

Research Article

Genetic Variability and Heritability of Yield and Yield Related Traits Among Bread Wheat (*Triticum Aestivum* L.) Accessions in West Shewa, Central Ethiopia

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Abstract

Bread wheat (*Triticum aestivum* L.) is a self-pollinated annual crop belongs to the family (Poaceae), tribe (Triticeae) and genus *Triticum*. Understanding the presence and magnitude of genetic variability is required as a prior condition for developing superior genotypes in breeding programs. This study aimed to assess the magnitude of genetic variability, heritability, genetic advance and identify promising bread wheat genotypes for further breeding. A total of 100 bread wheat genotypes were evaluated in alpha-lattice design with two replications in the 2021 main cropping season at Liban Jawi District, West Shewa Ethiopia. Analysis of variance showed that there was a significant difference ($p < 0.01$) among the genotypes for all studied traits. The highest genotypic and phenotypic coefficients of variations were observed for biomass yield, productive tillers, harvest index, grain yield and awn length whereas, low genotypic and phenotypic coefficients of variation were detected for days to heading, days to maturity and grain filling period. Broad sense heritability ranged from 55.55% for flag leaf width to 96.8% for awn length and Genetic Advance as a percent of Mean (GAM) ranged from 7.38% for number of days to maturity to 90.13% for awn length. Based on the present investigation among genotypes; genotypes viz 31790 (58.93 qt/ha), EBW192299 (57.97qt/ha), 33682(56.51 qt/ha) 34737 (55.38qt/ha and Acc.34159 (52.51 qt/ha) were identified as high yielders compared to another tested genotypes. However, further research is needed at least for one more year across multi-location.

Keywords: Bread wheat; Genetic advance; Heritability; Variability**Introduction**

Bread wheat (*Triticum aestivum* L.), is a self-pollinated annual crop which belongs to the family Gramineae (Poaceae), tribe *Triticeae*, genus *Triticum* and species *aestivum* [1]. It is an allohexaploid species with 3 different genome configurations (A, B, D) of 42 chromosomes ($2n=6x= 42$) and perfect flowers which enforced to reproduce as autogamous crop with 1-4% natural cross pollination [2]. The bread wheat is one of the oldest cereal crop regarded as the 'king of cereals' since it shares a large area under production, high productivity and holds a prominent position in the international food grain trade [3].

The bread wheat accounts about 95% of world-wide wheat production and the remaining 5% being tetraploid durum wheat used in pasta and semolina products [4]. The report on wheat production reveals that the world annual production was 765.4 million metric tons with average yield of 3.48 t/ha, and it accounts for nearly 30% of global cereal production. It was

identified as the first in production area and second in total production after maize and provides more nourishment than any other food crops [5].

In Ethiopia wheat is produced under rain fed conditions and nowadays broadly cultivated under irrigation. Wheat is widely grown in the high lands and mid-altitudes of Ethiopia. In spite of existence of wide agro-ecological suitable for wheat production; demand for wheat is increased because of population growth, urbanization, expansion of agro-industries in which wheat production is left behind by 25 to 30% to its demand in Ethiopia [6].

Wheat is the major essential cereal crop which occupying 1.79 million hectares of land with total production of 5.8 million tons and productivity was 3.046 t/ha in Ethiopia [7]. Wheat is one of the main food crops and has been the basic staple food [8]. Wheat has great importance for economic, commercial, in-

dustrial, diets for human beings and also using for livestock feed [9]. It is one of the most staple food and the main sources of calories in the major producing areas [10].

Presence of extensive variability gives a big chance for breeder to select desired material [11]. Genetic variability is important for breeder and farmers to develop new improved variety with good traits such as high yield, biotic and abiotic stress tolerance and improve nutrition quality. Genetic variability is also significant for conservation and breeding programs [12]. The genetic variability of cultivated crops and their wild relatives together form a potential and continued source for breeding new and better crop varieties [13].

During crop improvement program precise knowledge about genotype variability and association among desirable traits of breeding materials are the two prerequisite in which it is used to develop superior recombinant (Rauf, 2012). Knowledge of genetic diversity of a crop also helps the breeder in choosing desirable parents for the breeding program and gene introgression from distantly related germplasm.

The prerequisite for effective selection rely on genetic variability, heritability, genetic advance, genetic advance as percent of mean and correlation of grain yield with yield contributing traits [13]. Several genetic variability studies have been conducted on bread wheat based on quantitative and qualitative traits in order to select genetically superior parents for desirable traits [14].

Statement of Problem

There is high gap of productivity of wheat (3.046 tons/ha) in Ethiopia compared to other countries of the world like Germany (7.9 tons/ha), France (7.6 tons/ha), Egypt (6.4 tons/ha) [5]. The main wheat production limitations that affect the overall production and productivity are scarcity of improved varieties, use of low level of production inputs, poor agronomic practice, drought, poor soil fertility, diseases and insect pests [15]. Bread wheat is widely grown in West Shewa, intermediate highlands in general and at Liban Jawi in particular.

Besides, the existence of variation in the population alone is not adequate for improving suitable traits unless the genetic variability is well understood. Accurate estimates of phenotypic coefficient of variation, genotypic coefficients of variation, heritability and genetic advance are most important to guide future breeding strategies [16].

However, limited information is available on genetic variability and heritability of yield and yield related traits among bread wheat genotypes especially for large number of new accessions for further improvement.

Therefore, this research was conducted using one hundred different bread wheat genotypes with the following objectives:

General objective:

✓ To assess the variability and performance of bread wheat accessions to identify promising breeding materials.

Specific objectives:

- ✓ To assess the phenotypic variability among bread wheat accessions.
- ✓ To identify promising breeding materials.

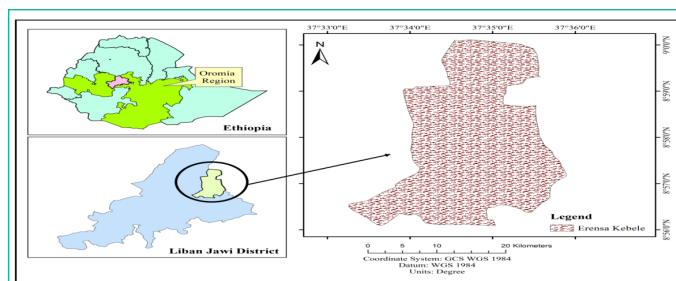


Figure 1: Map of the study area showing Ethiopia, Liban Jawi District and Erensa Kebele (study site) (Source: Adopted from Arc. GIS Computation and Ethiopian map, 2019).

