



# Genetic Variability Analysis of Agro-Morphological Traits among Bread Wheat (*Triticum aestivum* L.) Genotypes at Raya Valley of Southern Tigray, Ethiopia

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## ABSTRACT

Assessment of genetic variability in crop species is one of the major activities of plant breeding which helps to design breeding methods and/or selection of genotypes for further evaluation to meet the diversified goals. Therefore, this field experiment was conducted to assess the genetic variability in bread wheat genotypes. The field evaluation of 32 genotypes and 4 released varieties was conducted in 6 x 6 Triple Lattice Design at Mehoni Agricultural Research Station in 2017 cropping season. Results of analysis of variance revealed the presence of significant differences among genotypes for 12 quantitative traits. The variation observed among genotypes for grain yield ranged from 2.80 to 5.33 t ha<sup>-1</sup>. The four genotypes (QAFZAH-2/FERRIUG-2, KAUZ'S'/FLORKWA1//GOURMIA-3, ETBW5957 and SERI 82/SHUHA'S//PASTOR-2 had yield advantage of 7.58 to 12.21% over the high yielding check variety, GAMBO (4.75 t ha<sup>-1</sup>). Phenotypic (PCV) and genotypic (GCV) coefficient of variations ranged from 5.67 (plant height) to 14.74 (fertile tiller per plot) and 7.06 (days to maturity) to 19.08% (fertile tiller per plot), respectively. Heritability (H<sup>2</sup>) in broad sense and genetic advance as percent of mean (GAM) ranged between 41.46 (biomass yield) and 89.08 (days to heading) and 8.56 (plant height) and 24.09% (harvest index), respectively. High H<sup>2</sup> estimates coupled with moderate or high GAM for plant height, days to heading, days to maturity, spike length, grain yield, spikelets per spike and harvest index suggested the higher chance of improving these traits through selection of genotypes for high mean performance.

## 1. INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a hexaploid species with (2n=6x=42) having AABBDD with A, B and D genomes (Sleper and Poehlman, 2006). It is one of the oldest domesticated grain crops for 8000 years which native to Middle East. It has been

the basic staple food of many regions of the world, while it is grown under both irrigated and rain-fed conditions. It belongs to family Poaceae (formerly Graminae) (Yadawad *et al.*, 2015). World wheat production in 2017 was 743.2 million tons with average yield (3.34 t ha<sup>-1</sup>) and it accounts for nearly 30% of global cereal (FAO, 2017). The hexaploid bread wheat

accounts for 95% of the total wheat production; most of the remaining 5% is from tetraploid durum wheat (*T. turgidum* subsp. durum,  $2n=4x=28$ , AABB) (Shewry, 2009).

In Ethiopia, wheat is one of the major staple and strategic food security crops, and accounts for approximately 11% of the national calorie intake. Ethiopia is the second largest wheat producer in sub-Saharan Africa after South Africa. It is cultivated on 1.7 million hectares of land and has the production of 4.54 million tons with remain low productivity of  $2.67 \text{ t ha}^{-1}$  (CSA, 2017) in the country as compared to the world average yield ( $3.34 \text{ t ha}^{-1}$ ) (FAO, 2017).

Wheat is producing in Tigray regions which relatively lager as compared to other crop of the area. The total wheat area and production in Tigray region was 107,724.17 hectares and 212,867.26 tons with the average yield of  $1.98 \text{ t ha}^{-1}$ . Wheat stands second both in area and production among all crops followed by barely and *tef*. In the southern zone, the area coverage and productivity of wheat was 49,189.20 ha and 1,019,11.14 tons with the average yield of  $2.072 \text{ t ha}^{-1}$  respectively which is lower than from national (CSA, 2017).

Genetic improvement to develop varieties with high yield potential and resistance/tolerance to abiotic and biotic stresses, with acceptable end-use quality, is the most viable and environment-friendly option to sustainably increase wheat yield. Selection for grain yield improvement can only be effective if sufficient genetic variability is present in the genetic material (Ali *et al.*, 2008). Therefore, knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding program (Bisne, 2009). Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 1960; Falconer and Mackay, 1996). In order to bring the heritable improvements in economic characters through selection and breeding, estimation of genetic parameters must be made before starting a program. There are different techniques available to compute the genetic parameters and the index of transmissibility of characters (Waqar- Ul-Haq *et al.*, 2008).

The existence of variation alone in the population is not sufficient to improve desirable characters. High heritability is also needed to have better opportunity to select directly for the traits of interest. This is mainly because of the opportunity associated with high heritability incorrect identification and measurement of the genotypes based on phenotypic values and in avoiding errors in genotypic classification (Welsh, 1981). In breeding programs, selection is an integral part by which genotypes with high productivity in a given environment could be developed. However, selection for high yield is difficult because yield is the

end product of components of several characteristics, polygenic inheritance, and highly influenced by environment and genotype x environment interaction.

In the Southern Zone of Tigray Regional State, at mid and highland areas, some genetic variability studies in wheat genotypes have been made to develop varieties (Adhiena *et al.*, 2016). Raya Valley is the part of Southern Zone of Tigray Regional State; however, neither genetic variability studies in wheat genotypes nor introduction of improved wheat varieties were attempted. This is due to the insufficient rain fall to support the growth and yield production of wheat in the area and the largest part of the valley is at low altitude ( $\leq 1600 \text{ m.a.s.l.}$ ) experiencing warm to hot weather conditions. But, the dependence on rainfall alone in the area has in recent years been gradually replaced by supplemental irrigation and irrigated crop production. The number of farmers and investors using irrigation and supplemental irrigation is increasing. However, the absence of recommended varieties for the area remains as one of the major wheat production constraints in the area. Therefore, it is necessary to undertake research to develop wheat varieties for which genetic variability study is the first step. Thus, the present research was undertaken with the following objectives:-

- To assess genetic variability in selected bread wheat genotypes

### 3. MATERIALS AND METHODS

#### 3.1. Description of the Experimental Area

The study was carried at the research station of Mehoni Agricultural Research Center (MhARC) under supplemental irrigation in the 2017 main cropping season. Mehoni is located in Raya Valley in the northern parts of Ethiopia about 668 km from county's capital city of Addis Ababa, and about 120 km South of Mekelle, the capital city of Tigray regional state, Northern Ethiopia. Geographically, the experimental site is located at  $12^{\circ} 41'50'' \text{ N}$  latitude and  $39^{\circ} 42'08'' \text{ E}$  longitude with an altitude of 1578 m.a.s.l. The site receives mean annual rainfall of 750 mm with an average minimum and maximum temperature of  $22^{\circ} \text{ C}$  and  $32^{\circ} \text{ C}$ , respectively. The soil type and textural class of the experimental area is verty soil and clay loam respectively with pH of 7.9-8.1 (Hailelassie *et al.*, 2015).

