

# Integrative Assessment of Genetic Diversity, Population Structure, and Agronomic Trait Variation in Bread Wheat (*Triticum aestivum* L.) Using Principal Component and Cluster Analyses

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**Abstract:** Genetic diversity is essential for broadening the genetic base of wheat breeding and accelerating the development of high-yielding cultivars. In the present study, bread wheat (*Triticum aestivum* L.) genotypes were evaluated for agronomic, yield, and grain quality traits using analysis of variance, genetic parameter estimation, principal component analysis (PCA), and cluster analysis. Significant ( $P < 0.05$ ) variation was observed among genotypes for all evaluated traits, demonstrating the existence of substantial genetic variability. High heritability estimates for most agronomic and quality traits indicated that these characteristics are predominantly governed by genetic factors and can be effectively improved through selection. Principal component analysis identified five principal components with eigenvalues greater than 1.0, collectively explaining 79.4% of the total phenotypic variation. The first principal component contributed 26.5% of the total variation and was mainly associated with spike length, spikelets per spike, and grains per spike, identifying these traits as the major determinants of genetic divergence. Cluster analysis separated the genotypes into distinct groups with greater inter-cluster than intra-cluster distances, reflecting broad genetic diversity and providing opportunities for selecting genetically divergent parents. Genotypes UOS-7, UOS-11, and UOS-2 exhibited superior grain yield potential, whereas Pb-11, Galaxy-13, UOS-3, UOS-12, and UOS-11 showed desirable performance for key yield components, including tillering ability, grain number, and thousand-grain weight. Overall, the integration of genetic parameter analysis with multivariate statistical approaches effectively characterized the available diversity and identified promising parental materials for wheat improvement. These findings provide a valuable foundation for breeding programs aimed at enhancing grain yield, grain quality, and genetic gain in bread wheat.

**Keywords:** breeding; PCA; Cluster analysis; genotypes; heritability

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## 1. Introduction

Bread wheat is the well-known crop in the world. Wheat supplies 72% of calories and protein in daily food that is cheap source of energy (Iqbal and Naureen et al. 2022). Demand of wheat is increasing with expanding population. Development of wheat varieties is must to get higher yield potential per unit area (Mottaleb and Gideon et al. 2023). Wheat is the most critical food grain of Pakistan possessing the significant area under single harvest. About more than 10000 years ago, wheat was spread in South and Southwestern Asia (Singh and Anju et al. 2023).

Wheat is self-pollinated crop and its population after hybridization quickly achieves homozygosity which is extremely susceptible to ecological fluctuation (Krishnappa et al., 2022). Yield is an important character that shows the association of environment and genotype. Main objective of wheat breeding program is to develop high yield potential varieties (Mullualem and Alemu et al. 2024).

Genetic diversity signifies biochemical, molecular and phenotypic traits in species (Gomes and Cristina et al. 2025). In the breeding programme genetic diversity has a very great importance because diversity is the key of success for plant breeder (Mallor and Estela 2025). Biodiversity occurs between species and genetic diversity between populations of species (Secomandi and Guido et al. 2025). Wheat breeder is trying to get wide range of character that have impact on yield to develop genotypes from genetically diverge origin (Sharma and Vijay et al. 2025). In deciding the capability of genetically diverse lines and cultivars, wheat breeders need to observe a wide range of characters that have impact on yield. (Singh and Sapna et al. 2025).



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Determination for the good selection criterion is very important in wheat breeding programme. The genetic behavior of different traits is very important (Tu and Che-Tuo 2026). Different methods are used to measure the genetic components for transmissibility of traits (Hou and Jianghua et al. 2025). Heritability provides the knowledge to the plant breeders to know the trend of segregating generation for selection of desirable genotype (Vieira and Ana et al. 2025). High heritability along with high genetic advance with helps for suitable selection (Yali and Gudeta 2026). Heritability is determined from the ratio of phenotypic variance to genotypic variance that makes productive role for crop breeding (Mullualem and Alemu et al. 2025; Maqbool and Ishmal et al. 2026). Genetic advance is an important genetic parameter for the help of plant breeder during procedure of selection (Vieira and Ana et al. 2025).

Principal component analysis showed the variation among important components (Li 2025). Different components clarify the correlation and variation of characteristics in bread wheat genotypes. These components represent variation amongst characters like spike density and grain yield, individually (Sallam and Mostafa et al. 2026).

Cluster analysis is used to group the genotypes into different categories based on genetic similarities. On the basis of principal component analysis, cluster analysis ordered germplasm in different classes (Lemma and Chandra et al. 2026). It was also reported that selected genotypes can be grouped into different clusters due to presence of genetic variation among them (Bhatt and S.K. Verma et al. 2025). Based on above discussion the present study was planned to observe genetic difference among genotypes through principal component analysis and cluster analysis. The aims of current studies are to find the genetic diversity among advance breeding lines of wheat. To study the significant contribution by traits for further utilization in wheat breeding program to develop high yielding wheat varieties. To provide guidance to wheat breeder to determine the effect of yield components to enhance grain yield. The outcomes would be useful in provide source of selection and expanding the genetic base of the varieties for particular segregants.

## 2. Materials and Methods

Present study was conducted during the season of 2024-25 in the examination area of Department of Biotechnology, University of Okara. Seeds of 17 wheat advance lines and 3 commercial varieties as checks were collected from Department. of. Plant. Breeding and. Genetics, University. College of. Agriculture, University of Sargodha. These 20 genotypes were sown in the field to asses' genetic variation for various morphological traits that specifically impact on grain yield. The experiment was conducted on 21st November 2024 in RCBD with 3 replications in a plot size 9m<sup>2</sup> and row to row distance 30 cm. Up to maturity common cultural practices were taken.

### List of Wheat Genotypes with Parentage

| Genotype  | Parentage                                        |
|-----------|--------------------------------------------------|
| UO-1      | ATTILA/3*BCN//BAV92/3/PASTOR/4                   |
| UO-2      | ATTILA/3*BCN//BAV92/3/PASTOR/4                   |
| UO-3      | ATTILA/3*BCN*//BAV92/3/KIRITATI/WBLL1/4          |
| UO-4      | SA42/PARULA                                      |
| UO-5      | INQILAB91//SUNCO/TASMAN#8                        |
| UO-6      | MILAN/S87230//BA92/3/AKURI#1/4/MILAN/5/BAVIACORA |
| UO-7      | CHYAK1/GRACK                                     |
| UO-8      | ATTILA/3*BCN//BAV92/3/KRITATI/WBLLI/4            |
| UO-9      | CHYAK1/VILLA JUAREZ F2009                        |
| UO-10     | KACHU/PVN//KACHU                                 |
| UO-11     | WBLLI*2/BRAMBLING//CHYAK                         |
| UO-12     | KAUZ*3/MNV//MILAN/3/BAV92*2/4/KIRITARI           |
| UO-13     | CHIBIA//PRLII/CM65531/3/FISCAL/4/ND643           |
| UO-14     | KACHU//WBLLI*2/BRAMBLING                         |
| UO-15     | FRET2/TUKURU//FRET2/3/MUNAL#1                    |
| V-82003   | KRITATI/4/2*//WEAVER/TSL//WEAVER/3/WEAVER        |
| Pb-11     | AMSEL/ATTILA//INQ.91/PEW'S'                      |
| UO-18     | VEE/CMHTA.917//VEE/3/CMH83.2517/4/OASIS/2*BOR95  |
| Millat-11 | CHENAB2000/INQ.91                                |
| Galaxy-13 | PB96/87094//MH-97                                |

**Figure 1:** List of parentage of 20 bread wheat genotypes.

When 50% of spikes emerged the data for days to 50% heading was recorded from plot and then average was computed for further assessment.

Days to heading = Date of sowing to 50% heading.

When 50% plants physiologically matured and changed in peduncle (yellowish) the data for days to maturity was recorded. The average for days to maturity was computed for each genotype in each replication. Days to maturity were counted from date of sowing to date physiological maturity. Plant height was measured from soil surface level to the top of the spike excluding awns in centimeters by meter rod. Peduncle length of randomly three plants will be measured in centimeter by measuring the length between upper most node and base of spike and average was calculated. The length of spike was measured in centimeters from randomly three plants. It was measured from base of spike to its tip without awns. Mean was calculated. The spikelets were counted manually from randomly three spikes physically and average was calculated. Number of productive tillers were counted from each plot using meter square rod. 1000-grain weight was estimated from random sample of 1000 seeds obtained through seed counter. At the time of maturity, the spikes were harvested separately and number of grains was calculated from the average of three spikes. Each advance line from each plot was harvested and threshed. The grain yield was measured in grams utilizing electric balance.

Protein content was measured using OMEG analysis Bruns instrument Germany, 2008 at Cereal Technology lab Wheat Research Institute AARI Faisalabad. Moisture content was measured using OMEG analysis Bruns instrument Germany, 2008 at Cereal Technology lab Wheat Research Institute AARI Faisalabad. Gluten content was measured using OMEG analysis Bruns instrument Germany, 2008 at Cereal Technology Lab Wheat Research Institute AARI Faisalabad.

Starch content was measured using OMEG analysis Bruns instrument Germany, 2008 at Cereal Technology lab Wheat Research Institute AARI Faisalabad.

