D + E \\
V_r &= (1/4)D + (1/4)H_1 - (1/4)F + [(n+1)/2n]E \\
W_r &= (1/2)D - (1/4)F + (1/n)E \\
V_m &= (1/4)D + (1/4)H_1 - (1/4)H_2 - (1/2)F + (1/2n)E
\end{align*}
\]

Where

\[
\begin{align*}
V_p &= \text{Variance of the parents} \\
V_r &= \text{Mean of the } V_r \text{ for all the arrays} \\
V_m &= \text{Variance of arrays mean} \\
D &= \text{Components of variance due to additive effects of genes.} \quad = VoLo - E \\
H_1 &= \text{Components of variance due to dominance effects of genes.} \quad = VoLo - WoLoI + 4V_i L_i - (3n-2) E/n \\
H_2 &= H_t[1-(u-v)^2] \\
&= 4V_i L_i - 4V_o L_i - 2E
\end{align*}
\]
Where,

\[ u = \text{Proportion of positive genes in the parents.} \]
\[ v = \text{Proportion of negative genes in the parents.} \]
\[ F = \text{The mean of } F_i \text{ over the arrays.} \]

Where

\[ F_1 = \text{The covariance of additive and dominance effects in a single array.} \]
\[ = 2(VoLo-WoLo+V_I-L_I-Wr-Vr)-2(n-2) \frac{E}{n} \]
\[ h^2 = \text{Dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses)} \]
\[ = 4(MLI-MLo)^2-4(n-1) \frac{E}{n} \]
\[ E = \text{The expected environment component of variation.} \]
\[ = (\text{error S.S. + Replication S.S. /df}) / \text{number of replications.} \]

**Standard error:-**

In order to estimates the accuracy of the components \((D, H_1, H_2, F_1, h^2 \& E)\) of variance, the term of main diagonal of the matrix given by Hayman (1954b) with common multipliers \(S^2/n^5\) was used.

Where,

\[ S_2 = \frac{1}{2} \text{var (Wr-Vr)} \]

The formula being:

\[ S.E.(h) = \pm[S^2(4n^5 + 20n^4 - 16n^3 + 16n^2)/n^5]^{0.5} \]
\[ S.E.(H_1) = \pm[S^2(n^5 + 41n^4 - 12n^3 + 4n^2)/N^5]^{0.5} \]
\[ S.E.(H_2) = \pm[S^2(36n^4)n^5]^{0.5} \]
\[ S.E.(h^2) = \pm[S^2(16n^4 + 16n^2 - B2n + 16)/n^5]^{0.5} \]
\[ S.E.(E) = \pm[S^2(n^4/n^5)]^{0.5} \]
If the value of the parameters divided by its standard error exceeds 1.96, then it is significant.

**Other related parameters:-**

The mean degree of dominance was calculated as $(H_1/D)^{0.5}$. The proportion of genes with +ve and -ve effects was calculated as $H_2/4H_1$. The proportion of dominant and recessive gene groups which control the character estimated as $[(4DH_1)^{0.5} + F(4DH_1)^{0.5} – F]$, number of gene group as $h^2/H_2$ and the coefficient of correlation $(r)$ between the parented order of dominance $(W_r+V_r)$ and parented measurement $(Y_r)$ as ‘$r$’ were calculated.

**(B) Graphical Approach:-**

The graphical analysis was based on the variance and covariance value following the procedure given by Jinks and Hayman (1953) and later elaborated by Jink (1954,56) and Hayman (1954 a,b, 1957) and Askel and Johnson (1963).

The variance and covariance were calculated from the following statistics.

\[
\text{Parental mean} = \frac{\text{Sum of all parental values}}{\text{Total number of parents}}
\]

\[
= \frac{\text{Variance of parents (VP) = VoLo}}{1/(n-1) \left[\text{Sum of square of parental values – C.F.}\right]}
\]

Where,

\[
\begin{align*}
    n &= \text{Number of parents} \\
    \text{CF} &= \text{Correction factor} \\
    V_r &= \text{variance of each array} \\
    &= 1/(n-1) \left(\text{Sum of square of crosses involving particular, parent} – \text{CF}\right)
\end{align*}
\]
Where,

\[ CF = \frac{(\text{Sum of all ‘n’ crosses involving a particular line})^2}{\text{Number of crosses}} \]

Mean variance of the array (\(Vr\)) = \(\text{VIL}_I = 1/n (\Sigma vri)\)