When there was cessation of rainfall during the execution of the experiment, the crop was affected by moisture stress. During this time supplementary irrigate was provided using ground water resource to compensate the amount of water needed by the crop and also to provide the essential moisture for normal growth. This practice helps in alleviating the adverse effects of unfavorable rain patterns and improves crop yields. Therefore, amount of irrigation water to

supplement to each experimental plot was directed using drip irrigation which was installed in the experimental site, and the amount of water was measured using soil squeezed method to test soil moisture manually by hand and the irrigating started from booting stage at 55 days after sowing.

### 3.2. Experimental Plant Materials

A total of 36 bread wheat genotypes including four standard checks (Table.1) obtained from the National Wheat Research Program specifically from Werer (WARC) and Kulumsa (KARC) Agricultural Research Centers. The genotypes were selected based on adaptation to low moisture stress and classified under lowland types. In this experiment, four released for moisture stress bread wheat varieties were included as standard checks

**Table 1. List and pedigree of the thirty six bread wheat genotypes including four released varieties**

G*	Genotype (Pedigree)	Origin
G1	HUBARA-3*2/SHUHA-4	CIMMYT/ICARDA
G2	Atila-7	CIMMYT/ICARDA
G3	ETBW5535	EIAR/KARC
G4	ETBW5957	EIAR/KARC
G5	ATILA/AWSEQ-4	CIMMYT/ICARDA
G6	FENTALLE (CHECK)	CIMMYT/ICARDA
G7	ADEL-2	CIMMYT/ICARDA
G8	DAJAJ-1//VEE'S'/SAKER'S'	CIMMYT/ICARDA
G9	PASTOR-2/HUBARA-5	CIMMYT/ICARDA
G10	HIDDAB/ATTILA-7	CIMMYT/ICARDA
G11	PASTOR-2/HUBARA-3	CIMMYT/ICARDA
G12	HUBARA-5/ANGI-1	CIMMYT/ICARDA
G13	GAMBO (CHECK)	CIMMYT/ICARDA
G14	ANGI-2/HUBARA-3	CIMMYT/ICARDA
G15	ETBW 5898 (SET II C1)	EIAR/KARC
G16	QAFZAH-2/FERRIUG-2 (SET II C1)	CIMMYT/ICARDA
G17	TAGANA	CIMMYT/ICARDA
G18	JNRB.5/PIFED	CIMMYT/ICARDA
G19	KINGBIRD (CHECK)	EIAR/KARC
G20	OGOLCHO (CHECK)	EIAR/KARC
G21	ETBW5955 SET II C2)	EIAR/KARC
G22	REYNA-28	CIMMYT/ICARDA
G23	ETBW5963(SET II C3)	EIAR/KARC
G24	PRINIA-1//NESMA*2/14-/3/DUCULA	CIMMYT/ICARDA
G25	FRANCOLIN #1/BAJ #1	CMSS09B00490S-099M-099Y-2WGY-0B
G26	KAUZ'S'/FLORKWA1//GOUMRIA-3	CIMMYT/ICARDA
G27	BJY/COC//PRL/BOW/3/BLOYKA-1	CIMMYT/ICARDA
G28	KUBSA	CIMMYT/ICARDA
G29	PBW343*2/KUKUNA//KIRITATI	CIMMYT/ICARDA
G30	HUBARA-2/QAFZAH-21//DOVIN-2	CIMMYT/ICARDA
G31	INQALAB 91*2/TUKURU//WHEAR	CIMMYT/ICARDA
G32	ATILA*2//CHIL/BUC*2/3KUKUNA	CIMMYT/ICARDA
G33	SERI 82/SHUHA'S'//PASTOR-2 (SET I)	CIMMYT/ICARDA
G34	florkwa2/6/saker's'/5/rbs /anza/3/kvz/hys/ymh/tob /4/bow	CIMMYT/ICARDA
G35	katila17/deek2/8vee's'/7/cebeco148/3/ron/cha//nor67/5/hk/38m	CIMMYT/ICARDA
G36	attila 50y//attila/bcn/3/star*3/ musk-3	CIMMYT/ICARDA

Source: G\* = genotype code number used in the thesis.

### 3.3. Experimental Design and Layout

The field experiment was laid out in 6x6 triple Lattice design. The width of 1.2 m and length of 2.5 m and a total 3 m<sup>2</sup> area was allocated for each plot in each incomplete block of replication. Each plot had six rows at the spacing of 20 cm between rows, 0.5 m path between plots, 1 m spacing between sub-blocks (incomplete block) and 1.5 m distance between replications with total area of 19.5 m x 41.6 m. The net plot size of experimental plot was 1 m x 2.5 m (2.5 m<sup>2</sup>) since the plants in the two outer most rows were treated as border plants and excluded.

### 3.4. Land Preparation, Sowing and Management

The experimental field was prepared by using farm tractor plough. It was ploughed two times, the first at the beginning of May the second at the middle of June and the third manually using labor worker during planting in early July 2017.

The full dose of blended fertilizer recommended for the study area are NPSzn (19% N, 38%P: 7% S and 2.5% Zn) at the rate of 100 kg ha<sup>-1</sup> was applied as band application at planting time under supplemental irrigation. Nitrogen fertilizer in the form of Urea (46% N) at a rate of 150 kg ha<sup>-1</sup> was applied in two split doses; with half applied two weeks after sowing and remaining half after early booting stage. The seeds (125 kg ha<sup>-1</sup> rate) were sown by hand drilling in the rows as uniformly as possible. All other necessary field management practices were carried out as per the recommendations.

### 3.5. Data Collection

Data were collected both on plot and plant bases. The four central rows were used for data collection on plot basis, whereas 10 randomly selected plants from the four central rows of each plot were used for data collection on plant basis. Mean data of the 10 sample plants were used for data analyses.

#### 3.5.1. Data collected on plot basis

**Days to heading:** The number of days from the date of sowing to the stage where 50% of the plants have fully emerged spikes.

**Days to physiological maturity:** The number of days from the date of sowing to the stage where 90% of the plants in the plot reached physiological maturity.

**Grain filling period:** The number of days from heading to maturity obtained by subtracting the number of days to heading from the number of days to maturity.

**Thousand kernel weight (g):** The weight of one thousand randomly taken kernels from each experimental plot and adjusted to 12.5% moisture content.

