

*Full Length Research Paper*

## **Genetic variability studies on bread wheat (*Triticum aestivum* L.) genotypes**

**Alemu Dabi<sup>1\*</sup>, Firew Mekbib<sup>2</sup> and Tadesse Desalegn<sup>3</sup>**

<sup>1</sup>Department of Plant Breeding, Assosa Agricultural Research Center, Ethiopia.

<sup>2</sup>Department of Plant Breeding, Faculty of Agricultural Science, Haramaya University, Ethiopia.

<sup>3</sup>The German Society for International Cooperation (GIZ) GmbH, Addis Ababa, Ethiopia

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Thirty bread wheat genotypes were tested to assess the genetic variability, among studied genotypes using alpha-lattice design at Tongo sub-center of Assosa Agricultural Research Center and Kulumsa Agricultural Research Center in 2015. Analysis of variance revealed that there were statistically significant differences among the genotypes for most of the traits at individual and across locations. From the combined analysis of variance, significant ( $p \leq 0.05$ ) effect due to location, varieties and  $G \times E$  was observed for most of the traits. The varieties showed wider variability in mean grain yield of 1284.4-3788.7 kg ha<sup>-1</sup>, 2588.3-4683.3 kg ha<sup>-1</sup> and 1936.4 - 4095.6 at Tongo, Kulumsa and across location, respectively. Moderate PCV values (>10%) were obtained for grain yield, 1000 kernel weight, harvest index, tillers per plant and spikes per plant at individual location and across location including days to heading, above ground biomass yield, spike length and kernels per spike at Tongo and above ground biomass yield at Kulumsa. Similarly, moderate GCV values (>10%) were obtained for grain yield, 1000 kernel weight, tillers per plant and spikes per plant at individual location including days to heading, harvest index and kernels per spike at Tongo and above ground biomass yield at Kulumsa. Lower (<10%) was obtained for all traits across location. High heritability estimates (>80%) were obtained for days to heading (86.0%) and days to maturity (85.1%) at Tongo and days to heading (86.2 and 82.69%) and spikes length (80.1 and 82.85%) at Kulumsa and across location. But relatively high genetic advance (>20%) was obtained for grain yield (28.5%) and harvest index (24.3%) at Tongo. Moderate genetic advance (10-20%) was observed for 1000 kernel weight, spikes length and days to heading at individual location and across location including spikelets per spike, tillers per plant, above ground biomass, spikes per plant and plant height at individual location. Generally, it has been observed the presence of variability among the genotypes, heritability in the tested traits of the genotypes studied. Hence, Selection and hybridization on those genotypes based on the trait with high GCV, heritability and genetic advance can be recommended for farther yield improvement of bread wheat at respective location.

**Key words:** Heritability, genetic advance, traits, phenotypic, genotypic coefficient of variation.

### **INTRODUCTION**

Wheat (*Triticum aestivum* L.) is one of the world's major cereal crops and staple food of many regions grown under both irrigated and rain fed conditions. Unlike rice and maize, which prefer tropical environment, wheat is extensively grown in temperate regions occupying 17% of

all crop acreage worldwide. It is the staple food for 40% of the world's population (Goyal and Prasad, 2010; Peng et al., 2011). Currently it is also becoming most important cereals grown on a large scale (Fassil et al., 2000), because of its significance as cash crop, high level of

production per unit area, its major role in supplying the dietary requirements of the society. Wheat is the second only to rice which provides 21% of the total food calories and 20% of the protein for more than 4.5 billion people in 94 developing countries (Braun et al., 2010). Food consumption of wheat is projected at 488 million tonnes, 1.3% higher than in the 2014 season, keeping the average per capital level steady at 67.6 kg (FAO, 2015). Global wheat grain production must increase 2% annually to meet the requirement of consistently increasing world population (around 9 billion) till 2050 (Rosegrant and Agcaoili, 2010).

The leading wheat producing countries are China, India, United States, France, and Russia Federation (FAO, 2015). The Wheat Yield Consortiums an integral part of the wheat strategy to break the genetic yield barrier. In March 2012, 34 research organizations finalized a 10-year integrated research plan. The organizations agreed for sharing advanced scientific expertise, facilities and germplasm, to improve the wheat plant's photosynthesis, ear size and stalk strength working together to succeed in raising the genetic yield potential by up to 50% in the next 20 years. The wheat yield consortium findings will be incorporated into the wheat breeding platform, to deliver high-yielding varieties to farmers' fields in wheat target regions (CGIAR, 2013)

In Ethiopia, bread wheat is an introduced crop, although its time of introduction is immemorial (Hailu, 1991). Wheat can grow in the Ethiopian highlands, which are situated between 6° and 16°N and 35° and 42°E, at altitude ranging from 1500 to 3000 m. However, the most suitable altitude zones of wheat fall between 1900 and 2700 m.a.s.l (Bekele et al., 2000).

Wheat is an important staple food crop and the third highest source of grain-based calories behind corn and sorghum in Ethiopia. It accounts for a little more than 20% of the total calorie supply. 60% of production is used for household consumption, 20% is sold to the market, while the balance is used for seed, in-kind wages, animal feed and other uses. Wheat bran from commercial wheat millers is used as one of the ingredients in commercially-produced, compound animal feed (GAIN, 2015). It grows on 1.6 million hectares of production area with a total production of 3.8 million metric tons and ranks fourth in both area and production among cereal crops in different regions of Ethiopia (CSA, 2015). Ethiopian wheat production self-sufficiency is only 75% and the remaining 25% of wheat imported commercially and through food aid and shares of total cereal consumption is increased by 20% in recent year, making it the second most consumed cereal in Ethiopia after corn (USDA, 2016). Therefore, to meet the self-sufficiency, growing demand

of manufacturing industries and reduce the importing, increasing the yield potential would be the solution in the long-run. Farther more increasing wheat production is important to the economic stability and food security of Ethiopia.

Although the productivity of wheat has increased in the last few years in Ethiopia, it is still very low as compared to other wheat producing countries. The national average productivity is estimated to 2.4 tons/ha (CSA, 2015) which is by far below the world's average of 3.27 tons/ha (USDA, 2016). The low productivity is attributed to a number of factors including: Biotic (Diseases, insect pests, and weeds), abiotic (moisture, soil fertility, etc.) (Zegeye et al., 2001). Among biotic factors, rusts are the most important diseases of wheat, which cause up to 60% loss of wheat yield for leaf or stripe (yellow) rust and 100% loss for stem rust (Park et al., 2007). Wheat and rusts have coevolved for thousand years and resulted in the accumulation of wide spectrum of the pathogens in Ethiopia (Mengistu et al., 1991). Therefore, developments of new varieties which are resistance to different diseases and adaptable to environments with abiotic stress could be a solution for farther grain yield improvement in wheat.

Grain yield and its quality are the principal characters of a cereal crop (Ullah et al., 2010). They are complex quantitative characters, which are influenced by a number of yield contributing characters. Hence, the selection for desirable genotypes should not only be based on yield alone, and the other yield components should also be considered. Direct selection for yield is often misleading in wheat because wheat yield is polygenically controlled. For effective utilization of the genetic stock in crop improvement, information of mutual association between yield and yield components is necessary. It is therefore, necessary to know the correlation of various component characters with yield and among themselves. The correlation coefficients between yield and yield components usually show a complex chain of interacting relationship. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effects and illuminates the relationship in a more meaningful way. The success of a breeding program depends largely upon the amount of genetic variability present in the population and the extent to which the desired traits are heritable (Majumder et al., 2008).

Several genetic variability studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Daniel et al., 2011). Genetic improvement to develop varieties with high yield

\*Corresponding author. E-mail: alemu.dabi@ymail.com.

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potential and resistance/tolerance to a biotic and biotic stresses, with acceptable end-use quality, is the most viable and environment-friendly option to sustainably increase wheat yield. Such improvement of crops requires creation and introduction of genetic variation, inbreeding coupled with selection, and extensive evaluation of breeding materials at multiple locations to identify adapted and stable genotypes with desirable agronomic traits. Several genetic variability studies have been conducted on bread wheat at the different regions of Ethiopia (Adhiena, 2015; Awale et al., 2013; Gezahegn et al., 2015; Mitsiwa, 2013; Obsa, 2014). However, no variability studies have been conducted at Benishangul Gumze Regional State. Therefore, such information is essential for creation of genetic variation and further bread wheat improvement particularly, in the region and generally in the country. Therefore, the current study was carried out to estimate the genetic variability of bread wheat genotypes for yield and yield related traits.

## MATERIALS AND METHODS

### Experimental sites

The experiments were conducted at two locations, Kulumsa Agricultural Research Center (KARC) and Tongo, under Assosa Agricultural Research Center (AsARC) (Table 1).

