3. MATERIALS AND METHODS

The present investigation entitled "Studies on genetic variability and genotype-environment interaction in chickpea (Cicer arietinum L.)" was carried out using 45 chickpea (Cicer arietinum L.) genotypes in 12 environments at Janta Vedic College, Baraut, Baghat and S.V.B.P.U.A. & T., Meerut, U.P.

To identify the comparative behaviour of different genotypes at two locations, observations on plant basis for most of the quantitative traits were recorded on single plant basis at maturity stage. The relevant research work were carried out at the Research Farm of Janta Vedic College, Baraut, Baghat (U.P.) and Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.) during 2004-2005 and 2005-2006. Keeping in view, the objectives of this study defined earlier, the experimental and other technical programmes were formulated for estimating different stability parameters and variability in 45 chickpea genotypes.

The materials for this study consisted 45 genotypes of chickpea were obtained from S.V.B.P.U.A. & T., Meerut (U.P.).

The experimental and statistical methodologies adopted for the present investigation are described under:

3.1 ENVIRONMENTS AND EXPERIMENTS

The experiments consisting 45 genotypes were conducted in
Randomized Block Design with three replication during 2004-05 and 2005-06 at the Research Farm of Janta Vedic College, Baraut, Baghpat (U.P.) and Sardar Vallabhbhai Bhai Patel University of Agriculture and Technology, Meerut (U.P.) under different planting dates at Meerut and Baraut locations. The details of twelve environments are given below:

<table>
<thead>
<tr>
<th>Environment</th>
<th>Year</th>
<th>Location</th>
<th>Date of sowing</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>2004-05</td>
<td>Meerut</td>
<td>15th October</td>
</tr>
<tr>
<td>I</td>
<td>2004-05</td>
<td>Meerut</td>
<td>15th November</td>
</tr>
<tr>
<td>III</td>
<td>2004-05</td>
<td>Meerut</td>
<td>15th December</td>
</tr>
<tr>
<td>IV</td>
<td>2004-05</td>
<td>Baraut</td>
<td>22nd October</td>
</tr>
<tr>
<td>V</td>
<td>2004-05</td>
<td>Baraut</td>
<td>22nd November</td>
</tr>
<tr>
<td>VI</td>
<td>2004-05</td>
<td>Baraut</td>
<td>22nd December</td>
</tr>
<tr>
<td>VII</td>
<td>2005-06</td>
<td>Meerut</td>
<td>15th October</td>
</tr>
<tr>
<td>VIII</td>
<td>2005-06</td>
<td>Meerut</td>
<td>15th November</td>
</tr>
<tr>
<td>IX</td>
<td>2005-06</td>
<td>Meerut</td>
<td>15th December</td>
</tr>
<tr>
<td>X</td>
<td>2005-06</td>
<td>Baraut</td>
<td>22nd October</td>
</tr>
<tr>
<td>XI</td>
<td>2005-06</td>
<td>Baraut</td>
<td>22nd November</td>
</tr>
<tr>
<td>XII</td>
<td>2005-06</td>
<td>Baraut</td>
<td>22nd December</td>
</tr>
</tbody>
</table>