### 3. Statistical Method

The mean data for each trait was subjected to analysis of variance in order to determine the genotypic differences. Using the excel log function all %age data was transformed before the analysis. Means values of the traits was compared for significance through least significance differences at  $P \leq 0.05$ . Two distinctive statistical software, SPSS 16.0 and statistix 8.1 were utilized to determine the significance of traits and application of biometrical methods. The sample mean for each character in all the advance lines was computed on the basis of individual plant observations, as using the formula.

$$Y = \sum Y_i / n$$

Y = Sample means

$Y_i$  = Individual values

n = Number of observations

## Analysis of Variance (ANOVA)

| Source      | d.f.             | M.S.S               | Expected values of M.S.S. | Calculated F  |
|-------------|------------------|---------------------|---------------------------|---------------|
| Replication | $r - 1$          | $MSS_r (M_1)$       |                           | $(M_1 / M_3)$ |
| Genotype    | $g - 1$          | $MSS_g (M_2)$       | $\sigma_e^2 + \sigma_g^2$ | $(M_2 / M_3)$ |
| Error       | $(r - 1)(g - 1)$ | $MSS_e (M_3)$       | $\sigma_e^2$              |               |
| Total       | $(rg - 1)$       | $(M_1 + M_2 + M_3)$ |                           |               |

Where,

$r$  = Number of replications

$g$  = Number of genotypes

$MSS_r$  = Mean sum of squares due to replication

$MSS_g$  = Mean sum of squares due to genotypes (accessions)

$MSS_e$  = Mean sum of squares due to error

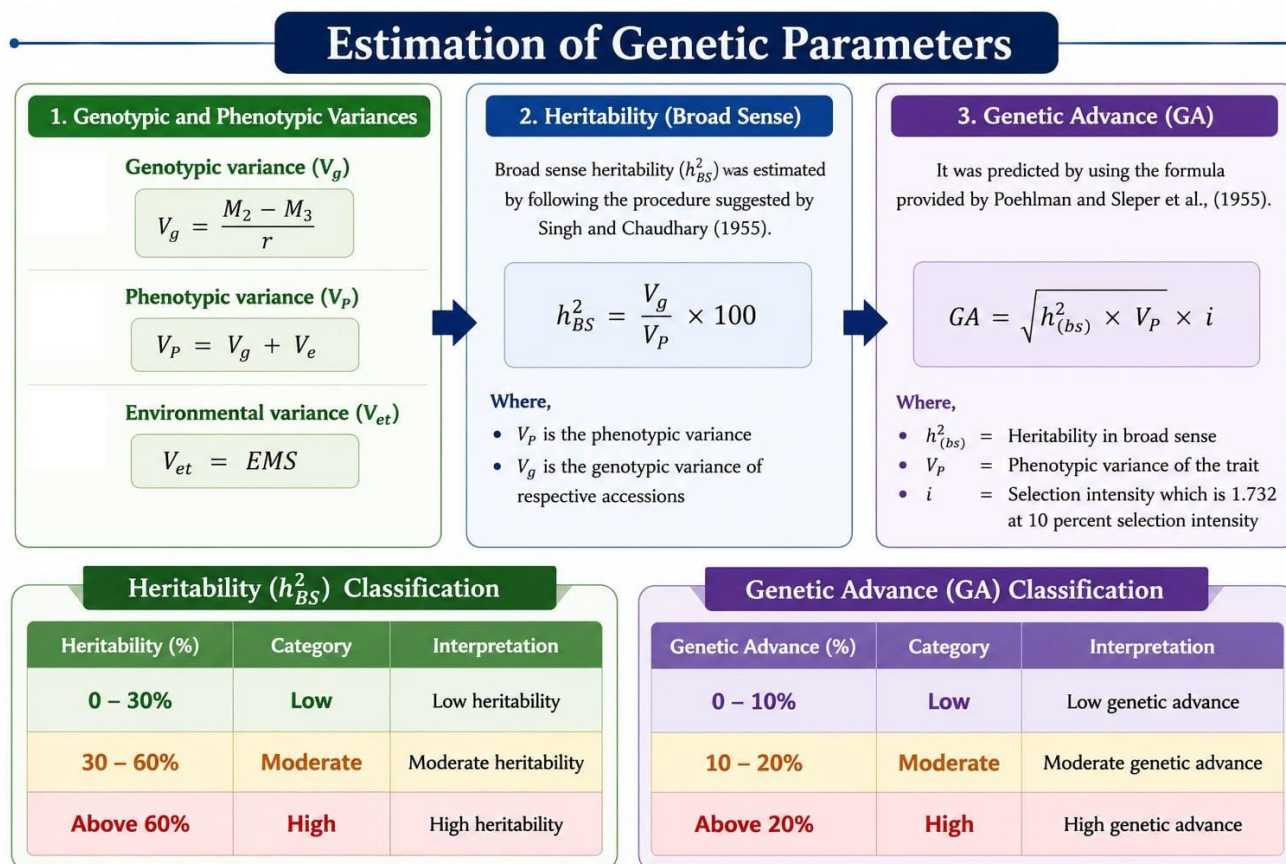
$\sigma_e^2$  = Error variance

$\sigma_g^2$  = Genotypic variance

**Figure 2.** Schematic representation of the analysis of variance (ANOVA) table used for evaluating genotype effects under a randomized complete block design (RCBD).

The above table presents the sources of variation, corresponding degrees of freedom (d.f), mean sum of squares (MSS), expected mean squares, and F-test statistics used to determine the significance of genotypic differences. Here,  $r$  denotes the number of replications,  $g$  the number of genotypes,  $MSS_r$  the mean sum of squares due to replication,  $MSS_g$  the mean sum of squares due to genotype,  $MSS_e$  the mean sum of squares due to error,  $\sigma_e^2$  the environmental (error) variance, and  $\sigma_g^2$  the genotypic variance.

Broad-sense heritability was categorized as low (0–30%), moderate (30–60%), and high (>60%), whereas genetic advance was classified as low (0–10%), moderate (10–20%), and high (>20%). These categories facilitate the assessment of the relative contribution of genetic factors to trait expression and the expected response to selection in breeding programs.



**Figure 3:** Classification of broad-sense heritability ( $H^2_{BS}$ ) and genetic advance (GA) used for interpreting genetic variability among maize genotypes.

#### 4. Principal Component Analysis (PCA)

PCA technique was used to observe interrelationships among variables (Bekele and Mebeaselassie et al. 2025). Principal component analysis (PCA) was used to know reliable information on how to classify groups of genotypes that have desirable yield traits for breeding programme (Azam and Mohammad et al. 2023). PCA is defined as “a method of data reduction to clarify the relationship between two or more traits and to distribute the total variance of the original traits into a limited number of uncorrelated new variables”. PCA can be used for two types of data matrix; a variance-covariance matrix and a correlation matrix. A correlation matrix standardizing the original data set is preferred with traits of different scales.

#### 5. Cluster Analysis

It is very simple statistical and numerical taxonomic technique was analyzed using the procedure of cluster with the help of computer software for windows. Cluster analysis is used to combine observations into clusters such that groups formed are similar within the groups and different from other groups due to some variables (Jaeger and David 2023).

A simplest method used to differentiate the entries using measurement that describes similarity or difference among the genotypes. By using cluster analysis, we can also formed groups of related variables. There are different ways to sort out cases into groups. There are many methods of clustering. Selection of a method depends on the size of the data to be evaluated. Hierarchical and non-hierarchical the most popular clustering methods (Kuzudisli and Burcu et al. 2023). In present study average data was analyzed by using Ward's Distance cluster analysis.

#### 6. Results and Discussion

The precession of the results provides by the valid experiment. The data was recorded for different characters and compiled for statistical analysis. For current study 20 wheat genotypes were used as experimental material.

The data of traits showed significant differences were further analyzed for heritability, genetic advance, principal component analysis and cluster analysis. Days to heading observed from 97.33 to 111. UOS-18 followed by UOS-4 had greatest mean values for days to heading (Table 1.1) while, UOS-15 showed minimum days to heading. Analysis of variance demonstrated that highly significant differences were present among bread wheat genotypes for days to heading (Table 1). Statistical significance and mean values are mentioned in the (Table 1). Grand mean value was 104.38. The presence of genetic variation was showed in material.

Highly significant differences exist between twenty wheat genotypes for days to maturity demonstrated by analysis of variance (Table 2). Days to maturity ranged from 159 to 153 days UOS-8 followed by UOS-6 had greatest mean values for days to maturity (Table 2.1). UOS-15 had least mean value 153 for days to maturity. Grand mean value was 156.65.

**Table 1:** Analysis of variance (ANOVA) for Days to heading

| SOV         | DF | SS     | MS    | F                   |
|-------------|----|--------|-------|---------------------|
| Replication | 2  | 0.53   | 0.26  | 0.075 <sup>ns</sup> |
| Genotypes   | 19 | 647.51 | 34.07 | 58.51 <sup>**</sup> |
| Error       | 38 | 22.13  | 0.58  |                     |
| Total       | 59 | 670.18 |       |                     |

(\* = Significant at 5% probability)

(\*\* = Highly Significant at 5% probability) Grand mean = 104.38

**Table 1.1:** Individual means comparison of treatment for days to heading

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-18    | 111.00 | a                  |
| UOS-4     | 108.67 | b                  |
| UOS-9     | 107.67 | bc                 |
| Galaxy-13 | 107.00 | cd                 |
| UOS-6     | 106.33 | de                 |
| UOS-8     | 106.33 | de                 |
| UOS-1     | 106.00 | def                |
| Pb-11     | 105.67 | ef                 |
| Millat-11 | 105.67 | ef                 |
| V-82003   | 105.00 | fg                 |
| UOS-2     | 105.00 | fg                 |
| UOS-7     | 104.33 | g                  |
| UOS-5     | 104.33 | g                  |
| UOS-10    | 103.00 | h                  |
| UOS-13    | 102.33 | hi                 |
| UOS-3     | 102.00 | hi                 |
| UOS-12    | 101.33 | i                  |
| UOS-11    | 99.33  | j                  |
| UOS-14    | 99.33  | j                  |
| UOS-15    | 97.33  | k                  |

Mean sharing the same letters are statistically similar ( $p > 0.05$ )

**Table 2:** Analysis of variance (ANOVA) for days to maturity

| SOV         | DF | SS     | MS    | F                   |
|-------------|----|--------|-------|---------------------|
| Replication | 2  | 19.9   | 9.95  | 9.66 <sup>ns</sup>  |
| Genotypes   | 19 | 224.3  | 11.80 | 11.38 <sup>**</sup> |
| Error       | 38 | 39.43  | 1.03  |                     |
| Total       | 59 | 283.65 |       |                     |

(\* = Significant at 5 % probability)

(\*\* = Highly Significant at 5% probability) Grand mean = 156.65

**Table 2.1:** Individual means comparison of treatment for days to maturity

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-8     | 159.67 | a                  |
| UOS-6     | 159.33 | a                  |
| UOS-12    | 159.33 | a                  |
| Pb-11     | 159.00 | a                  |
| UOS-10    | 158.67 | ab                 |
| UOS-14    | 158.33 | ab                 |
| Galaxy-13 | 158.00 | abc                |

|           |        |     |
|-----------|--------|-----|
| UOS-9     | 157.00 | bcd |
| UOS-13    | 157.00 | bcd |
| UOS-18    | 157.00 | bcd |
| V-82003   | 156.33 | cde |
| UOS-1     | 155.67 | def |
| UOS-4     | 155.67 | def |
| UOS-5     | 155.67 | def |
| UOS-2     | 155.00 | ef  |
| UOS-3     | 155.00 | ef  |
| UOS-7     | 154.67 | efg |
| Millat-11 | 154.67 | efg |
| UOS-11    | 154.00 | fg  |
| UOS-15    | 153.00 | g   |

Mean sharing the same letters are statistically similar ( $p>0.05$ )

Plant height is the most important character that was negatively related to yield indirectly effect grain yield in wheat. Development of short stature varieties has been desired due to lodging problems. By introducing short stature varieties grain yield was increased during green revolution. There were highly significance differences were determined for plant height.