The bread wheat genotypes to be studied were given in Table 2.

### Experimental design, data collected and field management

The trials were planted in July 04, 2015 at Kulumsa and August 18, 2015 at Tongo. Masood et al. (2008) reported Alpha lattice design provided smaller standard errors of differences, coefficients of variation and error mean squares as compared to randomized complete block design providing efficiency in comparing different entries/lines. Therefore in the current study, thirty genotypes were grown in alpha-lattice design with three replications. Each experimental unit consisted six rows of 2.5 m length with 20 cm spacing between rows. Data were collected from the central four rows for the parameters days to heading, days to maturity, grain filling period, grain yield, 1000 kernel weight, above ground biomass yield, harvest index, hectoliter weight and from randomly sampled plants for the characters; tillers per pant, plant height, kernel per spike, spikelet per spike, spike length and spikes per plant. 1.5 m alleys were left between reps. Non-experimental variables such as seed and fertilizer rates were used as recommended for the specific testing sites. Hence, 73/69 kg ha<sup>-1</sup> N/P<sub>2</sub>O<sub>5</sub> were used for Kulumsa and 60/69 kg ha<sup>-1</sup> N/P<sub>2</sub>O<sub>5</sub> for Tongo. A seed rate of 125 kg ha<sup>-1</sup> was used at both locations.

### Data analysis

#### Analysis of variance (ANOVA)

The analysis of variance (ANOVA) was performed using the SAS version 9.1.3 software for Alpha-Lattice Design. For each location and combined data over locations, analyses of variances, were done using the mean of ten sample plants for the characters like plant height, tillers per plant, spikelets per spike, spike length, kernels per spike and spikes per plant. However, plot values were used for the characters such as days to heading and maturity, grain

yield per hectare, harvest index, grain filling period, hectoliter weight, thousand kernels weight, and above ground biomass yield for analysis of variance. The Least Significant Difference (LSD) was used to compare two means at the 5 and 1% level of significance.

Individual locations ANOVA were computed using the following mathematical model:

$$Y_{ijl} = \mu + rj + gi + Pl(j) + \varepsilon_{ijl}$$

Where:  $Y_{ijl}$  = the observed value of the trait Y for the  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  replication;  $\mu$  = the general mean of trait Y;  $rj$  = the effect of  $j^{\text{th}}$  replication;  $gi$  = the effect of  $i^{\text{th}}$  genotypes and  $pl(j)$  = block within replicate effect;  $\varepsilon_{ijl}$  = the experimental error associated with the trait y for the  $i^{\text{th}}$  genotype in  $l^{\text{th}}$  block with in replication and  $j^{\text{th}}$  replication.

Combined ANOVA model:

$$Y_{ijk} = \mu + gi + Ej + GEij + Bk(j) + \varepsilon_{ijk}$$

Where,  $Y_{ijk}$  = observed value of genotype i in block k of location j;  $\mu$  = grand mean;  $Gi$  = effect of genotype i;  $Ej$  = environment or location effect;  $GEij$  = the interaction effect of genotype i with location/environment j;  $Bk(j)$  = effect of block k in location/environment j;  $\varepsilon_{ijk}$  = random error or residual effect of genotype i in block k of location j.

#### Estimation of phenotypic and genotypic parameters

$$\text{Genotypic variance } (\sigma_g^2) = \frac{MS_g - MS_e}{r} \quad (\text{Burton and De vane, 1953})$$

Where:  $MS_g$  = mean square due to genotypes,  $MS_e$  = error mean square,  $r$  = the number of replication, Environmental variance ( $\sigma_e^2$ ) = error mean square =  $MS_e$ , and Phenotypic variance ( $\sigma_p^2$ ) =  $\sigma_g^2 + \sigma_e^2$

Variance components for the data combined over locations were computed in a similar fashion as for individual locations by using the following formulae (Johnson et al., 1955)

$$\begin{aligned} \sigma_e^2 &= MS_e \\ \sigma_{gl}^2 &= \frac{MS_{gl} - MS_e}{r} \\ \sigma_g^2 &= \frac{MS_g - MS_{gl}}{rl} \\ \sigma_p^2 &= \sigma_g^2 + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_e^2}{lr} \end{aligned}$$

Where:  $\sigma_{gl}^2$  = Genetic by location interaction;  $MS_e$  = error mean square;  $MS_{gl}$  = genotype by location interaction mean square;  $MS_g$  = genotype mean square;  $r$  = replication and  $l$  = location

Coefficient of variation at phenotypic, genotypic and environmental levels was estimated as:

$$\begin{aligned} \text{Phenotypic coefficient of variation (PCV)} &= \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100 \\ \text{Genotypic Coefficient of variation (GCV)} &= \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100 \end{aligned}$$

Where:  $\bar{x}$  = grand mean of character.

**Table 1.** Experimental site analysis.

Site	Altitude	Latitude	Longitude	Annual rain fall (mm)	Average annual temperature (°C)
Tongo	1820	90 23.165° N	340 24 38°E	1316	24.3 - 26.6
Kulumsa	2200	8.08°N	39.08°E	832	9.78 - 23.12

**Table 2.** The listed of bread wheat genotypes to be studied.

Entry	Name	Pedigree/genotypes
1	Hidasse	ETBW5795(check 1)
2	ETBW 6861	WAXWING*2/HEILO
3	ETBW 8506	AGUILAL/FLAG-3
4	ETBW 8507	DURRA-4
5	ETBW 7120	QAFZAH-23/SOMAMA-3
6	ETBW 8508	REYNA-8
7	ETBW 7213	CHAM4/SHUHA'S/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB
8	ETBW 8509	REYNA-29
9	ETBW 7038	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA//TSI/VEE#5/4/CROC_1/AE.SQUARROSA (224)//2*OPATA
10	ETBW 8510	HIJLEEJ-1
11	ETBW 7058	ROLF07//TAM200/TUI/6/WBLL1/4/HD2281/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/TACUPETO F2001
12	ETBW 8511	BOW #1/FENGGANG 15/3/HYS//DRC*2/7C
13	ETBW 7147	CROC-1/AE.SQUARROSA(224)// OPATA/3/QAFZAH-21/4/SOMAMA-3
14	ETBW 8512	BABAX/LR42//BABAX*2/3/KURUKU/4/KINGBIRD #1
15	ETBW 7871	PAURAQ/4/PFAU/SERI.1B//AMAD/3/WAXWING
16	ETBW 8513	MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING
17	ETBW 6940	UTIQUE 96/FLAG-1
18	ETBW 8514	TUKURU//BAV92/RAYON/3/WBLL1*2/BRAMBLING/4/WBLL1*2/BRAMBLING
19	ETBW 7368	D. 56455
20	ETBW 8515	BECARD/3/PASTOR//MUNIA/ALTAR 84
21	ETBW 7364	ACSAD1115
22	ETBW 8516	KACHU/KIRITATI
23	ETBW 7194	VAN'S/3/CNDR'S//ANA//CNDR'S//MUS'S/4/TEVEE-5
24	ETBW 8517	FRNCLN*2/TECUE #1
25	ETBW 7101	KAMB2/PANDION
26	ETBW 8518	SUP152/AKURI//SUP152
27	ETBW 7872	QUAIU/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
28	ETBW 8519	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
29	ETBW 6937	AGUILAL/FLAG-3
30	Danda'a	DANPHE#1(check 2)

**Estimation of heritability in broad sense**

Heritability (H): in broad sense for all characters was computed using the formula given by Falconer (1989). Broad sense heritability (H) expressed as a percentage of the ratio of the genotypic variance ( $\sigma_g^2$ ) to the phenotypic variance ( $\sigma_p^2$ ) was estimated on genotype mean base (Allard, 1960) as:

$$\text{Heritability (H}^2\text{)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where:  $H^2$  = heritability in broad sense;  $\sigma_p^2$  = phenotypic variance;  
 $\sigma_g^2$  = genotypic variance