3.2 GENOTYPES

<table>
<thead>
<tr>
<th>S.N.</th>
<th>Genotypes</th>
<th>Pedigree</th>
<th>Types</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>GNG 1519</td>
<td>GNG 663 x GNG 925</td>
<td>Desi</td>
</tr>
<tr>
<td>2</td>
<td>WCG 4-1</td>
<td>Mutant of G 130</td>
<td>Desi</td>
</tr>
<tr>
<td>3</td>
<td>BG 256</td>
<td>(BG 62 x K 850-3/27) x (2250 x H 75-35)</td>
<td>Desi</td>
</tr>
<tr>
<td>4</td>
<td>WCG 97-28</td>
<td>Pusa 256 x Pusa Gaurav</td>
<td>Desi</td>
</tr>
<tr>
<td>5</td>
<td>PFGK 1218</td>
<td>FGK x FGK 869</td>
<td>Kabuli</td>
</tr>
<tr>
<td>6</td>
<td>GJG 0104</td>
<td>ICCV 92014 x ICCV 10</td>
<td>Desi</td>
</tr>
<tr>
<td>7</td>
<td>IPC 2001-1</td>
<td>BG 256 x L 532</td>
<td>Desi</td>
</tr>
<tr>
<td>8</td>
<td>CSJ 340</td>
<td>RSG 951 x RSG 901</td>
<td>Desi</td>
</tr>
<tr>
<td>9</td>
<td>GNG 1573</td>
<td>BG 1003 x GNG 149</td>
<td>Kabuli</td>
</tr>
<tr>
<td>10</td>
<td>CSJ 336</td>
<td>RSG 951 x RSG 585</td>
<td>Desi</td>
</tr>
<tr>
<td>No.</td>
<td>Variety</td>
<td>Description</td>
<td>Type</td>
</tr>
<tr>
<td>-----</td>
<td>---------------</td>
<td>-------------------------------------------------------</td>
<td>------</td>
</tr>
<tr>
<td>11</td>
<td>HK 00-299</td>
<td>(HK 95-94 x PNO 141) x HK 89-131</td>
<td>Kabuli</td>
</tr>
<tr>
<td>12</td>
<td>BGD 1020</td>
<td>(BDG 72 x Pusa 267) x (BG 1088 x ICC 14196)</td>
<td>Kabuli</td>
</tr>
<tr>
<td>13</td>
<td>IPC 2001-12</td>
<td>BG 364 x PGD 84-16</td>
<td>Desi</td>
</tr>
<tr>
<td>14</td>
<td>BG 2023</td>
<td>(KWR 108 x H 86-73) x (GF 91 x BG 369)</td>
<td>Desi</td>
</tr>
<tr>
<td>15</td>
<td>GNG 1577</td>
<td>BG 1003 x GNG 149</td>
<td>Kabuli</td>
</tr>
<tr>
<td>16</td>
<td>IPCK 305</td>
<td>ICCV 5 x ICCL 83007</td>
<td>Kabuli</td>
</tr>
<tr>
<td>17</td>
<td>HK 00-290</td>
<td>(HK 92-122 x HK 89-131)</td>
<td>Kabuli</td>
</tr>
<tr>
<td>18</td>
<td>H 00-191</td>
<td>GL 90169 x H 86-18</td>
<td>Desi</td>
</tr>
<tr>
<td>19</td>
<td>CSJK 9</td>
<td>RSGK 628 x DGM 538</td>
<td>Kabuli</td>
</tr>
<tr>
<td>20</td>
<td>BG 2030</td>
<td>BG 1088 x (ICCV 83003 x ICC 14196)</td>
<td>Kabuli</td>
</tr>
<tr>
<td>21</td>
<td>SCS 16</td>
<td>Local collection</td>
<td>Kabuli</td>
</tr>
<tr>
<td>22</td>
<td>BG 2027</td>
<td>Pusa 336 x (Avrodhi x WR 315)</td>
<td>Desi</td>
</tr>
<tr>
<td>23</td>
<td>CSJK 11</td>
<td>RSGK 628 x BG 1003</td>
<td>Kabuli</td>
</tr>
<tr>
<td>24</td>
<td>GJG 0106</td>
<td>ICCV 93001 x ICCV 10</td>
<td>Desi</td>
</tr>
<tr>
<td>25</td>
<td>WCG 2000-2</td>
<td>Pant G 114 x Pusa 244</td>
<td>Desi</td>
</tr>
<tr>
<td>26</td>
<td>BGD 1017</td>
<td>(Pusa 362 x BG 372) x (Avrodhi x Pusa 212)</td>
<td>Desi</td>
</tr>
<tr>
<td>27</td>
<td>GLK 21159</td>
<td>(ICCV 2 x ICCV 88507) x (ICCV 2 x ICC 7344)</td>
<td>Kabuli</td>
</tr>
<tr>
<td>28</td>
<td>BG 1053</td>
<td>Selection from ICCV 3</td>
<td>Kabuli</td>
</tr>
<tr>
<td>29</td>
<td>PBG 233</td>
<td>L 550 x H 86-18</td>
<td>Desi</td>
</tr>
<tr>
<td>30</td>
<td>GNG 469</td>
<td>Annagiri 1 x H 75-35</td>
<td>Desi</td>
</tr>
<tr>
<td>31</td>
<td>GLK 21143</td>
<td>GLK 88016 x FLIP 88-34C</td>
<td>Kabuli</td>
</tr>
<tr>
<td>32</td>
<td>L 550</td>
<td>PB 7 x Robat</td>
<td>Kabuli</td>
</tr>
<tr>
<td>33</td>
<td>BG 2031</td>
<td>(Avrodhi x Pusa 267) x (FLIP 88-47 x BG 1109)</td>
<td>Kabuli</td>
</tr>
<tr>
<td>34</td>
<td>IPCK 306</td>
<td>(Soba x ICCV 2) x Mocorito 88</td>
<td>Kabuli</td>
</tr>
<tr>
<td>35</td>
<td>HK 98-155</td>
<td>(ICCV 2 x Surutato 77)</td>
<td>Desi</td>
</tr>
<tr>
<td>36</td>
<td>WCG 3</td>
<td>Mutant of C 235</td>
<td>Desi</td>
</tr>
<tr>
<td>37</td>
<td>Surya</td>
<td>Mutant of G130</td>
<td>Desi</td>
</tr>
<tr>
<td>38</td>
<td>PFGK 1221</td>
<td>GLK 95095 x L 550</td>
<td>Kabuli</td>
</tr>
<tr>
<td>39</td>
<td>BGM 548</td>
<td>Mutant of ICC 5166</td>
<td>Desi</td>
</tr>
<tr>
<td>40</td>
<td>H 00-212</td>
<td>H 82-2 x C. reticulatum</td>
<td>Desi</td>
</tr>
<tr>
<td>41</td>
<td>BG 1003</td>
<td>Mutant of L 532</td>
<td>Kabuli</td>
</tr>
<tr>
<td>42</td>
<td>Sadbhavana</td>
<td>Mutant of C 235</td>
<td>Desi</td>
</tr>
<tr>
<td>43</td>
<td>GNG 1477</td>
<td>KPG 279-3 x GNG 469</td>
<td>Desi</td>
</tr>
<tr>
<td>44</td>
<td>WCG 10</td>
<td>Selection from G 130</td>
<td>Desi</td>
</tr>
<tr>
<td>45</td>
<td>WCG 97-15</td>
<td>PG 144 x Pusa 244</td>
<td>Desi</td>
</tr>
</tbody>
</table>
3.3 EXPERIMENTAL LAYOUT

Design : RBD (Randomized Block Design)
Number of genotypes : 45
Number of replication : 3 in each environment
Row to row distance : 30 cm
Plant to plant distance : 10 cm
Row length : 4 meter

Presowing irrigation was provided to ensure proper germination in all the experiments. The basal application of fertilizers (recommended doses) and standard package of agronomic practices was followed to obtain proper plant stand in the experiments.

