MATERIAL AND METHODS

MATERIAL:

The basic experimental material for this investigation comprised ten linseed cultivars selected on the basis of morphological diversity for different agronomic traits. Salient characteristics of the parental lines are listed in table 1. All possible crosses were made among these ten parents resulting in 45 $F_1$S produced during winter of 1992-93. Subsequently these $F_1$S were sown and selfed in production of $F_2$ seeds. The crossing plan used in producing $F_2$ has been presented in table 2.

METHODS:

Field Lay out:

A complete set of material consisting of 100 treatments (10 parent's, 45 $F_1$S and 45 $F_2$S) was grown in a randomised block with three replications at research farm of the Brahmanand Mahavidhyalaya, Rath (Hamirpur), U.P. The sowing was done on November 3, 1993. Parents, $F_1$S were sown in single rows whereas $F_2$S in two rows of 5 metre length. Row to row and plant to plant distances were kept at 50 and 10 cm/s respectively. All the cultural practices were adopted to raise the good crop.

Recording observations:

Observations were recorded for the following morphological characteristics on 10 randomly selected plants in the parental and $F_1$ populations. The observations were
recorded on their 13 biometric traits as described below in only tagged plants.

1. Days to flower:
   It was recorded as the period between seeding and opening 50% of the flower.

2. Days to maturity:
   It was recorded as period from seeding to complete maturity in days.

3. Days for reproductive period:
   It was calculated by reducing flowering time from the days to maturity.

4. Plant height:
   It was measured cm from the point of tillering to the top of the tallest shoot of the plant at the time of maturity.

5. No. of Primary Branches:
   The total number of primary branches arising from the base of the stem were counted at maturity.

6. No. of Secondary Branches:
   The total number of secondary fruit bearing branches arising from the primary branches including mother shoot were counted at the time of maturity.

7. No. of capsule per plant:
   All the seed bearing capsules on the selected plants were counted at the time of maturity.
8. No. of seeds per capsule:

Average of 10 randomly picked up capsules from each of the selected plants was taken for studying this trait and reaveraged as per plants selected for the study.

9. 1,000-seeds weight:

For determining the size, 1000 seeds were counted at random from the bulk yield of sampled plant of each treatment and weighted in g and calculated the mean 1000 seed weight in g.

10. Oil content:

The oil content in seed was measured treatment wise in each replication from bulk sample with the help of NMR and calculated in terms of percentage.

11. Fibre yield per plant:

After deseeding the stalk of selected plants were bulked treatmentwise from the bulk stalk, 100g sample of each treatment was allowed to ret around 40°C temperature in water for 5 days. Thereafter the treatmentwise stalk was sundried the fibre was extracted manually and after its weightment, mean fibre yield per plant was derived based on selected plants bulked for the purpose.

12. Harvest Index:

The harvest index was calculated with the ratio of grain yield (g) and total produce (g) and presented by this formula:

\[
\text{Harvest Index} = \frac{\text{Grain yield}}{\text{Total produce}} \times 100
\]
13. Grain yield per plant:

All the capsule hand picked from each plant, were threshed separately and clean seeds were weight in g and averaged based on plants selected.

Statistical Methods:

The data thus collected on parents, $F_1$ and $F_2$ were subjected to the following biometrical analysis.

1. To estimate components of genetic variance
2. To estimate variances of general & specific combining ability
3. To estimate general & specific combining ability effects
4. To estimate economic heterosis in $F_1$, hybrids and inbreeding depreciation incurred in $F_2$
5. To estimate the heritability excepted genetic gain in respect of attributes under study
6. To work out association among the characters under study at genotypic level.

