CHAPTER: III

MATERIALS AND METHODS

The present investigation was conducted to assess the genetic variability, correlation coefficient and path coefficient analysis in durum wheat. The study was carried out at the Wheat Research Station, Junagadh Agricultural University, Junagadh during Rabi 2016-17. Junagadh is situated at 21.5°N latitude and 70.5°E longitude with an elevation of 82.92 meters above the mean sea level. The soil of experimental site is medium black with pH 7.8. The weather during the growing season was favourable for normal growth and development of crop. The meteorological data for cropping season is presented in Appendix-I.

3.1 EXPERIMENTAL MATERIAL

The experimental material consisted of 40 diverse genotypes of wheat (Triticum durum) representing different geographic origin (Table 3.1). The pure seeds of these genotypes were obtained from the Wheat Research Station, Junagadh Agricultural University, Junagadh.

3.2 EXPERIMENTAL DETAILS

Forty genotypes of durum wheat were sown on 26th November, 2016 in a randomized block design with three replications at Wheat Research Station, Junagadh Agricultural University, Junagadh. Each line was sown in a single row plot of 3.0 m length with a spacing of 22.5 cm × 10 cm. The genotypes were randomly allotted to the plots in each replication. All the recommended agronomical practices along with necessary plant protection measures were followed timely for the successful raising of the crop.

3.3 CHARACTERS STUDIED

In each plot, five competitive plants were randomly selected and tagged excluding terminal ones to minimize border effects. The observations were recorded on these five randomly selected plants in each line and in each replication and their mean values were used for statistical analysis. The procedure adopted for recording the observations is described as under.
Table 3.1: List of genotypes used in the present study along with place of origin