3.4 CHARACTERS STUDIED

The observations for all the characters were recorded on five competitive plants in each genotype per replication and mean values per plant basis were obtained. The single plant observations were recorded on different genotypes in all the twelve environments.

3.4.1 Observations

Observations in each experiment were recorded on 5 competitive plants in each replication for each environment separately during both the years. All the thirteen agronomical traits used in the present study are given below:
1. Days to 50% flowering

The number of days taken from the date of sowing to the date of appearance of flowers on 50% plants of each genotype in the plot.

2. Days to maturity

Days to maturity was recorded when 75 per cent pods were physiologically mature. It was recorded on plant basis.

3. Plant height (cm)

Measured in cms from the ground level to the top of the plant.

4. Number of primary branches per plant

Total number of only pod bearing primary branches were recorded.

5. Number of secondary branches per plant

Total number of secondary pod bearing branches were recorded.

6. Height of first pod from the ground level (cm)

Measured in cms from the ground level to the first pod of main branch.

7. Number of pods per plant

Total number of seed bearing pods were counted.

8. Number of seeds per pod

Number of seed counted on 5 pods and averaged.

9. Number of seeds per plant

Total number of seeds per plant were counted from the sample of five competitive plants.
10. Biological yield per plant (g)

Dry weight per plant excluding roots was measured at the time of harvesting.

11. Grain yield per plant (g)

Grain yield was taken at the time of maturity from averaged over samples of five competitive plants.

12. Harvest index (%)

Harvest index was calculated by dividing the grain yield per plant (g) by the biological yield per plant (g) as described below:

\[
H.I. = \frac{\text{Total grain dry weight}}{\text{Total plant dry weight at harvest}} \times 100
\]

13. 100-seed weight (g)

Weight (g) of 100 dry seeds selected at random for each genotype separately.

3.5 STATISTICAL ANALYSIS

The statistical analysis was carried out for different experiments separately as per standard statistical procedures. Estimation of mean, variance, coefficient of variation, heritability and genetic advance was done as per method described by Snedecor and Cochran (1967) and usual analysis of variance was carried out as per statistical methods proposed by Panse and Sukhatme (1967). The stability analysis was carried out in accordance with Eberhart and Russell's (1966) and Perkins and Jinks (1968a). The mean data relating to various quantitative traits were subjected to the following statistical analysis:
3.5.1 ANALYSIS OF VARIANCE (ANOVA)

The analysis of variance was carried out for Randomized Block Design, for each of the environment separately. Difference among genotype for different characteristics were tested for significance by using analysis of variance technique (Panse and Sukhatme, 1954). Analysis of variance of the data was done on the basis of following model:

\[ Y_{ij} = \mu + g_i + b_j + e_{ij} \]

Where,

- \( Y_{ij} \) = phenotypic observation in \( i^{th} \) genotypes and \( j^{th} \) replication,
- \( \mu \) = general mean,
- \( g_i \) = \( i^{th} \) genotype effect,
- \( b_j \) = \( j^{th} \) block effect and
- \( e_{ij} \) = random error associated with \( i^{th} \) treatment and \( j^{th} \) replication.

The assumptions of the model are:

(a) All the observations are independent.

(b) Error involved in the population is normally and independently distributed with mean zero and variance \( \sigma^2 \).

(c) The different effects in the model are additive.

**Analysis of variance table**

<table>
<thead>
<tr>
<th>Source of variance</th>
<th>d.f.</th>
<th>Mean square (M.S.)</th>
<th>Expected (M.S.)</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>( (r-1) )</td>
<td>( MS_R )</td>
<td>( \sigma^2 e + g \sigma^2 r )</td>
<td>( MS_R / MS_E )</td>
</tr>
<tr>
<td>Genotypes</td>
<td>( (g-1) )</td>
<td>( MS_G )</td>
<td>( \sigma^2 e + r \sigma^2 g )</td>
<td>( MS_G / MS_E )</td>
</tr>
<tr>
<td>Error</td>
<td>( (r-1) (g-1) )</td>
<td>( MS_E )</td>
<td>( \sigma^2 e )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( (rg-1) )</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Where,

\[ r = \text{number of replications or blocks and} \]
\[ g = \text{number of treatments or genotypes}, \]

\( MS_R, MS_G \) and \( MS_E \) stand for the mean squares due to replications, genotypes and errors, respectively.

**ANALYSIS OF VARIANCE COMPONENTS**

The genotypic, phenotypic and error variance were calculated as follows:

1. **Genotypic variance**

   It is the variance contributed by the genetic cause of occurrence of difference an individual due to difference in their genetic make up. It was estimated by the formula given by Panse and Sukhatame (1954) for randomized block design

   \[ \sigma^2_g = \frac{M_g - M_e}{r} \]

   Where,

   \( \sigma^2_g = \text{genotypic variance} \)

   \( M_g = \text{Genotypic mean sum of squares of these characters}, \)

   \( M_e = \text{Error mean sum of squares of the characters and} \)

   \( r = \text{No. of replications.} \)

2. **Phenotypic variance**

   It is the sum of the variance contributed by genetic causes and environmental factors. It was calculated as under:

   \[ \sigma^2_p = \sigma^2_g + \sigma^2_e \]

   where,

   \( \sigma^2_p = \text{Phenotypic variance}, \)

   \( \sigma^2_g = \text{Genotypic variance and} \)

   \( \sigma^2_e = \text{Error variance.} \)
3. Error (environmental) variance

The mean square of error divided by the number of replications represented by variation attributed to the environmental cause.

$$\sigma^2_e = M_e$$

Where,

$$\sigma^2_e = \text{Error variance and}$$

$$M_e = \text{Error mean sum of square of the characters.}$$

3.5.2 Parameters of variability

3.5.2.1 Mean ($\bar{X}$)

The mean value of each character was worked out by dividing the totals by corresponding number of observations.

