Chapter-IV

EXPERIMENTAL FINDINGS

The data recorded on ten quantitative characters were subjected to the various statistical and geometrical analysis and the result obtained are described under the following heads:

1. Analysis of variance for the experiment

2. Components of variance analysed through
   (a) Graphical Analysis
   (b) Analytical Analysis

3. Combining ability variances

4. Estimates of general and specific combining ability effects

5. Heterosis

6. Heritability and genetic advance

1. ANALYSIS OF VARIANCE FOR THE EXPERIMENT

The analysis of variance for the design of experiment conducted in Randomized Complete Block Design was carried out under study for testing the difference among genotypes for all the ten characters. The mean square for all the ten characters are presented in Table 1a and 1b, 1c and 1d. Significant to highly significant differences were observed among the genotypes for all the characters under study. Parents showed significant differences for all the characters.

Crosses also showed significant differences for days to maturity, plant height, number of primary branches, day to flower, number of clusters per plant, number of
pods per cluster, number of seeds per pod, 100-grain weight, protein per cal (%) and yield per plant (g).

**Mean range and variability**

The mean values of the parents and crosses in respect of all the characters are presented in Appendix 1. The variability among parents and F1s and F2s for the characters under study is given in Table 2. The character-wise results are described as under:

**Days to flower**

The ranges of days to flower among the parents varied from 39.97 (PDM 84-139) to 46.53 (PDM 54) days. In F1, among the crosses it ranged from 39.10 (PDM 84-139 x K 92-140) to 53.90 (PS 16 x K 92-140) days. Parents K 1310, T 44 and Pusa 9531, K 92-140 were found to be early flowering in order of merit.

Whereas, crosses in F1 generation K 851 x PS 16, PDM 54 x K 1310, HUM 2 x K 1284, Pusa 9531 x K 1284, K 1310 x T 44, K 1284 x PS 16, HUM 2 x K 92-140 showed early flowering. In F2 it ranged from 40.73 (HUM 2 x T 44) to 49.57 (K 851 x PDM 54) days. Whereas, crosses in F2 generation K 851 x K 92-140, PDM 54 x HUM 2, PDM 54 x Pusa 9531, HUM 2 x T 44, Pusa 9531 x PDM 84-139, K 1310 x T 44, K 1284 x T 44, PDM 84-139 x PS 16 showed early flowering.

**Days to maturity**

Days to maturity ranged from 51.00 (K 1284) to 59.27 (PDM 54) days among parents, and 48.77 (K 851 x Pusa 9531) to 64.70 (PS 16 x K 92-140) days among F1 crosses, and 53.00 (K 1310 x K 1284) to 68.20 (K 851 x HUM 2) days among F2 crosses. The parents which showed early maturity were HUM 2, Pusa 9531, K 1284, PDM 84-139, K 92-140 were found to mature early and crosses in F1 are PDM 54 x HUM 2, PDM 54 x PDM 84-139, HUM 2 x PS 16, Pusa 9531 x PS 16, Pusa 9531 x K
92-140, K 1310 x K 92-140, PDM 84-139 x T 44, T 44 x K 92-140 and in F2 generation crosses K 851 x PDM 84-139, K 851 x PS 16, PDM 54 x HUM 2, PDM 54 x K 1310, PDM 54 x K 92-140, HUM 2 x Pusa 9531, HUM 2 x PDM 84-139, Pusa 9531 x K 1310, K 1310 x K 1284, K 1284 x PS 16, PDM 84-139 x PS 16, PS 16 x K 92-140 were found to mature early.

Plant height

The mean range of plant height among the parents varied from 8.87 (T 44) to 28.57 (HUM 2). Among the F1 crosses, it varied from 18.93 (Pusa 9531 x PDM 84-139) to 42.63 (PDM 54 x PDM 84-139) and among the F2 crosses it varied from 18.23 (PDM 84-139 x PS 16) to 37.27 (K 851 x Pusa 9631). The crosses showing tallness in F1 Pusa 9531 x K 1310, Pusa 9531 x K 92-140, K 1310 x K 92-140, K 1284 x K 92-140, PDM 84-139 x K 92-140. The crosses showing tallness in F2 K 851 x K 1310, PDM 54 x Pusa 9531, K 1284 x PDM 84-139, PDM 84-139 x T 44, PDM 84-139 x K 92-140, PS 16 x T 44.

Number of primary branches

The mean values for the characters ranged from 3.83 (HUM 2) to 6.30 (K 92-140) among parents and 4.27 (HUM 2 x Pusa 9531) to 6.83 (HUM 2 x PS 16) among F1 crosses and 3.47 (Pusa 9531 x PS 16) to 6.83 (K 1310 x T 44) among F2 crosses. The crosses, which showed more number of primary branches were K 851 x PDM 54, K 851 x HUM 2, K 851 x K 1310, PDM 54 x Pusa 9531, HUM 2 x K 1310, HUM 2 x PS 16, K 1310 x PS 16, K 1310 x K 92-140, in F1 crosses.

PDM 54 x HUM 2, PDM 54 x K 92-140, K 1310 x T 44, K 1310 x K 92-140, PDM 84-139 x K 92-140, HUM 2 x Pusa 9531, HUM 2 x PS 16 among F2 crosses, according to merit.
Number of cluster per plant

The number of cluster per plant among parents ranged from 5.37 (PDM 84-139) to 12.20 (K 1284) and in $F_1$ crosses it was recorded 4.67 (K851 x PDM 84-139) to 18.47 (K 1284 x PS 16) and in $F_2$ crosses it was recorded 5.43 (PDM 54 x K 1310) to 31.37 (K 851 x PDM 84-139). The crosses, PDM 54 x K 1284, HUM 2 x K 1310, HUM 2 x PDM 84-139, K 1284 x PS 16 in $F_1$ crosses and crosses K 851 x PDM 84-139, PDM 84-139 x PS 16, K 851 x K 1310, K 851 x K 92-140 in $F_2$ crosses showed more number of per cluster per plant to that order.

Number of pods per cluster

The number of pods per cluster among parents ranged from 4.00 (PDM 84-139) to 7.52 (PDM 54) and in $F_1$ crosses it was recorded 4.54 (PDM 54 x T 44) to 8.81 (HUM 2 x PDM 84-139) and in $F_2$ crosses it was recorded 4.24 (PS 16 x K 92-140) to 7.96 (K 1310 x PDM 84-139). The crosses in $F_1$ were K 851 x PS 16, PDM 54 x K 1310, HUM 2 x PDM 84-139, PDM 54 x K 1284, K 1284 x PS 16, PDM 84-139 x T 44 and in $F_2$ crosses K 851 x PDM 84-139, K 851 x K 92-140, Pusa 9531 x K 1310, K 1310 x K 1284, PDM 84-139 x PS 16, PS 16 x T 44, showed more number of pods per cluster to that order.