Results revealed plant height range was 83 to 109 cm. Grand mean value was 98.7cm. The genotype UOS-13 and UOS-18 produced maximum plant height 109 cm and 105.33 cm respectively. While shortest plant height 83 cm was measured from genotype UOS-4 (Table 3). Peduncle length is important morphological trait contributing to final yield of crop. Table 4 indicated highly significant differences among wheat genotypes. UOS-7 showed highest peduncle length (40 cm) followed by UOS-9 (39cm) while least peduncle length was 28.33 found in UOS-13 (Table 4.1). The grand mean value of peduncle length was 33.12cm.

**Table 3:** Analysis of variance (ANOVA) for plant height (cm)

| SOV         | DF | SS      | MS      | F       |
|-------------|----|---------|---------|---------|
| Replication | 2  | 22.53   | 11.26   | 4.36ns  |
| Genotypes   | 19 | 2031.52 | 106.922 | 41.40** |
| Error       | 38 | 98.13   | 2.58    |         |
| Total       | 59 | 2152.18 |         |         |

(\* = Significant at 5% probability.)

(\*\* = Highly Significant at 5% probability) Grand mean = 98.7cm

**Table 3.1:** Individual means comparison of treatment for plant height (cm)

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-13    | 109.00 | a                  |
| UOS-18    | 105.33 | b                  |
| UOS-11    | 104.00 | bc                 |
| UOS-15    | 104.00 | bc                 |
| UOS-12    | 103.67 | bc                 |
| Millat-11 | 102.33 | cd                 |
| Pb-11     | 102.00 | cd                 |
| Galaxy-13 | 102.00 | cd                 |
| UOS-2     | 100.67 | de                 |
| UOS-9     | 100.00 | de                 |
| UOS-7     | 99.33  | ef                 |
| UOS-1     | 97.33  | fg                 |
| V-82003   | 97.33  | fg                 |
| UOS-10    | 96.00  | g                  |
| UOS-8     | 95.67  | g                  |
| UOS-5     | 95.33  | g                  |
| UOS-14    | 95.00  | h                  |
| UOS-3     | 91.33  | h                  |
| UOS-6     | 91.00  | h                  |

UOS-4

83.00

I

**Table 4:** Analysis of. variance (ANOVA) for peduncle length (cm)

| SOV         | DF | SS    | MS    | F       |
|-------------|----|-------|-------|---------|
| Replication | 2  | 0.925 | 0.46  | 0.20ns  |
| Genotypes   | 19 | 755.4 | 39.76 | 18.01** |
| Error       | 38 | 83.9  | 2.20  |         |
| Total       | 59 | 840.3 |       |         |

(\*=Significant at 5% probability)

(\*\*=Highly Significant at 5% probability)Grand mean = 33.12cm.

**Table 4.1:** Individual means comparison of treatment for peduncle length (cm)

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-7     | 40.000 | a                  |
| UOS-9     | 39.000 | ab                 |
| Pb-11     | 38.667 | b                  |
| UOS-8     | 37.667 | bc                 |
| UOS-18    | 36.333 | cd                 |
| UOS-15    | 35.000 | cd                 |
| Galaxy-13 | 35.333 | d                  |
| UOS-12    | 32.000 | e                  |
| Millat-11 | 32.667 | e                  |
| UOS-2     | 32.667 | e                  |
| UOS-1     | 32.667 | e                  |
| UOS-6     | 32.000 | ef                 |
| UOS-3     | 31.000 | ef                 |
| UOS-14    | 31.667 | fg                 |
| V-82003   | 31.667 | fg                 |
| UOS-4     | 30.000 | gh                 |
| UOS-5     | 29.333 | gh                 |
| UOS-10    | 29.333 | h                  |
| UOS-11    | 28.333 | h                  |
| UOS-13    | 28.333 | h                  |

Mean sharing the same letters are statistically similar( $p>0.05$ )

Length of the spike had more contribution in genetic diversity of wheat genotypes then different characters. As showed in (Table 5) spike length showed highly significant differences among genotypes. Highest spike length 14.6 cm was recorded by the genotype UOS-18 followed by UOS-12 with spike length 13.67cm, while minimum spike length 9 cm was produced from check variety Millat-11 (Table 5). The grand mean value for spike length was 11.41 cm.

As mentioned in table 6 it is clear that highly significant differences were recorded among bread wheat genotypes and concluded that genetically diverse material was studied. For present study. Table 6.1 revealed that UOS-18 expressed greatest mean value of 24 spikelets per spike, while UOS-1 produced 23 spikelets per spike. Millat-11 had least number of spikelets per spike (15). Grand mean value was 18.6.

**Table 5:** Analysis of variance (ANOVA) for Spike length (cm)

| SOV         | DF | SS    | MS   | F      |
|-------------|----|-------|------|--------|
| Replication | 2  | 2.57  | 1.28 | 1.04ns |
| Genotypes   | 19 | 116.2 | 6.11 | 4.95** |
| Error       | 38 | 46.9  | 1.23 |        |
| Total       | 59 | 165.7 |      |        |

(\*=Significant at 15% probability)

(\*\*=Highly Significant at 15% probability)Grand mean = 11.41 cm

**Table 5.1:** Individual means comparison of treatment for spike length (cm)

| Genotypes | Mean | Homogeneous Groups |
|-----------|------|--------------------|
|-----------|------|--------------------|

|           |        |      |
|-----------|--------|------|
| UOS-18    | 14.667 | a    |
| UOS-12    | 13.667 | ab   |
| UOS-1     | 13.333 | abc  |
| Galaxy-13 | 13.000 | abc  |
| UOS-9     | 12.333 | bcd  |
| UOS-8     | 12.000 | bcde |
| UOS-7     | 12.000 | bcde |
| UOS-2     | 11.667 | cdef |
| UOS-6     | 11.667 | cdef |
| UOS-13    | 11.667 | cdef |
| UOS-10    | 11.000 | defg |
| UOS-11    | 11.000 | defg |
| Pb-11     | 11.000 | defg |
| UOS-5     | 10.833 | efgh |
| UOS-3     | 10.333 | efgh |
| UOS-4     | 10.333 | efgh |
| V-82003   | 10.333 | fgh  |
| UOS-14    | 10.000 | gh   |
| UOS-15    | 9.667  | gh   |
| Millat-11 | 9.000  | h    |

Mean sharing the same letters are statistically similar( $p>0.05$ )

**Table 6:** Analysis of variance (ANOVA) for spikelet per spike

| SOV         | DF | SS    | MS    | F       |
|-------------|----|-------|-------|---------|
| Replication | 2  | 1.30  | 0.65  | 0.47ns  |
| Genotypes   | 19 | 306.2 | 16.11 | 11.77** |
| Error       | 38 | 52.03 | 1.36  |         |
| Total       | 59 | 359.6 |       |         |

(\* = Significant at 5% probability)

(\*\* = Highly Significant at 5% probability) Grand mean = 18.6

**Table 6.1:** Individual means comparison of treatment for spikelet per spike

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-18    | 24.000 | a                  |
| UOS-1     | 23.000 | a                  |
| UOS-6     | 20.667 | b                  |
| Galaxy-13 | 20.000 | b                  |
| UOS-3     | 20.000 | bc                 |
| UOS-8     | 20.667 | bc                 |
| UOS-9     | 19.667 | bc                 |
| UOS-12    | 19.333 | bc                 |
| UOS-10    | 19.333 | bc                 |
| UOS-2     | 19.000 | bc                 |
| UOS-7     | 19.000 | bc                 |
| UOS-11    | 18.333 | cd                 |
| UOS-13    | 18.333 | cd                 |
| V-82003   | 17.000 | def                |
| UOS-5     | 16.668 | def                |
| UOS-14    | 16.667 | def                |
| Pb-11     | 16.667 | ef                 |
| UOS-15    | 16.333 | ef                 |
| UOS-4     | 16.000 | f                  |
| Millat-11 | 15.000 | fl                 |

Mean sharing the same letters are statistically similar ( $p>0.05$ )

Highly significant differences exist between wheat genotypes for number of spikes per meter<sup>2</sup> delighted from (Table 7). Spikes per meter<sup>2</sup> ranged from 1301 to 516. Pb-11 and Galaxy-13 had extreme number of spikes/m<sup>2</sup>. Most minimal number of tillers per meter<sup>2</sup> (301) were produced by UOS-10 (Table 7). Grand mean value was 408.68.

Analysis of variance demonstrated that highly significant differences for thousand grain weight among the genotypes were estimated (Table 8). Two wheat advance lines UOS-3 and UOS-11 displayed most extreme mean value 40.4 and 40.3g for 1000 grain weight respectively (Table 8.1). While least mean value 31.8g was showed by UOS-18 (Table 8.1). Grand mean with (36.62).