$$\bar{X} = \frac{\sum X_{ij}}{N}$$

Where,

$$X_{ij} = \text{Any observation in } i^{th} \text{ genotype and } j^{th} \text{ replication and}$$

$$N = \text{Total number of observations.}$$

3.5.2.2 Range

It is the difference between the lowest and the highest values for each character

$$R = H - L$$

Where,

$$H = \text{Highest value for the characters and}$$

$$L = \text{Lowest value for the characters.}$$

3.5.2.3 Standard error of mean

Standard error of difference of two means was calculated with the help of error mean square from the analysis of variance table.
Standard error (m±) = √\(\text{EMS}/r\)

Where,

\(\text{EMS} = \text{Error mean sum of square and}\)

\(r = \text{Number of replications.}\)

**3.5.2.4 Critical difference (CD)**

\[
\text{CD at 5%} = \frac{\sqrt{2 \text{EMS}}}{r} \times t \text{ value at error d.f. at 5% level of significance}
\]

Where,

\(r = \text{Number of replications and}\)

\(\text{EMS} = \text{Error mean of square.}\)

**3.5.2.5 Coefficient of variation**

Genotypic, phenotypic and environment coefficients of variation were estimated by the formula suggested by Burton and De Vane (1953) for each character as:

Genotypic coefficient of variation (G.C.V.) = \(\frac{\sqrt{V_{G}}}{\bar{X}} \times 100\)

Phenotypic coefficient of variation (P.C.V.) = \(\frac{\sqrt{V_{P}}}{\bar{X}} \times 100\)

Environment coefficient of variation (E.C.V.) = \(\frac{\sqrt{V_{E}}}{\bar{X}} \times 100\)

Where,

\(\bar{X}\) is the mean of that particular character and \(V_{G}\), \(V_{P}\) and \(V_{E}\) are the genotypic, phenotypic and environment variance, respectively.
3.5.2.6 Heritability in broad sense

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

\[ H = \frac{V_G}{V_P} \times 100 \]

Where,

\( H \) = Heritability (broad sense),
\( V_G \) = Genotypic variance and
\( V_P \) = Phenotypic variance.

3.5.2.7 Genetic advance expressed as percentage of mean

Estimates of appropriate variance components were substituted for the parameters to predict expected genetic gain as suggested by Lush (1949) and Johnson et al. (1955). The expected genetic advance was calculated at 5 per cent selection intensity for each character as:

Genetic advance (% of mean) = \[ \frac{K_{\sigma_P} H}{\bar{X}} \times 100 \]

Where, \( K_{\sigma_P} \) is the selection differential expressed in terms of phenotypic standard variations. Using 5 per cent selection in a large sample from a normally and independently distributed population, the value of selection intensity (\( K \)) is equal to 2.06 (Allard, 1960).

\[ H \quad = \quad \text{Heritability in broad sense, and} \]
\[ \bar{X} \quad = \quad \text{Mean value for that character over all the genotypes} \]

**CHARACTER ASSOCIATION**

3.5.3 Correlation coefficient analysis

The correlation coefficient were calculated from genotype, error
mean square and mean sum of products matrices obtained by the analysis of covariance. The expectation of phenotypic, genotypic and environmental mean sum of products were as follows:

<table>
<thead>
<tr>
<th>Source</th>
<th>d.f.</th>
<th>(M.S.P.)</th>
<th>Expectation of (M.S.P.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>(r-1)</td>
<td>M_r</td>
<td>(σ_{eij} + rσ_{gij})gij</td>
</tr>
<tr>
<td>Genotypes</td>
<td>(g-1)</td>
<td>M_{gij}</td>
<td>-</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1)(g-1)</td>
<td>M_{eij}</td>
<td>-</td>
</tr>
</tbody>
</table>

The estimates for genotypes covariance were worked out as follows from expectation of mean sum of products.

\[ σ_{gij} = \frac{(M_{p} - M_{eq})}{r} \]

Correlation coefficient

\[ r = \frac{\text{cov}(x,y)}{\sqrt{\text{v}(x)\times\text{v}(y)}} \]

Where,

- \( \text{cov}(x,y) \) is covariance between \( x \) and \( y \),
- \( \text{v}(x) \) is the variance of \( x \) and
- \( \text{v}(y) \) is the variance of \( y \)

**Test of significance of correlation coefficient**

For testing the significance of correlation coefficient the following formula was used:

\[ t = r\sqrt{\frac{n-2}{1-r^2}} \]

Where,

- \( r \) = Correlation coefficient and
- \( n \) = Total no. of observations.
This 't' value was tested against the table value of 't' at 5% and 1% value level of significance with (n-2) degree of freedom.