**Grain yield plot<sup>-1</sup>(g plot<sup>-1</sup>):** Grain yield in grams obtained from the central four rows of each plot, and adjusted to 12.5% moisture content.

**Grain yieldha<sup>-1</sup>(t ha<sup>-1</sup>):** Grain yield obtained from each plot was used to calculate grain yield in tons per hectare.

**Biomass yields (t ha<sup>-1</sup>):** The plants in the four central rows were harvested at the point of attachment to the ground, collected, sun-dried and weighed to obtain the biological yield.

**Harvest index (HI%):** Calculated on a plot basis, as the ratio of dried grain weight adjusted to 12.5% moisture content to the dried total above ground biomass weight and multiplied by 100.

#### 3.5.2. Data collected on plant basis

Data for the following characters were recorded on 10 randomly selected plants from each experimental plot. The averages of the ten plants in each experimental plot were used for data analysis.

**Plant height (cm):** This was measured from the soil surface to the tip of the spike excluding the awns at physiological maturity.

**Number of fertile tillers per plant:** The average number of fertile tillers per plant

**Kernels per spike:** The average number of kernels per spike

**Spikelet per spike:** The average number of spikelet per spike

**Spike length (cm):** This was measured in cm from the base of the spike to the top of the last spikelet excluding the awns.

**3.6. Data Analyses**

**3.6.1. Analysis of variance**

The data were subjected to analysis of variance (ANOVA) using SAS statistical software version (9.2)

(SAS, 2008) as per the expectations shown on Table 2. The comparison of mean performance of genotypes was done following the significance of mean squares using Duncan’s Multiple Range Test (DMRT).

**Table 2. Analysis of variance in triple lattice design and expected mean square**

Source of variation	DF	Sum of squares (SS)	Mean square MS= $\frac{SS}{df}$	Computed F	Expected mean squares
Replication	r – 1	SSR	MSR	$\frac{MSR}{MSE}$	$\sigma^2 + k\sigma b^2 + v\sigma r^2$
Treatment (unadj.)	k <sup>2</sup> – 1	SST (unadj.)	MST (unadj.)	$\frac{MST(unadj)}{MSE}$	$\sigma^2(\frac{k}{k+1}) m \sigma t^2$
Blocks within replication (adj.)	r(k-1)	SSB (adj.)	MSB (adj.)	$\frac{MSB(adj)}{MSE}$	$\sigma^2 + \sigma t^2 + k\sigma t^2$
Intra block error	(k-1)(rk-k-1)	SSE	MSE		a <sup>2</sup>
RCB Error	(t-1) (r-1)	SSe	MSe		$\sigma^2 e$
Total	rk <sup>2</sup> – 1	SSTO			

r = Number of replications. k<sup>2</sup> = Number of treatments, k = Number of plots in a block, SS = Sum square, MS = Mean square,  $\sigma^2$  = Variance, t = Number of genotypes, MSE = Mean squares for error and  $\sigma^2 e$ = Error variance.

Relative efficiency=  $\frac{\text{mean square error in RCBD design}}{\text{mean square error in tirriple lattice design}} \times 100$  according to (Gomez and Gomez (1984).

The characters that exhibited significant mean squares in general ANOVA were further subjected to genetic analyses. Phenotypic and genotypic variance and coefficient of variation, heritability, and genetic advance were computed using the Excel Microsoft Program. Genetic diversity was estimated from quantitative traits of genotypes using Euclidean distance computed by Statistical Software.

**3.6.2. Phenotypic and genotypic variability**

The phenotypic and genotypic variability of each quantitative trait were estimated as phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic coefficients of variation were computed using the formula suggested by Burton and de Vane (1953) as follows.

Genotypic variance ( $\sigma^2 g$ ) =  $\frac{M_{sg} - M_{se}}{r}$

Where,  $\sigma^2 g$  = genotypic variance,  $M_{sg}$ = mean square of genotype,  $M_{se}$  = mean square of error, r = number of replications

Phenotypic Variance ( $\sigma^2 p$ ) =  $\sigma^2 g + \sigma^2 e$

Where,  $\sigma^2 g$  = Genotypic variance,  $\sigma^2 e$  = Environmental variance in which Environmental variance = mean square of error and

$\sigma^2 p$  = phenotypic variance

$PCV = \left( \frac{\sqrt{\sigma_p^2}}{\bar{x}} \right) \times 100$

$GCV = \left( \frac{\sqrt{\sigma_g^2}}{\bar{x}} \right) \times 100$

Where: PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation = population mean of the character being evaluated

PCV and GCV values were categorized as low, moderate, and high values as indicated by Sivasubramaniah and Menon (1973) as follow. > 0 -

10% = Low, > 10 – 20% = Moderate; and > 20% = High

### 3.6.3. Heritability and genetic advance

Broad sense heritability values were estimated using the formula adopted from Falconer and Mackay (1996).

$$H^2 = (\sigma^2g/\sigma^2p) \times 100$$

Where,  $H^2$  = heritability in broad sense

$$\begin{aligned} \sigma^2p &= \text{phenotypic variance} \\ \sigma^2g &= \text{Genotypic variance} \end{aligned}$$

The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al.* (1955) as follows:-

> 0 - 30% = Low, > 30 – 60% = Moderate; and > 60% = High

### Expected genetic advance under selection (GA)

Genetic advance in absolute unit (GA) and as percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson *et al.* (1955) as:

$$GA = K * SDp * H^2;$$

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

### Genetic advance as percent of mean (GAM)

Genetic advance as percent of mean was estimated as follows:

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

Where, GAM = Genetic advance as percent of mean, GA = Genetic advance

$\bar{X}$  = Population mean of the character being evaluated

The GA as percent of mean was categorized as low, moderate and high as suggested by Johnson *et al.* (1955) as follows. 0 - 10% = Low, 10 – 20% = Moderate, and >20% = High

## 4. RESULTS AND DISCUSSION

### 4.1. Analysis of Variance

The analyses of variance (Table 3) showed highly significant differences ( $P < 0.01$ ) among wheat genotypes for all studied traits. Such considerable range of variations would provide a good opportunity for yield improvement. The results also justifies carrying out further genetic analysis by considering all (12) agro-morphology traits. Adhiena *et al.* (2016) conducted genetic variability study in 26 bread wheat genotypes considering twelve traits in Southern Zone of Tigray Regional State, at mid and highland areas. They reported the presence of significant differences among genotypes for all traits except for plant height and number of spikelets per plant. Many authors also revealed highly significant differences among all the wheat genotypes for all the characters (Mohammed *et al.*, 2011; Dergicho *et al.*, 2015; Gezahegn *et al.*, 2015). However, days to maturity, number of tillers per plant, biological yield and harvest index were not significantly different in durum wheat genotypes (Dawit *et al.*, 2012). This disparity may be due to the differences in the genotypes and test environments used in the different studies.