Materials and Methods

Description of the Study Area

The experiment was conducted at Liban Jawi District, West Shewa Zone, Oromia Regional State of Ethiopia. Liban Jawi is located at 173 km away from Addis Ababa and 47 km from Ambo town. The altitude of the district ranges from 1800 to 3098 m.a.s.l (meters above sea level) and receives an annual rain fall of 1000 mm to 1800 mm with average temperature of 10.4-29°C. It has three different agro-climatic conditions namely high land, moderate altitude and low land constituting 27%, 65% and 8%, respectively. The district is bordered in north by Chaliya and Mida Kegni district, in the south by Dire Inchini and Jibat district, in the east by Toke Kutaye district and in the west by Dano, Chaliya and Jibat district. The dominant soil type of the test site is loamy soil with PH of 6-7 (LJAO, 2021 unpublished data).

Planting Materials

A total of hundred bread wheat accessions were grown at Liban Jawi in 2021 cropping season. These bread wheat accessions were collected from different sources such as: Ethiopian Biodiversity Institute (EBI), Kulumsa Agricultural Research Center (KARC) and Holeta Agricultural Research Center (HARC). Nine released varieties (Alidoro, Dandaa, Digelu, Enkoy, Hidase, King bird, Kubsa, Ogocho and Wane) were used as check varieties (Table 1).

Experimental Design and Trial Management

The field experiment was carried out in 4x25 alpha lattice design with two replications during the main rainy season of 2021 at one location. The total area including border was 18.8 m x 17 m (319.6 m²) out of these effective trial area was 12.8 x 11 (140.8 m²). The replication had four blocks, in which each block contains twenty-five plots with two plots at the border were used to minimize the bordering effect. The plot per block dimension was 27 rows of 2 m length with 0.20 m row spacing. It means twenty-five (25) entries and two borders which were 27 rows applied per each block. Width of the block was 0.2 m x 27 which was 5.4 m per replication. The dimension of an individual block area was 5.4 m width x 2 m length (10.8m²). The spacing between blocks were 1 m and space between plots were 0.2 m. Terraces were formed over the block to protect the plot from soil erosion. The experimental field was well plowed four times before sowing and then planting rows were ready by exploitation of hand force row marker.

Planting was done by hand drilling method at a depth of 5 cm with the seed rate of 150 kg/ha. Planting was carried out at the first week of July. NPS and Urea fertilizers were applied at the rate of 100 kg/ha. Urea was applied in split application: first split (1/3) and the second split (2/3) of the total dose at plant-

Table 1: List and source of 100 bread wheat accessions grown in 2021.

| S.N | Accession | Source | S.N | Accession | Source | S.N | Accession | Source |
|-----|-----------|--------|-----|-----------|--------|-----|-----------|--------|
| 1 | 31169 | Amara | 35 | 33907 | Amara | 69 | 34737 | Tigray |
| 2 | 31224 | Oromia | 36 | 33909 | Amara | 70 | 34804 | Amara |
| 3 | 31257 | Oromia | 37 | 33911 | Amara | 71 | 34821 | Oromia |
| 4 | 31258 | Oromia | 38 | 33915 | Tigray | 72 | 34856 | Amara |
| 5 | 31296 | Amara | 39 | 33917 | Amara | 73 | 36255 | Oromia |
| 6 | 31394 | Oromia | 40 | 33919 | Amara | 74 | 36503 | Amara |
| 7 | 31395 | Oromia | 41 | 33921 | Amara | 75 | EBW192364 | KARC |
| 8 | 31430 | Amara | 42 | 33924 | Amara | 76 | EBW192398 | KARC |
| 9 | 31542 | Oromia | 43 | 33972 | Oromia | 77 | EBW192299 | KARC |
| 10 | 31543 | Oromia | 44 | 34029 | Amara | 78 | EBW192344 | KARC |
| 11 | 31600 | Oromia | 45 | 34037 | Amara | 79 | EBW192345 | KARC |
| 12 | 31551 | Oromia | 46 | 34039 | Amara | 80 | EBW192362 | KARC |
| 13 | 31554 | Oromia | 47 | 34043 | Oromia | 81 | EBW192610 | KARC |
| 14 | 31593 | Amara | 48 | 34045 | Amara | 82 | BW184033 | KARC |
| 15 | 31627 | Oromia | 49 | 34053 | Oromia | 83 | EBW192875 | KARC |
| 16 | 31630 | Oromia | 50 | 34073 | Amara | 84 | EBW192865 | KARC |
| 17 | 31632 | Oromia | 51 | 34086 | Amara | 85 | EBW192348 | KARC |
| 18 | 31643 | Oromia | 52 | 34097 | Oromia | 86 | EBW192489 | KARC |
| 19 | 31644 | Oromia | 53 | 34098 | Oromia | 87 | EBW192872 | KARC |
| 20 | 31786 | Amara | 54 | 34137 | Oromia | 88 | BWKU13383 | KARC |
| 21 | 31790 | Amara | 55 | 34145 | Oromia | 89 | EBW192398 | KARC |
| 22 | 31813 | Amara | 56 | 34152 | Amara | 90 | EBW194030 | KARC |
| 23 | 31818 | Amara | 57 | 34157 | Amara | 91 | EBW192870 | KARC |
| 24 | 33206 | Amara | 58 | 34159 | Amara | 92 | Alidoro | HARC |
| 25 | 33387 | Oromia | 59 | 34161 | Oromia | 93 | Danda,a | HARC |
| 26 | 33389 | Oromia | 60 | 34169 | Oromia | 94 | Digelu | KARC |
| 27 | 33516 | Amara | 61 | 34190 | Oromia | 95 | Enkoy | KARC |
| 28 | 33556 | Oromia | 62 | 34239 | SNNP | 96 | Hidase | KARC |
| 29 | 33597 | Amara | 63 | 34280 | Tigray | 97 | Kingbird | KARC |
| 30 | 33682 | Amara | 64 | 34667 | Oromia | 98 | Kubsa | KARC |
| 31 | 33794 | Amara | 65 | 34706 | Oromia | 99 | Ogolcho | KARC |
| 32 | 33828 | Amara | 66 | 34720 | Tigray | 100 | Wane | KARC |
| 33 | 33893 | Amara | 67 | 34728 | Tigray | | | |
| 34 | 33901 | Tigray | 68 | 34735 | Tigray | | | |