**Estimation of genetic advance**

Genetic advance in absolute unit (GA) and percent of the mean (GAM), were estimated in accordance with the methods illustrated by Johnson et al. (1955) as:

$$GA = K\sigma_p H$$

**Table 3.** Mean squares of the 14 traits of bread wheat genotypes tested at Kulumsa and Tongo in 2015/16.

Characters	Tongo						kulumsa					
	source				CV (%)	Efficiency	source				CV (%)	Efficiency
	Rep (DF=2)	Block(Rep) (DF=15)	Genotypes (DF=29)	Error (DF=43)			Rep (DF=2)	Block(Rep) (DF=15)	Genotypes (DF=29)	Error (DF=43)		
DH	17.54*	4.6	104.76**	5.37	4.2	0.96	5.73	2.6	43.21**	2.19	2.63	1.05
DM	3.1	6.86*	63.75**	3.52	1.8	1.24	4.43	9.11	30.34**	4.83	2.16	1.23
GFP	6.41	8.59	18.28**	4.52	4.31	1.23	7.23	4.78*	22.66**	6.2	5.47	0.94
PH	6.35478	17.41336	66.35**	14.32	5	1.06	90.65**	18.74**	69.68**	6.47	3.23	1.49
GY	160354	494552.51**	917407.72**	152281.2	13.62	1.58	687393.61*	231423.8	850298.88**	143794.7	10.39	1.16
TKW	33.6**	9.94	42.29**	5.63	7.09	1.2	3.33	13.29*	67.53**	5.68	5.5	1.35
HW	20.57*	6.01	16.34**	4.63	2.73	1.08	3.05	6.88*	11.90**	2.91	2.33	0.93
AGB	486111	2508648.6*	3800067.3**	1148792	9.22	1.31	975000	1905385	5689567**	1076804	9.59	1.2
HI	0.002*	0.001*	0.004**	5.83x10-4	9.84	1.24	0.01**	1.4X10-2**	5.6X10-2**	1.2X10-2	9.99	1.05
TPP	2.75**	0.58**	0.52**	0.2	15.59	1.49	2.67**	0.49**	0.60**	0.19	16.05	1.42
SPP	3.47**	0.51**	0.57**	0.2	16.45	1.42	2.91**	0.49**	0.47**	0.15	15.15	1.59
SL	1.20**	0.36*	1.66**	0.17	5.11	1.3	6.11**	0.99**	1.34**	0.1	3.79	3.24
SPS	1.6	0.85*	5.25**	0.85	5.16	1	0.89	0.68	3.65**	0.55	6.51	0.07
KPS	9.7	33.3	74.82**	14.28	9.29	1.34	16.02	28.68**	28.53**	8.89	4.06	1.58

DH, Days to heading; DM, Days to maturity; GFP, Grain filling period; GY, Grain yield; TKW, 1000 kernel weight; AGB, Above ground biomass (kg ha<sup>-1</sup>); HI, Harvest index; HW, Hectoliter weight; TPP, Tillers per plant; PH, Plant height (cm); SPS, Spikelets per spike; KPS, Kernels per spike; SL, Spike length; SPP; Spikes per plant. LSD= List significant difference; CV= Coefficient of variations.

Where, K=the standardized selection differential at 5% selection intensity ( $k=2.063$ );  $\sigma_p$  =phenotypic standard deviation on mean basis; H=heritability in broad sense.

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where: GAM= genetic advance as percent mean; GA=genetic advance under selection, and  $\bar{X}$  = Mean of the population in which selection employed.

## RESULTS AND DISCUSSION

### Analysis of variance of studied traits

Individual location (Table 3) and across locations (Table 4) ANOVA was carried out for 14

characters recorded at Tongo and Kulumsa. There was a highly significant difference among the genotypes for all traits including days to heading, days to maturity, grain filling period, plant height, grain yield, 1000 kernel weight, hectoliter weight, biological yield, harvest index, tillers per plant, spikes per plant, spikes length, spikelets per spike and kernels per spike studied at individual locations confirming the genetic variability for yield and its components. Obsa (2014) and Awale et al. (2013) also reported considerable genetic variability for grain yield and its component characters in studied bread wheat genotypes in Ethiopia. Other authors also reported considerable genetic variability for grain yield and its component characters in durum wheat (Khan et al., 2013;

Mohammed et al., 2011). Gezahegn et al. (2015) reported highly significant and significant differences among genotypes ( $P<0.01$ ) for days to heading, days to maturity, grain filling period, 1000 kernel weight, plant height, spike length, number of productive tillers per plant, number of spikelet's per spike and number of grains per plant, grain yield per plot, harvest index and hectoliter weight. However, Mitsiwa (2013) reported non-significant differences among bread wheat genotypes for plant height and spike length and Adhiena (2015) for plant height and number of tillers per plant.

Twelve quantitative characters which had homogeneous error variances were subjected for combined ANOVA over locations (Table 4).

Significant location effects were observed for all the traits except number of spike per plant indicating the differences in growth conditions exhibited at the two locations.

Mean squares of genotypes were significant ( $P \leq 0.01$ ) for all characters including days to heading, days to maturity, plant height, grain yield, 1000 kernel weight, hectoliter weight, harvest index, spikes per plant, spikes length, spikelets per spike and kernels per spike except for number of tillers per plant indicating variability in studied genotypes. Hence, selection could be effective for different quantitative characters or for inclusion in crossing program for creating variability. Such variability with in studied genotypes was also reported by Navin et al. (2014).

The location  $\times$  genotype interaction was significant for days to heading, days to maturity, plant height, grain yield, 1000 kernel weight, hectoliter weight, harvest index, spikes length, spikelets per spike and kernels per spike except number tiller per plant and spike per plant indicating different performance of bread wheat genotype across the two locations or genotypes responded differently to the different environmental conditions suggesting the importance of the assessment of genotypes under different environments in order to identify better performing genotypes for a particular environment. In accordance with Tesfaye et al. (2014) who reported significant differences among genotypes for most of the traits including day to heading, days to maturity, plant height, Septoria disease, thousand seed weight and hector liter weight across environments

## Mean, range and estimates of genetic parameters

### *Mean and range of grain yield and yield components*

Range and mean values for the 14 characters are shown in Tables 5 and 6 for Tongo and Kulumsa, respectively. The mean performance of the 30 genotypes for 14 traits is presented in Appendix Tables 5 and 6. Coefficients of variation (CV %) were used to compare the precision of the experimentation, that is, means with lower CV% for most of the characters revealed existence of reliability of the data (Gomez and Gomez, 1984). A range for days to heading at Tongo was 46 to 70 days with minimum values in genotypes ETBW 8518 and the maximum in ETBW 6940 with an average value of 55 days. 46.6% of the genotypes need above the grand mean (55 days) days to heading. The range for days to heading at Kulumsa was 48 to 66 days relatively narrow than days to heading at Tongo with minimum values in genotypes ETBW 8518 and the maximum in ETBW 7213 with an average value of 56 days. 30.0% of the genotypes need above the grand mean (56 days) days to heading. Days to maturity at Tongo and Kulumsa also ranged from 97 (ETBW 7101) to 117 (ETBW 6940) and 97 (ETBW 7101

and ETBW 8517) to 108 (ETBW 6940, ETBW 7147 and ETBW 7213) days, respectively, with an average value of 105 and 102 days, respectively, indicating that the tested genotypes were early to medium maturing category. Grain felling period ranged from 42 to 54.7 and 35 to 49 at Tongo and Kulumsa, respectively, indicating long grain filling period is required at Tongo relative to Kulumsa.

Plant height varied from 63.3 to 83.5 cm at Tongo and 67.2 to 88.7 cm at Kulumsa with a mean height of 75.7 and 78.8 cm, respectively. Number of tillers per plant and spikes per plant were ranged from 2 to 4 and 2 to 4, respectively, at Tongo with a mean of 3 for number of tillers per plant and 3 for number of spike per plant. Similarly, these traits ranged from 2 to 4 and 2 to 4, respectively, at Kulumsa with a mean of 3 for number of tillers per plant and 3 for number of spike per plant. Both number of tillers per plant and number of spike per plant showed similarity in values at both locations indicating most of the tillers were fertile. Spike length ranged from 6.6 to 9.7cm at Tongo and 6.7 to 10.0 cm at Kulumsa with a mean length of 7.9 and 8.5 cm, respectively. The mean number of spikelets per spike and number of kernel per spike were ranged 15 to 22 and 27 to 54, respectively, at Tongo with a mean of 18 for spikelet per spike and 41 for kernels per spike. Similarly, these traits ranged from 15 to 21 and 40 to 54, respectively, at Kulumsa with a mean of 18 for spikelet per spike and 46 for kernels per spike.

The mean 1000 kernel weight ranged from 24.7 g (ETBW 7194) to 38.7 g (ETBW 7364) with an average value of 33.5 g at Tongo and ranged from 27.6 g (ETBW 7058) to 51.3 g (ETBW 8518) with an average value of 43.3 g at Kulumsa. Hectoliter weight provides a rough estimate of flour yield potential in wheat and is important to millers just as grain yield is important to wheat producer. This variable ranged from 71.3 kg/hl (ETBW 8516) to 81.9 kg/hl (ETBW 8510) with an average value of 78.7 kg/hl at Tongo and ranged from 65.4 kg/hl (ETBW 8511) to 75.9 kg/hl (ETBW 8506) with an average value of 73.2 kg/hl at Kulumsa.