The relative efficiency of triple lattice design was greater than one for more than half quantitative traits but it was greater than 0.95 for all quantitative traits indicating triple lattice design is advantage as over RCBD in increasing in experimental precision (Table 3). Masood *et al.* (2008) and Idrees and Khan, (2009) reported alpha lattices design were on the average more efficient in reducing the experimental error and hence provide the efficient estimation of treatment contrasts. Thus, the present analysis were done by using triple lattice design. Coefficients of variation in percent were also used to compare the precision of the experimentation i.e. means with lower CV% for most of the characters revealed the reliability of the data collected from the experiment (Gomez and Gomez, 1984).

**Table 3. Mean squares from analysis of variance for twelve traits of thirty six bread wheat genotypes evaluated at Mehoni in 2017**

Traits	Replications(d.f =2)	Block Within replication (Adj.)(df=15)	Treatments (d.f=35)		Intra block Error (d.f=55)	RCBD Error	Rel. to effic. (%)	CV (%)
			(Unadj)	(Adj)				
Plant height (cm)	1293.51**	20.43**	94.92	91.22**	17.49	18.12	100.51	4.88
Days to heading	7.06**	4.82**	142.80	122.83**	4.04	4.21	100.64	2.80
Grain filling period (days)	2.26ns	5.71**	28.04	27.50**	6.12	6.08	98.39	8.59
Days to maturity	1.69ns	9.04**	157.00	132.74**	8.13	8.32	100.24	2.84
No. of fertile tillers/plant	0.11ns	0.07ns	0.50	0.38**	0.09	0.08	95.67	13.53
Spike length (cm)	0.14ns	0.24ns	2.70	2.17**	0.25	0.25	98.89	5.28
No. of spikelets/spike	0.22ns	0.98ns	7.31	6.48**	1.21	1.16	95.92	5.98
No. of kernels/ spike	15.53**	17.32**	65.39	56.24**	12.22	13.31	102.49	7.54
1000-kernel weight (g)	3.77ns	12.70**	58.66	53.33**	12.99	12.93	99.51	10.07
Grain yield (t/ha)	0.14ns	0.09ns	1.13	0.96**	0.12	0.12	94.46	8.38
Biomass yield (t/ha)	0.04ns	0.08ns	0.25	0.25**	0.10	0.09	95.31	10.26
Harvest index (%)	2.09ns	7.83**	82.19	74.19**	6.91	7.11	100.33	7.60

Note, \*\* and \* indicates highly significant at (1%) and significant at (5%) probability levels, respectively. DF= degree freedom

Rel.effic. = relative efficiency, RCBD=completely randomized design, CV= coefficient of variations and adj. and uadj. = adjusted or unadjusted treatment

## 4.2. Mean Performance of Genotypes

### 4.2.1. Phenology and Growth Characters

The genotypes variation for days to heading, grain filling period and days to maturity ranged from 58 to 81, 21 to 33 and 89 to 115, respectively. The mean performances of genotypes for plant height and number of fertile tillers per plot ranged from 74 to 97, and 1.4 to 2.9, respectively (Table 4). Adhiena *et al.* (2016) reported a wide range of variations among 26 bread wheat genotypes for days to heading ranged from 49.3 to 63 days with a mean of 56.9 days and days to maturity ranged from 102.7 to 129.7 days with a mean value of 114 days. Alemu *et al.* (2016) also reported wide range of variation between 48 and 66, and 97 and 108 for days to heading and days to maturity, respectively, among 30 bread wheat genotypes.

One (G1), three (G3) and two (G2) genotypes had mean performances lower than the earliest standard check (Kingbird) for days to heading, grain filling period and days to maturity, respectively (Table 4). None of new entry genotypes showed superiority over highest performing check (Gambo) for plant height while four genotypes had mean number of fertile tillers per plot greater than the highest performing check variety (Fentalle). Three (G3) and five (G5) genotypes were shorter than the check with shortest plant height among check varieties and low number of fertile tillers per plot, respectively. Among 36 genotypes, 47.22% exhibited days to heading lower than the genotypes mean indicating those genotypes were early heading as compared to the others (Table 4). Grain filling is also an important trait that ultimately affects the overall grain yield by increasing grain weight. The results in agreement with the findings of Mollasadeghi *et al.* (2012) in which days to heading and days to maturity showing similar parallelism to each other. However, some authors also reported non-significant differences among bread wheat genotypes for days to maturity and number of fertile tillers (Khan, 2013). This result suggested that the higher chance of selecting early genotypes which can escape the terminal moisture stress which is one of the wheat production problems in the study area. In this study, the genotypes with early heading also showed early maturity and late maturing ones exhibited correspondingly late days to heading. The differences of different authors report for the performance of bread wheat genotypes for maturity, plant height and number of fertile tillers for varied number of bread wheat genotypes might be due to the differences in the genetic factors carried by the genotypes included in each experiment, growing seasons and environments where the genotypes evaluated. The early maturity, plant height and number fertile tillers were reported as a function of both genetic and environmental factors (Berhanu, 2004; Obsa, 2014; Alemu *et al.*, 2016).

### 4.2.2. Spike, biomass, harvest index and grain yield characters

Traits like, the number of grains per spike is an important plant attribute that depends upon spike length, spikelets per spike and spike density. Accordingly, the wide genotypes variation for spike length, spikelets per spike, number of kernels per spike and thousand-kernel weight ranged from 7.6 cm to 11.4 cm, 15 to 22, 35 to 59, and 27g to 44g, within an average value of 9.46, 18.38, 46.10 and 35.79 respectively (Table 4). Similarly, Maqbool *et al.*, (2010) reported wide range of variation for plant height, grain filling period, number of spikelets per spike, biological yield, grain yield and thousand-kernel weight. The mean performances of genotypes for biomass yield ( $\text{plot}^{-\text{kg}}$ ) and harvest index were ranged from 2.1 to 3.5 and 21.9-42.1% respectively. Current modern wheat varieties have harvest index (HI) of c. 0.45-0.50 (spring type) and 0.50-0.55 (winter type), approaching its theoretical maximum value (c. 0.64 in winter wheat) (Foulkes *et al.*, 2011; Reynolds *et al.*, 2012). This wide ranges of mean values these traits depicted that bread wheat germplasm possess good amount of genetic variability.