Number of seeds per pod

The average number of seeds per pod varied from 6.58 (PS 16) to 11.41 (K 1284) and 5.61 (PDM 84-139 x K 92-140) to 11.87 (Pusa 9531 x K 92-140) and 4.96 (K 1284 x PDM 84-139) to 11.68 (PDM 84-139 x PS 16) among parents, $F_1$ crosses and $F_2$ crosses, respectively. The crosses with more number of seeds per pod were PDM 54 x HUM 2, PDM 54 x K 1310, PDM 54 x PDM 84-139, Pusa 9531 x PDM 84-139, Pusa 9531 x K 92-140, K 1310 x T 44, K 1284 x PS 16 and K 851 x PS 16, PDM 54 x Pusa 9531, Pusa 9531 x PDM 84-139, K 1310 x T 44, K 1284 x K 92-140, PDM 84-139 x PS 16 in $F_1$ and $F_2$ crosses, respectively according to merit.
100-grain weight (g)

The mean of 100-grain weight varied from 4.07 (T 44) to 5.40 (K 92-140) among the parents. The range among crosses was 3.64 (Pusa 9531 x PDM 84-139) to 5.62 (K 1310 x K 92-140) in F₁ and F₂, respectively. K 851 x K 1310, PDM 54 x HUM 2, PDM 54 x K 1310, PDM 54 x K 92-140, HUM 2 x Pusa 9531, PS 16 x T 44 and K 851 x HUM 2, K 851 x PDM 84-139, K 1310 x PDM 84-139, K 1310 x K 92-140, PS 16 x T 44 in F₁ and F₂ crosses showed 100-grain weight according to their merit.

Protein per cal (%)

The variability for protein content ranged from 16.86 per cent (HUM 2) to 20.94 per cent (PDM 54) among parents. Among F₁ crosses it ranged from 12.88 per cent (K 1310 x K 92-140) to 20.84 per cent (PDM 54 x PDM 84-139) and F₂ crosses it ranged from 12.38 per cent (PDM 54 x HUM 2) to 19.70 per cent (HUM 2 x K 1310). The crosses namely, K 851 x HUM 2, K 851 x K 1310, K 851 x T 44, PDM 54 x PDM 84-139, HUM 2 x K 1310, Pusa 9531 x K 1310, K 1310 x T 44, PS 16 x T 44, K 1284 x T 44, and K 851 x PDM 54, K 851 x PDM 84-139, PDM 54 x T 44, Pusa 9531 x K 1310, PDM 84-139 x T 44, PDM 84-139 x K 92-140, PS 16 x K 92-140 had maximum protein content as per that order in F₁ and F₂ crosses, respectively.

Yield per plant (g)

The average value of grain yield per plant ranged from 4.47 g (PS 16) to 11.63 g (K 1284) and 4.27 g (PDM 54 x Pusa 9531) to 15.83 g (K 1284 x T 44) and 4.43 g (HUM 2 x K 1310) to 11.97 g (PDM 54 x PDM 84-139) among parents, F₁ and F₂ crosses, respectively. Among the F₁ crosses, PDM 54 x K 1284, HUM 2 x Pusa 9531, HUM 2 x K 1284, Pusa 9531 x PS 16, K 1284 x T 44, were top yielders and among the F₂ crosses K 851 x HUM 2, PDM 54 x Pusa 9531, PDM 54 x PDM 84-139, Pusa 9531 x T 44, K 1310 x K 92-140, K 1284 x K 92-140 were top yielders according to their ranks.
2. COMPONENT OF VARIANCE

(a) Graphical analysis

The estimates of regression coefficient ‘b’, its standard error (Sb), deviation from zero (b-0) and from unity (b-1) values for different traits have been presented in Table 4 and Wr, Vr graphs for all the ten characters are presented in Fig. 1 to 10. The findings of graphical representation is explained character-wise, as under:

Days to flower

The regression coefficient ‘b’ differed non-significantly both from zero and unity but the value of $t^2$ was significant for the character in F1 but non-significant in F2.

The Vr, Wr graph for this character has been presented in Fig. 1. The regression line interrupted the Wr axis below the origin suggesting the operation of over dominance. The legends used for all the parents are 1 for K 851, 2 for PDM 54, 3 for HUM 2, 4 for Pusa 9531, 5 for K 1310, 5 for K 1284, 7 for PDM 84-139, 8 for PS 16, 9 for T 44, 10 for K 92-140. For this character (in F1) parent 1, 2, 3 showed excess of dominant genes, parent 10 exhibited excess of recessive genes. The remaining parent had almost equal proportion of dominant and recessive gene.

In F2 parent 4, 7, 8, 9 showed excess of dominant genes and parent 5, 6 showed excess of recessive genes and rest parent had almost equal proportion of dominant and recessive gene.

Days to maturity

The regression coefficient ‘b’ in F1 differed non-significant from zero and unity but the value of $t^2$ is significant.

In F2 the regression coefficient ‘b’ differed non-significant from zero and unity. The value of $t^2$ was significant.
DAYS TO FLOWER

Fig 1a (F1)

- Line of Unit Slope
- Actual regression line
- Array Points

Scale 1 Small Unit = 2

b = -0.04 ± 0.14

Fig 1b (F2)

Scale 1 Unit = 1

b = 0.95 ± 0.30

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 16
9. T44
10. K92-140
DAYS TO MATURITY

Fig 2a (F1)

--- Line of Unit Slope

Actual regression line

Array Points

Scale 1 part = 2 unit

b = -0.23 ± 0.16

Fig 2b (F2)

--- Actual regression line

Array Points

Scale 1 part = 2 unit

b = 0.04 ± 0.10

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 15
9. T44
10. K92-140
The Vr, Wr graph for days to maturity are given in Fig. 2. In F₁, the Wr axis was intersected by regression line on the origin point, which suggested the presence of complete dominance. Parent 2, 3, 4, 5, 7 showed excess of dominant genes while parent 6, 8, 10 showed excess of recessive genes. The remaining parent had almost equal proportion of dominant and recessive genes. The array points in scattered pattern, revealed the wide range of diversity in the parent.

In F₂ the Wr axis was intersected by regression line below the origin point which suggested the presence of over-dominance. Parents 7, 8, 9, 10 exhibited excess dominant genes while parent 3 and 2 showed excess of recessive genes. The remaining parents 1, 4, 5 and 6 had almost equal proportion of dominant and recessive genes.

