MATERIALS AND METHODS

The present experiment entitled "Varietal evaluation, Genetic divergence and Inter Character Correlation in Chickpea (Cicer arietinum L.) Under Late Sowing Conditions" involved 45 varieties and genotypes of chickpea (Cicer arietinum L.). Seeds of these varieties/genotypes were obtained from the Head, Pulses Research Laboratory, Genetics Division, I.A.R.I. New Delhi, and the Head, Department of Genetics and Plant Breeding, N. D. University of Agriculture and Technology, Kumarganj, Faijabad. These varieties/genotypes were being maintained at the Agricultural Research Farm of Sri Durga Ji Post Graduate College, Chandeshwar, Azamgarh (U.P.).

3.1. Experimental Site:

This investigation was made at the Agricultural Research Farm of S. D. J. Post Graduate college, Chandeshwar, Azamgarh U.P. It is situated near the college campus on the side of Azamgarh-Ghaziipur road at a distance of seven Km away from the Azamgarh district headquarters. Azamgarh district is situated in eastern U.P. at 26°4' "N" latitude, 83°11' longitude and at an elevation of 77.65m above the mean sea level.

3.2. Experimental Material:
The list of the 45 varieties/lines/genotypes of chickpea used in this experiment is given in Table (3.1).
3.3. Environments:

The experiment was conducted in two consecutive years viz., Rabi 2008-2009 and Rabi 2009-2010. These two years were considered as two environments, Year-I (2008-09) and Year-II (2009-10).

3.4. Lay Out of the Experiment:

This experiment was conducted in two consecutive years that constituted two environments. Experimental materials were sown on 17th Dec.2008 and 17th Dec. 2009 in a Randomized Block Design using 3 replications. Each of the 45 varieties/genotypes was sown in three rows of three meter length in each replication. Experimental sowing was done in the month of December (late sowing condition). Row -to-row and plant- to- plant distances were 30 cm and 10 cm, respectively. Before sowing of the experiments nitrogen @20 kg /ha, phosphorus @60kg/ha and potash @30kg/ha were applied as basal. All the necessary requirements of the crop such as irrigation and intercultural operations were fulfilled and the crop was maintained properly.

3.5. Observation:

At the time of flowering, randomly 10 plants were selected from each treatment in each replication and were tagged (labeled). Data were recorded for the following characters (Table 3.2).

3.6. Methods of Collection of Data:

1. Days to 50% Flowering:

Date on which 50% plants of a variety/genotype were in flowering was noted in each replication. Then number days taken from the date of sowing to the date of flowering were calculated.

2. Days to Maturity;

The numbers of days taken from sowing date to maturity date were calculated.

3. Plant height(cm);

The height of plant was measured from base to top of the plant at maturity, with the help of a meter scale.
Table 3.1: List of the varieties/genotypes of Chickpea (*Cicer arietinum* L.)