**Table 7:** Analysis of variance (ANOVA) for tillers per meter square

| SOV         | DF | SS      | MS    | F      |
|-------------|----|---------|-------|--------|
| Replication | 2  | 733     | 366.7 | 0.64ns |
| Genotypes   | 19 | 28253   | 1487  | 2.6**  |
| Error       | 38 | 21758.6 | 572.6 |        |
| Total       | 59 | 50744.6 |       |        |

(\* = Significant at 5% probability)

(\*\* = Highly Significant at 5% probability) Grand mean = 408.68

**Table 7.1:** Individual means comparison of treatment for tillers per meter square

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| Pb-11     | 516.33 | a                  |
| Galaxy-13 | 508.33 | ab                 |
| UOS-7     | 506.33 | ab                 |
| UOS-2     | 489.67 | ab                 |
| Millat-11 | 470    | ab                 |
| V-82003   | 466    | b                  |
| UOS-15    | 436.33 | c                  |
| UOS-6     | 425.00 | cd                 |
| UOS-4     | 422.67 | cd                 |
| UOS-1     | 406.67 | cde                |
| UOS-11    | 395.00 | de                 |
| UOS-12    | 394.67 | de                 |
| UOS-5     | 392.00 | def                |
| UOS-13    | 380.67 | efg                |
| UOS- 9    | 351.33 | fgh                |
| UOS-14    | 346.00 | gh                 |
| UOS- 3    | 327.33 | hi                 |
| UOS- 8    | 321.67 | hi                 |
| UOS-18hi  | 315.67 | hi                 |
| UOS-10    | 301.01 | il                 |

Mean sharing the same letters are statistically similar ( $p > 0.05$ )

**Table 8:** Analysis of variance (ANOVA) for 1000-grain weight (g)

| SOV         | DF | SS     | MS     | F       |
|-------------|----|--------|--------|---------|
| Replication | 2  | 0.001  | 0.0003 | 0.001ns |
| Genotypes   | 19 | 375.99 | 19.78  | 99.68** |
| Error       | 38 | 7.54   | 0.1985 |         |
| Total       | 59 | 383.5  |        |         |

(\* = Significant at 5% probability)

(\*\* = Highly Significant at 5% probability) Grand mean = 36.62

**Table 8.1:** Individual means comparison of treatment for 1000-grain weight (g)

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-3     | 40.45  | a                  |
| UOS-11    | 40.367 | a                  |
| UOS-2     | 40.337 | a                  |

|           |        |     |
|-----------|--------|-----|
| UOS-7     | 40.267 | a   |
| Galaxy-13 | 38.200 | b   |
| UOS-12    | 37.833 | bc  |
| Pb-11     | 37.533 | bcd |
| UOS-4     | 37.400 | cd  |
| V-82003   | 37.133 | cde |
| UOS-8     | 36.833 | def |
| UOS-9     | 36.500 | ef  |
| UOS-10    | 36.367 | f   |
| UOS-13    | 36.267 | fg  |
| UOS-14    | 35.600 | gh  |
| UOS-5     | 35.000 | h   |
| UOS-1     | 34.267 | i   |
| UOS-6     | 34.133 | i   |
| UOS-15    | 33.267 | j   |
| Millat-11 | 32.833 | j   |
| UOS-18    | 31.867 | k   |

Mean sharing the same letters are statistically similar ( $p > 0.05$ )

Number of grains per spike is the very important trait for determine grain yield and has significant effect on it. Results showed in table 9 that all genotypes had significant differences for number of grains per spike. The most extreme number of grains/spike was produced by the UOS-12 (55) followed by PB-11 (55) (Table 9.1). The wheat genotype which demonstrated the least number of grains per spike value was Millat-11 (33.6) took after by UOS-4 (Table 9). The grand mean worth for number of grains/spike was 46.73. Analysis of variance showed that highly significant variation was present among genotypes for grain yield/plot (Table 10). UOS-7 (4504g) showed most extreme grain yield/plot followed by UOS-11 (4314.3g) (Table 10.1). Least mean value for grain yield/plot was displayed by UOS-18 (3149.7g) (Table 10.1). Grand mean value for grain yield/plot was 3178 g.

**Table 9:** Analysis of variance (ANOVA) for number of grains per spike

| SOV         | DF | SS      | MS     | F       |
|-------------|----|---------|--------|---------|
| Replication | 2  | 2.03    | 1.017  | 0.24ns  |
| Genotypes   | 19 | 1969.73 | 103.67 | 24.94** |
| Error       | 38 | 157.97  | 4.16   |         |
| Total       | 59 | 2129.73 |        |         |

(\* = Significant at 5% probability)

(\*\* = Highly Significant at 51% probability) Grand mean = 46.73

**Table 9.1:** Individual means comparison of treatment for number of grains per spike

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| Pb-11     | 55.000 | a                  |
| UOS-12    | 55.000 | a                  |
| UOS-11    | 53.333 | ab                 |
| UOS-5     | 50.667 | bc                 |
| Galaxy-13 | 50.667 | bc                 |
| UOS-10    | 50.333 | bc                 |
| UOS-18    | 50.333 | bc                 |
| UOS-14    | 50.000 | bc                 |
| UOS-6     | 49.000 | cd                 |
| UOS-3     | 47.333 | cde                |
| UOS-8     | 47.333 | cde                |
| UOS-9     | 46.333 | de                 |
| UOS-1     | 45.667 | de                 |
| UOS-13    | 45.333 | ef                 |
| UOS-2     | 44.333 | ef                 |
| UOS-7     | 44.333 | ef                 |
| UOS-15    | 42.000 | fg                 |
| V-82003   | 38.667 | gh                 |
| UOS-4     | 35.333 | hi                 |

|           |        |    |
|-----------|--------|----|
| Millat-11 | 33.667 | il |
|-----------|--------|----|

Mean sharing the same letters are statistically similar (p>0.05)

**Table 10:** Analysis of variance (ANOVA) for grain yield/plot (g)

| SOV         | DF | SS        | MS     | F        |
|-------------|----|-----------|--------|----------|
| Replication | 2  | 3871      | 1936   | 0.40ns   |
| Genotypes   | 19 | 1.382E+07 | 727521 | 151.57** |
| Error       | 38 | 182391    | 4800   |          |
| Total       | 59 | 1.400E+07 |        |          |

(\*=Significant at 5% probability)

(\*\*=Highly Significant at 5% probability,)Grand mean. = 3178 g

**Table 10.1:** Individual means comparison of treatment for grain yield/plot (g)

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-7     | 4504.7 | a                  |
| UOS-11    | 4314.3 | b                  |
| UOS-2     | 4202.3 | bc                 |
| Galaxy-13 | 4147.3 | cd                 |
| UOS-1     | 4126.3 | cd                 |
| UOS-6     | 4058.7 | d                  |
| UOS-8     | 3855.7 | e                  |
| UOS-13    | 3835.7 | ef                 |
| V-82003   | 3811.7 | ef                 |
| UOS-14    | 3723.3 | fg                 |
| Pb-11     | 3660.3 | gh                 |
| Millat-11 | 3617.7 | gh                 |
| UOS-5     | 3549.0 | hi                 |
| UOS-9     | 3470.3 | ij                 |
| UOS-3     | 3405.7 | jk                 |
| UOS-12    | 3400.3 | jk                 |
| UOS-10    | 3331.0 | k                  |
| UOS-15    | 3182.0 | l                  |
| UOS-4     | 3178.0 | l                  |
| UOS-18    | 3149.7 | l                  |

Mean sharing. the same letters are statistically similar (p&gt;0.05)

For wheat and flour users' protein content is a key specification. Water absorption and gluten strength in relation to many processing properties protein content is also related to complete product components such as appearance and texture but for cakes and snacks low protein is required and for products of pan bread high protein is required. Results for protein (%) from ANOVA demonstrated that highly significant differences exist among twenty wheat genotypes (Table 11). Mean values are shown in table 4.11. Protein content ranged from 16 to 13.1(%). UOS-8 followed by UOS-13 gave greatest mean values for protein content (Table 11.1). UOS-18 produced least protein content as appeared. Grand mean value was 14.90.

For flour quality moisture content is essential. The moisture in wheat adjusted by flour millers to keep standard level before milling. Commonly moisture content is used (14 %). Moisture content also signifies storability. Flour with high moisture content is affected by bacteria, insect and mould which cause damage during storage while low moisture content in wheat and flour keeps more stable during storage. Moisture content in flour gives profitability in milling.

Highly significant variation exists between wheat genotypes for moisture percentage depicted from the (Table 12). Moisture percentage ranged from 10.26 to 12.16%. UOS-4 and UOS-18 had most extreme moisture percentage (Table 12.1). Most minimal moisture percentage was displayed by UOS-1 (10.2%). grand mean value was 11 percent.

**Table 11:** Analysis of variance (ANOVA) for protein %

| SOV         | DF | SS    | MS    | F       |
|-------------|----|-------|-------|---------|
| Replication | 2  | 0.032 | 0.016 | 0.5ns   |
| Genotypes   | 19 | 40.73 | 2.14  | 65.30** |
| Error       | 38 | 1.24  | 0.032 |         |
| Total       | 59 | 42.01 |       |         |

(\*=Significant at 5% probability.)