**Plant height**

In F₁, the deviation of regression coefficient ‘b’ was non-significant from zero and non-significant from unity. The value of $t^2$ was found to be significant.

In F₂, the deviation of regression coefficient ‘b’ was non-significant from zero and non-significant from unity also. The value of $t^2$ was found to be significant.

Vr, Wr graph presented in Fig. 3 showed that regression line intersected Wr axis below the point of origin indicating over dominance. Parents 3 and 1 showed excess dominant genes, parent 5 showed recessive genes for the character and parents 2, 4, 6, 7, 8, 9 and 10 had almost equal proportion of dominant and recessive genes.

**Number of primary branches**

In F₁ graph, the deviation of value of regression coefficient was significant from zero and non-significant from unity. The estimate of $t^2$ was also non-significant.

In F₂ graph, the deviation of value of regression coefficient was non-significant from zero and non-significant from unity. The estimate of $t^2$ was also non-significant.
PLANT HEIGHT (Cm)

Fig 3a (F1)
- Line of Unit Slope
- Actual regression line
- Array Points

Scale 1 part = 5 unit

b = 0.02 ± 0.09

Fig 3b (F2)

Scale 1 part = 2 unit

b = 0.95 ± 0.30

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 16
9. T44
10. K92-140
Number Of Primary Branches Per plant

**Fig 4a (F1)**

- Line of Unit Slope
- Actual regression line
- Array Points

Scale 1 part = .2 unit
b = -.37 ± .18

**Fig 4b (F2)**

Scale 1 part = .1 unit
b = .13 ± .33

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 16
9. T44
10. K92-140
In F₁, Vr, Wr graph for this trait has been presented in (Fig. 42) regression line cut the Wr axis above the origin point thereby suggesting partial dominance. Parent 4, 7, 9 showed excess of dominant genes, parent 6, 1 and 8 showed excess of recessive genes, while rest of the parents showed nearly equal proportion of dominant and recessive genes.

In F₂, Vr, Wr graph for this trait has been presented in Fig. 4a. Regression line cut the Wr axis above the origin point thereby suggesting partial dominance. Parents 4, 8, 1 showed excess of dominant genes, and parent 2, 3 showed excess of recessive genes, while other parents 5, 6, 7, 9 10 showed nearly equal proportion of dominant and recessive genes. The scattered array points suggested the presence of diversity among parents.

**Number of cluster per plant**

In F₁, the regression coefficient differed non-significantly from zero and non-significant from unity. Whereas, the estimates of $t^2$ was recorded non-significant.

The Vr, Wr graph (Fig. 5a) indicated the partial dominance for this character as the regression line intersected the Wr axis well above the part of origin.

The regression coefficient differed significantly from zero and non-significant from unity, whereas, the estimate of $t^2$ was recorded significant. The Vr, Wr graph (Fig. 5b) indicated the over dominance for this character as the regression line intersected the Wr axis well below the origin point.

Parents 4, 3, 9, 10, 2 exhibited excess of dominant genes. Parent 5, 6 showed excess of recessive genes while parent 1, 8 and 7 showed nearly equal proportion of dominant and recessive genes.
Number Of Clusters Per Plant

**Fig 5a (F1)**

- Line of Unit Slope
- Actual regression line
- Array Points

Scale: 1 part = 2 unit

\( b = 0.09 \pm 0.19 \)

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 16
9. T44
10. K92-140

**Fig 5 b (F2)**

Scale: 1 part = 10 unit

\( b = 0.07 \pm 0.02 \)
Number of pods per cluster

The regression coefficient differed non-significant from zero and unity. whereas, the estimate of $t^2$ was recorded non-significant. The $Vr$, $Wr$ graph (Fig. 6a) indicated the over-dominance for this character as the regression line intersected the $Wr$ axis well below the origin point.

Parents, 1, 2, 3, 5 and 7 showed excess of dominant genes while parent 4, 8, 6 and 10 showed excess of recessive gene and parent 9 exhibited equal number of dominant and recessive genes.

The regression coefficient differed non-significant from zero and unity. Whereas, the estimate of $t^2$ was recorded non-significant. The $Vr$, $Wr$ graph (Fig. 6b) indicated the partial dominance for this character as the regression line intersected the $Wr$ axis well above the origin point.

Parents, 1, 3, 4, 8 showed excess of dominant gene. Parent 5, 9 showed excess of recessive genes, while parents 2, 6, 7, 10 showed equal proportion of both dominant and recessive genes. The array points are seem to scattered pattern revealing the diversity among parents for the character.

Number of seeds per pod

In $F_1$, the value of regression coefficient was non-significant both from zero and from unity. The estimate $t^2$ was also non-significant.

The $Vr$, $Wr$ graph is presented in (Fig. 7a). The regression line intersected $Wr$ axis below the point of origin indicating over dominance. Parents 1, 3, 6, 9, 8 showed excess of dominant genes. Parent 7, 4 and 2 showed equal proportion of dominant and recessive genes. Parent 10 showed excess of recessive genes.

In $F_2$, the value of regression coefficient was non-significant both from zero and from unity. The estimate $t^2$ was significant.
Number Of Pods Per Plant

**Fig 6a (F1)**

- **Line of Unit Slope**
- **Actual Regression Line**
- Array Points

Scale 1 part: .1 unit
\( b = 0.08 \pm 0.31 \)

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 16
9. T44
10. K92-140

**Fig 6 b (F2)**

Scale 1 part: .1 unit
\( b = 0.22 \pm 0.21 \)
Number Of Seeds Per Pod

Fig 7 a (F1)

- Line of Unit Slope
- Actual regression line
- Array Points

Scale: 1 part = 1 unit
\[ b = -0.21 \pm 0.11 \]

Fig 7 b (F2)

Scale: 1 part = 1 unit
\[ b = -0.26 \pm 0.31 \]

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM-84-139
8. PS 16
9. T44
10. K92-140
The Yr, Wr graph is represented in (Fig. 7b). The regression line intersected Wr axis above the point of origin indicating partial dominance for all arrays. Parents 1, 9, 6, 10 and 3 showed excess of dominant genes. Parent 5 and 8 showed excess of recessive genes, while 2, 4 and 7 parents had equal proportion of dominant and recessive genes.

**100-grain weight (g)**

The value of ‘b’ differed non-significantly from zero as well as from unity. The value of $t^2$ was found to be significant (in $F_1$).