Above ground biomass showed a wide range of variation 9000 to 14166.7 kg ha<sup>-1</sup> with the mean value 11627.8 and 6000 kg ha<sup>-1</sup> to 15000 kg ha<sup>-1</sup> with the mean value 10816.7 kg ha<sup>-1</sup> at Tongo and Kulumsa, respectively. Harvest index (HI) has been used to describe the proportion of harvestable biomass. Current modern wheat varieties have HI of c. 0.45 to 0.50 (spring type) and 0.50 to 0.55 (winter type), approaching its theoretical maximum value (c. 0.64 in winter wheat) (Foulkes et al., 2011; Reynolds et al., 2012). In this study, harvest index ranged from 0.1 to 0.3 with an average value of 0.2 at Tongo and ranged from 0.2 to 0.4 with an average value of 0.3 at Kulumsa. The score of the variable was lower than its theoretical maximum value (0.64) at both locations.

Grain yield is the final result that can be studied through its yield components. Grain yield varied from

**Table 4.** Mean squares of the 12 traits of bread wheat genotypes tested across location in 2015/16.

Characters	Sources						Mean	CV
	Loc. (DF=1)	Rep(Loc.) (DF=4)	Block(Loc*Rep) (DF=30)	Genotype (DF=29)	Genotype *Loc (DF=29)	Error (DF=86)		
Days to heading	49.09**	20.44*	3.22ns	131.47**	16.496**	3.78	55.78	3.49
Days to maturity	328.05**	3.77ns	7.99*	80.75**	13.34**	4.18	103.18	1.98
Plant height	449.98**	48.50**	18.08ns	107.90**	28.12**	10.39	77.24	4.17
Grain yield	29555458.2**	423874.04*	362988.16**	1086233.14**	681473.46**	148038	3271	11.76
1000 kernel weight	4398.48**	18.47*	11.62**	90.54**	19.29**	5.65	38.41	6.19
Hectoliter weight	1363.89**	11.81*	4.08ns	21.298**	6.94*	3.77	75.97	2.55
Harvest index	0.44**	0.007**	0.0013	0.006**	0.0038**	0.0009	0.29	10.1
Tillers per plant	2.54**	6.29**	1.03**	0.43ns	0.34ns	0.28	2.77	19.42
Spikes per plant	0.91ns	6.33**	0.99**	0.51**	0.3ns	0.25	2.63	19.17
Spikes length	11.12**	3.65**	0.67**	2.75**	0.25*	0.13	8.2	4.46
Spikelets per spike	6.54**	1.25ns	0.76ns	7.03**	1.87**	0.7	18.08	4.63
Kernels per spike	1159.76**	12.86	30.99**	74.996**	28.36**	11.58	43.24	7.87

ns, \*\* and \* indicates non-significant, highly significant at 1% and significant at 5% probability levels, respectively. Rep = Replication; Loc = Location; CV = Coefficient of variations; DF= degree of freedom.

**Table 5.** Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as of mean for the 14 characters of bread wheat genotypes tested at Tongo in 2015/16.

Characters	Range	Mean $\pm$ S.E. mean	$\sigma^2g$	$\sigma^2p$	H <sup>2</sup>	GCV (%)	PCV (%)	GA	GA (%)
Days to heading	46.00-70.33	55.25 $\pm$ 0.73	33.13	38.50	86.04	10.42	11.23	10.89	19.71
Days to maturity	97.00-117.00	104.53 $\pm$ 0.595	20.08	23.60	85.07	4.29	4.65	8.43	8.06
Grain filling period	42.33-54.67	49.28 $\pm$ 0.35	4.59	9.11	50.36	4.35	6.12	3.10	6.29
Plant height	63.26-83.50	75.66 $\pm$ 0.60	17.34	31.66	54.77	5.50	7.44	6.29	8.31
Grain yield	1284.40-3788.70	2865.80 $\pm$ 74.4	255042.19	407323.35	62.61	17.62	22.27	815.22	28.45
1000 kernel weight	24.67-38.67	33.47 $\pm$ 0.47	12.22	17.85	68.44	10.45	12.63	5.90	17.63
Hectoliter weight	71.33-81.87	78.73 $\pm$ 0.33	3.90	8.53	45.76	2.51	3.71	2.73	3.46
Above ground biomass	9000.00-14166.70	11627.78 $\pm$ 164.5	883758.50	2032550.30	43.48	8.08	12.26	1264.57	10.88
Harvest index	0.13-0.30	0.25 $\pm$ 0.004	0.00125	0.00183	68.19	14.41	17.45	0.06	24.28
Tillers per plant	2.20-4.30	2.88 $\pm$ 0.0735	0.11	0.31	34.28	11.26	19.23	0.39	13.44
Spikes per plant	2.00-4.20	2.70 $\pm$ 0.0771	0.12	0.32	38.44	13.00	20.97	0.44	16.45
Spikes length	6.60-9.67	7.95 $\pm$ 0.0963	0.50	0.67	75.17	8.89	10.26	1.25	15.73
Spikelets per spike	15.16-21.53	17.89 $\pm$ 0.1812	1.47	2.32	63.22	6.77	8.51	1.96	10.98
Kernels per spike	27.47-54.07	40.7 $\pm$ 0.7144	20.18	34.46	58.56	11.04	14.42	7.01	17.23

$\sigma^2g$  = genotypic variance;  $\sigma^2p$  = phenotypic variance H<sup>2</sup> = Broad sense heritability; GCV = Coefficient of genotypic variance; PCV = coefficient of phenotypic variance; GA = genetic advance.

1284.4 kg ha<sup>-1</sup> to 3788.7 kg ha<sup>-1</sup> (mean of 2865.8 kg ha<sup>-1</sup>) and 2588.3 kg ha<sup>-1</sup> to 4683.3 kg ha<sup>-1</sup> (mean of 3676.2 kg ha<sup>-1</sup>) at Tongo and Kulumsa, respectively. The grain yield performance was better at Kulumsa indicating its potential for wheat production. Gezahegn et al. (2015) reported a wide variation of grain yield per hactar which ranged from 2115 kg ha<sup>-1</sup> (Menze) to 5955 kg ha<sup>-1</sup> (Alidoro) in bread wheat. In present study, genotypes ETBW 8514 (3788.7 kg ha<sup>-1</sup>), Hidasse (3654.4 kg ha<sup>-1</sup>) and ETBW 8513 (3615.2 kg ha<sup>-1</sup>) at Tongo and ETBW 7871 (4683.3 kg ha<sup>-1</sup>), Hidasse (4536.7 kg ha<sup>-1</sup>) and ETBW 7872 (4495 kg ha<sup>-1</sup>) at Kulumsa were found to be top yielders (Appendix Tables 1 and 2). The standard check Hidasse was best performed at both location.

### ***Estimates of genetic parameters***

The amount of genotypic and phenotypic variability that exist in a species is of utmost importance in breeding to select better varieties and initiating a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given genotypes. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability as well as genetic advance for selection of the traits studied are presented in Tables 5 to 7.

**Phenotypic and genotypic coefficients of variation:** In general, estimates of phenotypic coefficient of variation in this study were higher than their corresponding genotypic coefficient of variation indicating the influence of environment on the expression of these characters although the differences were small at both locations. Narrower difference between the values of GCV and PCV indicated that the environmental effect was small for the expression of these characters. According to Deshmukh et al. (1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate.

At Tongo the GCV ranged from 2.51% (Hectoliter weight) to 17.62% (Grain yield), whereas PCV ranged from 3.71% (Hectoliter weight) to 22.27% (Grain yield). Among all characters, moderate GCV and PCV values (>10%) were observed for days to heading (10.42 and 11.23%), grain yield (17.62 and 22.27%), 1000 kernel weight (10.45 and 12.63%), harvest index (14.41 and 17.45%), tillers per plant (11.26 and 19.23%), spikes per plant (13.00 and 20.97%), kernels per spike (11.04 and 14.42%), respectively, suggesting sufficient variability and thus scope for genetic improvement through selection for these traits. Navin et al. (2014) reported higher magnitude of GCV and PCV for grain yield per plant, harvest index, tillers per plant, spike length and test weight which support this finding. The rest of the

characters grouped under low phenotypic and genotypic coefficients of variation, indicating less scope of selection as they were under the influence of environment.