(\*\*=Highly Significant at 5% probability)Grand mean = 14.90

**Table 11.1:** Individual means comparison of treatment for protein %

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS-8     | 16.000 | a                  |
| UOS-13    | 15.933 | ab                 |
| UOS-14    | 15.767 | ab                 |
| V-82003   | 15.767 | ab                 |
| UOS-3     | 15.667 | bc                 |
| UOS-1     | 15.400 | cd                 |
| UOS-15    | 15.333 | d                  |
| UOS-12    | 15.300 | d                  |
| UOS-11    | 15.267 | d                  |
| UOS-7     | 15.233 | d                  |
| UOS-2     | 15.200 | d                  |
| UOS-10    | 15.133 | d                  |
| UOS-9     | 14.600 | e                  |
| UOS-6     | 14.500 | ef                 |
| UOS-5     | 14.333 | ef                 |
| UOS-4     | 14.233 | fg                 |
| Pb-11     | 14.033 | g                  |
| Galaxy-13 | 13.700 | h                  |
| Millat-11 | 13.567 | h                  |
| UOS-18    | 13.100 | il                 |

Mean sharing the same letters are statistically similar ( $p > 0.05$ )

**Table 12:** Analysis of variance (ANOVA) for moisture %

| SOV         | DF | SS    | MS    | F       |
|-------------|----|-------|-------|---------|
| Replication | 2  | 0.052 | 0.026 | 1.3ns   |
| Genotypes   | 19 | 12.47 | 0.65  | 31.42** |
| Error       | 38 | 0.79  | 0.020 |         |
| Total       | 59 | 13.32 |       |         |

(\* = Significant at 5% probability)

(\*\* = Highly Significant at 5% probability) Grand mean = 11

**Table 12.1:** Individual means comparison of treatment for moisture %

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS- 4    | 12.167 | a                  |
| UOS-18    | 11.600 | b                  |
| UOS- 6    | 11.400 | bc                 |
| Pb-11     | 11.300 | cd                 |
| UOS-10    | 11.233 | cd                 |
| UOS- 7    | 11.167 | cd                 |
| UOS- 8    | 11.167 | cd                 |
| V-82003   | 11.167 | cd                 |
| UOS- 2    | 11.133 | de                 |
| UOS- 5    | 11.133 | de                 |
| Millat-11 | 11.133 | de                 |
| UOS- 3    | 11.067 | de                 |
| UOS-15    | 10.900 | ef                 |
| Galaxy-13 | 10.900 | ef                 |
| UOS-13    | 10.767 | fg                 |
| UOS-11    | 10.533 | Gh                 |
| UOS- 9    | 10.400 | Hi                 |
| UOS-14    | 10.400 | Hi                 |
| UOS-12    | 10.333 | Hi                 |

|        |        |    |
|--------|--------|----|
| UOS- 1 | 10.267 | il |
|--------|--------|----|

iii Mean sharing the same letters are statistically similar ( $p > 0.05$ )

## 7. Gluten (%)

For elasticity and extensibility of flour dough gluten is responsible. In wheat the gluten test provides information on the quantities and estimates the quality of gluten. Highly significant differences exist between twenty wheat genotypes results revealed from analysis of variance for gluten percentage (Table 13). Statistical significance and mean values are appeared in the, (Table 4.13). Gluten percentage ranged from 22 to 33.3%. Millat-11 followed by UOS-3 had greatest mean values 22% for gluten percentage (Table 13.1). UOS-18 had least mean value 33.3% for gluten percentage (Table 13.1). Grand mean value 27.33%. Starch is very important component of wheat grain. It is necessary to measure starch viscosity properties. High viscosity of flour is preferred for Asian noodle products to make noodles with better texture. It is shown from the table 14 that highly significant contrasts exist between wheat genotypes for starch percentage. Starch percentage ranged from 50.8 to 53.2%. UOS-1 and UOS-12 had most extreme starch percentage 53.2 and 53%. Most minimal starch percentage 50% was produced by Millat-11. Grand mean value was 52.3 percent.

**Table 13:** Analysis of variance (ANOVA) for gluten %

| SOV         | DF | SS     | MS    | F      |
|-------------|----|--------|-------|--------|
| Replication | 2  | 6.53   | 3.26  | 0.97ns |
| Genotypes   | 19 | 508    | 26.73 | 8.01** |
| Error       | 38 | 126.8  | 3.33  |        |
| Total       | 59 | 641.33 |       |        |

(\* = Significant at 5% probability.)

(\*\* = Highly Significant at 5% probability) Grand mean = 27.33

**Table 13.1:** Individual means comparison of treatment for gluten %

| Genotypes | Mean   | Homogeneous Groups |
|-----------|--------|--------------------|
| UOS- 3    | 30.667 | ab                 |
| UOS-13    | 30.667 | ab                 |
| V-82003   | 30.667 | ab                 |
| UOS-14    | 30.000 | bc                 |
| UOS-8     | 29.667 | bcd                |
| UOS-1     | 28.667 | bcde               |
| UOS-12    | 28.667 | bcde               |
| UOS-10    | 28.000 | bcdef              |
| UOS-7     | 27.333 | cdefg              |
| UOS-11    | 27.333 | cdefg              |
| UOS-6     | 26.667 | defgh              |
| UOS-15    | 26.000 | efghi              |
| UOS- 9    | 26.000 | efghi              |
| UOS- 5    | 25.000 | fghij              |
| UOS- 4    | 24.667 | ghij               |
| UOS- 17   | 24.333 | ghij               |
| UOS- 20   | 23.667 | hij                |
| UOS- 2    | 23.333 | lj                 |
| UOS-18    | 22.000 | jm                 |
| UOS- 3    | 30.667 | ab                 |

Mean sharing, the same letters are statistically similar ( $p > 0.05$ )

**Table 14:** Analysis of variance (ANOVA) for starch %

| SOV         | DF | SS    | MS   | F       |
|-------------|----|-------|------|---------|
| Replication | 2  | 0.25  | 0.12 | 0.57ns  |
| Genotypes   | 19 | 20.39 | 1.07 | 50.09** |
| Error       | 38 | 0.81  | 0.21 |         |
| Total       | 59 | 21.47 |      |         |

(\* = Significant at 5% probability)

(\*\* = Highly Significant at 5% probability) Grand mean = 52.3

**Table 14.1:** Individual means comparison of treatment for starch %

| Genotypes | Mean     | Homogeneous Groups |
|-----------|----------|--------------------|
| UOS-1     | 53.200 a | a                  |
| UOS-12    | 53.067   | ab                 |
| Galaxy-13 | 52.967   | abc                |
| UOS-2     | 52.900   | bc                 |
| UOS-11    | 52.833   | bc                 |
| UOS-3     | 52.767   | cd                 |
| UOS-9     | 52.733   | cde                |
| UOS-5     | 52.567   | def                |
| Pb-11     | 52.500   | efg                |
| UOS-6     | 52.467   | fgh                |
| UOS-18    | 52.433   | fgh                |
| UOS-15    | 52.300   | gh                 |
| UOS- 7    | 52.233   | hi                 |
| UOS-4     | 52.233   | hi                 |
| UOS-14    | 52.233   | hi                 |
| UOS-8     | 52.000   | i                  |
| UOS-13    | 51.700   | j                  |
| V-82003   | 51.533   | j                  |
| UOS-10    | 51.467   | j                  |
| Millat-11 | 50.867   | k                  |

Mean sharing the same. letters are statistically similar ( $p > 0.05$ )

## 8. Heritability, Genetic Variability and Genetic Advance

This study showed high genetic advance and heritability for the traits. There is scope for the improvement of genotypes for the traits studied the percentage of genetic advance of mean showed. Genotypic and phenotypic variances, heritability, genetic advance for different characters have been shown in (Table 15) and discussed. Phenotypic and genotypic variances observed in wheat genotypes for days to heading were 11.74 and 11.16 respectively (Table 15). High heritability (95%) was observed with low genetic advance (5.78). Days to heading had significant association with grain yield. There is high heritability with low genetic advance exhibited favorable influence of environment rather than genotype and selection, may be fruitful in early. segregating generation.

Phenotypic and genotypic variances observed in wheat genotypes for days to maturity were. 4.62 and 3.59 respectively. High heritability (78%) was observed with low genetic advance 3.28 (Table 15). So the selection may not be affective. In wheat genotypes for plant height phenotypic and genotypic variances observed were 37.36 and 34.78 respectively. With moderate genetic advance (10.37) and high heritability 93.9% was observed. In this heritability is high and genetic advance is moderate so the selection will be fruitful.

**Table 15:** Heritability, genetic variability and genetic advance of wheat genotypes

| Variable                 | V <sub>G</sub> | V <sub>p</sub> | H <sup>2</sup> <sub>bs</sub> (%) | GA    |
|--------------------------|----------------|----------------|----------------------------------|-------|
| Days to heading          | 11.16          | 11.74          | 95                               | 5.78  |
| Days to maturity         | 3.59           | 4.62           | 78                               | 3.28  |
| Plant height             | 34.78          | 37.36          | 93.9                             | 10.37 |
| Peduncle length          | 12.52          | 14.78          | 85.12                            | 6.13  |
| Spike length             | 1.63           | 2.86           | 56.99                            | 2.19  |
| Spikelets per spike      | 4.92           | 6.28           | 78.34                            | 3.83  |
| Tillers per meter square | 304            | 876.6          | 34                               | 30    |
| 1000-grain weight        | 4.90           | 5.09           | 96                               | 3.82  |
| No of grain per spike    | 33.17          | 37.33          | 88.75                            | 9.92  |
| Grain yield/plot         | 0.240          | 0.245          | 97.05                            | 0.84  |
| Protein %                | 0.70           | 0.71           | 96                               | 1.42  |
| Moisture %               | 0.21           | 0.23           | 91                               | 0.76  |
| Gluten %                 | 7.80           | 11.13          | 70                               | 4.09  |
| Starch %                 | 0.29           | 0.50           | 58                               | 0.71  |

In wheat genotypes for peduncle length phenotypic and genotypic variances observed were 14.78 and 12.52cm respectively showed an effect of environmental interaction for the appearance of peduncle length. With low (6.13) genetic advance a high heritability (85.12%) was observed. There is high heritability with low genetic advance so the selection may not fruitful in early generation trait. Phenotypic and genotypic variances observed in wheat genotypes for spike length were 2.86 and 1.63 respectively. Moderate heritability (56.99%) was observed with (2.19) genetic advance. Moderate heritability showed to its medium transmission to next generation while low genetic advance also signified that spike length is highly influence by environmental effects and selection is ineffective in early segregating generation. Spike length is very important for the improvement of grain yield.

In wheat genotypes for spikelet per spike phenotypic and genotypic variances observed were 4.92 and 6.28 respectively. High heritability (78.34%) was observed with (3.83) genetic advance. There is high heritability with low genetic advance so the selection may not be fruitful in early generation for this trait.