3.5.4 PATH-COEFFICIENT ANALYSIS

The correlation coefficients were used to work out path-coefficient analysis. Path-coefficients were obtained according to Dewey and Lu (1959). A set of simultaneous equations in the following forms were solved:

\[ r_{1y} = p_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \ldots + r_{1x} p_{xy} \]
\[ r_{2y} = p_{2y} + r_{22} P_{2y} + r_{23} P_{3y} + \ldots + r_{2x} p_{xy} \]
\[ r_{ny} = p_{ny} + r_{n2} P_{2y} + r_{n3} P_{3y} + \ldots + r_{nx} p_{xy} \]

Where,

\[ r_{ny} = \text{Correlation coefficient of one character and yield,} \]
\[ p_{xy} = \text{Path-coefficient between the character and yield and} \]
\[ r_{n2}, r_{n3}, \ldots, r_{nx} = \text{Represent correlation coefficient of the character and each of other yield components in turn.} \]

The following correlation matrices were formed:

<table>
<thead>
<tr>
<th>Matrix A</th>
<th>Matrix B</th>
</tr>
</thead>
<tbody>
<tr>
<td>( r_{1y} )</td>
<td>1 ( r_{12}, r_{13}, \ldots, r_{1n} )</td>
</tr>
<tr>
<td>( r_{2y} )</td>
<td>( r_{21}, r_{23}, \ldots, r_{2n} )</td>
</tr>
<tr>
<td>( r_{3y} )</td>
<td>( r_{31}, \ldots, r_{3n} )</td>
</tr>
<tr>
<td>( \ldots )</td>
<td>( \ldots )</td>
</tr>
<tr>
<td>( r_{ny} )</td>
<td>( r_{n1}, r_{n2}, r_{n3}, \ldots )</td>
</tr>
</tbody>
</table>
The technique given by Goulden (1952) was followed for inversion of \((B^{-1})\) of B matrix.

Path coefficients \(P_{ij}\) were obtained as follows:

\[ P_{ij} = (B^{-1}) \times (A) \]

The indirect effects for a particular character through other characters were obtained by multiplication of direct path and particular correlation coefficient between these two characters, respectively.

Indirect effect = \(r_{ij} \times p_{iy}\)

Where,

\[ i = 1 \ldots n, \]
\[ j = 1 \ldots n, \]
\[ P_{iy} = p_{1y}, p_{2y}, \ldots, p_{ny} \text{ and} \]
\[ r_{ij} = \text{Correlation between two independent characters.} \]

The residual effect i.e. the variation in yield unaccounted for those associated was calculated from the following formula:

\[
\text{Residual effect (}\bar{X}\text{)} = \sqrt{1-R^2}
\]

Where,

\[
R^2 = P_{1y}r_{1y} + P_{2y}r_{2y} + \ldots + P_{ny}r_{ny}
\]

\(R^2\) is the squared multiple correlation coefficient and is the amount of variation in yield that can be accounted for by the yield component characters.

If the variance ratio ('t' value) for the given degree of freedom was less than table value at 5% and 1% level of significance, the differences between treatment were considered to be non-significant. But its variance ratio was
higher than the table value (13.26) degree of freedom, difference between treatments considered to be significant.

3.5.5 Genetic divergence analysis

The genetic divergence was computed by Mahalanobis, $D^2$ values comprised of following steps (Murty and Arunachalam, 1965).

1. A set of uncorrelated linear combination (y’s) was obtained by pivotal condensation of the common dispersion matrix of a set of correlated variables (x’s) (Rao, 1952). The common dispersion matrix was found with the help at error mean square and sum of products.

2. Using the relationship between y’s and x’s the mean value at different characters for each genotypes were transformed into the mean value of a set of uncorrelated linear combinations.

3. The $D^2$ values between $i^{th}$ genotypes for $k^{th}$ characters were computed as:

$$D^2_{ij} = \sum (Y_{it} - Y_{it})^2$$

4. The ‘K’ components of $D^2$ for each combination were ranked in descending order of magnitude.

5. The ranks were added up for each components $D^2$ overall combinations and the rank total was obtained.

3.5.5.1 Group constellation

Treating $D^2$ as the sum of squares of generalized distance, all genotypes were grouped into clusters was made following Tocker’s method (Rao, 1952).

In this method, the two populations having smallest distance from each other are considered first to which a third population having smallest average
D^2 value from the first two populations is added. Then comes the nearest forth population and so it goes on. At certain stage when it is felt that after adding a particular population, there is abrupt increase in the average D^2, this population is not added in that cluster. Similarly, a second cluster is formed. Thus, the process is continued till all the population are included into one or other cluster.

3.5.5.2 Average intra and inter-cluster distance

\[
\text{Average intra-cluster distance (D^2) = } \frac{\sum D_i^2}{n}
\]

Where,

\[
\sum D_i^2 = \text{Sum distance between all possible combinations and}
\]

\[
n = \text{Number of genotypes included in a cluster.}
\]

3.5.5.3 Intra-cluster mean values

The cluster mean for a particular character is the summation of mean values of lines included in a particular cluster divided by number of lines included in that cluster. These values were calculated separately for each character in each cluster.

3.5.5.4 Contribution of different characters towards divergence

The relative contribution of different characters to the total D^2 distance between each pair of genotypes was given a score of 1-10 (there were 10 characters) based on the magnitude of D^2 value due to each character (rank-1 represent the highest and rank-10 the lowest contribution).

Percentage of contribution of a character was calculated by standard method as suggested by Singh and Choudhary (1977).
Contribution of character $X$ (%) = \[ \frac{N(X) \times 100}{n(n-1)/2} \]

Where,

\[ N(X) = \text{Number of genotypic combinations which are ranked first for character 'X' out of the total genotypic contributions of } \frac{n(n-1)}{2} \text{ combinations} \]

and \( n = \text{Number of genotypes} \)

### 3.5.6 Phenotypic stability analysis

The mean values recorded for different characters in respect of 45 genotypes in 12 environments as well as pooled over the environments, were used for analysis of variance for phenotypic stability. Stability analysis made in this investigation followed the two approaches suggested by Eberhart and Russell's (1966) and Perkins and Jinks (1968a). The model used in these two different approaches are as follows:

#### 3.5.6.1 Eberhart and Russell's model (1966)

The approach is purely statistical one. The following model can be used to describe the performance of a variety over a series of environments.