Vr, Wr graph for this trait has been presented in (Fig. 8a). The Wr axis was intersected by regression line below the point of origin indicating over dominance. Parents 9, 4, 10, 6, 1 exhibited excess of dominant genes. Parent 5 and 7 exhibited excess of recessive genes. Parents 2, 3 and 8 showed equal proportion of dominant and recessive genes.

In $F_2$, the value of regression coefficient ‘b’ differed non-significantly from zero and from unity value of $t^2$ was recorded non-significant.

The Vr, Wr graph for 100-grain weight is presented in (Fig. 8b). The regression line intersected the Wr axis below the point of origin indicating the over dominance. Parents 6, 4 and 7 showed excess of dominant genes. Parents 2, 5, 8 and 3 showed excess of recessive gene while parents 1, 9 and 10 exhibited equal proportions of dominant and recessive genes. The array points found scattered showed diversity among parents.

**Protein per cal (%)**

In $F_1$, the value of ‘b’ was deviating non-significantly from zero and from unity also. The value of $t^2$ was recorded significant.
100 grain weight (gm)

Fig 8a (F1)

- Line of Unit Slope
- Actual regression line
- Array Points

Scale 1 part = .04 unit
b = .006 ± .22

Fig 8b (F2)

- 1. K851
- 2. PDM54
- 3. HUM2
- 4. Pusa 9531
- 5. K1310
- 6. K1284
- 7. PDM84-139
- 8. PS 16
- 9. T44
- 10 K92-140

Scale 1 part = .04 unit
b = .19 ± .17
Protein Per Calory (%)

Fig 9a (F1)
- Line of Unit Slope
- Actual regression line
- Array Points
Scale: 1 part = 1 unit
b = -0.09 ± 0.13

Fig 9b (F2)
Scale: 1 part = 1 unit
b = -0.51 ± 0.22

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 16
9. T44
10. K92-140
Yield Per Plant (g)

**Fig 10a (F1)**

- Line of Unit Slope
- Actual regression line
- Array Points

Scale: 1 part = 2 unit

$b = -0.02 \pm 0.28$

1. K851
2. PDM54
3. HUM2
4. Pusa 9531
5. K1310
6. K1284
7. PDM84-139
8. PS 16
9. T44
10. K92-140

**Fig 10b (F2)**

Scale: 1 part = 1 unit

$b = -0.15 \pm 0.25$
The Vr, Wr graph for protein content is presented in Fig. 9a. The regression line was interacted the Wr axis below the point of origin showing over dominance. The array points were found scattered revealing the diversity for protein content among parents. Parents 1, 3, 2, 6 and 5 exhibited excess of dominant genes. Parent 9 exhibited excess of recessive genes while parents 4, 7 and 8 exhibited equal proportion of dominant and recessive genes.

In F2, the value of ‘b’ was deviating non-significantly from zero and from unity also. The value of $t^2$ was recorded non-significant.

The Vr, Wr graph for protein content is presented in Fig 9b. The regression line was intersected the Wr axis below the point of origin showing over dominance. Parents 1, 6, 5, 10 and 3 exhibited excess of dominant genes. Parents 2, 4, 7 and 9 exhibited equal proportion of dominant and recessive genes. Parent 8 showing excess of recessive genes.

**Yield per plant (g)**

In F1, the regression coefficient deviated non significantly from zero and from unity also. The estimate of $t^2$ was non significant.

**(b) Analytical analysis**

Variance component analysis for crosses in respect of genetic component of variation was performed according to model proposed by Hayman (1954).

The estimates for all the component of variation ($D, H_1, H_2, F, h^2$ and $E$) along with their standard errors are given in Table 6.

For F1, the estimates of both additive ($D$) and dominance components ($H_1$ and $H_2$) were found to be highly significant for all the characters except days to flower, number of clusters per plant, number of seeds per pod and 100-grain weight which showed non-significant response to additive ($D$) component of variance. The magnitude
of $H_1$ and $H_2$ were found higher than the values of $D$ for all the characters showing the pre-dominance of non-additive genetic variance. Similarly, the magnitude of $H_1$ was higher than $H_2$ indicating the unequal distribution of positive and negative genes for all the characters.

For $F_2$, the estimates of both additive ($D$) and dominance components ($H_1$ & $H_2$) were found to be highly significant for all the characters except days to maturity, number of clusters per plant, number of pods per cluster, 100-grain weight and protein per cal., which showed non-significant response to additive ($D$) component of variance. The magnitude of $H_1$ and $H_2$ were found higher than the values of $D$ for all the characters showing the pre-dominance of non-additive genetic variance. Similarly, the magnitude of $H_1$ was higher than $H_2$ indicating the unequal distribution of positive and negative genes for all the characters.

The value of $F$ component were found positive for all the characters both in $F_1$ and $F_2$ significant values of $F$ were observed (for $F_2$) for days to flower and plant height which indicated that dominant alleles were more frequent for the expression of these traits. Positive but non-significant values of $F$ for other remaining characters both in $F_1$ and $F_2$ generation indicated the equal importance of dominant and recessive alleles.

The estimates of $h^2$ component were found significant and positive for $F_1$ generation for days to flower, days to maturity, plant height, protein per cal, yield per plant. In $F_2$ generation for days to flower, plant height, protein per cal. Negative but non-significant values were recorded for the characters (for $F_1$ generation) number of primary branches, 100-grain weight. In $F_2$ generation negative and non-significant values were recorded for number of primary branches. Significant and positive values of $h^2$ revealed the importance of dominant genes in heterozygous phase of the crosses. The estimate of $E$ were found significant for number of primary branches, in $F_1$ generation.
In $F_2$ generation, the estimate of $E$ were found significant for days to flower and number of primary branches. The non-significant response for $E$ was recorded in remaining characters.

For $F_1$ and $F_2$ generation, the mean degree of dominance $(H_1/D)^{0.5}$ values was found to be more than unity, for both $F_1$ and $F_2$ generation, for all the characters, indicating the presence of over-dominance.

For both $F_1$ and $F_2$ generation, asymmetrical distribution of positive and negative genes in the parents was observed for all the characters as the values of $(H_2/4 H_1)$ were found less than the theoretical value (0.25).

For both $F_1$ and $F_2$, the ratio of dominant and recessive genes $(4 DH_1)^{0.5} + F/ (4 DH_1)^{0.5} - F$ was recorded more than unity for all the traits, showing that the dominant genes were more frequent, than recessive genes.

In both $F_1$ and $F_2$, the ratio of $h^2/H_2$ was found to be less than one for days to flower, days to maturity, number of primary branches, number of clusters per plant, number of pods per cluster, number of seeds per pod, 100-grain weight, protein per cal, yield per plant. It pointed out that one major gene group was controlling the inheritance of these characters. The value was found to be more than one for plant height indicating that the inheritance of these character is governed by more than one gene groups.