At Kulumsa the GCV ranged from 0.11% (harvest index) to 13.57% (tillers per plant), whereas PCV ranged from 0.15% (harvest index) to 20.89% (tillers per plant). Moderate GCV and PCV values were observed for grain yield (10.32 and 14.59%), thousand-kernel weight (10.47 and 11.83%), above ground biomass yield (11.46 and 14.95%), tillers per plant (13.57 and 20.89%) and spikes per plant (12.65 and 19.50%), respectively. This indicated that selection will be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential. Similar results of moderate PCV and GCV has been reported for 1000 kernel weight and grain yield in wheat (Gezahegn et al., 2015). The characters days to maturity, grain filling period, plant height, hectoliter weight and harvest index were grouped under low phenotypic and genotypic coefficients of variation. The result is in line with the finding of Mohammed et al. (2011) and Gezahegn et al. (2015) for characters days to maturity, number of spikelets per spike and test weight showed low PCV and GCV (<5%) values. Mitsiwa (2013) also reported low PCV and GCV for grain filling period (1.82 and 1.59%) and days to maturity (3.63 and 3.50%), respectively.

The combined ANOVA results are presented in Table 7. Phenotypic coefficient of variability ranged from 2.89% (hectoliter weight) to 15.68% (spikes per plant). Genotypic coefficient of variability ranged from 2.89% (hectoliter weight) to 8.97% (1000 kernel weight). Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. Gezahegn et al. (2015), Gergana and Bozhidar (2015) and Navin et al. (2014) were reported similar result for all studied character. Low GCV (<10%) and moderate PCV (>10%) values were observed for grain yield (7.94 and 14.67%), 1000 kernel weight (8.97 and 10.73%), harvest index (6.60 and 12.43%), tillers per plant (4.32 and 14.81%) and spikes per plant (7.13 and 15.68%), respectively. Adhiena (2015) reported moderate PCV and GCV for spike length, number of grains per spike and harvest index. Similarly, Gezahegn et al. (2015) noted moderate phenotypic and genotypic coefficients of variation for 1000 kernel weight, grain yield and harvest index in sixty four bread wheat genotypes in Ethiopia which are in line with this finding for PCV. The lowest GCV and PCV values were observed for days to heading (7.85 and 8.63%), days to maturity (3.25 and 3.73%), plant height (4.72 and 6.00%), hectoliter weight (2.04 and 2.89%), spikelets per spike (5.13 and 6.56%), spikes length (7.87 and 8.65%) and kernels per spike (6.45 and 9.35%), respectively, indicating less scope of selection as they were under the influence of environment. The result is in line with the finding of Gezahegn et al. (2015) and Arati et al. (2015). Navin et al. (2014) reported higher PCV for grain yield



**Table 6.** Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as of mean for the 14 characters of bread wheat genotypes tested at Kulumsa in 2015/16.

Characters	Range	Mean $\pm$ S.E. mean	$\sigma^2g$	$\sigma^2p$	H <sup>2</sup>	GCV (%)	PCV (%)	GA	GA (%)
Days to heading	47.67 - 66.33	56.3 $\pm$ 0.45	13.67	15.86	86.20	6.57	7.07	7.08	12.58
Days to maturity	96.67 - 108.00	101.83 $\pm$ 0.41	8.50	13.33	63.76	2.86	3.59	4.80	4.72
Grain filling period	34.67 - 49.33	45.53 $\pm$ 0.38	5.49	11.68	46.97	5.15	7.51	3.31	7.28
Plant height	67.17 - 88.67	78.82 $\pm$ 0.7	21.07	27.54	76.51	5.82	6.66	8.28	10.51
Grain yield	2588.30 - 4683.30	3676.22 $\pm$ 68.8	143794.71	287589.42	50.00	10.32	14.59	553.17	15.05
1000 kernel weight	27.61 - 51.26	43.35 $\pm$ 0.59	20.62	26.29	78.41	10.47	11.83	8.30	19.14
Hectoliter weight	65.41 - 75.90	73.22 $\pm$ 0.27	3.00	5.90	50.73	2.36	3.32	2.54	3.47
Above ground biomass	6000 - 15000	10816.67 $\pm$ 183.84	1537587.8	2614391.40	58.81	11.46	14.95	1961.8	18.14
Harvest index	0.24 - 0.44	34.4 $\pm$ 0.006	0.00149	0.00267	55.80	0.11	0.15	0.06	0.17
Tillers per plant	1.93 - 4.33	2.73 $\pm$ 0.08	0.14	0.33	42.20	13.57	20.89	0.50	18.19
Spikes per plant	1.83 - 4.20	2.59 $\pm$ 0.08	0.11	0.26	42.10	12.65	19.50	0.44	16.94
Spikes length	6.67 - 10.00	8.45 $\pm$ 0.11	0.41	0.51	80.11	7.60	8.49	1.19	14.04
Spikelets per spike	14.73 - 20.53	18.27 $\pm$ 0.14	1.03	1.58	65.26	5.56	6.89	1.69	9.27
Kernels per spike	39.53 - 54.47	45.78 $\pm$ 0.49	6.55	15.44	42.41	5.59	8.58	3.44	7.51

$\sigma^2g$  = genotypic variance;  $\sigma^2p$  = phenotypic variance H<sup>2</sup> = Broad sense heritability; GCV= Coefficient of genotypic variance; PCV= coefficient of phenotypic variance; GA= genetic advance.

**Table 7.** Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as of mean for the 12 characters of bread wheat genotypes tested at across location in 2015/16.

Characters	Range	Mean $\pm$ S.E. mean	$\sigma^2gl$	$\sigma^2g$	$\sigma^2p$	H <sup>2</sup>	GCV (%)	PCV (%)	GA	GA (%)
Days to heading	46.83 - 66.83	55.78 $\pm$ 0.43	4.24	19.16	23.17	82.69	7.85	8.63	8.12	14.56
Days to maturity	96.83 - 112.50	103.18 $\pm$ 0.38	3.05	11.24	14.85	75.65	3.25	3.73	5.95	5.76
Plant height	66.93 - 85.47	77.24 $\pm$ 0.48	5.91	13.30	21.45	61.99	4.72	6.00	5.86	7.58
Grain yield	1936.40 - 4095.60	3271.01 $\pm$ 58.92	177811.85	67459.95	230384.82	29.28	7.94	14.67	286.71	8.77
1000 kernel weight	26.14 - 43.41	38.41 $\pm$ 0.53	4.54	11.88	16.98	69.96	8.97	10.73	5.88	15.31
Hectoliter weight	69.39 - 78.74	75.97 $\pm$ 0.30	1.06	2.39	4.81	49.79	2.04	2.89	2.23	2.93
Harvest index	0.19 - 0.36	0.29 $\pm$ 0.005	9.6x 10 <sup>-4</sup>	3.6 x10 <sup>-4</sup>	1.3x10 <sup>-4</sup>	28.21	6.60	12.43	0.02	7.15
Tillers per plant	2.23 - 3.82	2.77 $\pm$ 0.05	0.02	0.01	0.17	8.51	4.32	14.81	0.07	2.57
Spikes per plant	2.00 - 3.77	2.63 $\pm$ 0.05	0.02	0.04	0.17	20.66	7.13	15.68	0.17	6.61
Spikes length	7.10 - 9.70	8.20 $\pm$ 0.07	0.04	0.42	0.50	82.85	7.87	8.65	1.20	14.62
Spikelets per spike	15.20 - 20.55	18.08 $\pm$ 0.11	0.39	0.86	1.41	61.19	5.13	6.56	1.48	8.19
Kernels per spike	34.22 - 53.13	43.24 $\pm$ 0.47	5.59	7.77	16.36	47.51	6.45	9.35	3.92	9.07

$\sigma^2gl$  = genotype by environment interaction variance;  $\sigma^2g$  = genotypic variance,  $\sigma^2p$  = phenotypic variance; H<sup>2</sup> = broad sense heritability; GCV = Coefficient of genotypic variance; PCV = coefficient of phenotypic variance; GA = genetic advance.

per plant (28.43), tillers per plant (25.027), above ground biomass yield per plant (23.038), harvest index (23.03) and test weight (18.64) which contradicted this finding.

**Estimates of heritability:** Broad sense heritability ( $H^2$ ) which was estimated for the 14 character, ranged from 30.62 to 89.44% at Tongo and 35.82 to 87.81 at Kulumsa (Tables 5 and 6). Pramoda and Gangaprasad, (2007) categorized heritability estimates as low (<40%), medium (40-59%), moderately high (60-79%), and very high ( $\geq 80$ ). Accordingly, high heritability estimates were recorded (>80%) at Tongo for the characters; days to heading (86.04%) and days to maturity (85.07%) whereas medium to moderately high heritability were recorded for characters, grain filling period (50.36%), plant height (54.77%), grain yield (62.61%), 1000 kernel weight (68.44%), harvest index (68.19%), spikes length (75.17%), spikelets per spike (63.22%), kernels per spike (58.56%), hectoliter weight (45.76%) and above ground biomass yield (43.48%). The use of breeding will likely be successful in improving these traits or wheat genotype selections based on phenotype are effective. Low heritability estimates were recorded for tillers per plant (34.28%) and spikes per plant (38.44%) (Table 5).