<table>
<thead>
<tr>
<th>Sr. No.</th>
<th>Name of Genotype</th>
<th>Place of Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>AKDW-4905</td>
<td>PDKV, Akola, Maharashtra</td>
</tr>
<tr>
<td>2</td>
<td>DDW-40</td>
<td>IIWBR, Karnal, Haryana</td>
</tr>
<tr>
<td>3</td>
<td>DDW-39</td>
<td>IIWBR, Karnal, Haryana</td>
</tr>
<tr>
<td>4</td>
<td>GW-2014-565</td>
<td>SDAU, Vijapur, Gujarat</td>
</tr>
<tr>
<td>5</td>
<td>GW-2015-689</td>
<td>SDAU, Vijapur, Gujarat</td>
</tr>
<tr>
<td>6</td>
<td>GW-1330</td>
<td>SDAU, Vijapur, Gujarat</td>
</tr>
<tr>
<td>7</td>
<td>GW-1139</td>
<td>SDAU, Vijapur, Gujarat</td>
</tr>
<tr>
<td>8</td>
<td>GDW-1255</td>
<td>SDAU, Vijapur, Gujarat</td>
</tr>
<tr>
<td>9</td>
<td>HI-8770</td>
<td>IARI, RS, Indore, Madhya Pradesh</td>
</tr>
<tr>
<td>10</td>
<td>HI-8724</td>
<td>IARI, RS, Indore, Madhya Pradesh</td>
</tr>
<tr>
<td>11</td>
<td>HI-4728</td>
<td>IARI, RS, Indore, Madhya Pradesh</td>
</tr>
<tr>
<td>12</td>
<td>HI-8498</td>
<td>IARI, RS, Indore, Madhya Pradesh</td>
</tr>
<tr>
<td>13</td>
<td>HI-8787</td>
<td>IARI, RS, Indore, Madhya Pradesh</td>
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<td>14</td>
<td>HD-4730</td>
<td>IARI, New Delhi</td>
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<td>15</td>
<td>HD-3095</td>
<td>IARI, New Delhi</td>
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<tr>
<td>16</td>
<td>HD-4728</td>
<td>IARI, New Delhi</td>
</tr>
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<td>17</td>
<td>IWP-5070</td>
<td>IIWBR, Karnal, Haryana</td>
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<td>18</td>
<td>MACS-3744</td>
<td>ARI, Pune, Maharashtra</td>
</tr>
<tr>
<td>19</td>
<td>MACS-4054</td>
<td>ARI, Pune, Maharashtra</td>
</tr>
<tr>
<td>20</td>
<td>MACS-4049</td>
<td>ARI, Pune, Maharashtra</td>
</tr>
<tr>
<td>21</td>
<td>MPO-1329</td>
<td>JNKVV, Powarkheda, Madhya Pradesh</td>
</tr>
<tr>
<td>22</td>
<td>MPO-1215</td>
<td>JNKVV, Powarkheda, Madhya Pradesh</td>
</tr>
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<td>23</td>
<td>NIDW-706</td>
<td>MPKV, Niphad, Maharashtra</td>
</tr>
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<td>NIDW-653</td>
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<td>NIDW-1055</td>
<td>MPKV, Niphad, Maharashtra</td>
</tr>
<tr>
<td>26</td>
<td>NIDW-1038</td>
<td>MPKV, Niphad, Maharashtra</td>
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<td>27</td>
<td>PDW-291</td>
<td>PAU, Ludhiana, Punjab</td>
</tr>
<tr>
<td>28</td>
<td>PDW-233</td>
<td>PAU, Ludhiana, Punjab</td>
</tr>
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<td>29</td>
<td>PDW-347</td>
<td>PAU, Ludhiana, Punjab</td>
</tr>
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<td>30</td>
<td>PDW-350</td>
<td>PAU, Ludhiana, Punjab</td>
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<tr>
<td>31</td>
<td>PBND-4826</td>
<td>VNMKV, Parbhani, Maharashtra</td>
</tr>
<tr>
<td>32</td>
<td>RKD-305</td>
<td>MPUAT, Udaipur, Rajasthan</td>
</tr>
<tr>
<td>33</td>
<td>RKD-296</td>
<td>MPUAT, Udaipur, Rajasthan</td>
</tr>
<tr>
<td>34</td>
<td>RAJ-1555</td>
<td>SKRAU, Durgapura, Rajasthan</td>
</tr>
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<td>35</td>
<td>UAS-460</td>
<td>UAS, Dharwad, Karnataka</td>
</tr>
<tr>
<td>36</td>
<td>UAS-428</td>
<td>UAS, Dharwad, Karnataka</td>
</tr>
<tr>
<td>37</td>
<td>UPD-2949</td>
<td>GBPUAT, Pantnagar, Uttarakhhand</td>
</tr>
<tr>
<td>38</td>
<td>WHD-948</td>
<td>CCSHAU, Hisar, Haryana</td>
</tr>
<tr>
<td>39</td>
<td>WHD-933</td>
<td>CCSHAU, Hisar, Haryana</td>
</tr>
<tr>
<td>40</td>
<td>WSM-5723</td>
<td>PDKV, Akola, Maharashtra</td>
</tr>
</tbody>
</table>
(1) **Days to 50% flowering**
   Total number of days from the date of sowing to 50% emergence of main spike on plot basis was counted and expressed as days to 50% flowering.

(2) **Days to maturity**
   Number of days from date of sowing to 80% of plants tends to maturity was counted on plot basis.

(3) **Grain filling period (days)**
   Number of days from anthesis to grain maturity was counted on plot basis.

(4) **Plant height (cm)**
   The height of plant was measured in centimeters from the base of the plant to the tip of the main spike (excluding awns) at the time of maturity.

(5) **Number of productive tillers per plant**
   Number of tillers bearing spike was counted at the time of maturity.

(6) **Ear Length (cm)**
   Length from base to tip of the spike was measured in centimeters at the time of maturity.

(7) **Number of grains per main spike**
   This was measured by counting the number of grains from main spike of individual selected plants after harvesting and threshing.

(8) **Grain weight per main spike (g)**
   This was measured by weighing total number of grains from main spike in grams after threshing.

(9) **Grain yield per plant (g)**
   Total grains harvested from individual selected plants were weighed in grams.

(10) **Biological yield per plant (g)**
    After harvesting and drying of plant total biological yield per plant was recorded in grams by addition of total dry weight of plant and grain yield per plant.