Key: S.N: Serial Number; KARC: Kulumsa Agricultural Research; HARC: Holeta Agricultural Research Center

Table 2: Skeleton of analysis of variance table for alpha lattice design.

| SV | DF | Mean square | F values | Expected mean square |
|----------------|-----------|-----------------|----------------------|---|
| Replication(r) | r-1 | Ms _r | Ms _r /Mse | $\sigma_r^2 + \sigma_b^2 + \sigma_g^2 + \sigma_e^2$ |
| Block(rep) | r(b-1) | Ms _b | Ms _b /Mse | $r\sigma_b^2 + \sigma_g^2 + \sigma_e^2$ |
| Genotypes(g) | g-1 | Ms _g | Ms _g /Mse | $rb\sigma_g^2 + \sigma_e^2$ |
| Error | rg-rb-g+1 | Mse | | σ_e^2 |
| Total | rg-1 | Mst | | |

Key: SV: Source of Variation; DF: Degree of Freedom; r: number of Replication; b: Block; g: Genotypes; Ms_r: Mean Square of Replication; Ms_g: Mean Square of Genotypes; Ms_b: Mean Square of Block with in replication; Mse: Mean Square of Error; Mst: Mean Square of Total.

ing and mid tillering stages, respectively. Weeds were manually eradicated from the experimental field.

Data Collection

Data were collected both on plant and plot basis by random sampling technique with the use of descriptors for wheat [17].

Plant basis: Ten plants were randomly taken from the central plants for recording the following observations and the mean values for the treatments were computed.

Plant height (cm): The distance in cm between the ground level to the tip of the spike of ten plants (excluding the awns) at maturity were measured.

Number of productive tillers per plant (PT): The actual count of the fertile numbers of tillers of ten plants (spike bearing) per plant.

Spike length (cm): Length measured in cm from base of spike to the tip of the highest spikelet of ten plants (excluding the awns) in cm at maturity.

Spikelet per spike (SPS): Total number of spikelet on main spike of all ten plants were counted at the time of maturity and average was recorded.

Number of kernels per spike (KPS): Average number of seeds were recorded from the ten sampled plants.

Flag Leaf length (cm): Average length of the uppermost leaf on ten randomly selected plants at physiological maturity.

Flag Leaf width (cm): Average width of the uppermost leaf at widest point on ten randomly selected plants at physiological maturity.

Peduncle Length (cm): The length of peduncle from the last node to the tip of the peduncle during maturity on ten randomly tagged plants.

Table 3: Analysis of variance for 16 traits of bread wheat genotypes evaluated at Liban Jawi during 2021 growing season.

| Mean square | | | | | |
|-------------|---------------------|--------------------|-------------------|---------------|----------------|
| Traits | Replication (df= 1) | Block(rep) (df= 6) | Genotype (df= 99) | Error (df=93) | R ² |
| DH | 11.52 | 23.05 | 104.54** | 4.29 | 96.4 |
| DM | 95.22 | 61.12 | 55.94** | 6.74 | 90.7 |
| GFP | 44.18 | 9.25 | 32.45** | 7.53 | 83.6 |
| FLL | 36.52 | 14.83 | 22.77** | 2.89 | 90 |
| FLW | 0.02 | 0.09 | 0.09** | 0.04 | 84.6 |
| AL | 1.98 | 0.88 | 27.69** | 0.45 | 98.6 |
| PEL | 116.4 | 12.24 | 156.15** | 20.48 | 89.39 |
| PH | 2337 | 154.92 | 449.62** | 51.56 | 91.06 |
| SL | 12.61 | 1.24 | 3.12** | 0.46 | 89 |
| SPS | 8.08 | 3.54 | 5.65** | 1.28 | 83.9 |
| KPS | 1007.6 | 80.06 | 34.53** | 22.29 | 88.35 |
| BY | 1965.6 | 83.4 | 2719.9** | 55.46 | 98.17 |
| HI | 8.69 | 2.66 | 64.87** | 3.32 | 95.51 |
| TSW | 38.91 | 8.16 | 57.22** | 10.02 | 86.64 |
| PT | 12.1 | 0.18 | 3.28** | 0.2 | 94.9 |
| GY | 212.79 | 4.61 | 225.58** | 8.29 | 96.72 |

Key: **: highly significant at 0.01; df: Degree of Freedom; DH: Days to Heading; DM: Days to Maturity; GFP: Grain Filling Period; PH: Plant Height; SL: Spike Length; SPS: number of Spikelet Per Spike; KPS: number of Kernels Per Spike; BY: Biomass Yield quintal per hectare; HI: Harvest Index; TSW: Thousand Seed Weight; PT: Productive Tillers; FL: Flag Leaf length; FLW: Flag Leaf Width; AL: Awn Length; PEL: Peduncle Length and GY: Grain Yield quintal per hectare.

Table 4: Mean performance genotypes for selected traits among bread wheat genotypes valuated at Liban Jawi 2021/22.

| Bottom ten genotypes | | | | | | | | |
|----------------------|-----------|-------|----|-----------|-------|----|-----------|--------|
| No | Genotypes | GY | No | Genotypes | KPS | No | Genotypes | PH |
| 1 | 34667 | 6.86 | 1 | 33389 | 34.15 | 1 | EBW192344 | 75.57 |
| 2 | Ogolcho | 13.43 | 2 | 33556 | 39.6 | 2 | BW184033 | 76.05 |
| 3 | 33901 | 13.45 | 3 | 33924 | 39.85 | 3 | 31543 | 76.16 |
| 4 | Digelu | 14.09 | 4 | 31813 | 40.05 | 4 | EBW192364 | 77.23 |
| 5 | 34706 | 15.08 | 5 | 31600 | 40.45 | 5 | EBW192398 | 77.27 |
| 6 | 31542 | 16.43 | 6 | 33919 | 41.45 | 6 | EBW192345 | 77.55 |
| 7 | 33389 | 16.64 | 7 | 33516 | 41.8 | 7 | EBW194030 | 77.62 |
| 8 | EBW192872 | 16.75 | 8 | 34145 | 42.45 | 8 | EBW192362 | 78.18 |
| 9 | 33556 | 19.21 | 9 | Ogolcho | 42.45 | 9 | EBW192875 | 78.6 |
| 10 | 33972 | 19.45 | 10 | 31554 | 42.65 | 10 | EBW192348 | 79.85 |
| Top ten genotypes | | | | | | | | |
| 1 | 33828 | 48.99 | 1 | EBW192344 | 65.3 | 1 | 31542 | 120.75 |
| 2 | EBW192345 | 49.51 | 2 | 31786 | 66.25 | 2 | 31600 | 121.85 |
| 3 | King bird | 51.22 | 3 | EBW192870 | 67.55 | 3 | 34169 | 122.1 |
| 4 | Enkoy | 51.97 | 4 | EBW192364 | 68.75 | 4 | 34157 | 123.57 |
| 5 | Alidoro | 52.46 | 5 | 31543 | 70.65 | 5 | 31813 | 125 |
| 6 | 34159 | 52.51 | 6 | EBW192348 | 70.75 | 6 | 31643 | 126.2 |
| 7 | 34737 | 55.38 | 7 | EBW192398 | 70.8 | 7 | 33915 | 130.8 |
| 8 | 33682 | 56.51 | 8 | EBW192610 | 71 | 8 | 34098 | 133.55 |
| 9 | EBW192299 | 57.97 | 9 | 33893 | 73.2 | 9 | 34856 | 135.48 |
| 10 | 31790 | 58.93 | 10 | 34157 | 76.2 | 10 | 36255 | 135.5 |
| | Mean | 32.8 | | | 54.14 | | | 104.76 |
| | Min | 6.86 | | | 34.15 | | | 75.57 |
| | Max | 58.93 | | | 76.2 | | | 135.5 |
| | CV% | 8.78 | | | 6.13 | | | 6.85 |
| | LSD(0.05) | 5.72 | | | 9.37 | | | 14.26 |