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Name of varieties /genotypes</th>
<th>Obtained from</th>
<th>S. No.</th>
<th>Name of varieties /lines</th>
<th>Obtained from</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>486 -18</td>
<td>&quot;</td>
<td>25</td>
<td>ICCV -88503</td>
<td>&quot;</td>
</tr>
<tr>
<td>3</td>
<td>GCP -105</td>
<td>&quot;</td>
<td>26</td>
<td>BG -1103</td>
<td>IARI New Delhi</td>
</tr>
<tr>
<td>4</td>
<td>Vishal</td>
<td>&quot;</td>
<td>27</td>
<td>Pusa -372</td>
<td>&quot;</td>
</tr>
<tr>
<td>6</td>
<td>Udai</td>
<td>&quot;</td>
<td>29</td>
<td>KLB -97-5</td>
<td>IARI New Delhi</td>
</tr>
<tr>
<td>7</td>
<td>ICCV -15676</td>
<td>IARI New Delhi</td>
<td>30</td>
<td>NDL. 2-96-21</td>
<td>&quot;</td>
</tr>
<tr>
<td>8</td>
<td>ICC -11535</td>
<td>IARI New Delhi</td>
<td>31</td>
<td>KLB -97-8</td>
<td>&quot;</td>
</tr>
<tr>
<td>9</td>
<td>Anupam</td>
<td>&quot;</td>
<td>32</td>
<td>IPL-110</td>
<td>&quot;</td>
</tr>
<tr>
<td>10</td>
<td>BG -261</td>
<td>&quot;</td>
<td>33</td>
<td>KLB -97-7</td>
<td>&quot;</td>
</tr>
<tr>
<td>11</td>
<td>J.B. 315</td>
<td>&quot;</td>
<td>34</td>
<td>IPC -2002-36</td>
<td>&quot;</td>
</tr>
<tr>
<td>12</td>
<td>B.G. 209</td>
<td>&quot;</td>
<td>35</td>
<td>KLB-97</td>
<td>&quot;</td>
</tr>
<tr>
<td>13</td>
<td>BG -391</td>
<td>&quot;</td>
<td>36</td>
<td>Awarodhi</td>
<td>&quot;</td>
</tr>
<tr>
<td>14</td>
<td>Green -112</td>
<td>&quot;</td>
<td>37</td>
<td>BG-203</td>
<td>&quot;</td>
</tr>
<tr>
<td>15</td>
<td>BG-1108</td>
<td>&quot;</td>
<td>38</td>
<td>Pusa-256</td>
<td>&quot;</td>
</tr>
<tr>
<td>16</td>
<td>BG -376</td>
<td>&quot;</td>
<td>39</td>
<td>ICRISAT-3074</td>
<td>N.D.U.A.T. Faizabad</td>
</tr>
<tr>
<td>17</td>
<td>BG -2019</td>
<td>&quot;</td>
<td>40</td>
<td>BG-1105</td>
<td>IARI New Delhi</td>
</tr>
<tr>
<td>18</td>
<td>BG -1101</td>
<td>&quot;</td>
<td>41</td>
<td>BG-1053</td>
<td>&quot;</td>
</tr>
<tr>
<td>19</td>
<td>BG -390</td>
<td>&quot;</td>
<td>42</td>
<td>ICRISAT-3073</td>
<td>N.D.U.A.T. Faizabad</td>
</tr>
<tr>
<td>20</td>
<td>EC -539009</td>
<td>N.D.U.A.T. Faizabad</td>
<td>43</td>
<td>BG-1073</td>
<td>IARI New Delhi</td>
</tr>
<tr>
<td>21</td>
<td>BG -1107</td>
<td>IARI New Delhi</td>
<td>44</td>
<td>K-850</td>
<td>N.D.U.A.T. Faizabad</td>
</tr>
<tr>
<td>22</td>
<td>Pusa -1088</td>
<td>IARI New Delhi</td>
<td>45</td>
<td>H.O.O.108</td>
<td>IARI New Delhi</td>
</tr>
<tr>
<td>23</td>
<td>BG -1044</td>
<td>IARI New Delhi</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Table 3.2: List of characters taken in the experiments

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Character</th>
<th>Symbol</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><strong>Physiological characters</strong></td>
<td></td>
</tr>
<tr>
<td>1.</td>
<td>Days to 50% flowering.</td>
<td>DF</td>
</tr>
<tr>
<td>2.</td>
<td>Days to maturity</td>
<td>DM</td>
</tr>
<tr>
<td></td>
<td><strong>Morphological characters</strong></td>
<td></td>
</tr>
<tr>
<td>3.</td>
<td>Plant height (cm)</td>
<td>PH</td>
</tr>
<tr>
<td>4.</td>
<td>Leaf length (cm.)</td>
<td>LL</td>
</tr>
<tr>
<td>5.</td>
<td>Number of leaflets per leaf</td>
<td>NL/L</td>
</tr>
<tr>
<td>6.</td>
<td>Leaflet length (cm.)</td>
<td>LtL</td>
</tr>
<tr>
<td>7.</td>
<td>Width of leaflet (cm.)</td>
<td>WL</td>
</tr>
<tr>
<td>8.</td>
<td>Number of primary branches per plant</td>
<td>NPB</td>
</tr>
<tr>
<td>9.</td>
<td>Number of secondary branches per plant</td>
<td>NSB</td>
</tr>
<tr>
<td>10.</td>
<td>Number of pods per plant</td>
<td>NP/P</td>
</tr>
<tr>
<td>11.</td>
<td>Pod length, (cm)</td>
<td>PL</td>
</tr>
<tr>
<td>12.</td>
<td>Pod width (cm.)</td>
<td>PW</td>
</tr>
<tr>
<td>13.</td>
<td>Number of seeds per pod.</td>
<td>NS/P</td>
</tr>
<tr>
<td>14.</td>
<td>100-seed weight (g)</td>
<td>100.SW</td>
</tr>
<tr>
<td>15.</td>
<td>Seed yield per plant (g)</td>
<td>YPP</td>
</tr>
</tbody>
</table>
4. **Leaf length (cm);**
Average size leaves were taken from the selected plant and the length of leaf (Compound leaf) was measured from leaf base to the leaf tip.