In $F_1$ generation, the coefficient of correlation between parental order of dominance $(Wr + Vr)$ and parental measurement $(Yr)$ was found to be negative for days to flower, days to maturity, plant height, number of primary branches, number of cluster per plant, number of pods per cluster, number of seeds per pod and yield per plant. In $F_2$ generation for negative for plant height, number of clusters per plant, number of pods per cluster, 100-grain weight and rest characters were exhibited positive value of ‘$r$’ positive genes were mostly dominant for the traits with negative ‘$r$’
value, negative genes were mostly dominant for the traits with positive correlation coefficient value.

3. COMBINING ABILITY VARIANCES

The mean sum of squares due to general and specific combining ability variance for all the ten characters viz.; days to flower, days to maturity, plant height, number of primary branches, number of clusters per plant, number of pods per cluster, number of seeds per pod, 100-grain weight, protein per cal, yield per plant in Table 5. The variance due to general combining ability (gca) were highly significant for all the characters in \( F_1 \) generation. In \( F_2 \) generation variance due to general combining ability (gca) were highly significant for all characters except number of primary branches and number of pods per cluster. Variance due to specific combining ability (sca) were also highly significant for all the characters except number of primary branches, number of clusters per plant in \( F_1 \) generation. For \( F_2 \) generation variance due to specific combining ability (sca) were highly significant for all the characters except 100 grain weight.

4. ESTIMATES OF COMBINING ABILITY EFFECTS

(i) General combining ability effects

The estimates of general combining ability effects for all the ten characters are given in Table 8 and their character wise observation are given below:

Days to flower

In mung bean early flowering is preferred hence parents having negative estimates of general combining ability effects were considered desirable. Significant negative gca effects were recorded in \( F_{15} \) generation in parents, Pusa 9531, K 1310, K 1284, T 44, PDM 84-139, HUM 2. In \( F_{28} \) generation the parents showing negative significant gca effects are Pusa 9531, K 1310, PDM 84-139, PS 16 and T 44.
Days to maturity

Similar to early flowering, early maturity is also desirable hence. In F<sub>1</sub>s generation parents with negative and significant gca effect were considered good. Parents HUM 2, Pusa 9531, K 1284, PDM 84-139 had negative and highly significant values which may be considered as most desirable type for breeding purpose at earliness.

Parents showing positive and significant gca effects are K 851, PDM 54, K 1310, PS 16, T 44, K 92-140. In F<sub>2</sub>s generation parents with negative and significant gca effects are Pusa 9531, K 1284, PDM 84-139 and K 92-140.

Plant height

In F<sub>1</sub>s generation significant positive gca effects were observed in parents, K 85, PDM 54, HUM 2 and which showed that these parents were good combiners for tallness while, Pusa 9531, K 1284, PS 16, T 44 having negative and significant gca effect was considered to be good source for dwarfness.

In F<sub>2</sub>s generation parents showing negative and significant effects are Pusa 9531, K 1310, K 1284, PS 16, T 44 and K 92-140. The parents showing positive significant gca effects were K 851, PDM 54, HUM 2.

Number of primary branches

In F<sub>1</sub>s generation the desirable parents for more number of primary branches were K 851, PS 16 and K 92-140 as they produced significant positive gca effects.

In F<sub>2</sub>s generation, the desirable parents for more number of primary branches were K 851, Pusa 9531, T 44, K 92-140 as they produced significant positive gca effects.
**Number of clusters per plant**

In F₁ generation the parents PDM 54, HUM 2, K 1284, PDM 84-139 and K 92-140 had positive and significant gca effects. These parents were taken as desirable for more number of clusters per plant.

In F₂ generation the parents showing positive and significant gca effects are K 851, PDM 84-139 and T 44.

**Number of pods per cluster**

In F₁ generation the parents PDM 54, HUM 2, Pusa 9531 had positive and significant gca effects. These parents were taken as desirable for more number of pods per plant.

In F₂ generation the parents K 851, PDM 54, HUM 2, T 44 had positive and significant gca effects.

**Number of seeds per pod**

In F₁ generation parents, except K 851, T 44 and K 92-140 all parents showed positive and significant effects for more number of seeds per pod.

In F₂ generation parents Pusa 9531, K 1284, T 44, K 92-140 exhibited significant and positive gca effect.

**100-grain weight (g)**

The parents K 851, PDM 54, HUM 2, PDM 84-139 and K 92-140 exhibited significant positive estimates of gca effects and thus, these parents were considered as useful for large seed size in F₁ generation.

In F₂ generation, the parents K 851, HUM 2, K 1310 and K 92-140 exhibited significant positive estimates of gca effects.
**Protein per cal (%)**

In F₁s generation the positive and significant gca effects were recorded in parents, K 851, PDM 54, HUM 2, K 1310, PDM 84-139 for protein content. Thus, these parents were desirable for high protein content.

In F₂s generation the positive and significant gca effects were recorded in parents, K 851, PDM 54, K 1310, PDM 84-139, PS 16, T 44, K 92-140 for protein content.

**Yield per plant**

For high grain yield per plant, the parents PDM 54, HUM 2, Pusa 9531, K 1284 are desirable in F₁s generation, they produced significant positive effects.

In F₂s generation parents PDM 54, Pusa 9531, K 1310, PDM 84-139, PS 16, T 44, K 92-140 they produced significant positive gca effects.

**(ii) Specific combining ability effects**

In order to identify good cross combinations which are expected to give desirable recombinants, the specific combining ability effects of all the crosses were worked out for all the characters and are presented in Table 9 characterise results are described as under:

**Days to flower**

In F₁s generation range of estimates of sca effect for days to flower varied from -5.56 to 6.66 of 45 crosses. The crosses had significant negative sca effects were, K 851 x Pusa 9531, K 851 x PS 16, PDM 54 x K 1310, HUM 2 x K 92-140, Pusa 9531 x PS 16, K 1310 x T 44, K 1284 x PS 16, PDM 84-139 x K 92-140.
In F₂s generation the crosses had significant negative sca effects were, K 851 x K 92-140, PDM 54 x HUM 2, PDM 54 x Pusa 9531, PDM 54 x PS 16, HUM 2 x T 44, Pusa 9531 x PDM 84-139, K 1284 x PS 16.

**Days to maturity**

The estimates of sca effects ranged from −7.18 to 6.87. The crosses found significant superior for earliness were, K 851 x Pusa 9531, K 851 x PS 16, PDM 54 x K 1310, PDM 54 x PDM 84-139, PDM 54 x PS 16, K 1310 x K 92-140, PDM 84-139 x T 44 in F₁s generation.