Key: GY: Grain Yield (qt/ha); KPS: Kernels Per Spike; PH: Plant Height (cm); CV: Coefficient of Variation; LSD: Least Significance Difference.

Awn Length (cm): Awn length from the end of spike to the tip of the awn was measured and average for ten randomly tagged plants were recorded.

Plot basis: The data on the following attributing traits were collected on the basis of the plots.

Days to 50% heading (DH): It was recorded by counting the number of days from sowing to the date when at least 50% of the heads in the plot fully exerted from the boom or flowered.

Grain filling period (GFP): It was the result obtained from the number of days to maturity minus the number of days to heading.

Days to 90% maturity: Recorded by counting the number of days from sowing to the days when 90% of the heads in the plot were physiologically matured.

Grain yield per plot (g): Moisture was adjusted to the standard moisture content at 12.5% moisture basis after threshing using moisture tester and the adjusted yield per plot was converted to quintal per hectare.

Thousand seed weight (g): The weight(g) of 1000 seeds from randomly sampled seeds per plot measured by using sensitive balance.

Biological yield or biomass (g): Was determined by weighing the total air dried above ground biomass of the plot and converted to quintal per hectare.

Harvest index(%): It was calculated by dividing grain yield per plot to total above ground dry biomass yield per plot and then multiplied by hundred.

Data Analysis

Analysis of Variance (ANOVA)

All data were subjected to analyses of variance (ANOVA) using general linear model (GLM) a procedure of SAS statistical version 9.4 software [18]. Least Significance Difference (LSD) were used to separate differences in parameters means of genotypes where significant variation was observed at 5% probability level.

Analysis of variance was done by means of the following model:-

$$Y_{ijl} = \mu + \tau_i + \gamma_j + \rho_l(j) + \varepsilon_{ijl}$$

Where; μ is the overall (grand) mean, τ_i is the effect due to the i th treatment, ($i=1, 2, 3, \dots, t$), γ_j is the effect due to the j th replication, and ($j=1, 2, \dots, r$), $\rho_l(j)$ is block inside replicate effect, ε_{ijl} is that the error term wherever the error terms, are independent observations from an approximately normal distribution with mean = 0 and constant variance $\sigma^2 \varepsilon$.

Estimation of Variance Components: The presences of genotypic and phenotypic variations that exist in a crop species are essential in initiating a breeding program. They were estimated to observe the extent of variability between the genotypes. The phenotypic and genotypic variability of each trait were estimated as phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic coefficients of variation were estimated by utilizing the formula suggested by Burton and Devane (1953) [19] as follows:

$$\text{Environmental variance}(\sigma^2_e) = \text{MSe}; \text{Genotypic variance}(\sigma^2_g) =$$

Table 5: The range and mean performance of bread wheat genotypes for 16 traits.

| Traits | Range | | | | Mean | CV (%) | LSD (0.05) |
|--------|-----------|---------|-----------|---------|--------|--------|------------|
| | Entry | Minimum | Entry | Maximum | | | |
| DH | 34706 | 58 | 33389 | 101.5 | 77.69 | 2.67 | 4.11 |
| DM | EBW192362 | 114.5 | 33389 | 145 | 122.63 | 2.12 | 5.16 |
| GFP | 31169 | 37 | EBW192364 | 57.5 | 44.96 | 6 | 5.45 |
| PH | EBW192344 | 75.57 | 31542 | 135.5 | 104.76 | 6.85 | 14.26 |
| SL | 34667 | 5.55 | 34157 | 14.55 | 9.67 | 7.01 | 1.34 |
| SPS | 31395 | 15.45 | 31818 | 24.2 | 18.44 | 6.13 | 2.24 |
| KPS | 33389 | 34.15 | 34157 | 76.2 | 54.14 | 8.72 | 9.37 |
| BY | 34667 | 36.25 | 34159 | 243.75 | 151.78 | 4.91 | 14.79 |
| HI | 31542 | 9.36 | EBW192348 | 37.59 | 21.88 | 8.33 | 3.62 |
| TSW | Ogolcho | 22.69 | 34169 | 56.28 | 40.88 | 7.74 | 6.28 |
| PT | 34667 | 2.1 | 34137 | 8.4 | 4.99 | 8.9 | 0.89 |
| FLL | EBW192362 | 19.7 | 33597 | 36.1 | 28.8 | 5.91 | 3.38 |
| FLW | EBW192362 | 1.05 | 34053 | 1.95 | 1.47 | 12.94 | 0.38 |
| AL | 34667 | 0 | 33911 | 15.58 | 8.31 | 8.07 | 1.33 |
| PEL | EBW192362 | 27.13 | 34169 | 63.2 | 48.76 | 9.28 | 8.99 |
| GY | 34667 | 6.86 | 31790 | 58.93 | 32.8 | 8.78 | 5.72 |

Key: GY: Grain Yield (qt/ha); KPS: Kernels Per Spike; PH: Plant Height (cm); CV: Coefficient of Variation; LSD: Least Significance Difference.