The variance of the mean of arrays

\[ (Vm) = \text{VOL}_I \]

\[ = \frac{1}{n-1} [(\text{Mean of the crosses involving first parent})^2 + \text{---} + (\text{mean of the crosses involving } n^{th} \text{ parent})^2 - (\text{Grand mean})^2/n] \]

Covariance between parents & their offspring,

\[ Wr = \frac{1}{n-1} [(\text{sum of the product of } i^{th} \text{ cross with } j^{th} \text{ parent}) - (\text{product of the sum of } i^{th} \text{ cross with sum of } j^{th} \text{ parents}/n)] \]

\[ = \frac{1}{n-1} [(P_1)^2 + (P_1)(P_2) + (P_1)(P_3) + \text{----} (P_1)(P_n)] [(\text{Sum of the crosses involving a particular parent}) (\text{Sum of } n \text{ parents})/n] \]

Mean covariance between mean of the parents & the array

\[ (Wr) = \text{WoLoI} = \frac{1}{n} \Sigma Wri \]

The differences between the mean of the parents

The differences between the mean of the parents and mean of their \(n^2\) progeny = \((\text{MLI} - \text{MLo})^2\)

\[ = \left[ \frac{1}{n} \{ 1/n(\text{Grand total}) - (\text{Sum of } n \text{ parental values}) \} \right]^2 \]

The expected environment components of variance

\[ = E; \text{ It is calculated as with ungroup randomization suggested by Askel and Johnson (1963)} \]

\[ E = \left( \frac{\text{Replication SS + Error SS}}{\text{Replication df + Error d.f.}} \right) / \text{Number of replications}. \]
Testing the validity of Hypothesis:-

The following tests are made as per procedure described by Hayman (1954 a,b)

(a) Uniformity test of (Wr, Vr) using ‘t’ test at 4 and (n-2) degree of freedom

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

Which is an F with 4 & (n-2) degree of freedom. A significant value of ‘t’ would indicate the non-uniformity of Wr, Vr & thus invalidates the hypothesis postulated.

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

\[ b = \frac{\text{Cov. (Wr Vr)}}{\text{Var. (Vr)}} \]

Where,

\[ \text{Cov. (Wr Vr)} = \frac{[\Sigma Vr \times Wr - \Sigma Vr \times \Sigma Wr/n]}{(n-1)} \]

\[ \text{Var (Vr)} = \frac{[\Sigma Vr^2 - (\Sigma Vr)^2/n]}{(n-1)} \]

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

\[ \text{S.E.}(b) = \left[(\text{Var. Wr-b Cov. Wr Vr) / Var. Vr(n-2)}) \right]^{0.5} \]

Where,

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

Now, the significant value of b from zero and unity was tested by using ‘t’ value for (n-2) degree of freedom.

\[ H_0:b = 0 = (b-0) / SE (b) \]

\[ H_0:b = 1 = (1-b) / SE (b) \]
These pairs of \((W_r, V_r)\) 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 from unity \((1-b)\) against table value of ‘t’ for \((n-2)\) degree of freedom. In the absence of non-allelic interaction, \(W_r\) is related to \(V_r\) by straight line of unit slope.

**Wr, Vr Graph:**

The relationship of \(W_r\) with \(V_r\) provides some useful informations regarding parents. The \(W_r\) values are plotted against the corresponding value of \(V_r\) for a particular character. The limiting parabola is plotted by obtaining \(W_{ri}\) values against \(V_{ri}\) from the following relationship:-

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

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

For drawing regression line, we require \(W_{rei}\) values, which are calculated as follows:

\[
W_{rei} = W_r - bV_r + bV_{ri}
\]

Where,

\[
\begin{align*}
W_r & = \text{Mean of } W_r \text{ for all the arrays.} \\
V_r & = \text{Mean of } V_r \text{ for all the arrays.} \\
W_{rei} & = \text{Expected value of } W_r \text{ corresponding to } V_r. \text{By plotting of intercept of the regression line with } W_r \text{ ordinate, i.e. } a \text{ is obtained by the following equation:}
\end{align*}
\]

\[
a = \bar{W}_r - b\bar{V}_r
\]
(C) Combining ability analysis:-

The combining ability was worked out by the procedure by Griffings (1956) method –2, model –1. In this method, two steps are involved in the analysis of data. The first step consists of analysis of data for testing the null hypothesis that is no genotypic differences among F₁'s and parents are established, it is nuded to provide further to the second step of analysis i.e. combining ability analysis which is assumed as-

\[ X_{ijkl} = \mu + g_i + g_j + g_{ij} + 1/bc \Sigma k \Sigma l e_{ijkl} \]