5. **Number of leaflets per leaf;**
Numbers of leaflets per leaf were counted from each selected plant.

6. **Leaflet length(cm);**
Length of three leaflets was measured in each selected plant and then average was calculated.

7. **Width of leaflet (cm);**
Width of leaflets (already selected for length measurement) was measured with the help of a scale.

8. **Number of primary branches per plant;**
Number of primary branches per plant was counted in every selected plant and average was calculated.

9. **Number of secondary branches per plant;**
Numbers of secondary branches/plant (arising from primary branches) were counted in every selected plant and average was calculated.

10. **Number of Pods per plant;**
Pods were counted from each selected plant.

11. **Pod length;**
Pod length was counted in each selected plant and average was calculated

12. **Pod width (cm.);**
Width of pod was measured with the help of Vernier Calipers.

13. **Number of seeds per pod;**
At the time of threshing, seeds were counted in 3 pods from each selected plant and then mean was calculated

14. **100-seed weight (g);**
100 seeds were counted randomly from every variety/genotype from each replication and were weighed on a Triple Beam Balance.

15. Seed yield per plant (g);
Total seeds from each selected plant of all the treatments in all the replication were weighed and mean was calculated.

3.7. Biometrical (Statistical) Analysis:

The data recorded for each character from randomly selected plants were used to calculate mean value. The replication-wise mean values were subjected to the following statistical and biometrical analysis.

3.7.1. Analysis of Variance:

It was done according to Panse and Sukhatme (Panse and Sukhatme 1967). The general formula and procedure are given below.

\[
\text{Correction factors (C.F.) = } \frac{GT^2}{N}
\]

Where \( GT \) = grand total; \( N \) = total number of plots or observation.

\[
\text{Sum of squares due to block or replication (R.S.S.) =}
\]
\[
\frac{(\sum R_1^2 + \sum R_2^2 + \sum R_3^2)}{(\text{Number of Treatments})} - \text{(C.F.)}
\]

\[
\text{Sum of squares due to treatments (Tr. S. S.) =}
\]
\[
\frac{(\sum Y_1^2 + \sum Y_2^2 + \sum Y_3^2 + \cdots + \sum Y_{45}^2)}{(\text{Number of Replications})} - \text{C.F.}
\]

\[
\text{Total sum of squares (T.S.S.) =}
\]
\[
(X_1^2 + X_2^2 + X_3^2 + \cdots + X_{45}^2) - \text{(C.F.)}
\]

\[
\text{Sum of Square due to error =}
\]
\[
(Total \ S. \ S.) - (R. \ S. \ S. + Tr. \ S. \ S.)
\]

Details of analysis of variance table are given in Table 3.3.
### Table 3.3: Analysis of variance table

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Source of Variation</th>
<th>Degree of Freedom</th>
<th>Sum of Square (s.s.)</th>
<th>Mean sum of Squares M.S.S or MS</th>
<th>F – Value (Variance ratio)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Replication (r)</td>
<td>(r-1)</td>
<td>Rep. S. S.</td>
<td>S. S. r/(r-1)=MS(r)</td>
<td>M.S.(r)/MS e=F</td>
</tr>
<tr>
<td>2.</td>
<td>Treatment (t)</td>
<td>(t-1)</td>
<td>Tr. S. S.</td>
<td>S.S. t/(t-1)=MS(t)</td>
<td>M.S(t)/M Se =F</td>
</tr>
<tr>
<td>3.</td>
<td>Error (e)</td>
<td>(r-1)(t-1)</td>
<td>Error S. S.</td>
<td>S.S. error/(r-1)(t-1)=MS (e)</td>
<td>-</td>
</tr>
</tbody>
</table>

#### 3.7.2. Test of Significance:

The calculated “F” value was compared with the Table “F” value. Higher calculated “F” values than the table “F” value at 0.05 (5%) probability level indicated that the varietal differences regarding the particular character were significant. When the calculated “F” value was greater than “F” value at 0.01 (1%) probability levels, the differences were considered highly significant.