Table 5: The range and mean performance of bread wheat genotypes for 16 traits.

| Traits | Range | | | | Mean | CV (%) | LSD (0.05) |
|--------|-----------|---------|-----------|---------|--------|--------|------------|
| | Entry | Minimum | Entry | Maximum | | | |
| DH | 34706 | 58 | 33389 | 101.5 | 77.69 | 2.67 | 4.11 |
| DM | EBW192362 | 114.5 | 33389 | 145 | 122.63 | 2.12 | 5.16 |
| GFP | 31169 | 37 | EBW192364 | 57.5 | 44.96 | 6 | 5.45 |
| PH | EBW192344 | 75.57 | 31542 | 135.5 | 104.76 | 6.85 | 14.26 |
| SL | 34667 | 5.55 | 34157 | 14.55 | 9.67 | 7.01 | 1.34 |
| SPS | 31395 | 15.45 | 31818 | 24.2 | 18.44 | 6.13 | 2.24 |
| KPS | 33389 | 34.15 | 34157 | 76.2 | 54.14 | 8.72 | 9.37 |
| BY | 34667 | 36.25 | 34159 | 243.75 | 151.78 | 4.91 | 14.79 |
| HI | 31542 | 9.36 | EBW192348 | 37.59 | 21.88 | 8.33 | 3.62 |
| TSW | Ogolcho | 22.69 | 34169 | 56.28 | 40.88 | 7.74 | 6.28 |
| PT | 34667 | 2.1 | 34137 | 8.4 | 4.99 | 8.9 | 0.89 |
| FLL | EBW192362 | 19.7 | 33597 | 36.1 | 28.8 | 5.91 | 3.38 |
| FLW | EBW192362 | 1.05 | 34053 | 1.95 | 1.47 | 12.94 | 0.38 |
| AL | 34667 | 0 | 33911 | 15.58 | 8.31 | 8.07 | 1.33 |
| PEL | EBW192362 | 27.13 | 34169 | 63.2 | 48.76 | 9.28 | 8.99 |
| GY | 34667 | 6.86 | 31790 | 58.93 | 32.8 | 8.78 | 5.72 |

Key: C.V: Coefficient of Variation; LSD: Least Significant Difference; DH: Days to Heading; DM: Days to Maturity; GFP: Grain Filling Period; PH: Plant Height (cm); SL: Spike Length (cm); SPS: Spikelet Per Spike; KPS: Kernel Per Spike; BY: Biomass Yield (qt/ha); HI: Harvest Index; TSW: Thousand Seed Weight; PT: Productive Tillers; FLL: Flag Leaf Length (cm); FLW: Flag Leaf Width (cm); AL: Awn Length (cm); PEL: Peduncle Length (cm) and GY: Grain Yield (qt/ha).

MSG-MSe/r; Phenotypic variance (σ^2p)= $\sigma^2g + \sigma^2e$.

Where, σ^2g = genotypic variance Msg= mean square of genotype Mse= mean square of error r= number of replications σ^2e = Environmental variance, σ^2p = phenotypic variance and r= replication.

Phenotypic coefficient of variation(PCV)= $\sqrt{\sigma^2p/x} \times 100$

Genotypic coefficient of variation(GCV)= $\sqrt{\sigma^2g/x} \times 100$

Where, PCV represent Phenotypic coefficient of variation, GCV represent Genotypic coefficient of variation and x represent population average of the trait. According to Sivasubramaniah and Menon (1973) PCV and GCV values were classified as high (>20%), medium (10-20%) and low (0-10%) [20].

Estimation of Broad Sense Heritability and Expected Genetic Advance: Broad sense heritability values were estimated using the formula adopted from Falconer and Mackay (1996). $H^2b = \sigma^2g / \sigma^2p \times 100$ Where: H^2b = heritability in broad sense, σ^2g = genotypic variance, σ^2p = phenotypic variance.

According to Johnson *et al.* (1955) the percentage of heritability was classified as low (0-30%), moderate (30-60%) and high (>60%). Estimation of genetic advance in (GA) and genetic advance as percentage of means (GAM) were estimated as described by Johnson *et al.* (1955) [21] as:

Genetic advance(GA)= $K \sigma p H^2b$

Where, GA= Genetic advance σp = Phenotypic standard deviation on mean basis; H^2b = Heritability in the broad sense. K= the standardized selection differential at 5% selection intensity (2.063).

Genetic Advance as percentage of Mean (GAM)

Genetic Advance as percentage of Mean (GAM) was estimated as follows:

GAM = $GA/x \times 100$

Where, GAM= Genetic advance as percentage of mean GA= Genetic advance, and x= mean of population. According to

Table 6: Variance and genetic parameters of bread wheat traits evaluated at West Shewa.

| No | Trait | δ^2g | δ^2e | δ^2p | GCV % | PCV % | ECV% | H ² b % | GA | GAM |
|----|-------|-------------|-------------|-------------|-------|-------|------|--------------------|-------|-------|
| 1 | DH | 50.12 | 4.29 | 54.41 | 9.11 | 9.49 | 2.66 | 92.11 | 14 | 18.02 |
| 2 | DM | 24.6 | 6.74 | 31.34 | 4.04 | 4.56 | 2.11 | 78.49 | 9.05 | 7.38 |
| 3 | GFP | 12.46 | 7.53 | 19.99 | 7.85 | 9.94 | 6.09 | 62.33 | 5.75 | 12.79 |
| 4 | PH | 199.03 | 51.56 | 250.59 | 13.47 | 15.11 | 6.85 | 79.42 | 25.94 | 24.76 |
| 5 | SL | 1.33 | 0.46 | 1.79 | 11.93 | 13.83 | 7.04 | 74.30 | 2.05 | 21.19 |
| 6 | SPS | 2.18 | 1.28 | 3.46 | 8 | 10.08 | 6.13 | 63.00 | 2.41 | 13.07 |
| 7 | KPS | 6.12 | 22.29 | 28.41 | 14.19 | 17 | 8.72 | 69.58 | 13.2 | 24.38 |
| 8 | BY | 1332.22 | 55.46 | 1387.68 | 24.05 | 24.54 | 4.91 | 96.00 | 73.77 | 48.60 |
| 9 | HI | 30.77 | 3.32 | 34.09 | 25.35 | 26.68 | 8.32 | 90.26 | 10.87 | 49.68 |
| 10 | TSW | 23.6 | 10.02 | 33.62 | 11.88 | 14.18 | 7.73 | 70.19 | 8.38 | 20.49 |
| 11 | PT | 1.54 | 0.2 | 1.74 | 24.87 | 26.43 | 9.02 | 88.50 | 2.4 | 48.09 |
| 12 | FLL | 9.94 | 2.89 | 12.83 | 10.9 | 12.44 | 5.90 | 77.47 | 5.7 | 19.79 |
| 13 | FLW | 0.05 | 0.04 | 0.09 | 15.21 | 20.40 | 13.6 | 55.55 | 0.34 | 23.13 |
| 14 | AL | 13.62 | 0.45 | 14.07 | 44.41 | 45.14 | 8.06 | 96.80 | 7.49 | 90.13 |
| 15 | PEL | 67.83 | 20.48 | 88.31 | 16.89 | 19.27 | 9.27 | 76.80 | 14.88 | 30.52 |
| 16 | GY | 108.64 | 8.29 | 116.93 | 32.57 | 32.97 | 8.78 | 92.91 | 20.72 | 63.17 |