Three genotypes; viz ATILA\*2//CHIL/BUC\*2/3KUKUNA, ETBW5535 and ETBW5963 (SET II C3) genotypes with longer spike length than the check (Gambo), the longest spike length among check varieties. High number of kernels per spike was recorded for genotypes 6 and 9 respectively than the standard check (Gambo) (Table 4). Eight, twenty nine and thirty three entry genotypes showed superior for spikelets per spike than highest performing check (Gambo). Among 36 genotypes, 25% of the genotypes showed highest thousand-kernel weight than the highest performing check (Ogolcho) variety. In the present result for thousand kernel weight, comparative result with Obsa (2014) report for 1000-seed weight with values ranging from 25 to 46.67 g with a mean value of 39.67g.

Grain yield per plant is also a character of prime importance and of special interest to a wheat breeder. Accordingly, highly significant variability was observed among genotypes for grain yield  $\text{t ha}^{-1}$ , which ranged from 2.9 to 5.3 with the mean value of 4.18  $\text{t ha}^{-1}$  and coefficient of variation of 8.38%. Depending on the mean performances, genotypes such as QAFZAH-2/FERRIUG-2 (SET II C1), KAUZ'S'/FLORKWA1//GOUMRIA-3, SERI 82/SHUHA'S'/PASTOR-2 (SET I) and ETBW5957HUBARA-3\*2/SHUHA-4 had mean performances higher than the highest performing check variety (Gambo=4.75  $\text{t ha}^{-1}$ ) for grain yield ( $\text{t ha}^{-1}$ ) with 5.33, 5.16, 5.15 and 5.11 while lower yielder were obtained from genotypes G30 (3.33  $\text{t ha}^{-1}$ ), G11 (2.98  $\text{t ha}^{-1}$ ) and G8 (2.87  $\text{t ha}^{-1}$ ) (Table 4). Generally, the range of variation was wide for all the characters studied. Berhanu *et al.* (2017) conducted genetic variability among 49 bread wheat genotypes at Axum,



Northern, Ethiopia and reported a wide range of grain yield from 2.37 to 5.44 t ha<sup>-1</sup> with a mean of 3.95 t ha<sup>-1</sup> and the maximum grain yield obtained was 5.44 t ha<sup>-1</sup> and 5.37 t ha<sup>-1</sup>, 4.64 t ha<sup>-1</sup>) and 4.56 t ha<sup>-1</sup> respectively. Gezahegn *et al.* (2015) reported a wide variation of grain yield per hectare which ranged from 2.11 to 5.95t ha<sup>-1</sup> while Alemu *et al.* (2016) also

reported that 2.59 to 4.68 t ha<sup>-1</sup> and 1.28 to 3.79 tones ha<sup>-1</sup> at Kulumsa and Tongo site for bread wheat in Ethiopia respectively. Regarding biomass yield, 25% of the genotypes were greater than the highest biomass yielder check Gambo (13.08 t ha<sup>-1</sup>). These high yielding genotypes could be utilized in further breeding.