\[ Y_{ij} = \mu_i + B_i I_j + \delta_{ij} \]

Where,

\[ Y_{ij} = \text{The variety mean of the } i^{th} \text{ genotype at the } j^{th} \text{ environment (where, } i = 1, 2, \ldots \text{; } j = 1, 2, \ldots, n) \]

\[ \mu_i = \text{Grand mean of the } i^{th} \text{ genotype over all the environments,} \]
\[ B_i = \text{Regression coefficient that measures the linear response of the } i^{\text{th}} \text{ genotype to varying environments,} \]

\[ I_j = \text{Environmental index obtained as the mean of all the genotypes at the } j^{\text{th}} \text{ environment minus the grand mean, i.e. } I_j = \left( \sum_i Y_{ij} / g \right) - \left( \sum_i \sum_j Y_{ij} / gn \right) \]

\[ \delta_{ij} = \text{Deviation from regression of the } i^{\text{th}} \text{ genotype in } j^{\text{th}} \text{ environment.} \]

Where,

\[ \sum I_j = 0, \]

\[ \sum Y_{ij} = \text{Total of all the genotypes at the } j^{\text{th}} \text{ environment,} \]

\[ \sum \sum Y_{ij} = \text{Grand total,} \]

\[ g = \text{Number of genotypes and} \]

\[ n = \text{Number of environments.} \]

In this approach the model provides a mean of partitioning the genotype x environment interaction into two parts, viz.,

1. The variation due to the linear response of the genotype to varying environment indices (sum of square due to regression).

2. The unexplainable variations from the regression on the environmental index \((S^2{\delta i})\).

With this model, the sum of square due to environment and genotype-environment interactions are partitioned into environment (linear) and deviation from regression.
### Analysis of variance for joint regression analysis as per model of Eberhart and Russell (1966)

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>Sum of square (S.S.)</th>
<th>M.S.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotypes (G)</td>
<td>g-1</td>
<td>(1/n \sum Y_i^2 - (\sum Y_i)^2/ng)</td>
<td>(MS_1)</td>
</tr>
<tr>
<td>Environments (E)</td>
<td>n-1</td>
<td>(1/n \sum Y_i^2 - (\sum Y_i)^2/ng)</td>
<td></td>
</tr>
<tr>
<td>G x E</td>
<td>(g-1)(n-1)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>E + G x E</td>
<td>g(n-1)</td>
<td>(\sum \sum Y_{ij}^2 - \sum Y_i^2/n)</td>
<td></td>
</tr>
<tr>
<td>E (linear)</td>
<td>1</td>
<td>(1/g(\sum Y_{ij})^2/\sum Y_i^2)</td>
<td></td>
</tr>
<tr>
<td>G x E (linear)</td>
<td>g-1</td>
<td>(\sum (\sum Y_{ij})^2/\sum Y_i^2 - \text{Env.(L)} S.S)</td>
<td>(MS_2)</td>
</tr>
<tr>
<td>Pooled deviation</td>
<td>g(n-2)</td>
<td>(\sum \sum S_{ij}^2 / (\text{VSS-Regr. S.S.}))</td>
<td>(MS_3)</td>
</tr>
<tr>
<td>Genotype-1</td>
<td>n-2</td>
<td>([\sum Y_i^2 - (Y_i)^2/n] - [\sum Y_{ij}^2/\sum Y_i^2])</td>
<td></td>
</tr>
<tr>
<td>Genotype-g</td>
<td>n-2</td>
<td>([\sum Y_{si}^2 - (Y_s)^2/n] - [\sum Y_{si}^2/\sum Y_i^2])</td>
<td></td>
</tr>
<tr>
<td>Pooled error</td>
<td>ng(r-1)</td>
<td>(\sum [S_j^2/(r-1)(g-1)n]/r)</td>
<td>(S^2_e)</td>
</tr>
</tbody>
</table>

Where,

\(r, n\) and \(g\) indicate the number of replications, environments and genotypes, respectively. \(S^2_e\) is the mean square due to pooled error which were calculated as:

\[S^2_e = \sum [S_j^2/(r-1)(g-1)n]/r\]

Where,

\(S_j^2 = \text{Error sum of square at the } j^{th} \text{ location.}\)
3.5.6.1.1 Estimation of stability parameters for individual genotypes

The stability parameters of individual genotypes were calculated as suggested by Eberhart and Russell’s (1966) which are described below:

A. Environmental Index ($I_j$)

$$I_j = (\sum_i Y_{ij}/g) - (\sum_j Y_{ij}/gn)$$

Where,

$I_j$ = Environmental index,

$\sum_i Y_{ij}$ = Total of all the genotypes at $j^{th}$ environment,

$g$ = Number of genotypes,

$\sum_j Y_{ij}$ = Grand total and

$n$ = Number of environments.

B. Regression coefficient ($b_j$)

The coefficient of regression ($b_j$) of the performance of each genotype in various environments on the environmental indices over all the genotypes under study was calculated as:

$$b_j = \frac{\sum_i Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

$b_j$ = Regression coefficient,

$\sum_j I_j^2$ = The sum of square of environmental indices which is common to each value of $b_j$,

$\sum_i Y_{ij} I_j$ = The sum of products of environmental index $(I_j)$ with the corresponding mean ($\bar{X}$) of that variety at each
location. These values may be obtained in the following manner:

\[(\bar{X}) \ (l_j) = (\sum_i Y_{ij} \ l_j) = S\]

Where,

\[(\bar{X}) = \text{Matrix of means},\]

\[(l_j) = \text{Vector for environmental index and}\]

\[(S) = \text{Vector for sum of products, i.e. } \sum_i Y_{ij} \ l_j\]