Key: DH: Days to Heading; DM: Days to Maturity; GFP: Grain Filling Period; PH: Plant Height; SL: Spike Length; SPS: Spikelet Per Spike; KPS: kernels per Spike; GY: Grain Yield; BY: Biomass Yield; H: Harvest Index; TSW: Thousand Seed Weight; PT: Productive Tillers; FLL: Flag Leaf Length; FL: Flag Leaf Width; AL: Awn Length; PEL: Peduncle Length; δ^2g : Genotypic Variance; δ^2e : Environmental Variance; δ^2p : Phenotypic Variance; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; H²b: Broad Sense Heritability; GA: Genetic Advance and GAM: Genetic Advance as percent of Mean

Johnson *et al.* (1955) Genetic advance as percentage of mean (GAM) was classified as low (0-10%), moderate (10-20%) and high (>20%).

Results And Discussion

Analysis of Variance (ANOVA)

Analysis of variance (ANOVA) showed highly significant difference ($P < 0.01$) among the 100 bread wheat genotypes for all the studied traits (days to 50% heading, days to maturity, grain filling period, plant height, spike length, spikelet per spike, kernel per spike, biomass yield, harvest index, thousand seed weight, productive tillers, flag leaf length, flag leaf width, awn length, peduncle length and grain yield (Table 3).

The results of analysis of variance showed existence of adequate amount of variability among bread wheat accessions for yield and its components. This will provide an opportunity for a breeder to select best bread wheat genotypes through selection, as variability within population is a basic prerequisite for plant breeding program.

Many authors also reported the existence of significant variation among bread wheat genotypes for different traits. Kalimullah *et al.* (2012) reported that, highly significant difference ($p < 0.01$) among forty-one bread wheat genotypes with respect to days to heading, days to maturity, grain filling period, plant height, thousand seed weight, biomass yield and grain yield [22].

Similarly, Adhiena *et al.* (2016) reported significant difference among 64 bread wheat genotypes for days to heading, days to maturity, grain filling period, number of tillers per plant, spike length, number of kernels per spike, thousand kernel weight, biomass yield, harvest index and grain yield. Likewise, significant difference for days to heading, days to maturity, grain filling period, biomass yield, harvest index, thousand kernel weight, plant height, fertile tiller per plant, spike length, number of spikelet per spike, number of kernel per spike and grain yield were observed as reported by [23-25].

Mean and Ranges of Bread Wheat Genotypes for Studied Traits

According to the result of descriptive statistics indicated,

there were a wide range of variations among the genotypes studied (Table 4). The genotypes showed considerable variation in days to heading and maturity. Date of heading of the genotypes ranged from 58 to 101 days while number of days to maturity ranged from 114.5 to 145 days. Average number of days to heading and days to maturity were 77.69 days and 122.63 days respectively. Among the genotypes, the earliest heading was 34706 (58 days), EBW-192299 (60 days), EBW192344 (61 days), 31551 (62 days), Kingbird (62 days), 31554 (63 days). However, genotypes such as 33389 (101.5 days), 31542 (91 days), 31813 (91 days), 31818 (90 days), 34157 (89 days) and 31600 (89 days) had late heading period.

The shortest time for maturity was recorded for EBW192362, Ogoicho, EBW192299 (114.5 days) followed by EBW192865, 31551, 34706 (115 days) however; accessions 33389 had the longest time for maturity (145 days) followed by 31818 (140 days). Knowing days to heading and maturity is among the most important attributes that need to be considered in selecting genotypes in terminal stress conditions [26].

The result of present study agrees with the findings of Tesfaye *et al.* (2014) who reported the presence of high variation among the genotypes for days to heading and maturity. Yohannes *et al.* (2020) also reported wide range of variation among bread wheat genotypes for days to heading and days to maturity. Accession number 31169 was the earliest to fill the grain with 37 days, which is 20.5 days earlier than late grain filling period followed by 34086 and 33911 that had 38 days for grain filling period. However, EBW192364 was late to fill the grain with 57.5 days followed by accession number 34706 (57 days) and Kingbird (56.5 days) [27].

The studied genotypes also showed extensive range of variability in their spike length (5.55-14.55 cm), spikelet per spike (15.45-24.2), kernels per spike (34.15-76.2), biomass yield (36.25-243.75 qt/ha), harvest index (9.36-37.59), thousand seed weight (22.69-56.28g), productive tillers (2.1-8.4), flag leaf length (19.7-36.1), flag leaf width (1.05-1.95), awn length (0-15.58) and peduncle length (27.13-63.2) with mean values 9.67, 18.44, 54.14, 151.78, 21.88, 40.88, 4.99, 28.8, 1.47, 8.31 and 48.76 respectively. Mean plant height ranged from 75.57-135.5 cm with the grand mean 104.76 cm. The maximum plant height (cm) was detected for genotypes

36255(135.5), 34856(135.48)34098(133.55), 33915(130.8), 31643(126.2) while the minimum number was noted for genotypes EBW192344 (75.57 cm), BW184033 (76.05 cm), 31543 (76.16 cm), EBW192364 (77.23 cm), EBW192398 (77.27 cm), EBW192345 (77.55 cm) (Table 4) In line with present study, (Yaqoob, 2016) reported high range of variation for plant height.