In F₂s generation the crosses showing negative significant sca effects are K 851 x PDM 84-139, K 851 x PS 16, K 851 x T 44, K 851 x K 92-140, PDM 54 x HUM 2, PDM 54 x Pusa 9531, HUM 2 x Pusa 9531, HUM 2 x K 92-140, K 1310 x K 1284, PDM 84-139 x PS 16.

**Plant height**

The range of sca effects among F₁ hybrids varied from 0.36 to 12.93. For tallness the cross combinations namely, K 851 x PDM 54, K 851 x HUM 2, K 851 x K 1310, K 851 x PDM 84-139, K 851 x T 44, PDM 54 x Pusa 9531, PDM 54 x PS 16, HUM 2 x Pusa 9531, HUM 2 x K 1310, Pusa 9531 x K 1310, Pusa 9531 x T 44, K 1310 x PS 16, K 1284 x K 92-140, PS 16 x K 92-140, T 44 x K 92-140 exhibited positive and significant sca effects.

The range of sca effects among 0.81 to 11.72 F₂s generation the positive significant combinations are K 851 x HUM 2, K 851 x Pusa 9531, K 851 x PDM 84-139, K 851 x K 92-140, PDM 54 x PS 16, PDM 54 x T 44, HUM 2 x K 1284, HUM 2 x T 44, Pusa 9531 x K 1310, Pusa 9531 x K 1310, Pusa 9531 x PS 16, K 1310 x K 1284, K 1310 x T 44, K 1310 x K 92-140, K 1284 x PDM 84-139, K 1284 x K 92-140, PDM 84-139 x T 44.
**Number of primary branches**

For the character among F₁ hybrid the range of sea effects varied from -1.94 to 1.79. The crosses showed significant positive gca effects are K 851 x PDM 54, K 851 x HUM 2, K 851 x K 1284, PDM 54 x Pusa 9531, PDM 54 x PDM 84-139, HUM 2 x PS 16, Pusa 9531 x PDM 84-139, K 1310 x K 92-140, K 1284 x K 92-140, T 44 x K 92-140.

In F₂'s generation the crosses showed significant and positive sea effects are K 851 x PDM 54, K 851 x Pusa 9531, K 851 x PS 16, PDM 54 x HUM 2, PDM 54 x K 92-140, HUM 2 x Pusa 9531, Pusa 9531 x K 1310, K 1310 x T 44, K 1310 x K 92-140, PDM 84-139 x K 92-140.

**Number of cluster per plant**

The crosses recorded positive and significant sea effects in F₁ hybrids for the character number of cluster per plant in the range of -3.97 to 7.05. The crosses exhibited significant positive sea effects are K 851 x T 44, K 851 x K 92-140, PDM 54 x HUM 2, PDM 54 x K 1284, PDM 54 x PDM 84-139, HUM 2 x K 1310, HUM 2 x PDM 84-139, Pusa 9531 x PDM 84-139, K 1310 x PDM 84-139, K 1284 x PS 16, PS 16 x T 44.

In F₂'s generation the crosses exhibited significant positive sea effects are, K 851 x K 1310, K 851 x PDM 84-139, K 851 x K 92-140, PDM 54 x PDM 84-139, HUM 2 x Pusa 9531, Pusa 9531 x K 1310, Pusa 9531 x T 44, K 1310 x T 44, K 1284 x PDM 84-139 and PDM 84-139 x PS 16.

**Number of pods per cluster**

The estimates of sea effects varied from -1.75 to 2.95 among F₁ hybrids. The crosses recorded positive and significant sea effects for the character are, K 851 x HUM 2, K 851 x PS 16, K 851 x K 92-140, PDM 54 x K 1310, PDM 54 x K 1284.
HUM 2 x PDM 84-139, Pusa 9531 x PDM 84-139, K 1310 x PDM 84-139, K 1310 x T 44, PS 16 x T 44.

The estimates of sea effects varied from 1.29 to 2.55 among F₂s crosses. The crosses showed significant and positive heterosis are, K 851 x PDM 84-139, K 851 x K 92-140, PDM 54 x K 92-140, HUM 2 x K 92-140, Pusa 9531 x K 1310, K 1310 x K 1284, K 1310 x PDM 84-139, K 1284 x K 92-140, PS 16 x T 44.

**Number of seeds per pod**

The estimates of sea effects varied from -4.93 to 3.76 among F₁ hybrids. The cross combinations PDM 54 x HUM 2, PDM 54 x K 1310, PDM 54 x PDM 84-139, HUM 2 x PDM 84-139, Pusa 9531 x PDM 84-139, Pusa 9531 x K 92-140, K 1310 x T 44 and K 1284 x PS 16.

In F₂s generation the crosses which are significant positive sea effects are K 851 x HUM 2, K 851 x PS 16, K 851 x K 92-140, PDM 54 x PS 16, HUM 2 x K 92-140, Pusa 9531 x K 1284, Pusa 9531 x PDM 84-139, K 1310 x K 1284, K 1310 x PS 16, K 1310 x T 44, K 1284 x K 92-140, PDM 84-139 x PS 16.

**100-grain weight (g)**

The range of estimates of sea effects for the characters 100-grain weight varied from -1.07 to 1.53 among F₁ hybrids. The crosses showed positive significant sea effects are K 851 x Pusa 9531, K 851 x K 1310, K 851 x PDM 84-139, PDM 54 x T 44, HUM 2 x Pusa 9531, HUM 2 x K 1284, K 1310 x K 1284, K 1310 x PDM 84-139, K 1284 x PS 16, K 1284 x K 92-140, PS 16 x T 44.

Among F₂s generation the crosses exhibited positive significant sea effects are K 851 x HUM 2, K 851 x K 1310, K 851 x PDM 84-139, PDM 54 x HUM 2, HUM 2 x PS 16, Pusa 9531 x K 1284, K 1310 x PDM 84-139, K 1310 x K 92-140, K 1284 x T 44, PDM 84-139 x T 44.
**Protein per cal (%)**

The estimates of sea effects varied from -4.63 to 4.66 among F1 hybrids. The crosses showed significant positive sea effects are, K 851 x HUM 2, K 851 x Pusa 9531, K 851 x K 1310, K 851 x PS 16, PDM 54 x PDM 84-139, PDM 54 x T 44, HUM 2 x Pusa 9531, HUM 2 x K 92-140, K 1310 x K 1284, K 1310 x PS 16, K 1284 x PS 16, PDM 84-139 x T 44, PDM 84-139 x K 92-140, PS 16 x T 44.