1. Estimation of components of genetic variance:

The estimation of components of genetic variance was carried out for each character for testing null hypothesis, using following statistical model.

\[ F_{ijk} = u + V_{ij} + b_k + e_{ijk} \]

\[(i, j = 1, \ldots, t, \quad k = 1, \ldots, b)\]
Where,

\[ P_{ijk} = \text{The phenotypic of } ijk^{th} \text{ observation} \]
\[ u = \text{the population mean} \]
\[ b_k = \text{the block effect} \]
\[ e_{ijk} = \text{the error term for } ijk^{th} \text{ observation} \]

On the basis of above model, the data obtained were first subjected to randomized block analysis. The skeleton of analysis of variance is given below:

<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>Block</td>
<td>(b-1)</td>
<td>( M_b )</td>
<td>( M_b M_e ) For ( b-1 ), ( (b-1)(t-1) ) d.f.</td>
</tr>
<tr>
<td>Treatment</td>
<td>(t-1)</td>
<td>( M_t )</td>
<td>( M_t M_e ) For ( t-1 ), ( (b-1)(t-1) ) d.f.</td>
</tr>
<tr>
<td>Between Parents</td>
<td>(P-1)</td>
<td>( M_p )</td>
<td>( M_p M_e ) For ( P-1 ), ( (b-1)(t-1) ) d.f.</td>
</tr>
<tr>
<td>Between ( F_1 ) crosses</td>
<td>(( F_1-1 ))</td>
<td>( M_{F_1} )</td>
<td>( M_{F_1} M_e ) For ( F_1-1 ), ( (b-1)(t-1) ) d.f.</td>
</tr>
<tr>
<td>Between ( F_2 ) crosses</td>
<td>(( F_2-1 ))</td>
<td>( M_{F_2} )</td>
<td>( M_{F_2} M_e ) For ( F_2-1 ), ( (b-1)(t-1) ) d.f.</td>
</tr>
<tr>
<td>Parents Vs ( (F_1 + F_2) )</td>
<td>1</td>
<td>( M_{S_1} )</td>
<td>( M_{S_1} M_e ) For 1, ( (b-1)(t-1) ) d.f.</td>
</tr>
<tr>
<td>( F_1 ) Vs ( F_2 )</td>
<td>1</td>
<td>( M_{S_2} )</td>
<td>( M_{S_2} M_e ) For 1, ( (b-1)(t-1) ) d.f.</td>
</tr>
<tr>
<td>Error</td>
<td>( (b-1)(t-1) )</td>
<td>( M_e )</td>
<td></td>
</tr>
</tbody>
</table>
Test of Significance:

The mean squares due to various components were tested using F-test comparing the observed value of variance ratio with its expected value at desired probability level based on degree of freedom for different sources and degree of freedom for error. The mean squares due to interactions based on one degree of freedom were tested against the same error as for the other sources of variation.

2. Analysis of components of variance:

The analysis was made as per method suggested by Hayman (1954). The expectations in biometrical scale for various statistics worked out as given by him are as follow-

\[
V_0L_0 = \hat{D} + \hat{E}' \\
W_r = \frac{\frac{1}{2}D-\frac{1}{2}F_r+\hat{E}'}{n} \\
W_0L_{0L} = \frac{\frac{1}{2}D-\frac{1}{2}F+\hat{E}'}{n} \\
V_r = \frac{\frac{1}{2}D-\frac{1}{2}F_r+\hat{H}_1+(\hat{E}'+\frac{1}{2}(n-1)\hat{E}')}{n} \\
V_1L_1 = \frac{\frac{1}{2}D-\frac{1}{2}F+\hat{H}_1+(\hat{E}'+\frac{1}{2}(n-1)\hat{E}')}{n} \\
V_0L_1 = \frac{\frac{1}{2}D-\frac{1}{2}F+\frac{1}{2}H_1+\frac{1}{2}H_2+(\hat{E}'+\frac{1}{2}(n-2)\hat{E}')}{n^2} \\
(m_{L1}-m_{L0})^2 = \frac{\frac{1}{4}H_2^2+(n-1)((n-1)\hat{E}'+\hat{E}')}{n^3}
\]