Grain yield of the bread wheat genotypes were showed wide range of variability (58.93 qt/ha to 6.86 qt/ha) with mean of (32.8 qt/ha) as indicated in (Table 4). The highest grain yield were recorded for genotypes 31790 (58.93 qt/ha), EBW192299 (57.97 qt/ha), 33682 (56.51 qt/ha), 34737 (55.38 qt/ha), 34159 (52.5 qt/ha), whereas lowest grain yield recorded for genotypes 34667 (6.86 qt/ha), Ogocho (13.43 qt/ha), 33901(13.45 qt/ha), Digelu (14.09 qt/ha) and 34706 (15.08 qt/ha). Alemu *et al.* (2017) also reported high range of variation among genotypes for grain yield. Generally, the result showed the presence of genetic variability among the genotypes for grain yield and yield component traits. This provides an opportunity for bread wheat improvement through selection for the target area [28].

Consequently, high variability for 16 traits in one hundred bread wheat genotypes implied that there was reasonably sufficient variability which provides ample scope for selecting superior and desired genotypes. In general, ranges of variation was wide for all the traits studied. In agreement with the present finding, Tesfaye *et al.* (2014) observed high range of variation for grain yield, thousand kernel weight, plant height and days to heading.

Maqbool *et al.* (2010) reported wide range of variation for plant height, grain filling period, number of spikelet per spike, biomass yield, grain yield and thousand kernel weight. Moreover, Fellahi *et al.* (2013) reported large variation for grain yield, thousand kernel weight and number of kernels per spike. Based on their mean performance in quintal per hectare, genotypes 31790 (58.93), EBW192299 (57.97), 33682 (56.51), 34737(55.38) and 34159 (52.51) were found to be top yielders (Appendix 1). These high yielding genotypes may be used in further wheat improvement programs [30].

Estimation of Variance Components

Estimate of phenotypic variance (δ^2p), genotypic variance (δ^2g), environmental variance (δ^2e), Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) and Environmental Coefficient of Variation (ECV) were provided in Table 6. A higher magnitude of differences between phenotypic and genotypic variances was ascertained among the traits.

The highest value of phenotypic variance was computed for biomass yield qt/ha (1387.68) while the lowest was for flag leaf width (0.09). Similarly, genotypic variances were in the ranges between (1332.22) for biomass yield qt/ha and (0.05) for flag leaf width.

Generally, the values calculated for a phenotypic variance were over the corresponding genotypic variance for all traits. The environmental variance was also observed higher for traits such as plant height, kernel per spike, biomass yield and peduncle length. This indicates that there was a larger influence of environmental factors on the phenotypic expression of these traits.

According to Burton and Devane (1953), PCV and GCV values more than 20% are regarded as high; values between 10 and 20% to be medium and value less than 10% are considered to

be low. Phenotypic Coefficient of Variation (PCV) ranged from 4.56% for days to maturity to 45.14% for awn length while Genotypic Coefficient of Variation (GCV) ranged from 4.04% for days to maturity to 44.41 % for awn length. From the analyzed bread wheat genotype traits with high value (>20) of phenotypic coefficient of variation were awn length (45.14%), grain yield (32.97%), harvest index (26.68%), productive tillers (26.43%) and biomass yield (24.54%). Similarly, the maximum value of GCV (>20) also obtained from awn length (44.41%), grain yield (32.57%), harvest index (25.35%), productive tillers (24.87%) and biomass yield (24.05%).

These high results of PCV and GCV with little difference revealed that the genotypes reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters would be possible. Likewise, Tarekegn *et al.* (1994) reported high PCV and GCV for grain yield, biomass and harvest index in wheat. Furthermore, Wolde *et al.* (2016) observed high value of PCV and GCV for grain yield, harvest index and productive tillers per plant in wheat [31].

Low values (<10) of PCV and GCV are obtained for the traits of days to heading, days to maturity and grain filling period. This indicates that those traits were less scope of selection as they were narrow for their variability and practically difficult for their improvement. Likewise, Yohannes *et al.* (2020) reported similar findings for days to heading, grain filling period and days to maturity in bread wheat.

Among the sixteen traits studied moderate (10–20) values of PCV and GCV are obtained for traits namely number of kernels per spike, flag leaf length, spike length, thousand seed weight, plant height and peduncle length. This showed that selection may be effective based on these traits.

In line with present result, Degewione and Alamerew, (2013) reported moderate PCV and GCV for thousand seed weight, number of kernels per spike, spike length and plant height in 26 bread wheat genotypes. Number of spikelet per spike was found to be moderate for PCV while low for GCV whereas flag leaf width was found to be high for PCV while moderate for GCV [32].

Generally the PCV values were relatively higher than GCV values for all the traits suggesting environmental influence on the genotypes for the expression of the characters. Similar finding was reported by [3,33]. However, closeness between the values of both parameters showing less effect of environmental to the phenotypic expression. This result agreed with the findings of Abinisa *et al.*; (2011) and Tsegaye *et al.*; (2012). Out of sixteen traits moderate ECV was observed from single trait flag leaf width (13.6%) whereas all the left traits had minimum ECV indicating that low environmental variance [34,35].

Estimate of Heritability and Expected Genetic Advance

Heritability describes the portion of variability that is transferred from parents to offspring. Broad sense heritability is the ratio of the genotypic variance to the total phenotypic variance [36]. Assessment of heritable and non-heritable components in the total variability is vital in adopting suitable breeding method. Heritability estimate indicates the likelihood and extent to that improvement is feasible through selection [36]. GCV and heritability would give better information about the efficiency of selection [19]. The estimated broad sense heritability and genetic advance for 16 quantitative traits was presented in Table 6.

The heritability was categorized as low (0-30%), moderate (30-60%) and high (>60%) as described by [36]. Heritability in broad sense ranged from 55.55% for flag leaf width to 96.8% for awn length.

High heritability that is supported by moderate and high genetic advance indicated that almost probably the heritability of those characters is because of additive gene effects and selection may well be effective for these characters [37].

Based on these categories traits such as grain filling period (62.33%), spikelet per spike (63%), kernels per spike (69.58%), thousand seed weight (70.19%), spike length (74.3%), peduncle length (76.8%), flag leaf length (77.47%), days to maturity (78.49%), plant height (79.42%), productive tillers (88.5%), harvest index (90.26%), days to heading (92.11%), grain yield (92.91%), biomass yield (96%) and awn length (96.8%) showed high heritability. High heritability of these traits indicated that the variation observed was mainly under genetic control in which they are less influenced by environment and the possibility of progress from selection. For those characters which exhibited high heritability, selection could be easy.