\( i,j = 1,2,3 \ldots \ldots \ldots \ldots \ldots \ldots n; \)

\( k = 1,2,3 \ldots \ldots \ldots \ldots \ldots \ldots b; \)

\( l = 1,2,3 \ldots \ldots \ldots \ldots \ldots \ldots c) \)

Where,

\( X_{ijkl} \) = the mean of \( ij^{th} \) genotypes over \( k \& l \)

\( \mu \) = the population mean

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

\( g_j \) = the gca effect of \( j^{th} \) parent,

\( S_{ij} \) = The specific combining ability (sca) for the cross between \( i^{th} \) & \( j^{th} \) parents such as \( S_{ij} = S_{ji} \),

\( b \) = Number of replications.

\( c \) = Number of plants per replication.

\( e_{ijkl} \) = The environmental effect (mean error effect) associated with the \( ijk^l \) individual observations on \( i \)th individual in \( k \)th block with \( i \)th as female parent and \( j \)th as male parent. The analysis of variance (ANOVA) table for combining ability with expectation of mean sum of squares (ms) is as follows-
### ANOVA table for combining ability:

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Df</th>
<th>SS</th>
<th>MS</th>
<th>Expectation of MSS</th>
<th>F test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gca</td>
<td>(n-1)</td>
<td>Sg</td>
<td>Mg</td>
<td>$\sigma^2_g + \sigma^2_s + (n+2) \sigma^2_g$</td>
<td>Mg/Me</td>
</tr>
<tr>
<td>Sca</td>
<td>n(n-1)/2</td>
<td>Sc</td>
<td>Me</td>
<td>$\sigma^2_e + \sigma^2_s$</td>
<td>Ms/Me</td>
</tr>
<tr>
<td>Error</td>
<td>(b-1)(c-1)</td>
<td>Se</td>
<td>Me</td>
<td>$\sigma^2_e$</td>
<td></td>
</tr>
</tbody>
</table>

Where,

- $gca = \text{General combining ability}$
- $sca = \text{Specific combining ability}$
- $b = \text{Number of replications}$
- $c = \text{Number of treatments (Parents + F1s)}$

- $Sg = 1/(n+2)[\Sigma(x_i + x_{ii})^2 - 4/n X^2]$
- $SS = \Sigma k\Sigma jX_{2ij} - 1/(n+2) \Sigma i(X_i - X_{ii})^2 + 2/(n +1)(n +2)x^2$
- $\sigma^2_g = 1/(n+2)(Mg - Me)$
- $\sigma^2_s = Ms - Me$
- $\sigma^2_e = Me$

Where,

- $Sg = \text{the sum of square due to gca}$
- $Ss = \text{the sum of square due to sca}$
- $Se = \text{the sum of square due to error}$
- $Mg = \text{the mean sum of square due to gca}$
- $Ms = \text{the mean sum of square due to sca}$
- $Me = \text{the MSS of error obtained from ANOVA table}$
- $\sigma^2_g = \text{Estimates of gca}$
- $\sigma^2_s = \text{Estimates of sca}$
- $\sigma^2_e = \text{Estimates of error}$
The various effects were estimated as follows:

(a) Estimation of gca effects:

gca effects of $i^{th}$ parent,

$$g_i = \frac{1}{n+2} \left[ \sum (x_i + x_{ii}) - 2/n \right]$$

Where,

- $x_i$ = Row total for $i^{th}$ parent.
- $x_{ii}$ = Diagonal value of $i^{th}$ parent as a male.
- $n$ = Number of parents.

(b) Estimation of sca effects:

sca effect of $ii^{th}$ cross,

$$S_{ij} = X_{ij} - \left[ \frac{1}{n+2} (X_i + X_{ii} + X_j + X_{jj}) + 2/(n+1)(n+2) \right]$$

Where,

- $X_{ij}$ = diagonal value of $ij^{th}$ cross
- $X_i$ = raw total of $j^{th}$ parent.
- $X_j$ = diagonal value of $j^{th}$ parent
- $n$ = number of parents.
Estimation of standard error:-