For tillers per meter square phenotypic and genotypic variances observed in wheat genotypes were 876.6 and 304 respectively. Greater difference between genotypic and phenotypic variance indicated that this trait is highly environmental factor involve for this trait. Low heritability (34%) was observed with high genetic advance (30). low heritability with high genetic advance showed that this trait is governed by additive gene affects. Low heritability is being exhibited due to high environmental effects. Selection may be rewarding for this trait influence by environment but the selection is favorable for this trait in early segregating generation for genetic improvement of crop plant. This was due to the difference in the experimental material.

Phenotypic and genotypic variances observed in wheat genotypes for 1000-grain weight was 5.09 and 4.90 respectively. Phenotypic variance is nearly similar to genotypic variance reflected the least effect of environment for the determination of 1000 grain weight. High heritability (96%) was observed with (3.82) genetic advance. There is high heritability with low genetic advance so the selection may be useful for this trait in letter generation. High heritability means greater transmission of inheritance to the next generation.

Phenotypic and genotypic variances observed in wheat genotypes for number of grains per spike were 37.33 and 33.17 respectively. High heritability (88.75%) was observed with genetic advance (9.92). Selection may be affective in later generation. Phenotypic and genotypic variances. observed in wheat genotypes for grain yield per plot were 0.245 and 0.240 irrespectively. Smaller difference showed least effect of environment. High heritability (97.05%) was observed with (0.84) genetic advance. selection may useful in latter generation.

Phenotypic and genotypic variances observed in wheat genotypes for protein content were 0.71 and 0.70 respectively. Smaller difference showed least environmental affect. High heritability (96%) was observed with high genetic advance (1.42). There is high heritability with low genetic advance so the selection will not useful in early generation. Phenotypic and genotypic variances observed in wheat genotypes for moisture content were 0.23 and 0.21 respectively. Smaller difference showed least environmental affect. High heritability (91%) was observed with low genetic advance (0.76). There is high heritability with low genetic advance so the selection may be useful in later generation.

Phenotypic and genotypic variances observed in wheat genotypes for gluten content were 11.13 and 7.80 respectively. High heritability (70%) was observed with high genetic advance (4.09). There is high heritability with low genetic advance so the selection is favorable for this trait in early segregation generation. Phenotypic and genotypic variances observed in wheat genotypes for starch content were 0.50 and 0.29 respectively. Moderate heritability (58%) was observed with low genetic advance (0.71). Moderate heritability showed to its medium transmission to next generation while low genetic advance also signified that starch percentage is highly influence by environmental effects and selection is ineffective. in early segregating generation.

Mean sharing the same. letters are statistically similar ( $p > 0.05$ )

## 9. Principal Component Analysis (PCA)

Principal component analysis (PCA) was carried out to categorize the genotypes on the basis of genetic similarities. The data matrix of 14x20 was prepared for the analysis. The mean data was analyzed by using principal component analysis (PCA) through statistic software. PCA studied each group of genotypes to estimate. the relationship between yield and its component. Level of difference between first PC and different PCs was to some degree higher. It showed that germplasm used for analysis had limited genetic base. In first principal component showed an eigen value 3.45 and 26.5% variance was obtained (Table 16). In that PC, spikelet per spike, spike length, starch percentage, number of grains/spike peduncle length and days to heading had the most significant value that contributed to high yield. The PC 1 showed constructive results for all characteristics with the exception of gluten, moisture, protein percentage and spikes per meter square that indicated negative impacts on yield (Table 16).

**Table 16:** Eigen value, % total variance and cumulative variance % of principal components with respect to 20 wheat genotypes

| Principal component | Eigen value | Variance % | Cumulative variance % |
|---------------------|-------------|------------|-----------------------|
| PC1                 | 3.45        | 26.5       | 26.5                  |
| PC2                 | 2.6         | 20.7       | 47.2                  |
| PC3                 | 1.7         | 13.1       | 60.3                  |
| PC4                 | 1.3         | 10.6       | 71                    |
| PC5                 | 1.09        | 8.3        | 79.4                  |

Second PC represented 20.7 % variance and 47.2% cumulative variance with Eigen value 2.6 (Table 16). Grain yield, plant height, number of grain/spike, protein, starch content and 1000-grain weight were the significant contributor for variation in this principal component.

In third principal component 60.3% cumulative variance was seen alongside 13.1% individual variance. PC3 showed (1.7) Eigen value Spike length, number of grain per spike, days to maturity/ and protein and gluten percentage were the negative contributor of variation. In third PCs grain yield, plant height, peduncle length, tillers per meter square and 1000-grain weight were shown positive impacts (Table 17).

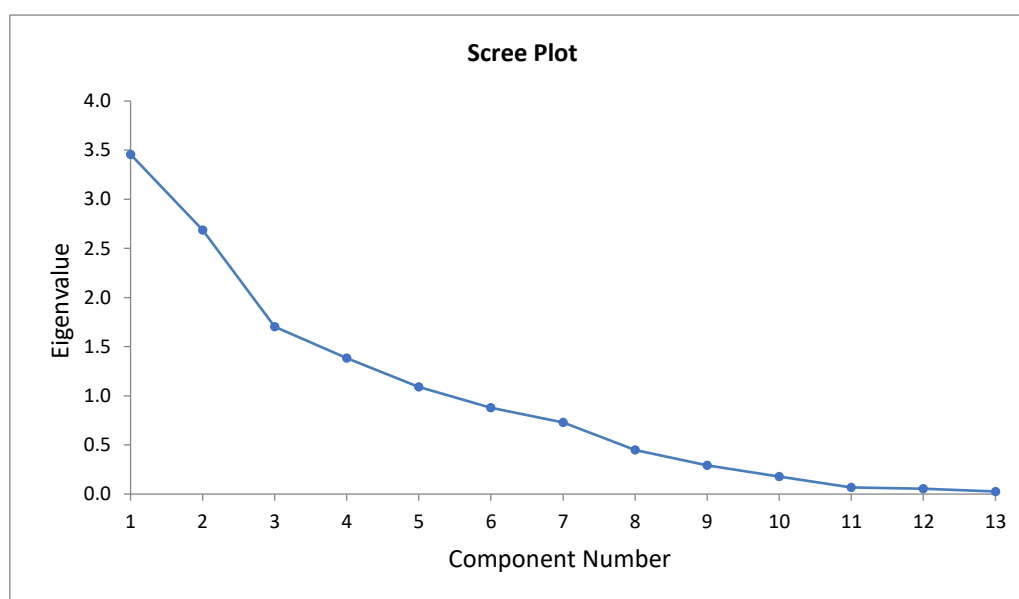
**Table 17:** Principal Components (PCs) for fourteen characters in 20 wheat genotypes

| Plant Character            | IPC1    | IPC2    | IPC3    | PC4     | PC51    |
|----------------------------|---------|---------|---------|---------|---------|
| Days to heading            | 0.2469  | -.04421 | 0.0399  | 0.0779  | -.03060 |
| Days to maturity           | 0.2226  | -0.0231 | -0.3235 | 0.1221  | -0.4308 |
| Plant height               | 0.1203  | 0.2005  | 0.0692  | -0.6855 | 0.0680  |
| Peduncle length            | 0.2280  | -0.1124 | 0.2085  | -0.2539 | -0.3492 |
| Spike length               | 0.4852  | 0.0317  | -0.0769 | -0.0680 | -0.1172 |
| Spikelet per spike         | 0.4307  | 0.0473  | -0.1641 | 0.0486  | -0.1483 |
| Tillers per meter square   | -0.0399 | -0.0654 | 0.6017  | -0.1596 | -0.0837 |
| 1000-Grain weight          | 0.0107  | 0.2911  | 0.3470  | 0.4482  | -0.1291 |
| Number of grains per spike | 0.3400  | 0.2723  | -0.1438 | 0.0647  | 0.1963  |
| Grain yield/plot           | 0.0836  | 0.2613  | 0.4611  | 0.0499  | -0.3295 |
| Protein (%)                | -0.1780 | 0.4391  | -0.1174 | 0.2096  | -0.2507 |
| Moisture (%)               | -0.0640 | -0.4833 | 0.0957  | 0.2996  | -0.0085 |
| Gluten (%)                 | -0.3371 | 0.2085  | -0.2275 | -0.1172 | -0.4466 |

Fourth principal component showed 71% combined variance alongside eigen value 1.3 (Table 16). 1000-grain weight, starch percentage and days to maturity were the real donor of variation in fourth PC. Plant height and peduncle length demonstrated negative impacts. The genotypes were poor for plant height (Table 17).

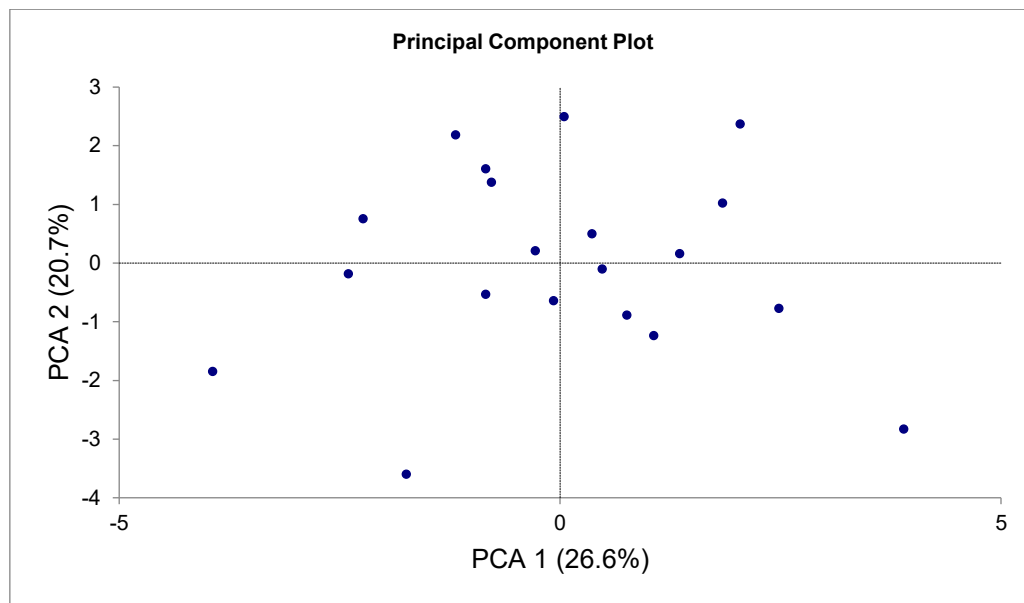
Fifth principal component showed 79.4% combined variance alongside Eigen value 1.09 (Table 16). Plant height, starch percentage and number of grains per spike were the real donor of variation in fifth PC. /Peduncle length, /days to heading, /days to maturity, /grain yield and spike llength demonstrated negative impacts. These genotypes were poor for gluten percentage (Table 17).