#### 3.7.3. Critical difference (C.D):

It was calculated as “Standard error of difference or S.E. (d) x t values” at error degree of freedom. \( \sqrt{C.D.} = S.E. (d) \times t \)

Where, \[ S.E. (d) = \sqrt{\frac{2 \times M.S. Error}{No. of Replications}} \]

\( t \) = t value at error degrees of freedom at 0.05 or 0.01 probability level.

#### 3.7.4. Variability and Genetic Parameters:

Genotypic Variance = \( (\sigma^2 g) \): It was calculated by the following formula

\[
\text{Genotypic variance} \ (\sigma^2 g) = \frac{M.S. Treatment - M.S. Error}{No. of Replications}
\]
Error variance \( (\sigma^2_e) = M.S.\ Error \)

Phenotypic variance \( (\sigma^2_p) = \sigma^2_g + \sigma^2_e \)

3.7.4.1. Genotypic Coefficient of Variation (GCV):

It was calculated according to the formula given by Burton (1952)

\[
G.C.V.(\%) = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100
\]

3.7.4.2. Phenotypic Coefficient of Variation (PCV):

\[
P.C.V.(\%) = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100
\]

Where

\[
\bar{X} = \text{General mean (grand mean) of the character} = \frac{\text{Grand Total}}{N}
\]

3.7.4.3. Heritability:

Heritability was calculated in broad sense according to the formula suggested by Hanson et al. (1956).

\[
\text{Heritability}(\%) = \frac{\text{Genotypic variance} (\sigma^2_g)}{\text{Phenotypic variance} (\sigma^2_p)} \times 100
\]

3.7.4.4. Genetic advance under selection (Gs):

The expected genetic advance was calculated according to the formula given by Johnson et al. (1955).

\[
\text{Genetic Advance under selection} (Gs) = \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p} \times K
\]

Gs = Heritability \times Phenotypic standard deviation \times K

Where

\[
K = \text{selection differential (a constant) which is 2.06 at 5\% selection intensity.}
\]

\[
\text{Heritability Fraction} = \frac{\sigma^2_g}{\sigma^2_p}
\]

Phenotypic standard Deviation \( = \sqrt{\sigma^2_p} \)
3.7.4.5. Genetic advance (% of mean):

It was calculated by the following formula.

\[
G.A. \text{ (% of mean)} = \frac{\text{Genetic Advance (Absolute)}}{\bar{X}} \times 100
\]

Where \( \bar{X} \) = Grand mean of the character.

3.7.5. Correlation coefficient:

Correlation coefficients were calculated from variance and covariance component.

The method given in Singh and Chaudhary (1985) was used for the calculation of simple correlation coefficients. Sum of products and mean sum of product were calculated to find out covariance.

Analysis of Covariance table is given below.

3.7.5.1. Analysis of covariance

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Source of Variation</th>
<th>Degree of freedom</th>
<th>Sum of products (S.P.)</th>
<th>Mean sum of products (M.S.P.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Replication</td>
<td>(r-1)</td>
<td>X</td>
<td>X/(r-1)</td>
</tr>
<tr>
<td>2.</td>
<td>Treatment</td>
<td>(t-1)</td>
<td>Y</td>
<td>Y/(t-1)</td>
</tr>
<tr>
<td>3.</td>
<td>Error</td>
<td>(r-1)(t-1)</td>
<td>Z</td>
<td>Z/(r-1)(t-1)</td>
</tr>
</tbody>
</table>

Error Covariance \( (Cov^e. xy) = M.S.P. \) Error

Genotypic Covariance \( (Cov^g. xy) = \frac{(M.S.P. \text{Treatment} - M.S.P. \text{Error})}{\text{Number of Replications}} \)