**Table 4. Mean performance of thirty six bread wheat genotypes evaluated at Mehoni in 2017**

G*	HD	GFP	MD	PHT	FTPP	SL	SPS	KPS	TKW(g)	GY(t/ha)	BY(kg p)	Hi (%)
G1	70.00 <sup>h-k</sup>	29.33 <sup>ah</sup>	99.33 <sup>g-j</sup>	82.88 <sup>e-h</sup>	2.57 <sup>a-d</sup>	9.21 <sup>g-l</sup>	19.13 <sup>b-f</sup>	46.53 <sup>b-l</sup>	32.73 <sup>g-m</sup>	4.75 <sup>a-d</sup>	3.30 <sup>a-c</sup>	36.35 <sup>c-k</sup>
G2	78.67 <sup>a-c</sup>	26.67 <sup>dj</sup>	105.33 <sup>c-f</sup>	85.34 <sup>d-f</sup>	2.27 <sup>d-i</sup>	10.55 <sup>b-d</sup>	19.47 <sup>b-d</sup>	49.60 <sup>b-e</sup>	35.33 <sup>c-l</sup>	3.83 <sup>h-m</sup>	3.03 <sup>a-c</sup>	31.85 <sup>j-n</sup>
G3	73.33 <sup>e-i</sup>	25.00 <sup>gk</sup>	98.33 <sup>g-k</sup>	94.23 <sup>ab</sup>	2.07 <sup>d-k</sup>	10.37 <sup>a-c</sup>	19.27 <sup>b-d</sup>	49.67 <sup>b-e</sup>	30.87 <sup>j-m</sup>	4.59 <sup>b-g</sup>	3.00 <sup>a-c</sup>	37.92 <sup>a-g</sup>
G4	65.67 <sup>lm</sup>	24.00 <sup>i-j</sup>	89.67 <sup>o</sup>	83.32 <sup>d-h</sup>	2.60 <sup>ac</sup>	8.90 <sup>i-o</sup>	15.00 <sup>k</sup>	39.73 <sup>jk</sup>	42.13 <sup>a-c</sup>	5.15 <sup>ab</sup>	3.10 <sup>a-d</sup>	41.53 <sup>a-c</sup>
G5	78.00 <sup>a-d</sup>	29.00 <sup>a-h</sup>	107.00 <sup>b-d</sup>	87.55 <sup>b-f</sup>	1.90 <sup>h-n</sup>	10.20 <sup>c-f</sup>	18.67 <sup>b-g</sup>	47.67 <sup>b-g</sup>	29.20 <sup>l-k</sup>	4.11 <sup>e-j</sup>	3.20 <sup>a-d</sup>	32.19 <sup>h-n</sup>
G6	68.33 <sup>k-l</sup>	29.67 <sup>a-g</sup>	98.00 <sup>g-l</sup>	94.87 <sup>ab</sup>	2.67 <sup>ab</sup>	10.06 <sup>c-g</sup>	17.87 <sup>c-h</sup>	48.90 <sup>b-e</sup>	31.20 <sup>j-m</sup>	4.26 <sup>e-i</sup>	3.17 <sup>a-d</sup>	33.66 <sup>f-l</sup>
G7	71.00 <sup>f-k</sup>	21.33 <sup>k</sup>	92.33 <sup>m-o</sup>	81.60 <sup>e-h</sup>	2.9 <sup>a</sup>	8.29 <sup>m-q</sup>	15.17 <sup>j</sup>	35.30 <sup>k</sup>	38.33 <sup>a-h</sup>	4.10 <sup>e-j</sup>	2.70 <sup>dc</sup>	38.51 <sup>a-f</sup>
G8	80.67 <sup>ab</sup>	33.00 <sup>a</sup>	113.67 <sup>a</sup>	83.97 <sup>d-h</sup>	1.37 <sup>n</sup>	10.20 <sup>c-f</sup>	22.30 <sup>a</sup>	58.43 <sup>a</sup>	35.77 <sup>b-k</sup>	2.87 <sup>o</sup>	3.07 <sup>a-d</sup>	23.40 <sup>pq</sup>
G9	77.67 <sup>ad</sup>	30.67 <sup>a-f</sup>	108.33 <sup>bc</sup>	90.12 <sup>bd</sup>	2.67 <sup>ab</sup>	8.81 <sup>j-o</sup>	18.50 <sup>b-g</sup>	52.93 <sup>ab</sup>	33.53 <sup>e-m</sup>	4.05 <sup>f-j</sup>	3.20 <sup>a-d</sup>	31.85 <sup>h-n</sup>
G10	59.67 <sup>po</sup>	29.67 <sup>a-g</sup>	89.33 <sup>o</sup>	74.34 <sup>l</sup>	2.53 <sup>a-e</sup>	7.55 <sup>q</sup>	17.00 <sup>f-k</sup>	40.97 <sup>h-k</sup>	43.87 <sup>a</sup>	4.71 <sup>b-e</sup>	2.80 <sup>b-d</sup>	42.10 <sup>a</sup>
G11	81.11 <sup>a</sup>	33.33 <sup>a</sup>	114.67 <sup>a</sup>	78.40 <sup>g-i</sup>	1.60 <sup>k-n</sup>	7.74 <sup>pq</sup>	17.43 <sup>e-i</sup>	40.07 <sup>l-k</sup>	35.00 <sup>d-l</sup>	2.98 <sup>no</sup>	3.47 <sup>a</sup>	21.85 <sup>q</sup>
G12	71.00 <sup>t-k</sup>	27.00 <sup>c-j</sup>	98.00 <sup>g-l</sup>	85.42 <sup>d-t</sup>	2.47 <sup>a-t</sup>	9.02 <sup>h-m</sup>	18.73 <sup>b-g</sup>	45.63 <sup>d-j</sup>	38.40 <sup>a-h</sup>	4.34 <sup>c-g</sup>	2.93 <sup>a-d</sup>	37.07 <sup>a-h</sup>
G13	73.33 <sup>e-i</sup>	24.67 <sup>h-k</sup>	98.00 <sup>g-l</sup>	97.43 <sup>a</sup>	2.00 <sup>e-l</sup>	10.72 <sup>a-c</sup>	19.93 <sup>bc</sup>	52.93 <sup>ab</sup>	37.53 <sup>b-j</sup>	4.75 <sup>a-d</sup>	3.27 <sup>a-d</sup>	36.35 <sup>c-j</sup>
G14	69.67 <sup>i-k</sup>	26.33 <sup>e-j</sup>	95.00 <sup>l-m</sup>	84.67 <sup>d-h</sup>	2.07 <sup>d-k</sup>	8.98 <sup>h-n</sup>	19.13 <sup>b-f</sup>	48.17 <sup>b-g</sup>	32.07 <sup>g-m</sup>	4.51 <sup>c-g</sup>	3.00 <sup>a-c</sup>	37.64 <sup>a-g</sup>
G15	69.33 <sup>i-l</sup>	23.67 <sup>kj</sup>	93.00 <sup>l-o</sup>	85.26 <sup>df</sup>	2.50 <sup>a-f</sup>	9.63 <sup>e-j</sup>	17.80 <sup>c-h</sup>	43.73 <sup>d-j</sup>	39.87 <sup>a-e</sup>	4.68 <sup>b-f</sup>	3.00 <sup>a-c</sup>	39.19 <sup>a-e</sup>
G16	61.00 <sup>n-p</sup>	30.67 <sup>a-f</sup>	91.67 <sup>m-o</sup>	89.75 <sup>be</sup>	2.67 <sup>ab</sup>	9.24 <sup>g-k</sup>	15.80 <sup>h-i</sup>	42.20 <sup>g-j</sup>	42.60 <sup>ab</sup>	5.33 <sup>a</sup>	3.3 <sup>ab</sup>	39.56 <sup>a-e</sup>
G17	79.33 <sup>ab</sup>	28.67 <sup>a-h</sup>	108.00 <sup>bc</sup>	93.38 <sup>ac</sup>	2.27 <sup>d-i</sup>	9.83 <sup>d-h</sup>	19.40 <sup>b-d</sup>	44.23 <sup>d-j</sup>	35.33 <sup>c-l</sup>	3.52 <sup>j-m</sup>	3.43 <sup>a</sup>	25.64 <sup>o-k</sup>
G18	77.00 <sup>be</sup>	31.67 <sup>a-c</sup>	108.67 <sup>bc</sup>	93.93 <sup>ab</sup>	1.70 <sup>j-n</sup>	8.95 <sup>h-o</sup>	19.63 <sup>bc</sup>	52.27 <sup>bc</sup>	32.33 <sup>g-m</sup>	4.25 <sup>e-i</sup>	3.43 <sup>a</sup>	30.94 <sup>k-n</sup>