From the initial five PCs it was observed that gluten percentage, spike length and number of spikes per meter square had most reduced value in these PCs. Moreover, high estimations of PC5 and PC4 showed that genotypes could be selected from these groups for good hybridization program. The scatter plot explains the association among different clusters (Fig 1). A large number of genotypes with changeable genetic diversity could be explained with the help of different morph-physiological characters or relationship among the genotypes. PC 1 and PC 2 contributing about 47.26% to the total variance were plotted to study the relations among different clusters with PC-1 on X-axis and PC-2 on Y-axis (Fig 2).



**Figure 4:** Scree plot of principal component analysis between Eigen values and principal components

Cluster analysis grouped and differentiated the genotypes on the basis of variation present among them for various characters. In current study, 20 wheat genotypes were used for clustering on the basis of 14 yield parameters i.e. plant height, peduncle length, days to heading, days to maturity, spike length, spikelet per /spike, tiller per meter square, 1000-grain weight, number of /grain per spike, grain yield per plot, protein, moisture, gluten and starch percentage.

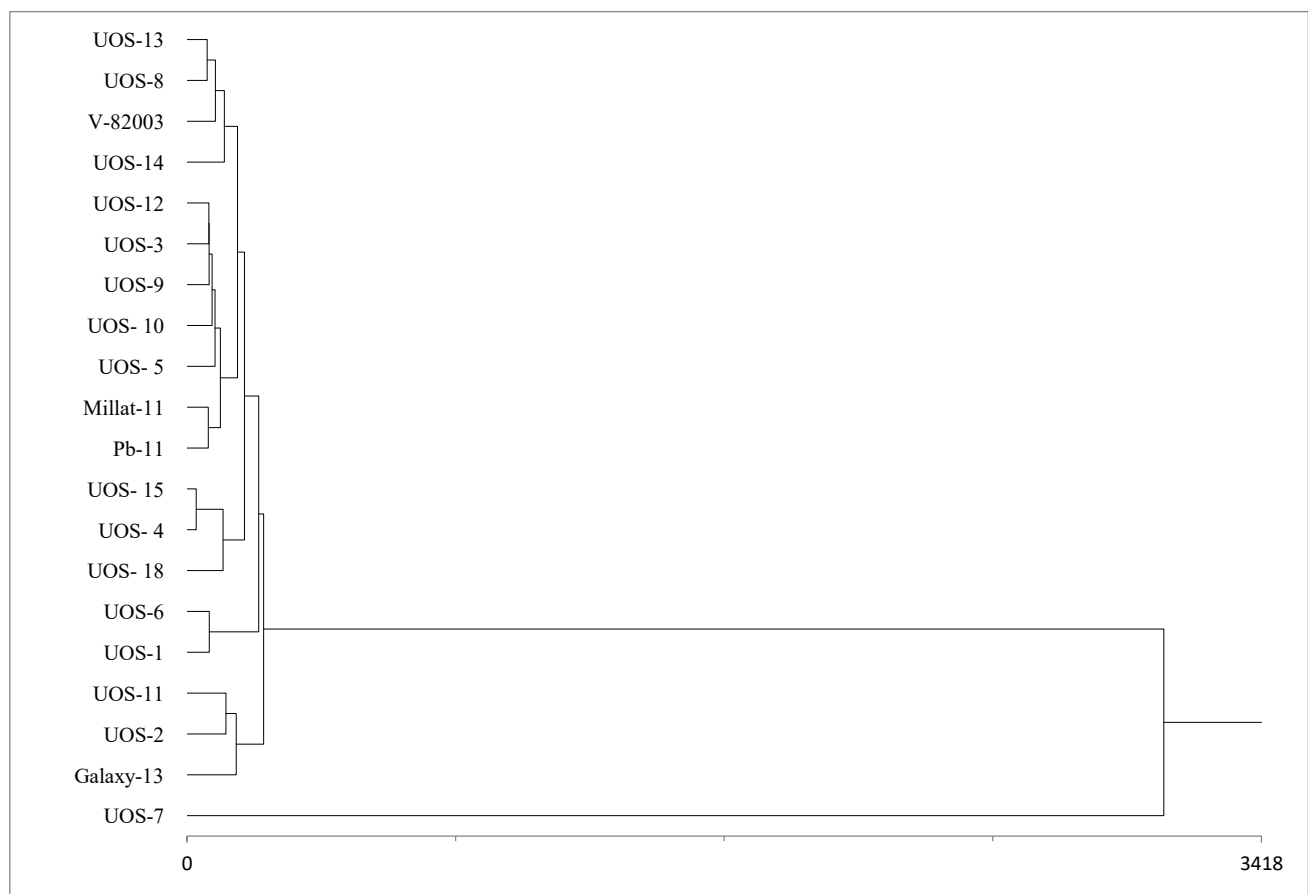


**Figure 5:** Biplot graph of twenty genotypes of wheat base on fourteen morphological traits

### 10. Cluster Analysis

Cluster analysis grouped and differentiated the genotypes on the basis of variation present among them for various characters. In current study, 20 wheat genotypes were used for clustering on the basis of 14 yield parameters i.e. plant height, peduncle length, days to heading, days to maturity, spike length, spikelet per /spike, tiller per meter square, 1000-grain weight, number of /grain per spike, grain yield per plot, protein, moisture, gluten and starch percentage.

Researchers worked on clustering for genetic diversity. Group 10 and 9 were the most similar groups among all 27 groups.



**Figure 6:** Dendrogram using Ward's Method

Data regarding cluster analysis is presented in (Fig.3). Based on ID2 values 20 wheat genotypes were grouped into V clusters. This indicated that cluster I comprised of four genotypes i.e. UOS-13, UOS-8, V-82003 and UOS-14. Cluster II comprised of seven

genotypes which were UOS-12, UOS-3, UOS-9, UOS-10, UOS-5, Millat-11 and Pb-11. Cluster III comprised of three genotypes i.e. UOS-15, UOS-4, and UOS-18. Cluster IV comprised of only two genotypes UOS-6 and UOS-1. While cluster V comprised of four genotypes which were UOS-11, UOS-12, Galaxy-13 and UOS-7.

Dendrogram displayed distance between the clusters, it was found that cluster II and cluster IV were the most diverse clusters indicating that their members had great genetic diversity for the characters under study. Cluster III and cluster V were the least diverse for the selected characters. It indicated that both the clusters had very small genetic diversity. Local check variety Galaxy-13 was present in cluster V. In cluster II a variety Millat-11 and UOS-12, UOS-3, UOS-9 and UOS-10 were the diverse genotypes while Millat-11 and Pb-11 were same. Cluster I contain those genotypes which had highest value of traits plant height, days to maturity and protein percentage while cluster II contain those genotypes which had highest value of traits 1000-grain weight, number of grain per spike, tillers per meter square and gluten percentage. Cluster III contain those genotypes which had highest value of traits days to heading, spike length, spikelet per spike and moisture percentage. Cluster IV contain those genotypes which had highest value of starch percentage and cluster V contain the genotypes which had highest value of traits peduncle length and grain yield.

**Table 18:** Average inter and intra cluster distances of 20 wheat genotypes

|             | Cluster I. | Cluster II | Cluster III | Cluster IV | Cluster V |
|-------------|------------|------------|-------------|------------|-----------|
| Cluster I.  |            | 385.180    | 725.100     | 948.684    | 577.601   |
| Cluster II  | 385.180    |            | 1108.689    | 1326.189   | 958.379   |
| Cluster III | 725.100    | 1108.689   |             | 247.475    | 157.589   |
| Cluster IV  | 948.684    | 1326.189   | 247.475     |            | 372.821   |
| Cluster V   | 577.601    | 958.379    | 157.589     | 372.821    |           |

The data on intra and inter cluster distance have been presented in (Table 18) among different clusters. Maximum inter cluster distance was 1326.18 among cluster II and cluster IV followed by 1108.6 in cluster II and III. Minimum inter cluster distance 157.5 was observed in cluster V and III. Cluster with large inter cluster distance showed that the genotypes include in this cluster had the greater diversity and the crossing between the genotypes in these cluster were expected to desirable recombinant.

Variation level found in present genotypes shows high potential for developing wheat genotypes for different desirable morphological traits.

## 11. Conclusions

Analysis of variance showed that there is huge variation among genotypes for all traits studied. These genotypes could be utilized for future breeding program to exploit genetic diversity. As concerned performance of genotypes for different traits; UOS-18 has taken maximum days to heading. UOS-15 has taken minimum days to heading while maximum days to maturity has taken by UOS-8 and minimum days to maturity has taken by UOS-15. Maximum value for plant height, peduncle length, spike length, tillers/meter square, spikelet per spike, number of grain per spike, grain yield and 1000 grain weight were showed by UOS-13, UOS-7, UOS-18, Pb-11, UOS-18, Pb-11, UOS-3 and UOS-7 respectively. High protein content was produced by UOS-8, high moisture content by UOS-4, high gluten and starch content produced by Millat-11 and UOS-1.