At Kulumsa high heritability estimates were recorded (>80%) for the characters; days to heading (86.20%) and spikes length (80.11%) indicating that the variation observed were mainly under genetic control and were less influenced by the environment and the possibility of progress from selection. Moderate heritability were recorded for days to maturity (63.76%), plant height (76.51%), grain yield (57.99%), 1000 kernel weight (78.41%), hectoliter weight (50.73%), above ground biomass yield (58.81%), harvest index (55.80%), kernels per spike (65.25%). The result of harvest index, grain yield and hectoliter weight were in line with Gezahegn et al. (2015). Medium heritability estimates were recorded ( $\leq 50$ %) for the characters; grain filling period (46.97%), spikelets per spike (42.41%) tillers per plant (42.20%), spikes per plant (42.10%) indicating that the variation observed were mainly due to influence of the environment.

For combined analysis the estimated heritability for the studied traits is presented in Table 7. The heritability values ranged from 8.51 to 82.85 %. High heritability (>80%) was computed for days to heading and spike length indicating selection could be fairly easy and improvement is possible using these traits in breeding. Adhiena (2015) reported high heritability for days to heading which support this finding. Similarly, Gergana and Bozhidar (2015) and Desheva and Cholakov (2014) reported high heritability value for spike length. In the same year Gergana and Bozhidar (2015) reported high estimates of heritability (above 60%) for five characters spike length with awns (74.93%), spike length without awns (80.48%), spikelets per spike (63.96%), grain weight per spike (67.47)% and thousand grain weight (73.51%) in their study on variability, heritability, genetic

advance and associations among characters in emmer wheat genotypes. Medium to moderate heritability was recorded for days to maturity (75.65%), plant height (61.99%), 1000 kernel weight (69.96%), hectoliter weight (49.79%), spikelets per spike (61.19%) and kernels per spike (47.51%). Arati et al. (2015), Navin et al. (2014) and Ali et al. (2008) also reported high heritability estimates for grain yield per plant, number of seeds per spike, plant height and 1000 seed weight which support the present findings. Low heritability was recorded for the characters grain yield (29.28%), harvest index (28.21%), tiller per plant (8.51%) and spikes per plant (20.66%). This result is contradicted with the finding of Gergana and Bozhidar (2015) who reported high heritability for tillers per plant and spikes per plant. Selection may be considerably difficult or virtually impractical for less heritable due to the masking effect of the environment.

**Estimates of expected genetic advance:** Genetic advance as percent mean was categorized as low (0-10%), moderate (10-20%) and high 20% and above (Johnson et al., 1955). Accordingly, the expected genetic advance as the percent of means expressed as a percentage of the mean ranged from 3.46% for hectoliter weight to 28.45% for gain yield at Tongo (Table 5). High GAM was observed in grain yield (28.45%) and harvest index (24.28%). In accordance with finding of Arati et al. (2015) and Navin et al. (2014) who reported similar result with this study. GAM was moderate for days to heading (19.71%), 1000 kernel weight (17.63%), above ground biomass yield (10.88%), tillers per plant (13.44%), spikes per plant (16.45%), spikelets per spike (15.73%) and kernels per spike (10.98%). GAM was low for days to maturity, grain filling period, plant height and hectoliter weight.

At Kulumsa the expected genetic advance expressed as a percentage of the mean ranged from 0.17% for harvest index to 19.14% for 1000 kernel weight (Table 6), indicating that selecting the top 5% of the base population could result in an advance of 0.17 to 19.14% over the respective population mean. GAM was moderate for 1000 kernel weight plot (19.14%) followed by spikelets per spike, tillers per plant, above ground biomass yield, spikes per plant, spikes length, days to heading, plant height in conformity with the findings by Gezahegn et al. (2015) and Awale.et al. (2013) for the traits, 1000 kernel weight per plot (20.13%), grain yield (14.85%), days to 50% heading (14.70%) and number of grains per plant(14.65%) except for harvest index (15.68%).

Genetic advance expressed as percentage of mean from the combined analysis (Table 7) was moderate for days to heading (14.56%), 1000 kernel weight (15.31%) and spikes length (14.62). Gergana and Bozhidar (2015) reported moderate for spikes length (31.83%) and thousand grains weight (33.76%). Mohammed et al. (2011) and Navin et al. (2014) also reported high genetic advance (as percentage of mean) for grain yield and yield related traits like thousand kernel weight and harvest

index which are similar with the present finding. Awale et al. (2013) reported high genetic advance for days to heading, grain filling period, number of tillers, 1000 seed weight, plant height, peduncle length and spike length which are similar with this study except for number of tillers and grain filling period. This suggested selection could be effective in genotypes for these traits and the possibility of improving bread wheat grain yield through direct selection for grain yield related traits. Low genetic advance as percent of the means were recorded for the characters grain yield, harvest index, plant height, spikes per plant, spikelets per spike and kernels per spike, days to maturity, hectoliter weight and tillers per plant. The result is not in line with finding of Gergana and Bozhidar (2015) who reported high genetic advance as a percent of the mean for the characters, number of productive tillers per plant and plant height which are low in this study. Characters like days to heading, 1000 seed weight and spike length showed high heritability coupled with moderate genetic advance. Therefore, these characters should be given top priority during selection breeding in wheat. The results are in accordance with reports of Navin et al. (2014) for the character 1000 kernels weight and Desheva and Cholakov (2014) for spike length indicated that heritability was due to additive gene effects and selection may be effective in early generations for these traits. Gezahegn et al. (2015) reported that high heritability couple with moderate genetic advance as percent of mean for days to 50% heading (82.06 and 14.70%), 1000 kernel weight (74.28 and 20.13%), plant height (69.43 and 10.27%) and spike length (63.66 and 10.34%), respectively, which support the present study. High heritability associated with low genetic advance was exhibited by days to maturity (85.93 and 9.26). This may be because of predominance of non-additive gene action in the expression of this character. The high heritability of these traits was due to favorable influence of environment rather than genotypic and selection for these traits may not be rewarding.

## Conclusion

The study revealed the existence of significant genetic variability among the tested genotypes and heritability for different traits confirmed possibility to increase wheat productivity in target area. Attention should be given for traits which has moderate to high heritability and genetic advance in order to bring an effective response of grain yield improvement. Hence, selection and hybridization on those genotypes based on the trait with high GCV, heritability and genetic advance can be recommended for farther yield improvement of bread wheat at respective location.

## CONFLICTS OF INTERESTS

The authors have not declared any conflict of interests.

## REFERENCES

- Adhiena M (2015). Genetic variability and association among seed yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes at Oflla district, northern Ethiopia. Msc. Thesis, Haramaya University, Ethiopia.
- Ali Y, Babar MA, Javed A, Philippe M, Zahid L (2008). Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) Germplasm. Pakistan Journal of Botany 40(5):2087-2097.
- Allard RW (1960). Principles of plant breeding. Wiley and Sons. Inc. New York.
- Arati Y, Hanchinal RR, Nadaf HL, Desai SA, Suma B, Rudra NV (2015). Genetic variability for yield parameters and rust resistance in F<sub>2</sub> population of wheat (*Triticum aestivum* L.). International Quarterly Journal of Life Science 10(2):707-710.
- Awale D, Takele D, Mohammed S (2013). Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. International Research Journal of Agricultural Sciences 1(2):19-29.
- Bekele HH, Verkuijji WM, Tanner DG (2000). Adaptation of improved wheat technologies in Addaba and Dodola Woredas of the Bale highlands of Ethiopia. CIMMYT/EARO, Addis Ababa, Ethiopia.
- Braun HJ, Atlin G, Payne T (2010). Multi-location testing as a tool to identify plant response to global climate change. In: Reynolds MP, ed. Climate Change and Crop Production. Surrey: CABI. pp. 115-138.
- Burton GW, Devane EH (1953). Estimating heritability in Tall Fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal 45:487-488.
- Consultative Group on International Agricultural Research (CGIAR) (2013). Wheat Annual progress report. Research program on wheat.
- Central Statistics Agency (CSA) (2015). Agricultural sample survey report on area, production and yield of meher season crops for private peasant holdings. Statistical bulletin 578, CSA, Addis Ababa, Ethiopia.
- Daniel H, Mebrahtom M, Tsige G (2011). Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. Journal of Central European Agriculture 12(2):344-352.
- Desheva G, Cholakov T (2014). Variability, heritability and genetic progress for some Yield components in common winter wheat genotypes (*Triticum aestivum* L.) Genetics and Plant Physiology 4(3-4):191-200.
- Deshmukh SN, Basu MS, Reddy PS (1986). Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of ground nut. Indian Journal of Agricultural Science 56:515-518.
- Diers BW, Mcvetty PBE, Osborn TC (1996). Relationship between heterosis and genetic distance based on RFLP markers in oilseed rape (*Brassica napus* L.). Crop Science 36:79-83.
- Falconer, D. S. 1989. Introduction to Quantitative Genetics. 3rd ed. Longman, Essex, UK, pp. 275-276.
- Food and Agriculture Organization (FAO) (2015). Food and Agriculture Organization of the United Nations online database <http://www.fao.org/giews/>. Accessed, 4, February.
- Fassil K, Teklu E, Teklu T, Assefa G (2000). On farm demonstration of improved durum wheat varieties under enhanced drainage on Vertisols in central highlands of Ethiopia. In: Eleventh Regional Wheat Workshop for Eastern, Central and Southern Africa. CIMMYT, Addis Ababa, Ethiopia.
- Foulkes MJ, Slafer GA, Davies WJ, Berry PM, Sylvester-Bradley R, Martre P, Calderini DF, Griffiths S, Reynolds MP (2011). Raising yield potential of wheat. III. Optimizing partitioning to grain while maintaining lodging resistance. Journal of Experimental Botany 62:469-486.
- Global Agricultural Information Network (GAIN) (2015). Assessments of commodity and trade issues by USDA staff. GAIN, Ethiopia, ET-1503.
- Gergana D, Bozhidar K (2015). Study on variability, heritability, genetic advance and associations among characters in emmer wheat genotypes (*Triticum dicoccon* Schrank). Journal of Biological Science and Biotechnology SE/ONLINE:221-228
- Gezahegn F, Sentayehu A, Zerihun T (2015). Genetic variability studies