This is as a result of there would be a close correspondence between the genotype and the phenotype because of the relative minor contribution of the environment to the phenotype. Similarly, Khan *et al.* (2017) stated high heritability value for plant height, spikelet per spike, spike length, thousand seed weight and grain yield in bread wheat [38].

Likewise, Adhiena *et al.* (2016) reported high heritability for days to heading, kernels per spike, thousand seed weight, days to maturity and grain filling period. Muhammad *et al.* (2017) also reported high heritability for spike length, thousand seed weight, biomass yield, grain yield and harvest index. In similar way, Nishant *et al.* (2018) reported high heritability for thousand seed weight and awn length and Destaw *et al.* (2020) reported high heritability for productive tiller and plant height [23,37,39,40]. Moderate heritability values were recorded for flag leaf width (55.55%) which suggested that selection should be delayed to more advance generation for this trait. The utility of heritability increases when it used to estimate genetic advances [21]. A high heritability estimate does not necessarily mean high genetic gain (genetic advance) [41].

Although heritability estimates provide basis for selection on the phenotypic performance, the estimates of heritability and GAM should always be considered simultaneously, because high heritability will not always be associated with high GAM [21].

Johnson *et al.* (1955) classified Genetic Advance as the percentage of the Mean (GAM); values from 0%-10% are low, from 10%-20% moderate and 20% and above are high. The present study showed high genetic advance as percent of mean for thousand seed weight (20.49%), spike length (21.19%), flag leaf width (23.13%), kernels per spike (24.38%), plant height (24.76%), peduncle length (30.52%), productive tillers (48.09%), biomass yield (48.6%), harvest index (49.68%), grain yield (63.17%) and awn length (90.13%) as suggested by [21].

Kali mullah *et al.* (2012) reported high value of genetic advance as percent of mean for plant height, kernels per spike, biomass yield and thousand seed weight. Arya *et al.* (2017) reported high value of genetic advance as percent of mean for spike length, biomass yield, kernels per spike and harvest index. Nishant *et al.* (2018) reported high value of genetic advance as

percent of mean for thousand seed weight, peduncle length and awn length [22,40,42].

The moderate value was recorded for grain filling period (12.79%), spikelet per spike (13.07%), days to heading (18.02%) and flag leaf length (19.79%) whereas the minimum was recorded for days to maturity (7.38) (Table 6). Munir *et al.* (2007) reported moderate values of genetic advance as percentage of mean for spikelet per spike. Birhanu *et al.* (2017) also reported moderate genetic advance as percentage of mean for grain filling period and days to heading which support the present findings [43,44].

Genetic Advance (GA) in absolute unit shows the improvement of traits in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity [41]. Estimates of GA for grain yield was 20 qt/ha indicating that, whenever we select the best 5% high yielding genotypes as parents, mean grain yield of progenies could be improved by 20 qt/ha. Similarly, the GA values for biomass yield, plant height, day to maturity, thousand seed weight and harvest index, were 73.77 qt/ha, 25.94 cm, 9.05 days, 8.38 g and 10.87 %, respectively (Table 6).

From the studied traits high heritability coupled with high genetic advance as percent of mean were recorded for thousand seed weight, spike length, plant height, kernels per spike, peduncle length, productive tillers, biomass yield, harvest index, grain yield and awn length.

This shows that these characters do not seem to be a lot of influenced by environmental factors and significant improvement for these traits could be accomplished through direct selection and also these traits are considered to be directed by additive genes [45]. Kali mullah *et al.* (2012) reported high heritability coupled with high genetic advance as percent of mean for plant height, kernels per spike, biomass yield and thousand seed weight. Arya *et al.* (2017) reported high heritability coupled with high genetic advance as percent of mean for spike length, biomass yield and harvest index. Likewise, Nishant *et al.* (2018) reported high heritability coupled with high genetic advance as percent of mean for thousand seed weight and awn length.

High heritability coupled with moderate genetic advance as percent of the mean was observed for days to heading, grain filling period, spikelet per spike and flag leaf length. Moderate heritability coupled with high genetic advance as percent of the mean was observed for flag leaf width indicating improving the trait through selection would be effective. High heritability may not essentially result in increased genetic advance. In this study, days to maturity (78.49%) showed high estimate of heritability, however, it exhibited low estimate of genetic advance as percentage of mean (7.38%).

This is the indication of non-additive gene actions. If a trait is governed by non-additive gene action, it may be give high heritability but showed low genetic advance as percentage of mean, whereas, if trait is directed by additive gene action heritability and genetic advance as percentage of mean could be high [45].

Conclusions and Recommendation

Knowledge on the extent of genetic variability is important in plant breeding program as it provide the basis for selection. In present thesis work, a total of 100 bread wheat genotypes were evaluated for their variability during the main cropping season

of 2021 in West Shewa, central Ethiopia. The experiments were laid out using alpha lattice design with two replications. The analysis of variance revealed highly significant variations among the genotypes for all characters studied. The presence of significant variability among the genotypes suggested that possibility of improving the traits through direct and indirect selections as variability within population is the basic prerequisite for crop improvement.

Higher phenotypic over genotypic coefficient of variation were observed for all traits with range of GCV 4.04 for number of days to maturity to 44.41 for awn length, PCV 4.56 for number of days to maturity to 45.14 for awn length. Broad sense heritability 55.55 for leaf width to 96.8 for awn length and genetic advance as percent of mean 7.38 for number of days to maturity to 90.13 for awn length. Productive tillers, biomass yield, harvest index, grain yield and awn length showed higher GCV along with higher heritability and genetic advance as percentage of mean and thus such traits are controlled by additive gene action and could be improved through recurrent selection. However, days to maturity had higher heritability and lower genetic advance as percentage of mean. Such trait mostly governed by non-additive gene types and could not fix through selection.

The present results suggest that traits namely; productive tillers, biomass yield, harvest index, grain yield and awn length had high heritability and high genotypic coefficient of variation coupled with high genetic advance as percentage of mean and could be improved through selection. Based on the current results, genotypes namely; 31790 (58.93 qt/ha), EBW192299 (57.97 qt/ha), 33682 (56.51 qt/ha), 34737 (55.38 qt/ha) and 34159 (52.51 qt/ha) were identified as high yielders genotypes compared to other tested genotypes. However, it is important to emphasize that the results and conclusions made are based on the data obtained from one-year field evaluation at single location. Therefore, evaluation of these genotypes in three to four replications across at least six locations would be necessary in order to get the comprehensive results.

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