C. Deviation from regression \((S^2 di)\)

The deviation from linear regression \((S^2 di)\) was calculated as follow:

\[S^2 di = [\sum_i (\delta_{ij}^2/(n-2))] - (S^2 e/r)\]

Where,

\[n = \text{No. of environments,}\]

\[S^2 e = \text{Estimate of pooled error for variance of a variety mean at the j}^{\text{th}} \text{ location,}\]

\[r = \text{Number of replications and}\]

\[\sum_i \delta_{ij}^2 = [\sum_i Y_{ij}^2 - (Y_j)^2/n] - [\sum_i Y_{ij} \ l_j]^2 / \sum_i l_j^2\]

3.5.6.1.2 Test of significance

A. Testing of sources of analysis of variance

I. The significance of difference among the genotype means i.e.

\[H_0 = \mu_1 = \mu_2 = \ldots... \ldots... = \mu_g\]

Can be tested by the 'F' test.
'F' = \frac{MS_1/MS_3}{Mean square due to pooled deviation} = \frac{Mean square due to genotypes}{Mean square due to pooled deviation}

Tested against 'F' table value at (g-1), (n-1) g(n-2) d.f at 5% and 1% level of significance.

II. The hypothesis that there are no differences among genotypes for their regression on the environmental index.

H_0 = b_1 = b_2 = \ldots = bg

Can be tested approximately by the 'F' test

'F' = \frac{MS_2/MS_3}{Mean square due to pooled deviation} = \frac{Mean square due to G \times E (linear)}{Mean square due to pooled deviation}

Tested against 'F' table value at (g-1), g(n-2) d.f at 5% and 1% level of significance.

Note: MS_3 was tested against S^2_e. In case MS_3 was non-significant, S^2_e and MS_3 were pooled to test the remaining sources of variation.

B. Testing of b_i

The hypothesis that any regression coefficient does not differ from unity or zero is tested by appropriate 't' test.

't' = \frac{(b_i - 1)/SE(b_i)}{at (n-2) d.f.}

S.E. (b_i) = \frac{M.S. due to pooled deviation of \text{i}^{th} \text{ variety}}{\sum \sum \Sigma_i l_j^2}

Where,
M.S. due to pooled deviation of \( i^{th} \) variety = \( \delta_{ij}^2 / n-2 \) with \( n-2 \) d.f.

C. Testing of \( b \)

\[
F = b^2 \times \frac{\sum I_j^2}{MS_e} \text{ at } (n-2) \text{ d.f.}
\]

Where,

\( b = \) Regression coefficient,

\( \sum I_j^2 = \) Sum of squares of environmental indices and

\( MS_e = \) Pooled error M.S.

C. Testing of \( S^2_{di} \)

Significance of deviation from regression \( S^2_{di} \) was tested by calculating 'F' value.

\[
'F' = \frac{(\sum \delta_{ij}^2 / n-2)}{S^2 e} \text{ at } (n-2) \text{ and } n(r-1) \text{ (g-1) d.f.}
\]

Where,

\( \sum \delta_{ij}^2 = \) Pooled deviation

If both the regression coefficient and diversion from regression are significant, regression coefficient is again tested as follows:

\[
F = (b^2 \frac{\sum I_j^2}{\sum \sigma_{ij}^2}) / n-2 \text{ at } (n-2) \text{ d.f.}
\]

Estimation of mean of \( b \), \( SE_{(b)} \), \( SE_{(Mean)} \) and population mean.

Mean of \( b = \overline{b} = \frac{\Sigma b_i}{g} \)

\[
SE_{(b)} = \sqrt{\frac{MS \text{ due to pooled deviation}}{\frac{\sum \delta_{ij}^2}{\sum I_j^2}}}
\]
\[
\text{SE}_{\text{mean}} = \sqrt{\frac{\text{MS due to pooled deviation}}{\text{Number of environment} - 1}}
\]

\[
\text{Population mean (} \mu \text{)} = \sqrt{\frac{\text{Grand total}}{\text{Number of observations}}}
\]

**Stable genotype**

A genotype with unit regression coefficient \((bi=1)\) and the deviation not significantly different from zero \((S^2 di = 0)\) is said to be the stable one.

**3.5.6.2 Perkins and Jinks (1968a) model**

This is a combined statistical and genetical approach. The biometrical genetic model is given by:

\[
Y_{ij} = \mu + d_i + e_j + g_{ij} + e_{ij}
\]

Where,

- \(Y_{ij}\) = mean of \(i^{th}\) variety in the \(j^{th}\) environment,
- \(\mu\) = General mean over all the genotypes and environments,
- \(d_i\) = Additive genetic effect,
- \(e_j\) = Additive environmental effect,
- \(g_{ij}\) = \(G \times E\) interaction effect and
- \(e_{ij}\) = Residual error variation of \(i^{th}\) variety in \(j^{th}\) environment.