(11) **Harvest index (%)**
    It was calculated in percentage by using the following formula:
    \[
    \text{Harvest index (\%)} = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100
    \]

(12) **100-grain weight (g)**
    A random sample of 100 grains per plot from each replication was counted and weighed in grams.


3.4 STATISTICAL ANALYSIS

The replication-wise mean values of five randomly selected plants in each entry were used for the statistical analysis for different character under study. The data recorded for various characters were statistically analyzed at the Computer Cell, Department of Genetics and Plant Breeding, College of Agriculture, J.A.U., Junagadh for the various parameters viz., genetic variability, genotypic and phenotypic correlations and path coefficient analysis.

3.4.1 Analysis of variance

The analysis of variance for randomized block design (RBD) was done for each character as per Panse and Sukhatme (1967). The statistical model used for analysis of variance was based on the following linear model.

\[ Y_{ij} = \mu + r_i + g_j + \sigma_{ij} \]

Where,

- \( Y_{ij} \) = Yield of \( j^{th} \) genotype in \( i^{th} \) replication
- \( \mu \) = General mean
- \( r_i \) = Effect of \( i^{th} \) replication
- \( g_j \) = Effect of \( j^{th} \) genotype
- \( \sigma_{ij} \) = Uncontrolled random error associated with \( j^{th} \) genotype in \( i^{th} \) replication

The format of analysis of variance is given as under in Table 3.2.

**Table 3.2: Analysis of variance for experimental design**

<table>
<thead>
<tr>
<th>Source</th>
<th>d.f.</th>
<th>Mean sum of squares</th>
<th>Expected mean squares</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>(r-1)</td>
<td>( M_r )</td>
<td>( \frac{1}{\sigma^r} + \frac{g^2}{\sigma^g} )</td>
</tr>
<tr>
<td>Genotypes</td>
<td>(g-1)</td>
<td>( M_g )</td>
<td>( \frac{2}{\sigma^g} + \frac{r^2}{\sigma^r} )</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1)(g-1)</td>
<td>( M_e )</td>
<td>( \frac{2}{\sigma^e} )</td>
</tr>
</tbody>
</table>

Significance of replications mean sum of square \((M_r)\) and genotypes mean sum of square \((M_g)\) was tested against error mean sum of square \((M_e)\).
3.4.2 Estimation of components of variance

The phenotypic, genotypic and error variances were estimated as follows:

\[ \sigma_e^2 = M_e \]

\[ \sigma_g^2 = \frac{(M_g - M_e)}{r} \]

\[ \sigma_p^2 = \sigma_g^2 + \sigma_e^2 \]

Where,

\( r \) = Number of replications

\( g \) = Number of genotypes

\( M_g \) = Mean sum of square due to genotypes

\( M_r \) = Mean sum of square due to replications

\( M_e \) = Mean sum of square due to error

\( \sigma_e^2 \) = Error variance

\( \sigma_g^2 \) = Genotypic variance

\( \sigma_p^2 \) = Phenotypic variance

The standard error of mean (S.Em.) was calculated using following formula:

\[ \text{S.Em.} = \sqrt{\frac{\sigma_e^2}{r}} \]

The critical difference (C.D.) for comparing mean of any two genotypes was computed using following formula:

\[ \text{C.D.} = \text{S.Em.} \times \sqrt{2} \times 't' \]

Where,

\( 't' \) = Table value of ‘t’ at 5% level of significance and error degree of freedom.

The coefficient of variation (CV) was determined as per under given formula:

\[ \text{C.V.} (%) = \frac{\text{CV}}{X} \times 100 \]

Where,

\( \overline{X} \) = Mean of the character.
1) **Phenotypic Range**

It is the difference between maximum value and minimum value in a particular trait.

\[ \text{Range} = \text{Maximum value} - \text{Minimum value} \]

While comparing the range of different traits, it is necessary to make it unitless. Hence, coefficient of range was calculated as per the following formula:

\[ \text{Coefficient of range (\%)} = \frac{\text{Range}}{\text{Maximum value + Minimum value}} \times 100 \]

2) **Phenotypic coefficient of variation (PCV \%)**

The phenotypic coefficient of variation, which measures the magnitude of phenotypic variation present in a particular character, was estimated as per the formula suggested by Burton and De Vane (1953).