G19	58.33 <sup>op</sup>	32.00 <sup>ab</sup>	90.33 <sup>no</sup>	74.55 <sup>i</sup>	1.93 <sup>g-l</sup>	8.20 <sup>n-q</sup>	15.80 <sup>ij</sup>	45.37 <sup>d-j</sup>	37.00 <sup>a-j</sup>	3.34 <sup>m-o</sup>	2.13 <sup>e</sup>	39.19 <sup>a-e</sup>
G20	57.67 <sup>p</sup>	32.67 <sup>a</sup>	90.33 <sup>no</sup>	84.23 <sup>fh</sup>	2.57 <sup>a-d</sup>	8.35 <sup>l-q</sup>	16.00 <sup>h-j</sup>	40.30 <sup>h-j</sup>	38.80 <sup>a-g</sup>	4.34 <sup>e-i</sup>	2.67 <sup>d</sup>	41.03 <sup>a-b</sup>
G21	79.33 <sup>ab</sup>	29.00 <sup>a-h</sup>	108.33 <sup>bc</sup>	87.87 <sup>b-f</sup>	2.03 <sup>d-l</sup>	11.07 <sup>ab</sup>	18.97 <sup>b-t</sup>	44.33 <sup>d-j</sup>	41.13 <sup>a-d</sup>	3.73 <sup>l-m</sup>	3.17 <sup>a-d</sup>	29.55 <sup>m-o</sup>
G22	59.33 <sup>op</sup>	32.67 <sup>a</sup>	92.00 <sup>m-o</sup>	77.35 <sup>hi</sup>	2.50 <sup>a-f</sup>	8.57 <sup>k-p</sup>	16.70 <sup>h-k</sup>	41.80 <sup>g-j</sup>	33.50 <sup>e-m</sup>	3.42 <sup>l-o</sup>	2.73 <sup>dc</sup>	31.94 <sup>j-n</sup>
G23	63.33 <sup>nm</sup>	30.67 <sup>a-f</sup>	94.00 <sup>j-o</sup>	86.12 <sup>c-f</sup>	2.20 <sup>d-i</sup>	9.54 <sup>g-i</sup>	18.50 <sup>b-g</sup>	43.13 <sup>e-j</sup>	37.07 <sup>a-j</sup>	4.50 <sup>c-g</sup>	2.70 <sup>dc</sup>	41.91 <sup>ab</sup>
G24	62.00 <sup>no</sup>	33.00 <sup>a</sup>	95.00 <sup>j-n</sup>	73.70 <sup>l</sup>	2.53 <sup>a-e</sup>	8.11 <sup>o-q</sup>	17.07 <sup>e-j</sup>	41.53 <sup>g-j</sup>	38.80 <sup>a-h</sup>	4.11 <sup>e-j</sup>	2.87 <sup>a-d</sup>	35.98 <sup>d-k</sup>
G25	74.00 <sup>d-h</sup>	26.33 <sup>e-j</sup>	100.33 <sup>f-i</sup>	85.65 <sup>d-g</sup>	1.97 <sup>g-l</sup>	10.18 <sup>c-f</sup>	18.90 <sup>b-f</sup>	49.50 <sup>b-e</sup>	26.87 <sup>m</sup>	4.25 <sup>e-i</sup>	3.07 <sup>a-d</sup>	34.54 <sup>e-m</sup>
G26	71.67 <sup>f-k</sup>	31.00 <sup>a-e</sup>	102.67 <sup>d-g</sup>	83.84 <sup>d-h</sup>	2.37 <sup>a-h</sup>	9.70 <sup>d-i</sup>	19.20 <sup>b-e</sup>	48.37 <sup>b-f</sup>	37.53 <sup>a-j</sup>	5.16 <sup>ab</sup>	3.27 <sup>a-d</sup>	39.47 <sup>a-e</sup>
G27	70.67 <sup>g-k</sup>	26.00 <sup>f-j</sup>	96.67 <sup>h-m</sup>	85.23 <sup>df</sup>	2.10 <sup>d-k</sup>	8.57 <sup>k-p</sup>	18.60 <sup>b-g</sup>	46.07 <sup>c-j</sup>	31.60 <sup>j-m</sup>	4.74 <sup>a-e</sup>	3.23 <sup>a-d</sup>	36.59 <sup>b-j</sup>
G28	77.67 <sup>a-d</sup>	27.67 <sup>b-j</sup>	105.33 <sup>c-f</sup>	89.57 <sup>be</sup>	1.97 <sup>g-l</sup>	10.45 <sup>b-e</sup>	19.27 <sup>b-d</sup>	52.57 <sup>a-c</sup>	28.67 <sup>m</sup>	4.40 <sup>e-h</sup>	3.17 <sup>a-d</sup>	35.06 <sup>e-l</sup>
G29	81.00 <sup>ab</sup>	30.00 <sup>a-f</sup>	111.00 <sup>ab</sup>	88.97 <sup>b-f</sup>	1.60 <sup>k-n</sup>	9.10 <sup>h-l</sup>	20.40 <sup>b</sup>	48.33 <sup>b-f</sup>	41.40 <sup>a-d</sup>	3.47 <sup>k-n</sup>	3.43 <sup>a</sup>	25.58 <sup>o-q</sup>
G30	75.00 <sup>cf</sup>	31.33 <sup>a-d</sup>	106.33 <sup>b-e</sup>	62.13 <sup>eh</sup>	1.97 <sup>g-l</sup>	9.08 <sup>h-m</sup>	19.70 <sup>bc</sup>	48.20 <sup>b-f</sup>	40.40 <sup>a-e</sup>	3.33 <sup>m-o</sup>	2.97 <sup>a-d</sup>	28.08 <sup>n-p</sup>
G31	72.67 <sup>fj</sup>	28.67 <sup>a-h</sup>	101.67 <sup>e-h</sup>	88.22 <sup>bf</sup>	1.73 <sup>i-n</sup>	10.20 <sup>c-f</sup>	18.23 <sup>b-g</sup>	43.50 <sup>e-j</sup>	31.73 <sup>g-m</sup>	3.51 <sup>j-n</sup>	2.70 <sup>dc</sup>	32.73 <sup>g-n</sup>
G32	78.33 <sup>ac</sup>	33.00 <sup>a</sup>	111.33 <sup>ab</sup>	89.07 <sup>bf</sup>	1.43 <sup>nm</sup>	11.38 <sup>a</sup>	19.10 <sup>b-f</sup>	43.93 <sup>d-j</sup>	31.40 <sup>j-m</sup>	4.11 <sup>e-j</sup>	3.40 <sup>ab</sup>	30.24 <sup>l-o</sup>
G33	74.00 <sup>dg</sup>	27.67 <sup>b-j</sup>	101.67 <sup>e-h</sup>	88.67 <sup>bf</sup>	2.40 <sup>a-h</sup>	10.27 <sup>b-f</sup>	19.97 <sup>bc</sup>	49.77 <sup>b-e</sup>	39.67 <sup>a-t</sup>	5.11 <sup>a-c</sup>	3.27 <sup>a-d</sup>	39.14 <sup>a-e</sup>
G34	68.67 <sup>jl</sup>	31.33 <sup>a-d</sup>	100.00 <sup>g-j</sup>	83.9 <sup>dh</sup>	2.73 <sup>ab</sup>	10.04 <sup>c-g</sup>	18.83 <sup>b-g</sup>	45.43 <sup>d-j</sup>	40.00 <sup>a-e</sup>	4.41 <sup>d-g</sup>	3.07 <sup>a-d</sup>	36.12 <sup>d-k</sup>
G35	72.67 <sup>fj</sup>	27.67 <sup>b-j</sup>	100.33 <sup>f-i</sup>	85.5 <sup>o</sup>	2.30 <sup>c-h</sup>	9.41 <sup>g-k</sup>	18.83 <sup>b-g</sup>	46.73 <sup>b-h</sup>	37.67 <sup>a-j</sup>	4.02 <sup>h-l</sup>	2.73 <sup>dc</sup>	36.82 <sup>a-i</sup>
G36	74.33 <sup>dg</sup>	26.33 <sup>e-j</sup>	100.67 <sup>t-i</sup>	83.13 <sup>dh</sup>	1.50 <sup>n-l</sup>	9.54 <sup>e-j</sup>	17.87 <sup>c-h</sup>	50.37 <sup>b-c</sup>	29.47 <sup>l-m</sup>	3.85 <sup>h-m</sup>	2.73 <sup>dc</sup>	35.22 <sup>e-l</sup>