The expected value of components were obtained by least square computation (and assuming that \( \hat{E} = \hat{E}' \))

\[
\hat{D} = V_0L_0 - \hat{E}' \\
\hat{F} = 2V_0L_0 - 4W_0L_{0L} - 2(n-2)\hat{E}'/n \\
\hat{H}_1 = V_0L_1 - 4W_0L_{0L} + V_1L_1 - (3n-2)\hat{E}'/n \\
\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\hat{E}' \\
\hat{H}^2 = 4(m_{L1}-m_{L0})^2 - 4(n-1)\hat{E}'/n^2 \\
\hat{F}_r = 2(V_0L_0 - W_0L_{0L} - V_1L_1 - W_r - V_r) - 2(n-2)\hat{E}'/n
\]
The above statistics and components are defined as follow:

\[ V_{O_O} \] = Variance of parents

\[ V_r \] = Variance of the array \(^{rth}\) array

\[ V_{1L_1} \] = mean variance of array

\[ W_r \] = The covariance between the parent and their off-springs in one array \(^{rth}\) array

\[ W_{O-O1} \] = The mean covariance between the parents and arrays

\[ V_{O-L_1} \] = The variance of the mean of arrays

\[ (m_{L1} - m_{O1})^2 \] = the difference between the mean of the parents and mean of their \(n^2\) progenies.

\[ \hat{D} \] = components of variation due to additive effects of genes

\[ \hat{H}_1 \] = components of variation due to dominance effect of the genes

\[ \hat{H}_2 = \hat{H}_1 (1-(u-v)^2) = 4V_{1L_1} - 4V_{O-L_1} - 2\hat{E} \]

Where, \(u\) = Proportion of positive genes in parents

\(v\) = Proportion of negative genes in parents

(or of the genes with positive (negative) effects and where, \(u+v=1\))

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

\[ \hat{F} \] = The mean of \(Fr\) over the array, where \(Fr\) is the covariance of additive and dominance effects in the single array
\( \hat{E} \) = The expected environmental component or variation as with ungrouped randomization as suggested by AKsel and Johnson (1963)

(Block SS + Error SS/Block d.f. + Error d.f.)

The uniformity of \( W_r - V_r \) would indicate the validity of the hypothesis postulated by Hayman (1954) which was tested by the 't' on \( n-2 \) degree of freedom with the following formula:

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

Significance of \( t^2 \) indicates the failure of hypothesis.

Standard error of estimation:

In order to estimate the accuracy of the estimates of the components of variation, the use of equation

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

was made along with the terms of the main diagonal of the covariance matrix given by Hayman (1954) as corresponding multipliers and the values as functions of the 'n' the parental number. Assuming the corresponding multipliers as \( \hat{CD}, \hat{CF}, \hat{CH}_1, \hat{CH}_2, \hat{Ch}^a \) and \( \hat{CE} \) the standard error are:

\[
\begin{align*}
\text{SE} \ \hat{D} &= (S^2 \times \hat{CD})^{\frac{1}{2}} \\
\text{SE} \ \hat{F} &= (S^2 \times \hat{CF})^{\frac{1}{2}} \\
\text{SE} \ \hat{H}_1 &= (S^2 \times \hat{CH}_1)^{\frac{1}{2}} \\
\text{SE} \ \hat{H}_2 &= (S^2 \times \hat{CH}_2)^{\frac{1}{2}} \\
\text{SE} \ \hat{h}_2 &= (S^2 \times \hat{Ch}^2)^{\frac{1}{2}} \\
\text{SE} \ \hat{E} &= (S^2 \times \hat{CE})^{\frac{1}{2}}
\end{align*}
\]
The significance of estimates $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, and $\hat{E}$ was tested by 't' at 44 degree of freedom.