Phenotypic Covariance \( (Cov^p. xy) = (Cov^g. xy) + (Cov^e. xy) \)

3.7.5.2. Phenotypic Correlation Coefficient \( (r^p xy) \) :

\[
\text{Phenotypic Correlation Coefficient} \ (r^p xy) = \frac{(Cov^p. xy)}{\sqrt{(\sigma^2 px) \times (\sigma^2 py)}}
\]

Where
\( \sigma^2 px \) = Phenotypic variance of character \( x \)
\( \sigma^2 py \) = Phenotypic variance of character \( y \)
\( Cov^p. xy \) = Phenotypic covariance of character \( x \) and \( y \)
3.7.5.3. Genotypic Correlation Coefficient ($r_{xy}^g$):

\[
Genotypic\ Correlation\ Coefficient\ (r_{xy}^g) = \frac{(Cov^g, xy)}{\sqrt{(\sigma^2 gx) \times (\sigma^2 gy)}}
\]

Where,
- $\sigma^2 gx$ = Genotypic variance of character $x$
- $\sigma^2 gy$ = Genotypic variance of character $y$
- $Cov^g, xy$ = Genotypic covariance of character $x$ and $y$

3.7.5.4. Test of significance of phenotypic correlation:

It was tested by comparing the correlation coefficient with the Table value at $(n-2)$ degree of freedom, where “$n$” represents the paired observation i.e. number of varieties/genotypes (Hayes et al. 1955).

3.7.6. Path Coefficients Analysis:

A Path coefficient is simply a standardized partial regression coefficient and as such measures the direct influences of one variable upon another and permits the partition of correlation coefficient into component of direct and indirect effects. The use of this method requires a cause and effects situation among the variables and the estimates.

3.7.6.1. (I) Calculation of Direct Effect:

The correlation coefficients of the 14 characters with yield/plant were partitioned into direct and indirect effects (Dewey and Lu 1959). Seed yield/plant was considered as effect (or dependent character), while other 14 characters were considered as cause (or independent characters). The direct paths were worked out with the help of the following equations.

\[
r_{1,15} = P_1 r_{1,1} + P_2 r_{1,2} + P_3 r_{1,3} + P_4 r_{1,4} + P_5 r_{1,5} + P_6 r_{1,6} + P_7 r_{1,7} + P_8 r_{1,8} + P_9 r_{1,9} + P_{10} r_{1,10} + P_{11} r_{1,11} + P_{12} r_{1,12} + P_{13} r_{1,13} + P_{14} r_{1,14}
\]

\[
r_{14,15} = P_1 r_{14,1} + P_2 r_{14,2} + P_3 r_{14,3} + P_4 r_{14,4} + P_5 r_{14,5} + P_6 r_{14,6} + P_7 r_{14,7} + P_8 r_{14,8} + P_9 r_{14,9} + P_{10} r_{14,10} + P_{11} r_{14,11} + P_{12} r_{14,12} + P_{13} r_{14,13} + P_{14} r_{14,14}
\]

Here “$r$” is the correlation coefficient between the character pair involved and the “$P$” is the direct effect of the character on yield.
3.7.6.2. (II) Calculation of Indirect Effect:
The computation of direct indirect effect was made as per formula given below.

Indirect effect = \( r_{ij} \times P_{ij} \)

Where

\[ i = 1, \ldots, n \]

\[ j = 1, \ldots, n \]

\[ P_{ij} = P_{iy} - P_{yi} \]

3.7.6.3. (III) Calculation of Residual Factor

The residual factor (x) is given by the following formula (Singh and Chaudhary 1985).

\[ P^2x = 1 - P_{ij} x r_{ij} x P_{yj} \]

3.7.7. Genetic Divergence (\( D^2 \))

Genetic divergence studies were made using 15 characters of Chickpea. The Mahalanobis \( D^2 \) statistic (Mahalanobis 1936, Rao 1952) was estimated using computer package INDOSTAT Based on the \( D^2 \) values the varieties/genotypes were grouped into clusters with the help of Tocher's method (Rao 1952). The contribution of different character were calculated and each characters was ranked on the basis of

\[ d_i = V^i - V^k \] Values

Rank I was given to the highest mean difference and rank \( P = (15) \) to the lowest difference.