These effects are defined as follows:

\[
\mu = \frac{Y_{..}}{st}
\]

\[
e_j = \frac{(Y_{.j})}{t} - \mu
\]
\( d_i = (Y_i/s) - \mu \)

\( g_{ij} = Y_{ij} - \mu - d_i - e_j \)

Where,

\( s \quad \text{The total number of environments and} \)

\( t \quad \text{The total number of genotypes} \)

It is known that G x E interaction of any variety is a linear function of environmental value, that is

\( g_{ij} = \beta_i e_j + \delta_{ij} \)

So the model becomes

\( Y_{ij} = \mu + d_i + e_i + B_i e_i + \delta_{ij} + e_{ij} \)

\( Y_{ij} = \mu + d_i + (1 + \beta_i) e_j + \delta_{ij} + e_{ij} \)

In comparison to Eberhart and Russell's model, the regression coefficient in this approach is different in the sense that Perkins and Jinks proposed to calculate the regression of genotype *x* environment interaction value on the environmental index. In terms of this model, the earlier model of Eberhart and Russell's is thus regression of \((e_i + g_{ij})\) on \(e_j\). The regression of \(e_j\) on \(e_j\) being one, and regression of \(g_{ij}\) on \(e_j\) being \(B_i\), the bi value of Eberhart and Russell's model is thus:

\[ b_i = 1 + B_i \]

\[ B_i = b_i - 1 \]

\( s^2 d_i \) remains the same as in Eberhart and Russell's model. Thus, the relative ranking of different genotypes in this model remains the same as in Eberhart and Russell's model.

**Analysis of variance**

The total variance is divided into various sources:
S.S. Line \((S_g) = (\Sigma_i Y_i^2 / n) - (\bar{y}^2 / ng)\)

S.S. due to environment (S.S. due to joint regression):
\[ S_E = (\Sigma_j Y_j^2 / g) - (\bar{Y}_j^2 / ng) \]

Note: It is the same as S.S. due to genotypes \(x\) environment interaction
(linear) of Eberhart and Russell's model.

Now, total S.S. due to \(g \times e\) interaction is calculated using following
formula:
\[ S_{GE} = \Sigma_i \Sigma_j Y_{ij}^2 - (1/n) (\Sigma_j Y_j^2) - (1/n) (\Sigma_i Y_i^2) + (1/ng) (\bar{y}^2) \]

This S.S. is further divided into two parts i.e.

(i) S.S. due to heterogeneity between regressions, which is the same as
\(S_{GE}\) (linear) of Eberhart and Russell's model.

(ii) Remainder S.S. which is the same as S.S. due to pooled deviation of
Eberhart and Russell's model.

S.S. due to heterogeneity:
\[ S_h = \frac{\Sigma_i [\Sigma_j Y_{ij}^2 \{ (Y_{ij} / g) - (\bar{y} / ng) \}]^2}{\Sigma_j \Sigma_i Y_{ij}^2} - S_E \]

It is the same as S.S. \(G \times E\) (linear) in Eberhart and Russell's model.

Remainder S.S.
\[ S_r = S_{GE} - S_h \]

It is same as pooled deviation in Eberhart and Russell's model.

Test of significance

(i) To test the significance of differences among line:

Mean square due to line
\[ F = \frac{\text{Mean square due to line}}{\text{Mean square due to Line in Env.}} = \frac{M_1}{M_3} \]
tested against 'F' table value at (g-1), (g-1) (g-1) d.f. at 5% and 1% level of significance

**Analysis of variance table**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>Sum of square (S.S.)</th>
<th>M.S.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lines (difference between genotypes)</td>
<td>g-1</td>
<td>(1/n \sum_i Y_i^2 - (\bar{y}^2/ng))</td>
<td>(M_1)</td>
</tr>
<tr>
<td>Environments (E) (joint regression)</td>
<td>n-1</td>
<td>(\sum_j Y_j^2/g - (\bar{Y}^2/ng))</td>
<td>(M_2)</td>
</tr>
<tr>
<td>Line x Environment</td>
<td>(g-1)(n-1)</td>
<td>(\sum_i \sum_j Y_{ij}^2 - (1/n) (\sum_i Y_i^2)) (- (1/g)(\sum_j Y_j^2) + (1/ng) (\bar{Y}^2))</td>
<td>(M_3)</td>
</tr>
<tr>
<td>Heterogeneity between regression</td>
<td>g-1</td>
<td>(\frac{\sum_i (\sum_j Y_{ij}) (Y_j/g) - (\bar{Y}/ng))^2}{\sum_j Y_{ij}^2} - S.S.E.)</td>
<td>(M_4)</td>
</tr>
<tr>
<td>Remainder</td>
<td>(g-1) (n-2)</td>
<td>S.S.(g \times E) - S.S. due to heterogeneity</td>
<td>(M_5)</td>
</tr>
<tr>
<td>Pooled error</td>
<td>ng(r-1)</td>
<td>(\sum_j [S_{ij}^2/(r-1)(g-1)n]n/r)</td>
<td>(M_6)</td>
</tr>
</tbody>
</table>

(ii) To test the significance of environment (joint regression):

\[
F = \frac{\text{Mean square due to Env. (Joint Reg.)}}{\text{Mean square due to g x e}} = \frac{M_2}{M_3}
\]

tested against 'F' table value at (n-2), (g-1) (n-1) d.f. at 5% and 1% level of significance.

(iii) To test the significance of line x environment:

\[
F = \frac{\text{Mean square due to line x environment}}{\text{Mean square due to error}} = \frac{M_3}{M_6}
\]
tested against 'F' table value at \([(g-1) (n-1)] [ng (r-1)]\) d.f. at 5% and 1% level of significance.

(iv) To test the significance of heterogeneity between regression

\[
F = \frac{\text{Mean square due to heterogeneity between reg.}}{\text{Mean square due to error}} = \frac{M_4}{M_6}
\]

3.5.7 The chickpea (Cicer arietinum L.) genotypes will be screened for similarity and diversity with respect to adaptation reactions over the given range of environments as proposed by Singh and Gupta (1984), Singh (1985) and Singh (2001) based on correlation coefficients \((r^2\text{ and } r^3)\). Correlation coefficients \((r^2\text{ and } r^3)\) were estimated by utilizing the methods given by (Dewey and Lu, 1959).