Related statistics of components of variance:

$(\hat{H}_1/\hat{D})^{\frac{1}{2}} = \text{Mean degree of dominance}$

$\hat{H}_2/4\hat{H}_1 = \text{Proportion of positive and negative effects of genes in the parents}$

\[
\frac{(4\hat{D}\hat{H}_1)^{\frac{1}{2}} + \hat{F}}{(4\hat{D}\hat{H}_1)^{\frac{1}{2}} - \hat{F}} = \text{Proportion of dominant and recessive genes in the parents, } \hat{F} \text{ being insignificantly different from zero.}
\]

$\hat{h}^2/\hat{H}_2 = \text{No. of group of genes which control the character and exhibit dominance.}$

(iii) Combining ability analysis:

The combining ability analysis was carried out by the procedure suggested by Griffing (19565) for method 2, Model 1, as this model assumes that both the varieties and block effects are fixed but environmental effect is random variable and the experimental material is considered as the population itself about which the inferences are to be drawn. It compares combining ability of the parents when themselves are used as testers to detect the superior combinations. It is also assumed that error is independently and normally distributed with the mean zero and error variance $\sigma^2_e$. The mathematical model for combining ability analysis is assumed to be:
\[ X_{ijkl} = u + g_i + j + S_{ij} + \frac{l}{bc} \cdot e_{ijkl} \cdot k_i \]

\((i, j = 1, 2, \ldots, \ldots, p, \nonumber\)

\(k = 1, 2, \ldots, \ldots, b, \nonumber\)

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

Where,

\(u\) = the population mean \nonumber\)

\(g_i\) = the general combining ability (g.c.a.) of \(i^{th}\) parent \nonumber\)

\(g_j\) = the g.c.a. of the \(j^{th}\) parent \nonumber\)

\(S_{ij}\) = the specific combining ability (s.c.a.) for the cross between the \(i^{th}\) and \(j^{th}\) parents such that \(S_{ij} = S_{ji}\) \nonumber\)

\(e_{ijkl}\) = the environmental effect associated with the \(ijkl^{th}\) individual observation on \(i^{th}\) individual in \(k^{th}\) block in the \(l^{th}\) plot with \(i^{th}\) as a female parent and \(j^{th}\) as male parent. \nonumber\)

The usual restrictions such as \(\xi g_i = 0\) and \(\xi S_{ij} = S_{ij} = 0\) (for each \(i\)) are imposed. \nonumber\)

The analysis of variance table for method 2, model 1 (parents and one set of \(F_1\)es are included but not reciprocal \(F_1\)es) with expectations of mean sum of squares is as follows:
<table>
<thead>
<tr>
<th>Source d.f.</th>
<th>S.S.</th>
<th>M.S.</th>
<th>Expectation of M.S.S.</th>
<th>'F' test</th>
</tr>
</thead>
<tbody>
<tr>
<td>g.c.a. P-1</td>
<td>S_g</td>
<td>M_g</td>
<td>$6^2_e + (P+2)(1/P-1) \ i g_i^2$</td>
<td>$M_e^2$ for P-1, m.d.f.</td>
</tr>
<tr>
<td>s.c.a. P(P-1)/2</td>
<td>S_s</td>
<td>M_s</td>
<td>$6^2_e + 2/P(P-1)$</td>
<td>$M_s^2 M_e$ for P(P-1)/2 m.d.f.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>$S_{ij}^2$</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>$i j$</td>
<td></td>
</tr>
<tr>
<td>error</td>
<td>M</td>
<td>S_e</td>
<td>$M_e$</td>
<td>$6^2_e$</td>
</tr>
</tbody>
</table>

Where,

$S_g = \frac{1}{P+2} \sum_{i} (X_i + X_{ii})^2 - 4/PX^2/2$  

$S_s = \sum_{ij} X_{ij}^2 - 1/P + 2 \frac{1}{4} (X_i + X_{ii})^2 + 2(P+1)(P+2) X - 2$  

and

$M_e = M_e / bc$

Where,

- $b$ = number of replications
- $c$ = number of observations per plot
- $M_e$ = the error m.s.s. obtained from previous ANoVA
- $S_g$ = the sum of squares (S.S.) due to g.c.a.
- $S_s$ = the sum of squares (S.S.) due to s.c.a.
- $p$ = the number of parents
- $X_i$ = total of array involving $i^{th}$ as female
- $X_{ii}$ = the value of the $i^{th}$ parent of the array
- $X_{..}$ = the grand total
\[ X_{ij} \] = the value of the cross with \( i \)th as female and \( j \)th as male parents.