- in bread wheat (*Triticum Aestivum* L.) genotypes at Kulumsa Agricultural Research Center, South East Ethiopia. *Journal of Biology, Agriculture and Healthcare* 5:2224-3208.
- Gomez KA, Gomez AA (1984). *Statistical Procedures for Agricultural Research*, 2<sup>nd</sup> edit. John Wiley and Sons, New York.
- Goyal A, Prasad R (2010). Some important fungal diseases and their impact on wheat production. In: Arya A, PerellóAEV (eds) *Management of fungal plant pathogens*. CABI (H ISBN 9781845936037). P 362.
- Hailu GM, Tanner DG, Mengistu H (1991). Bread wheat Breeding and Genetics Research in Ethiopia: A Historical Perspective, Addis Ababa, IAR/CIMMYT.
- Idrees N, Khan MI (2009). Design improvement using uniformity trials experimental data. *Pakistan Journal of Agricultural Science* 46(4):2076-0906.
- Johnson HW, Robinson HF, Comstock RF (1955). Genotypic and Phenotypic correlation in soybean and their implication in selection. *Agronomy Journal* 47:477-483.
- Khan AA, Alam MA, Alam MK, Alam MJ, Sarker ZI (2013). Correlation and path analysis of durum wheat (*Triticum turgidum* L. var. *Durum*). *Bangladesh Journal of Agricultural Research* 38(3):515-521.
- Majumder DAN, Shamsuddin AKM, Kabir MA, Hassan L (2008). Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. *Journal of Bangladesh Agricultural University* 6(2):227-234.
- Masood MA, Faroo K, Mujahid Y, Anwar ZM (2008). Improvement in precision of agricultural field experiments through design and analysis. *Pakistan Journal of Life and Social Science* 6(2):89-91.
- Mengistu H, Getaneh W, Yeshe A, Rebka D, Ayele B (1991). Wheat pathology research in Ethiopia. *Wheat Research* pp.173-218.
- Mitsiwa A (2013). Genetic variability and association among agronomic characters in some wheat (*Triticum aestivum* L.) genotypes in Arsi zone, Oromia region, Ethiopia. Msc. Thesis, Haramaya University, Ethiopia.
- Mohammed A, Amsalu A, Geremew B (2011). Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. *durum*) genotypes. *African Journal of Agricultural Research* 6(17):3972-3979.
- Navin K, Shailesh M, Vijay K (2014). Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). *Journal Bioscience Discovery* 5(1):64-69.
- Obsa CH (2014). Genetic variability among bread wheat (*Triticum aestivum* L.) genotypes for growth characters, yield and yield components in Bore district, Oromia regional state. Msc. Thesis, Haramaya University, Ethiopia.
- Park RF, Bariana HS, Wellings CS (2007). Stem rust of wheat in Australia. Preface *Australian Journal of Agricultural Research* 58:469.
- Peng J, Sun D, Nevo E (2011). Wild emmer wheat, *Triticum dicoccoides*, occupies a pivotal position in wheat domestication. *Agricultural Journal of Crop Science* 5:1127-1143.
- Pramoda HP, Gangaprasad S (2007). Biometrical basis of handling segregation population for improving productivity in onion (*Allium cepa* L.). *Journal of Asian Horticulture* 3(4):278-280.
- Reynolds M, Bonnett D, Chapman SC, Furbank RT, Manès Y, Mather DE, Parry MAJ (2012). Raising yield potential of wheat. I. Overview of a consortium approach and breeding strategies. *Journal of Experimental Botany* 62:439-452.
- Rosegrant MW, Agcoili M (2010). Global food demand, supply and food prospects. International food policy research Institute, Washington, D.C., USA.
- Tesfaye T, Tsige G, Tadesse D (2014). Genetic variability, heritability and genetic diversity of bread wheat (*Triticum aestivum* L.) genotype in western Amhara region, Ethiopia. *Wudpecker Journal of Agricultural Research* 3(1):026-034.
- United States Department of Agriculture (USDA) (2016). *World Agricultural Production* 22:3.
- Zegeye T, Taye G, Tanner D, Verkuiji H, Agidie A (2001). Adoption of improved bread wheat varieties and inorganic fertilizer by small-scale farmers in Yelmana Densa and Farta districts of Northwestern Ethiopia. EARO and CIMMYT.

## Appendix

Table 1. Mean performance of 30 bread wheat genotypes tested at Kulumsa.

ENT	Genotypes	DTH	DTM	GFP	PTH	GY	TKW	HLW	BY	HI	TPP	SPP	SL	SPS	KPS
1	Hidasse	56.67	103	46.33	76.67	4536.7	48.81	73.01	11333	0.40	4.33	3.93	7.2	14.73	43.27
2	ETBW 6861	59	104	45	78.33	3845	40.54	73.44	10333	0.37	2.20	2.17	9.43	18.47	49.53
3	ETBW 8506	52.67	97.33	44.67	69.83	2640	44.39	75.90	6000	0.44	2.60	2.43	8.13	16.87	40.8
4	ETBW 8507	55	101.33	46.33	72.5	3151.7	48.28	68.97	10667	0.30	3.00	2.13	8.43	17	41.47
5	ETBW 7120	55.67	105	49.33	82.17	4001.7	46.55	72.66	11333	0.35	2.30	2.27	8.7	19.13	42.47
6	ETBW 8508	56.33	103.67	47.33	67.17	2876.7	41.66	74.53	10000	0.29	2.20	1.83	6.67	17.87	39.63
7	ETBW 7213	66.33	108	41.67	83.67	3538.3	35.65	72.58	11333	0.31	1.93	1.83	9.03	20.53	48.73
8	ETBW 8509	58	106	48	79	3753.3	34.05	73.05	11000	0.34	2.60	2.40	8.17	19.57	52.2
9	ETBW 7038	49.33	97.67	48.33	72.83	3625	45.98	75.16	10500	0.34	2.27	2.23	7.5	18.13	42.83
10	ETBW 8510	52.33	99	46.67	69.67	4126.7	42	75.61	10833	0.38	2.70	2.40	9.2	18.77	44.6
11	ETBW 7058	56.33	100.33	44	88.67	3563.3	46.42	72.93	10833	0.33	2.13	2.10	8.27	17.73	39.53
12	ETBW 8511	63	97.67	34.67	83.83	2588.3	27.61	65.41	10833	0.24	3.13	2.33	9.1	20.27	47.63
13	ETBW 7147	65.67	108	42.33	87	4016.7	34.58	68.47	15000	0.27	3.50	3.50	9.5	18.6	45.2
14	ETBW 8512	51.67	97.33	45.67	74	2935	44.04	73.52	10167	0.29	2.23	2.23	7.47	18.23	47.27
15	ETBW 7871	55.67	99.67	44	81.67	4683.3	44.42	74.48	11500	0.41	2.70	2.47	8.17	19.2	41.5
16	ETBW 8513	56.67	104.33	47.67	83	3215	44.27	74.71	11000	0.29	2.93	2.73	8.9	18.8	48.27
17	ETBW 6940	60	108	48	87.83	4011.7	39.39	73.11	11167	0.36	2.73	2.67	9.2	18.4	46.17
18	ETBW 8514	55.67	101.67	46	76.17	3998.3	45.37	74.35	11000	0.37	2.47	2.40	7.77	17.07	46.93
19	ETBW 7368	56	99.67	43.67	78.5	3790	46.69	75.47	10667	0.36	2.47	2.37	10	18.13	49.1
20	ETBW 8515	54.33	100.33	46	79.17	3730	44.65	73.97	12333	0.31	4.23	4.20	8.5	18.8	54.47
21	ETBW 7364	56.33	102.33	46	76	3308.3	46.21	72.93	9667	0.35	3.00	2.90	8.77	17.8	45.97
22	ETBW 8516	54.67	101	46.33	72.5	3935	49.45	73.91	10500	0.37	3.07	2.87	8.4	17.87	50.73
23	ETBW 7194	62.33	102.33	40	79.83	4180	36.74	72.93	11333	0.37	1.97	1.97	7.93	19.07	45.4
24	ETBW 8517	55.67	100.33	44.67	76.83	3958.3	45.65	73.63	11167	0.36	2.9	2.9	8.23	16.1	43.9
25	ETBW 7101	52.67	96.67	44	79	2753.3	45.6	73.75	9000	0.31	3.27	3.23	8.87	19.47	44.63
26	ETBW 8518	47.67	97	49.33	71	4168.3	51.26	74.89	9667	0.44	2.37	2.17	8	18.47	46.33
27	ETBW 7872	58	104	46	88.67	4495	43.8	74.37	14000	0.32	2.43	2.27	9.17	18.13	47.13
28	ETBW 8519	53.67	100	46.33	77.33	4018.3	46.51	73.27	10500	0.39	2.47	2.57	7.53	17.97	46.23
29	ETBW 6937	56.67	106	49.33	87.5	3350	43.23	73.7	9500	0.36	2.53	2.4	9.87	18.6	45.97
30	Danda'a	55	103.33	48.33	84.37	3493.3	46.81	71.95	11333	0.31	2.37	2.23	7.37	18.27	45.4
<b>Mean</b>		56.3	101.83	45.53	78.82	3676.2	43.35	73.22	10817	0.34	2.7	2.54	8.45	18.27	45.78
<b>CV</b>		2.63	2.16	11.42	3.23	10.39	5.5	2.33	9.59	9.99	16.05	15.15	3.79	6.51	4.06
<b>LSD at 5%</b>		2.44	3.62	4.1	4.19	624.4	3.92	2.81	1708.7	0.06	0.7141	0.6329	0.53	4.91	1.22
<b>LSD at 1%</b>		3.26	4.84	5.48	5.6	834.45	5.24	3.75	2283.5	0.08	0.95	0.85	0.7	6.56	1.63