\[ \text{PCV (\%)} = \sqrt{\frac{\sigma_p^2}{\bar{X}}} \times 100 \]

Where,
- PCV (\%) = Phenotypic coefficient of variation
- \( \sigma_p^2 \) = Phenotypic variance
- \( \bar{X} \) = Mean of the character

3) **Genotypic coefficient of variation (GCV \%)**

The genotypic coefficient of variation, which measures the magnitude of genotypic variation present in a particular character, was estimated as per the formula suggested by Burton and De Vane (1953).

\[ \text{GCV (\%)} = \sqrt{\frac{\sigma_g^2}{\bar{X}}} \times 100 \]

Where,
- GCV (\%) = Genotypic coefficient of variation
- \( \sigma_g^2 \) = Phenotypic variance
- \( \bar{X} \) = Mean of the character

4) **Heritability (Broad sense)**

Heritability in broad sense, which is the ratio of genotypic variance (\( \sigma_g^2 \)) and phenotypic variance (\( \sigma_p^2 \)), was calculated by using the formula suggested by Allard (1960).
Genetic advance (GA)
The expected genetic advance at 5% selection intensity was estimated by using formula as suggested by Allard (1960).

\[
GA = k \times \sigma_p \times h^2
\]

Where,
- \(GA\) = Genetic advance under selection
- \(K\) = Selection differential (value of \(k\) at 5% selection intensity is 2.06)
- \(\sigma_p\) = Phenotypic standard deviation
- \(h^2\) = Heritability value of the character

Genetic advance per cent of mean
The genetic advance expressed as per cent of mean was calculated as under:

\[
\text{Genetic advance as per cent of mean} = \frac{\text{Genetic advance (GA)}}{\text{Mean of character (X)}} \times 100
\]

3.4.3 Correlation coefficients
Correlation coefficient is the measurement of relationship between two or more series of variables. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while phenotypic correlation includes both genotypic as well as environmental influences. The phenotypic and genotypic correlation coefficients of all the pair of characters were worked out as per Al-Jibouri et al. (1958). The data were subjected to covariance analysis from which different components of mean sum of products were estimated.
The format of analysis of covariance is given as under in Table 3.3.

<table>
<thead>
<tr>
<th>Source</th>
<th>d.f.</th>
<th>Mean sum of products</th>
<th>Expectation of mean sum of products</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>((r-1))</td>
<td>(MP_r)</td>
<td>-</td>
</tr>
<tr>
<td>Genotypes</td>
<td>((g-1))</td>
<td>(MP_g)</td>
<td>(\text{Cov}<em>{e1.2} + r \text{Cov}</em>{g1.2})</td>
</tr>
<tr>
<td>Error</td>
<td>((r-1) (g-1))</td>
<td>(MP_e)</td>
<td>(\text{Cov}_{e1.2})</td>
</tr>
</tbody>
</table>
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Where,

\[ r = \text{Number of replications} \]
\[ g = \text{Number of genotypes} \]
\[ \text{Cove}_{1.2} = \text{Environment covariance between first and second characters} \]
\[ \text{Cov}_{g1.2} = \text{Genotypic covariance between first and second characters} \]

1) **Genotypic covariance (Cov}_{g1.2)**
\[ \text{Cov}_{g1.2} = (\text{MP}_g - \text{MP}_e)/r \]

Where,

\[ \text{MP}_g = \text{Mean sum of product due to genotypes between first and second characters} \]
\[ \text{MP}_e = \text{Mean sum of product due to error between first and second characters} \]
\[ r = \text{Number of replications} \]

2) **Error covariance (Cov}_{e1.2)**
\[ \text{Cov}_{e1.2} = \text{MP}_e \]

Where,

\[ \text{MP}_e = \text{Mean sum of product due to error between first and second characters} \]

3) **Phenotypic covariance (Cov}_{p1.2)**
\[ \text{Cov}_{p1.2} = \text{Cov}_{g1.2} + \text{Cov}_{e1.2} \]