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

\[
\text{S.E.(} \hat{g}_i \text{)} = [(n-1)\sigma^2_e/n(n+2)]^{0.5} = \sqrt{\text{var}(gi)}
\]

\[
\text{S.E.(} \hat{S}_{ii} \text{)} = [(n^2+n+2) \sigma^2_e/(n-1)(n+2)]^{0.5} = \sqrt{\text{var}(sii)}
\]

\[
\text{S.E.}(\hat{g}_i-\hat{g}_j) = [2\sigma^2_e/(n+2)]^{0.5} = \sqrt{\text{var}(gi-gj)}
\]

\[
\text{S.E.}(\hat{S}_{ij}) = [2(n-1)\sigma^2_e/(n+2)]^{0.5} = \sqrt{\text{var}(Sij)}
\]

\[
\text{S.E.}(S_{ij}-S_{ij}) = [2(n-2)\sigma^2_e/(n+2)]^{0.5} = \sqrt{\text{var}(Sij-Sij)}
\]

\[
\text{S.E.}(S_{ij}-S_{ik}) = [2(n+1)\sigma^2_e/(n+2)]^{0.5} = \sqrt{\text{var}(Sij-Sik)}
\]

\[
\text{S.E.}(S_{ij}-S_{ki}) = [2n\sigma^2_e/(n+2)]^{0.5} = \sqrt{\text{var}(Sij-Ski)}
\]

Where,

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

In order to compare the mean of various entries, the critical difference (CD) was calculated as follows-

\[\text{CD} = \text{SE (difference)} \times 't' \text{ value}\]

Where,

\[t = \text{table value, 5\% & 1\% at error degree of freedom.}\]

Degree of dominance:-

The average degree of dominance was calculated using the formula as suggested by Kempthorne and Curnow (1961).

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

Where,

\[\sigma^2_s = \text{estimated variance due to sca}\]
\[\sigma^2_g = \text{estimated variance due to gca}\]
(3) Estimation of Heterosis

Heterosis in terms of increase or decrease in the performance of $F_1$ over the superior parent and mid parent was calculated by the formula.

Heterosis (%) over superior parent = $\frac{\overline{F_1} - \overline{SP}}{\overline{SP}}$ x 100

Heterosis (%) over mid parent = $\frac{\overline{F_1} - \overline{MP}}{\overline{MP}}$ x 100

Where,
- $\overline{F_1}$ = Mean value of $F_1$
- $\overline{SP}$ = Mean value of superior parent
- $\overline{MP}$ = Mean value of mid parent

Test of significance:-

Significance of heterosis over superior and mid parent was tested by using simple ‘t’ test.

Where,
- $SE$ = Standard error difference between two treatment mean to be compared.
- $Me$ = Error mean squares obtained from the ANOVA.
- $r$ = Number of replication

In order to compare the mean of various entries, the CD was calculated by the following formula:
CD = SE x t (‘t’ value at 5% and 1%)

\[
\begin{align*}
\text{‘t’ value (SP)} &= \frac{F_1 - SP}{S.E.} ; \quad \text{‘t’ value MP} = \frac{F_1 - MP}{S.E.}
\end{align*}
\]

(4) Estimation of selection parameters:-

The selection parameters, namely variability, heritability and genetic advance were calculated to analysis the suitability of the selection of efficient genotypes.

(a) Estimation of variability:-

The mean sum of square for error was substracted from the mean sum of squares due to strains for obtaining the genotypic variance which was calculated according to the method as suggested by Burton (1952) and phenotypic variance calculation method as suggested by Burton and Devane (1953).

Environmental variance \((\sigma^2_e) = E\)

Phenotypic variance \((\sigma^2_{ph}) = (\sigma^2_g + \sigma^2_e)\)

\[
\sqrt{\sigma^2_g}
\]

Genotypic coefficient of variation = \(\frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100\)

Where,

\(V\) = Strain mean square,

\(E\) = error mean square,

\(r\) = Number of replications and

\(\bar{X}\) = general mean of the character
(b) Estimation of heritability

Coefficient of heritability (in narrow sense) in F1 generation was calculated by formula proposed by Crumpacker and Allard (1962) which is given as below-

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

Heritability (\%) = Heritability coefficient (h^2) \times 100

Where,

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

D, H1, F and E are components of variances

(c) Estimation of genetic advance:

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

\[\text{GA} = (k)(h^2)(\sigma^2pH)\]

And Genetic advance in % over mean of the character was calculated as

\[\text{GA (\%)} = \frac{\text{G.A.} \times 100}{\overline{X}}\]

Where,

\[\text{GA} = \text{Estimate of genetic advance.}\]

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

\[\sigma^2pH = \text{Phenotypic standard deviation}\]

\[k = \text{Selection differential constant at 5\% selection intensity i.e.} k-2.06.\]

\[\overline{X} = \text{Population mean of the character concurred.}\]