**Table 2.** Mean performance of 30 bread wheat genotypes tested at Tongo.

ENT	Genotypes	DH	DM	GFP	PTH	GY	TKW	HW	BY	HI	TPP	SPP	SL	SPS	KPS
1	Hidasse	50	101	51	75.27	3654.4	38	79.23	13000	0.28	4.3	4.2	7.03	15.67	37.27
2	ETBW 6861	59	106.67	47.67	76.1	3293.7	30.67	78.97	12666.7	0.26	2.77	2.5	7.83	17.73	38.67
3	ETBW 8506	47.33	97	49.67	70.1	3287.7	35.33	81.17	11500	0.28	3.37	3.03	6.69	15.77	35.33
4	ETBW 8507	47.67	97.67	50	73.27	2828.3	37.33	79.93	10833.3	0.26	2.97	2.97	7.2	15.17	37
5	ETBW 7120	53.67	106	52.33	72.63	2441.2	38	78.3	11000	0.22	3.37	3.17	8.27	18.63	27.47
6	ETBW 8508	50	102.67	52.67	66.7	2019.9	36	81.17	10333.3	0.2	2.53	2.43	7.53	17.43	28.8
7	ETBW 7213	67.33	114.33	47	79.17	3410	30	78.2	14166.7	0.24	2.2	2.03	9.3	20.13	47.9
8	ETBW 8509	63	111	48	79.37	3019.8	29.33	79.37	13333.3	0.23	2.93	2.77	8.4	21.53	54.07
9	ETBW 7038	47.67	99	51.33	69.5	2650.6	33.33	80.77	10000	0.27	3.63	3.6	7.13	16.67	43.27
10	ETBW 8510	50.67	99	48.33	73.67	3003.5	32	81.87	11666.7	0.26	2.3	2.07	8	18.1	45.37
11	ETBW 7058	55	104.67	49.67	75.57	2815.8	34.67	78.83	11000	0.25	3.6	3.47	7.4	16.9	32.3
12	ETBW 8511	63.33	109	45.67	73.3	1284.4	24.67	73.37	10000	0.13	2.83	2.73	8.8	19.7	43.93
13	ETBW 7147	65	112.33	47.33	75.87	2867.5	28.67	75.23	12000	0.24	2.8	2.57	8.23	18.13	38.17
14	ETBW 8512	48.67	99	50.33	78.33	3180.4	36	80.03	11000	0.29	2.47	2.37	7.2	16.53	43.77
15	ETBW 7871	61.67	104	42.33	77.13	3420.4	31.33	81.03	12333.3	0.28	2.5	2.43	8.3	18.07	41.73
16	ETBW 8513	60	110.67	50.67	78.63	3615.2	37.33	80.9	12333.3	0.29	2.77	2.57	8.37	20	46.33
17	ETBW 6940	70.33	117	46.67	78.57	2614.5	30.67	75.9	13500	0.19	2.93	2.47	9.2	20.3	45.13
18	ETBW 8514	55.67	104.33	48.67	79.37	3788.7	36.67	80.3	12666.7	0.3	2.43	2.27	8.13	19.03	41.57
19	ETBW 7368	55.67	103	47.33	83.5	3242.5	34.67	81.7	12000	0.27	2.4	2.2	9.4	18.5	43.23
20	ETBW 8515	50.33	100	49.67	73.23	2428.2	33.33	77.77	10833.3	0.22	2.63	2.37	7.17	15.9	44.23
21	ETBW 7364	54.33	106	51.67	74.03	2896.3	38.67	78.43	11833.3	0.25	2.7	2.37	7.5	18.27	33.07
22	ETBW 8516	49	102	53	70.37	1923.8	28	71.33	9000	0.21	2.77	2.6	7.97	17.93	42.2
23	ETBW 7194	64.33	108.33	44	73.2	1625.9	24.67	75.5	10833.3	0.15	2.57	2.03	7.5	17.33	36.93
24	ETBW 8517	58	106.67	48.67	80.87	3265	35.33	78.57	12666.7	0.26	3.17	3.5	8.2	17.27	43.37
25	ETBW 7101	48	97	49	78.33	2873	32.67	79.37	10666.7	0.27	2.87	2.53	7.83	17.57	39.5
26	ETBW 8518	46	97.33	51.33	63.27	2594.6	35.33	78.97	9833.3	0.27	2.43	2.4	6.6	15.93	35.63
27	ETBW 7872	56.33	104	47.67	82.27	3342.2	37.33	81.47	12500	0.26	2.83	2.4	9.67	18.87	47.67
28	ETBW 8519	48	100	52	73.3	3157.6	36	77.77	11166.7	0.28	3	2.87	7.3	16.7	43.5
29	ETBW 6937	57	111.67	54.67	81.53	2817.2	30.67	79.27	12833.3	0.21	2.63	2.4	9.13	19.6	44.47
30	Danda'a	54.67	104.67	50	83.4	2611.9	37.33	77.1	11333.3	0.23	3.83	3.6	7.27	17.23	39.13
Mean		55.26	104.53	49.28	75.66	2865.8	33.47	78.73	11627.8	0.25	2.88	2.7	7.95	17.89	40.7
CV		4.2	1.8	4.31	5	13.62	7.09	2.73	9.22	9.84	15.59	16.45	5.11	5.16	9.29
LSD at 5%		3.82	3.09	3.5	6.23	642.57	3.91	3.54	1764.9	0.04	0.74	0.73	0.67	6.22	1.52
LSD at 1%		5.1	4.13	4.68	8.33	858.72	5.22	4.73	2358.6	0.05	0.99	0.98	0.89	8.32	2.03

DH, Days to heading; DM, Days to maturity; GFP, Grain filling period; GY, Grain yield; TKW, 1000 kernel weight; AGB, Above ground biomass (kg ha<sup>-1</sup>); HI, Harvest index; HW, Hectoliter weight; TPP, Tillers per plant; PH, Plant height (cm); SPS, Spikelets per spike; KPS, Kernels per spike; SL, Spike length; SPP, Spikes per plant. LSD= List significant difference; CV= Coefficient of variations.