**Estimates of Various Effects:**

The various effects were estimated as follows:

\[ \hat{g}_i = \frac{1}{P+2} [X_i + X_{ii} - 2/PX..] \]

S.C.a. effect of \( ij \)th cross:

\[ \hat{\delta}_{ij} = X_{ij} - \frac{1}{P+2}(X_i + X_{ii} + X_{jj}) + 2/((P+1)+(P+2)X..) \]

**Estimated Variances of the estimates of the effect and their variances**

\[ \text{Var}(\hat{g}_i) = \frac{P - 1}{P(P+2)} \frac{6^2}{e} \]

\[ \text{Var}(\hat{\delta}_{ij}) = \frac{(P+P+2)}{(P+1)(P+2)} \frac{6^2}{e}, \text{ where } i \neq j \]

\[ \text{Var}(\hat{g}_i - \hat{g}_j) = \frac{2}{P+2} \frac{6^2}{e}, \text{ where } i \neq j \]

\[ \text{Var}(\hat{\delta}_{ii} - \hat{\delta}_{jj}) = \frac{2(P-2)}{P+2} \frac{6^2}{e}, \text{ where } i \neq j \]

\( 6^2 = M_e \) taken as error M.S.S. from the combining ability analysis, \( \hat{g}_i \) and \( \hat{\delta}_{ij} \) are the estimates of the general and specific combining ability effects, respectively and \( P, X_i, X_{ii}, X.. \) and \( X_{ij} \) are the same as explained earlier except that \( X_j \) = total of the array involving \( j \)th as a male and \( X_{jj} \) = the value of \( j \)th parent of the array.
Test of significance of g.c.a. and s.c.a. effects:

The hypothesis $H_0 (\hat{g}_i = 0)$ for all i's and $H_0 (\hat{s}_{ij} = 0)$ for all i and j are tested by the 't' test on corresponding error degree of freedom, with suitable level of significance.

$$t = \frac{\hat{g}_i - 0}{\text{Se} (\hat{g}_i )}$$

$$t = \frac{\hat{s}_{ij} - 0}{\text{SE}(\hat{s}_{ij})}$$

respectively

Estimation of Heterosis and inbreeding depression:

It was calculated in relation to economic parent of the zone using the following formula:-

$$\text{Heterosis over economic parent in percentage} = \frac{\bar{F}_1 - \bar{EP}}{\bar{EP}} \times 100$$

where, $\bar{F}_1$ = the mean of the $F_1$ generation

$\bar{EP}$ = the mean of economic parent

Test of Significance:

Significance of heterosis was tested by the method suggested by Panse and Sukhatme (1961) SE of difference between any two values

$$(\text{EP}) = \sqrt{\frac{2 \text{VE}}{r}}$$

where,

$\text{VE} = $ error variance

$r = $ number of replications

$\text{C.D.} = \text{SE} \times 't'$ ( 't' value at 0.05 and 0.01)
The coefficient of inbreeding depression has been worked out by the formula as given below:

Inbreeding depression in percentage \[= \frac{F_1 - F_2}{F_1} \times 100\]

where, \(F_1\) = the mean of \(F_1\) generation
\(F_2\) = the mean of \(F_2\) generation

Test of significance:

The significance of the inbreeding depression was tested by the following formula:

\[t = \frac{\text{Estimate}}{\text{S.E. of estimate}}, \text{ for corresponding error d.f. at } P = 0.05 \text{ and } 0.01\]

\[\text{SE} = \sqrt{M_e[1/(b+1)/(b-1)(t-1)]}\]

where,
\(M_e\) = error mean sum of squares
\(b\) = number of blocks
\(t\) = number of treatments

5. Estimation of Selection parameter:

The selection parameters viz, heritability and genetic advances were calculated to analyse the suitability of direct and indirect selections. These parameters were estimated by the following procedures:
(a) Direct Selection Parameters:

Heritability:

Heritability in narrow sense was calculated by the following formula suggested by Crumpacker and Allard (1962), which is based on the component analysis in $F_1$ generation:

$$h^2 = \frac{1/4 \hat{D}}{1/4 \hat{D} + 1/4 \hat{H}_1 - 1/4 \hat{F} + \hat{E}}$$

and in $F_2$ generation it was calculated by the following formula suggested by Verhalen and Murray (1969) as:

$$h^2 = \frac{1/4 \hat{D}}{1/4 \hat{D} + 1/16 \hat{H}_1 - 1/8 \hat{F} + \hat{E}}$$

where,

$h^2$ = estimate of heritability coefficient and
$
\hat{D}, \hat{H}_1, \hat{F}$ and $\hat{E}$ are the same components as explained earlier.

Genetic Advance:

Genetic advance was calculated by the following formula:

$$GA = Kn^2 \frac{6}{
\overline{p}}$$

Genetic advance in percentage over mean of the character:

$$\frac{GA}{\overline{x}} \times 100$$

where,

GA = estimate of genetic advance
\[ K = \text{Selection differential at a particular intensity viz, 2.06 at 5 percent selection intensity as given by lush (1945)} \]

\[ \sigma_{Ph}^2 = \text{Phenotypic standard deviation.} \]

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

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

(b) Indirect Selection Parameters:

Correlation:

Correlations were calculated using the following formula

\[ r (x_1, x_2) = \frac{\text{Cov. } x_1, x_2}{\sqrt{V(x_1) \cdot V(x_2)}} \]

where,

\[ r = (x_1, x_2) \text{ is the correlation between } x_1 \text{ and } x_2 \]

\[ \text{cov.} = (x_1, x_2) \text{ is the covariance between } x_1 \text{ and } x_2 \]

\[ V(x_1) = \text{is the variance of } x_1 \]

\[ V(x_2) = \text{is the variance of } x_2 \]

Correlation coefficient:

The correlation coefficient between the variances were compared with the help of following formula:

Genotypic correlation coefficient:

Genotypic correlation coefficient was calculated by the following formula as suggested by Robinson et al. (1951).
Genotypic correlation = \[ \frac{\text{Genotypic covariance}}{\sqrt{\text{G.V. for (X) X G.V. for(Y)}}} \]

G.V. for X = Genotypic Variance for X
G.V. for Y = Genotypic Variance for Y

X & Y are two variables.

(a) GENOTYPIC COVARIANCE = \[ \frac{\text{M.S.P. treatment (ry)} - \text{M.S.P. error(xy)}}{r} \]

(b) GENOTYPIC VARIANCE OF Y = \[ \frac{\text{M.S.S. treatment (Y)} - \text{M.S.S. error(Y)}}{r} \]

Phenotypic correlation coefficient:

It was calculated by the following formula Robinson et al. (1951).

Phenotypic correlation = \[ \frac{\text{Phenotypic covariance}}{\sqrt{\text{Ph.V. for(X) X Ph.V. for(Y)}}} \]

where,

Ph.V. for X = Phenotypic Variance for X
Ph.V. for Y = Phenotypic Variance for Y

X and Y are two variables.

Test of Significance:

The significance of correlation coefficient was tested with the help of a statistical table by Fisher and Yates, at (n-2) degree of freedom.