The crosses among F2s generation showed significant positive sea effects are, K 851 x PDM 54, K 851 x HUM 2, K 851 x PS 16, PDM 54 x PS 16, PDM 54 x T 44, HUM 2 x K 1310, HUM 2 x PDM 84-139, Pusa 9531 x K 1310, K 1284 x PS 16, K 1284 x K 92-140, PDM 84-139 x T 44, PDM 84-139 x K 92-140, PS 16 x K 92-140.

**Yield per plant (g)**

Among F1 hybrids, sea effects for yield per plant varied from -6.00 to 5.39. The crosses found to have significant positive sea effect are K 851 x HUM, PDM 54 x HUM 2, PDM 54 x K 1284, PDM 54 x PDM 84-139, PDM 54 x T 44, HUM 2 x Pusa 9531, HUM 2 x K 1284, HUM 2 x PDM 84-139, Pusa 9531 x PS 16, Pusa 9531 x T 44, Pusa 9531 x K 92-140, K 1310 x T 44, K 1284 x PS 16, K 1284 x K 92-140, T 44 x K 92-140.

The crosses among F2 generation exhibited significant positive sea effects are, K 851 x HUM 2, K 851 x K 92-140, PDM 54 x Pusa 9531, PDM 54 x T 44, HUM 2 x PS 16, Pusa 9531 x T 44, K 1310 x K 1284, K 1310 x PDM 84-139, K 1310 x T 44, K 1310 x K 92-140, K 1284 x K 92-140, PDM 84-139 x PS 16, PS 16 x T 44.

5. HETEROSIS

Heterosis was calculated as per cent increase or decrease in F1 over better parent and economic heterosis over standard variety (K 851).
The estimates of heterosis are of practical utility only when hybrids are superior over the best existing cultivar. Different varieties included in this study had different desirable traits. Therefore, the heterosis was calculated over better parent for each combination. Variety K 851 had more desirable traits along with its high adaptable nature and regarded as best existing variety, so economic heterosis was calculated over standard parent K 851.

Estimates of heterosis in F₁ over better parent and economic heterosis in per cent have been presented in Table 1 and their character-wise explanation is as under:

**Days to flower**

Since early flowering is preferred hence heterosis was estimated over better parent, the crosses showing negative heterosis which are considered desirable. The range of heterobeltiosis varied from −0.16 to 27.12 per cent. Out of 45 crosses, thirty crosses showed significant heterosis irrespective of positive and negative values. Out of them only four crosses namely K 851 x PS 16, PDM 54 x PDM 84-139, Pusa 9531 x PDM 84-139 and PDM 54 x K 1310 in order of merit, recorded negative and significant heterobeltiosis for earliness.

Economic heterosis ranged from −1.72 to 0.112 per cent. Crosses namely K 851 x Pusa 9531, K 851 x PS 16, PDM 54 x K 1310, PDM 54 x T 44, HUM 2 x K 92-140, K 1310 x K 1284, K 1284 x PS 16, PDM 84-139 x PS 16, PDM 84-139 x K 92-140 and T 44 x K 92-140 in order of merit, recorded negative and significant heterosis for earliness.

**Days to maturity**

Similar to days to flowering early maturity is also desirable. The magnitude of heterosis for days to maturity varied from −15.43 to 20.56 per cent. 34 crosses showed significant heterosis. Out of which, two hybrids showing significant negative heterosis for early maturity were, K 851 x Pusa 9531, K 1310 x PDM 84-139 in that order.
The range of economic heterosis varied from -9.68 to 1.39 per cent. Of 25 significant heterotic crosses, the negative significant economic heterosis present in crosses, namely, K 851 x Pusa 9531, K 851 x K 1310, PDM 54 x PS 16, PDM 54 x K 92-140, HUM 2 x Pusa 9531, HUM 2 x K 1284, Pusa 9531 x K 1284, Pusa 9531 x PDM 84-139, Pusa 9531 x K 92-140, K 1310 x K 1284, K 1310 x K 92-140, K 1284 x T 44, PDM 84-139 x PS 16, PS 16 x T 44, PS 16 x K 92-140 in that order for early maturity.

**Plant height**

Heterobeltiosis varied from -7.82 to 226.00 per cent. Hybrids, K 851 x PDM 54, exhibited significant and negative heterobeltiosis.

Economic heterosis for plant height ranged from -29.99 to 47.00 per cent of 32 crosses which are significant, the crosses namely, K 851 x PDM 54, K 851 x HUM 2, PDM 54 x HUM 2, Pusa 9531 x PS 16, Pusa 9531 x K 92-140, K 1284 x PDM 84-139, K 1284 x K 92-140, PDM 84-139 x PS 16, T 44 x K 92-140, PS 16 x K 92-140 in order of merit, recorded positive and significant economic heterosis.

**Number of primary branches**

The range of heterobeltiosis and economic heterosis varied from -40.21 to 78.26 per cent and -36.29 to 21.25 per cent, respectively. Out of 18 significant crosses, the crosses namely, PDM 54 x Pusa 9531, PDM 54 x PDM 84-139, PDM 54 x PS 16, K 1284 x PDM 84-139, PDM 84-139 x PS 16, showed positive and significant heterobeltiosis.

The crosses namely Pusa 9531 x K 92-140, K 1284 x PS 16, PDM 84-139 x PS 16, PDM 84-139 x T 44, T 44 x K 92-140 exhibited positive and significant economic heterosis.
**Number of clusters per plant**

For this trait heterobeltiosis observed from -42.62 to 117.39 per cent of 30 crosses the crosses, namely, K 851 x PDM 54, K 851 x K 1284, PDM 54 x T 44, HUM 2 x T 44, Pusa 9531 x K 1284, K 1310 x PS 16, K 1310 x T 44, PDM 84-139 x T 44, T 44 x K 92-140 showed negative and significant heterobeltiosis.

Economic heterosis for this trait ranged from -27.99 to 50.27 per cent of 28 crosses, the crosses namely, K 851 x K 92-140, PDM 54 x K 1310, PDM 54 x K 1284, PDM 54 x K 92-140, HUM 2 x K 1310, HUM 2 x K 1284, HUM 2 x K 92-140, Pusa 9531 x K 1284, Pusa 9531 x K 92-140, K 1310 x K 1284, PDM 84-139 x PS 16, PDM 84-139 x K 92-140, PS 16 x T 44 showed positive and significant economic heterosis.

**Number of pods per cluster**

For this trait heterobeltiosis observed from -32.97 to 58.53 per cent. The crosses with maximum heterobeltiosis in order of merit were, K 851 x PDM 54, K 851 x PS 16, PDM 54 x PDM 84-139, HUM 2 x PDM 84-139, K 1310 x K 1284, K 1310 x PDM 84-139, PDM 84-139 x K 92-140.