The genotypic and phenotypic variances and covariances were used for calculating the genotypic and phenotypic correlation coefficients, respectively (Al-Jibouri et al., 1958).

a) **Genotypic correlation coefficient (r}_{g1.2)**
\[ r_{g1.2} = \frac{\text{Cov}_{g1.2}}{\sqrt{\sigma^2_{g1}\cdot\sigma^2_{g2}}} \]

Where,

\[ \text{Cov}_{g1.2} = \text{Genotypic covariance between first and second characters} \]
\[ \sigma^2_{g1} = \text{Genotypic variance for first character} \]
\[ \sigma^2_{g2} = \text{Genotypic variance for second character} \]

b) **Phenotypic correlation coefficient (r}_{p1.2)**
\[ r_{p1.2} = \frac{\text{Cov}_{p1.2}}{\sqrt{\sigma^2_{p1}\cdot\sigma^2_{p2}}} \]
Where,

\[ \text{Cov}_{p1.2} = \text{Phenotypic covariance between first and second characters} \]

\[ \sigma^2_{p1} = \text{Phenotypic variance for first character} \]

\[ \sigma^2_{p2} = \text{Phenotypic variance for second character} \]

The significance of the correlation values at \((n-2)\) degrees of freedom was tested by adopting the formula suggested by Panse and Sukhatme (1967).

**3.4.4 Path Coefficient Analysis**

Path coefficient is a standardized partial regression coefficient and measures the direct and indirect influence of one variable upon another thereby permitting the separation of the correlation coefficient into the component of direct and indirect effects.

The path coefficient analysis was carried-out as per the method suggested by Dewey and Lu (1959). Genotypic correlation coefficients of 11 variables with grain yield were used to estimate the path coefficient for the direct effects of various independent characters on yield. The direct effects designated as \(p\) were calculated by increasing the underlying correlation matrix as per Doolittle method described by Steel and Torrie (1960).

\[ r_{1y} = P_{1y} + P_{2y} r_{1.2} + \ldots, + P_{11y} r_{1.11} \]

\[ r_{2y} = P_{1y} r_{1.2} + P_{2y} + \ldots, + P_{11y} r_{2.11} \]

\[ \ldots, + \ldots, + \ldots, + \ldots, + \ldots, + \ldots, + \ldots, + \ldots, + \ldots, + \ldots, + \ldots, \]

\[ r_{11y} = P_{1y} r_{1.11} + P_{2y} r_{2.11} + \ldots, + P_{11y} \]

Where,

\(r_{1y}, r_{2y}, r_{3y}, \ldots, r_{11y}\) are the genotypic correlations of days to 50\% flowering, days to maturity, grain filling period, plant height, number of productive tillers per plant, ear length, number of grains per main spike, grain weight per main spike, biological yield per plant, harvest index and 100-grain weight, respectively, with grain yield per plant.

\(P_{1y}, P_{2y}, P_{3y}, \ldots, P_{13y}\) are the direct effects of characters \(viz.,\) days to 50\% flowering, days to maturity, grain filling period, plant height, number of productive tillers per plant, ear length, number of grains per main spike, grain weight per main spike, biological yield per plant, harvest index and 100-grain weight respectively.
The coefficient of determination was calculated by using the following relationship:

\[ 1 = P_{1,y}^2 + 2P_{1,y} r_{1,2}P_{2,y} + 2P_{1,y} r_{1,3}P_{3,y} + 2P_{1,y} r_{1,4}P_{4,y} + 2P_{1,y} r_{1,5}P_{5,y} + 2P_{1,y} r_{1,6}P_{6,y} + 2P_{1,y} r_{1,7}P_{7,y} + 2P_{1,y} r_{1,8}P_{8,y} + 2P_{1,y} r_{1,9}P_{9,y} + 2P_{1,y} r_{1,10}P_{10,y} + 2P_{1,y} r_{1,11}P_{11,y} + \ldots + P_{10,y}^2 + 2P_{10,y} r_{10,11}P_{11,y} + P_{11,y}^2 + R^2 \]

The residual variation (R) is variation in dependent character i.e. grain yield due to uncontrolled causes was estimated by subtracting this value from unity.