Genetic variation was estimated among genotypes for the traits under study. Smaller difference between genotypic and phenotypic variance for all the traits except tillers per meter square and gluten percentage was estimated. These traits were least effective by environment but tiller per meter and gluten percentage were highly influence by environmental factors. High heritability was estimated for traits days to heading, days to maturity, plant height, peduncle length, spikelet per spike, number of grains per spike, grain yield/plot, 1000 grain weight, protein, moisture and gluten content and reflected to greater transmission of inheritance to next generation. Moderate heritability was found for the traits spike length and starch content while low heritability was estimated for tillers/meter square. High genetic advance was measured for the traits; tillers per meter square and moderate genetic advance was measure for traits days to heading, plant height, peduncle length, number of grains per spike and low genetic advance was measured for days to maturity, spike length, spikelet per spike, 1000-grain weight, grain yield/plot, protein, moisture, starch and gluten percentage. The traits with high heritability indicated that the selection will be more useful for genetic improvement for that trait.

As concerned principal component analysis out of 14 components first five PCs exhibited more than 1 Eigen value and 79.4% cumulative variation. In the first principal component spikelet per spike, spike length, and number of grains per spike were most important. First component contributed 26.5% variation. In PC2 variation was obtain 20.7% which was mainly caused by plant height, protein content, number of grains/spike, gluten content and /1000-grain weight. PC3 showed 13.1% variation mainly by tillers per meter square, 1000-grain weight, peduncle length and grain yield. In PC4 variation was obtained 10.6% mainly caused by 1000-grain weight, moisture, protein and starch content. PC5 showed 8.3% variation mainly caused by number of grains per spike.

As regarded cluster analysis higher estimation of inter cluster distance was observed between cluster II and cluster IV. Cluster II poses maximum number of genotypes and cluster IV poses minimum number of genotypes. Inter cluster distance was higher than intra cluster distance which indicated wide genetic diversity among the genotypes of different cluster than those of same cluster. Higher the genetic distance between the cluster wider is the genetic diversity between genotypes. The combination of parents in hybridization was determined by mean performance, genetic distance and cluster pattern based on the genetic divergence and superiority with respect to any of the traits. On the basis of performance of genotypes UOS-7, UOS-11, UOS-2 are recommended for high yield potential. The varieties Pb-11, Galaxy-13, UOS-7, and UOS-2 are recommended to utilize for the improvement of tillers. For the improvement of grain weight UOS-3, UOS-11, UOS-2 and UOS-7 may be used in breeding programme. Pb-11, UOS-12, and UOS-11 may be utilize for increasing grain numbers. Selection may be focus on the traits; number of tillers, with short stature

plant for affective breeding programme. PCA indicated that five important component accounted for 79.4% variation among traits in wheat genotypes. First component assigns 26.5% variation between traits and designated as spike length and spikelet/spike. Thus, grain number can be improved by spike length and spikelet per spike. Genotypes included in cluster II may be utilized for the enhancement of grain yield.

## References

- Azam, Mohammad Golam, and Mohammad Amir Hossain et al. 2023. Genetic analyses of mungbean [*Vigna radiata* (L.) Wilczek] breeding traits for selecting superior genotype (s) using multivariate and multi-traits indexing approaches. *Plants* 12: <https://www.mdpi.com/2223-7747/12/10/1984>
- Bekele, Bantayehu, and Mebeaselassie Andargie et al. 2025. Characters associations and principal component analysis for quantitative traits of Sesame (*Sesamum indicum* L.) genotypes from Ethiopia. *Ecological Genetics and Genomics* 35. <https://www.sciencedirect.com/science/article/pii/S2405985425000369>
- Bhatt, Ashish, and S.K. Verma et al. 2025. Assessment of crop genetic diversity utilizing multivariate analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes. *Legume Research* 48: 1987-1994. <https://arccjournals.com/journal/legume-research-an-international-journal/LR-5375>
- Gomes Marques, Ines, and Cristina Vieites-Blanco et al. 2025. Phenotypic variation and genetic diversity in European *Alnus* species. *Forestry: An International Journal of Forest Research* 98: 332-343. <https://academic.oup.com/forestry/article/98/3/332/7716273>
- Hou, Wanli, and Jianghua et al. 2025. As a reservoir of antibiotic resistance genes and pathogens, the hydrodynamic characteristics drive their distribution patterns in Lake Victoria. *Environmental Pollution* 370:1-11. <https://www.sciencedirect.com/science/article/pii/S0269749125002763>
- Iqbal, Muhammad Javid, and Naureen Shams et al. 2022. Nutritional quality of wheat. *Wheat. Rijeka, Croatia: IntechOpen*. <https://www.intechopen.com/chapters/81564>
- Jaeger, Adam, and David Banks. 2023. Cluster analysis: A modern statistical review. *Wiley Interdisciplinary Reviews: Computational Statistics* 15. <https://wires.onlinelibrary.wiley.com/doi/10.1002/wics.1597>
- Krishnappa, Gopalareddy and Bhudeva Singh Tyagi et al. 2022. Wheat breeding. *Fundamentals of field crop breeding: Nature*: 39-111. [https://link.springer.com/chapter/10.1007/978-981-16-9257-4\\_2](https://link.springer.com/chapter/10.1007/978-981-16-9257-4_2)
- Kuzudisli, Cihan, and Burcu Bakir-Gungor et al. 2023. Review of feature selection approaches based on grouping of features. *PubMed Central*. <https://pmc.ncbi.nlm.nih.gov/articles/PMC10358338/>
- Lemma, Koricho, and Chandra Sekhar Singh et al. 2026. Assessment of Genetic Divergence in Naked Barley (*Hordeum vulgare* L.) Genotypes Using Cluster and Principal Component Analysis. *Research Squar*. <https://assets-eu.researchsquare.com/files/rs-8993040/v1/bd887ad1-4f4a-4176-96d0-a2a1498adf93.pdf>
- Li, Shaoshu. 2025. Momentum, volume and investor sentiment study for us technology sector stocks—A hidden markov model based principal component analysis. *PloS one* 20. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0331658>
- Mallor, Cristina and Estela Luna. 2025. The genetic diversity of the Spanish vegetable Genebank BGHZ-CITA: conservation and utilization. *Plant Gene Banks: Genetic Resources Collections, Conservation and Sustainable Utilization*. [https://link.springer.com/rwe/10.1007/978-981-99-4236-7\\_109-2](https://link.springer.com/rwe/10.1007/978-981-99-4236-7_109-2)
- Manzoor, Imran, and Kotb A. Attia et al. 2025. Assessment of Nutritional and Agro morphological Traits in Zea mays Inbred Lines for Aflatoxin Resistance Using the Side Needle Inoculation Technique. *Phytopharmacology Research Journal* 4: 43–53. <https://ojs.prjn.org/index.php/prjn/article/view/84>
- Maqbool, Zaina, and Ishmal Malik et al. 2026. CRISPR in Wheat: Patents, Breeding Advances, and Emerging Challenges. *Trends in Intellectual Property Research* 4: 11-23. <https://doi.org/10.69971/tipr.4.1.2026.103>
- Mottaleb, Khondokar Abdul, and Gideon Kruseman et al. 2023. Projecting wheat demand in China and India for 2030 and 2050: Implications for food security. *Frontiers in Nutrition* 9: <https://www.frontiersin.org/journals/nutrition/articles/10.3389/fnut.2022.1077443/full>
- Mullualem, Destaw, and Alemu Tsega et al. 2024. Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. *Heliyon* 10: <https://www.sciencedirect.com/science/article/pii/S2405844024089497>
- Mullualem, Destaw, and Alemu Tsega et al. 2025. Phenotypic Variability, Heritability, and Performance Evaluation of Bread Wheat (*Triticum aestivum* L.) Genotypes for Grain Yield and Yield-Related Characters in North West Ethiopia. *Advances in Agriculture* 1: <https://onlinelibrary.wiley.com/doi/10.1155/aia/1499833>
- Sallam, Ahmed, and Mostafa Hashem et al. 2026. Genetic and phenotypic associations between peduncle characteristics and spike productivity in wheat under drought and normal conditions. *Theoretical and Applied Genetics* 139: <https://link.springer.com/article/10.1007/s00122-025-05140-2>
- Secomandi, Simona, and Guido Roberto Gallo et al. 2025. Pangenome graphs and their applications in biodiversity genomics. *Nature Genetics* 57: 13-26. <https://www.nature.com/articles/s41588-024-02029-6>
- Sharma, Anoushka and Vijay Rana et al. 2025. Genetic variability and correlation studies based on diverse wheat panel for grain yield and related attributes under north-western Himalayan conditions. *Vegetos*: 1-12. <https://link.springer.com/article/10.1007/s42535-025-01400-0>
- Singh, Charan and Sapna Yadav et al. 2025. Wheat drought tolerance: unveiling a synergistic future with conventional and molecular breeding strategies. *Plants* 14: <https://www.mdpi.com/2223-7747/14/7/1053>

- Singh, Sanjay Kumar and Anju Mahendra Singh et al. 2023. Wheat: origin, history, and production practices. *1st Edition, Wheat science, CRC Press*: 1-32. <https://www.taylorfrancis.com/chapters/edit/10.1201/9781003307938-1/wheat-sanjay-kumar-singh-anju-mahendru-singh-om-prakash-gupta-pradeep-kumar-singh>
- Tu, Hui-Ning and Che-Tuo Liao. 2026. A Modified Bayesian Optimization Approach for Determining a Training Set to Identify the Best Genotypes from a Candidate Population in Genomic Selection. *Journal of Agricultural, Biological & Environmental Statistics* 31: 1-22. <https://link.springer.com/article/10.1007/s13253-024-00632-y>
- Vieira, Rafael Augustao and Ana Paula Oliveria Nogueira et al. 2025. Optimizing the selection of quantitative traits in plant breeding using simulation. *Frontiers in plant science* 16: <https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2025.1495662/full>
- Yali, Werkissa and Gudeta Nepir. 2026. Assessment of genetic variation, heritability, and genetic advance among elite sorghum [*Sorghum bicolor* (L) Moench] genotypes for yield and yield associated traits under moisture stress areas. *Reproduction and Breeding* 6: 21-26. <https://www.sciencedirect.com/science/article/pii/S2667071225000596>