Economic heterosis for this character ranged from -21.98 to 28.50 per cent. The positive and significant economic heterosis recorded in crosses, namely, K 851 x PS 16, HUM 2 x T 44, K 1310 x PS 16, K 1310 x K 92-140, K 1284 x T 44, PDM 84-139 x PS 16, PS 16 x T 44.

**Number of seeds per pod**

The magnitude of heterobeltiosis and economic heterosis for this character ranged from -54.91 to 66.02 per cent and -58.49 to 28.95 per cent, respectively. Out of 45 crosses, 25 crosses showed significant heterobeltiosis. Of which the crosses namely, PDM 54 x Pusa 9531, Pusa 9531 x PDM 84-139, Pusa 9531 x K 92-140, K 1284 x T
44, K 1284 x K 92-140, PDM 84-139 x PS 16 showed negative and significant heterobeltiosis.

For economic heterosis the crosses namely, K 851 x Pusa 9531, K 851 x K 1310, PDM 54 x K 1284, HUM 2 x PDM 84-139, K 1310 x K 1284, K 1310 x T 44, PS 16 x T 44 showed positive and significant economic heterosis.

**100-grain weight**

The observed heterosis over better parent ranged from -33.17 to 41.46 per cent, out of 45 crosses, 31 crosses showed significant heterobeltiosis and crosses namely, PDM 54 x HUM 2, PDM 54 x K 1310, K 851 x K 1310, PDM 54 x PDM 84-139, PDM 54 x K 92-140, HUM 2 x Pusa 9531, HUM 2 x K 1284, K 1284 x T 44, PS 16 x T 44, T 44 x K 92-140 with positive and significant heterobeltiosis.

The magnitude of economic heterosis ranged from -5.86 to 43.85 per cent. Out of 45 crosses, only 37 crosses showed significant economic heterosis. The crosses namely, PDM 54 x HUM 2, PDM 54 x Pusa 9531, PDM 54 x K 92-140, Pusa 9531 x PS 16, Pusa 9531 x K 92-140, K 1310 x PS 16, K 1310 x K 92-140, K 1284 x K 92-140, T 44 x K 92-140 showed significant and positive economic heterosis.

**Protein per cal (%)**

The range of heterobeltiosis for this trait was recorded between -38.90 to 28.00 per cent. Out of 45 crosses, 38 crosses showed significant heterobeltiosis for protein content, but only crosses namely, HUM 2 x Pusa 9531, HUM 2 x K 1284, HUM 2 x K 92-140, K 1284 x PS 16, PDM 84-139 x PS 16, PS 16 x T 44 found with significant and positive heterobeltiosis.

Economic heterosis ranged from -9.71 to 10.34 per cent. The crosses namely, K 851 x K 1310, K 851 x K 92-140, HUM 2 x PS 16, K 1284 x PS 16, K 1284 x K 92-140, PS 16 x K 92-140 exhibited positive and significant economic heterosis.
Yield per plant (g)

The heterobeltiosis for the character yield per plant was observed from -40.69 to 158.86 per cent. Out of 45 crosses, 29 crosses showed significant heterobeltiosis and crosses namely, K 851 x HUM 2, PDM 54 x K 1284, HUM 2 x K 1284, HUM 2 x PDM 84-139, Pusa 9531 x T 44, PDM 84-139 x PS 16 showed maximum heterobeltiosis in order of merit.

The economic heterosis ranged from -69.57 to 60.38 per cent. The crosses namely, K 851 x PDM 54, HUM 2 x Pusa 9531, HUM 2 x K 1284, HUM 2 x PDM 84-139, PS 16 x T 44, K 1310 x K 92-140 exhibited significant and positive economic heterosis.

6. HERITABILITY AND GENETIC ADVANCE

The estimates of narrow sense heritability and expected genetic advance as percentage of mean for different characters under study are presented in Table 2.16. Heritability estimates in narrow sense have been categorized according to Robinson (1965) as follows:

<table>
<thead>
<tr>
<th>Heritability Level</th>
<th>Percentage Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low heritability</td>
<td>below 10 per cent</td>
</tr>
<tr>
<td>Medium heritability</td>
<td>10 to 30 per cent</td>
</tr>
<tr>
<td>High heritability</td>
<td>above 30 per cent</td>
</tr>
</tbody>
</table>

Among F₁ crosses

Medium heritability was recorded for days to flower, day to maturity, plant height, number of primary branches, number of cluster per plant, number of pods per cluster, number of seeds per pod, 100-grain weight, yield per plant, low heritability was observed for protein per cal.
Among F$_2$ crosses

High heritability was recorded for days to flower, plant height, medium heritability was observed for days to maturity, number of primary branches, number of pods per cluster, number of seeds per pod, 100-grain weight, protein per cal., yield per plant, low heritability was recorded for number of clusters per plant.

The expected genetic advance in per cent over mean was high for number of primary branches, plant height, number of clusters per plant, number of pods per cluster, number of seeds per pod, medium for 100-grain weight, protein per cal., yield per plant and low for days to flower, days to maturity in F$_1$ and F$_2$ crosses, respectively.

In F$_1$ crosses, high heritability coupled with medium to high genetic advance was recorded for plant height, number of pods per plant, number of primary branches and in F$_2$ crosses are days to flower, plant height, number of pods per cluster and number of seeds per pod.

**CORRELATION COEFFICIENT**

The estimates of phenotypic and genotypic correlation coefficients between all possible pairs involving all the 10 characters separately for first and second filial generations were computed. The correlations between grain yield and other yield contributing traits and among the traits themselves are presented in Table 17-18.

In general, the magnitude of genotypic coefficient of correlations were found to be considerably more than the phenotypic correlations in both the generations for all the traits. This indicates a strong inherent association amongst most of the characters taken into consideration. A perusal of data revealed that out of all possible combinations of correlation coefficient, the significant association were recorded three in parents and one in F$_2$ generations. Among these the significant and positive values were recorded only one in parents and one in F$_2$. Whereas, significant negative values were obtained two in parents.
In parents number of seeds per pod is significant and negatively associated with plant height ($r_p = -0.716^*$$). Number of clusters per plants is negatively and significantly associated with plant height ($r_p = -0.685^*$$). Number of seeds per pod is significantly and positively associated with number of cluster per plant ($r_p = 0.717^*$$).

In $F_2$ yield per plant is significantly and positively associated with number of seeds per pod ($r_p = 0.643^*$$).