Source: G\* = genotype code number used in the table, Mean values in column of each trait followed by similar letter(s) had non-significant difference at P<0.05  
 TKW=Thousand-kernel weight, BY=biomass yield (kgplot<sup>-1</sup>), GY=grain yield t ha<sup>-1</sup>, HI=Harvest index.

### 4.3. Estimates of Variance Components

#### 4.3.1. Phenotypic and genotypic variability

Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population. PCV and GCV values were categorized as low (0 - 10%), moderate (10 - 20%) and high (> 20%) by Sivasubramaniam and Menon (1973). Accordingly, the genotypes coefficient of variation (GCV) ranged from 5.67% for the plant height to 14.74% for number of fertile tillers plant<sup>-1</sup>, whereas the phenotypic variation (PCV) ranged from 7.06% for days to maturity to 19.08% for number of fertile tillers plant<sup>-1</sup> (Table 5). In the present study, none of the traits had high PCV and GCV values. Whereas traits with moderate PVC value were number of kernels per spike, number of fertile tiller per plant, grain filling period, thousand-kernel weight, grain yield, Biomass yield, and harvest index. Considering the GCV estimates, number of fertile tillers per plant, thousand-kernel weight, grain yield, and harvest index exhibited moderate values. Moderate GCV coupled with moderate PCV was observed for number of productive tillers per plant, thousand-kernel weight, grain yield and harvest index, indicating the effectiveness of selection based on the phenotypic performance of the genotypes. The studied characters that had low GCV values were plant height, days to heading, grain filling period, days to maturity, spike length, number of spikelets per spike, number of kernels per spike and biomass yield while for PCV were plant height, days to heading, days to maturity, spike length and number of spikelets per spike, suggesting the difficulty in hereditary genetic material of these traits through plant breeding.

Similar observations showing moderate values for the phenotypic and genotypic coefficients of variation in wheat were reported by Kolakar *et al.* (2012), Mohammed *et al.* (2011) and Berhanu *et al.* (2017) for grain yield, biomass yield, plant height, peduncle length, number of productive tillers per meter, spike length, number of spikelets per spike, number of grains per spike and 1000-grain weight; with the indication that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. In contrary to the current finding, Berhanu *et al.* (2004) reported that higher GCV and PCV values were observed for grain yield, thousand-kernel weight, harvest index, tillers per plant, spikes per plant, spike length, kernels per spike and grain protein yield while similar lowest GCV and PCV values (< 5 %) were observed for days to maturity in bread wheat.

The phenotypic coefficient of variation was relatively greater than the genotypic coefficient of variation for all the traits; however, the magnitude of the difference was small for all traits expect for number of fertile tillers. This indicated narrow range of genotypic variability along with

less influence of environment for the expression of the traits, and the results revealing moderate GCV and PCV indicate there is still some possibility for the improvement the characters. Similar results depicting closer values of the PCV to the GCV estimates for most characters thereby showing little environmental effect on the expression of the characters were also reported by Dawit *et al.* (2012) and Adhiena *et al.* (2016).

#### 4.3.2. Estimates of heritability and expected genetic advance

In the present study, the broad sense heritability estimates ranged from 41.46% for biomass yield to 89.08% for days to heading (Table 5). High heritability (>60%) noticed for days to heading (89.08%) followed by days to maturity (82.02%), grain yield (76.31%), harvest index (73.85%), spike length (72.83%), and number of spikelets per spike (65.16). The obtained results were also in accordance with results of Dergicho *et al.* (2015) who reported high heritability was observed for studied characters such as, days to heading, thousand-grain weight, grain filling period, days to maturity, spike length, and number of spikelets per spike in 68 bread wheat germplasm. The other authors also reported similar results in which high heritability were recorded for spike length, number of grain per spike and grain yield per plot in wheat were reported (Ali *et al.*, 2008; Kolakar *et al.*, 2012; Desheva and Cholakov, 2014). But, the present finding was disagreement with the result of Gezahegn *et al.* (2015) who were reported moderate and low heritability values for harvest index, grain yield per plot and biomass yield. Moderate heritability values were also recorded for all the remaining of traits. This result suggests that selection could be easy and improvement is possible using selection breeding for these traits. In agreement with the current result, Berhanu *et al.* (2017) reported moderate heritability for grain filling period, kernels per spike, plant height, biomass, thousand-kernel weight in bread wheat genotypes.

The expected genetic advanced expressed as a percentage of the mean varied between 8.56% for plant height and 24.09% for harvest index (Table 5), indicating that selecting the top 5% of the base population could result in an advance of 8.56% to 24.09% over the respective population. Genetic advance as a percentage of the mean was high for harvest index (24.09%) followed by number of tiller per plant (23.47%), and grain yield (23.22%). Traits like spike length, number of spikelets per spike, days to heading, days to maturity, grain filling period, thousand-kernel weight, number of kernels per spike and biomass yield were showed moderate genetic advance as percent of mean. It was also moderate for days to heading (12.21%) and days to maturity (12.00%). This result implied that the high and moderate values of these traits showed the traits were under genetic controls which help for true selection for

wheat breeding improvement. This is because of high values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh, 1993).

The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.*, 1955). Accordingly, high heritability coupled with high genetic advance as percent of mean were also found for grain yield (76.31%, 23.22%) and harvest index (73.85%, 24.09%). Dergicho *et al.* (2015) reported similar findings for high heritability associated with high genetic advance for grain yield per plot and harvest index which supports the present findings. High heritability coupled with moderate genetic advance as percent of mean were noticed for days to heading, days to maturity, number of spikelets per spike and spike length. Moderate heritability associated with high genetic advance was observed for number of fertile tillers per plant, whereas moderate heritability coupled with moderate genetic advance as percent of mean was observed for grain filling period, number of kernels per spike, thousand-kernel weight and biomass yield. These are simply inherited traits indicates that most likely the heritability is due to additive gene effects. Therefore, these characters could be useful criteria for selection and may be effective in early generations for these traits. Mohammed *et al.* (2011) and Berhanu *et al.* (2017) also reported similar results, showing relatively high

estimates of genetic advance (as percentage of mean) for grain yield and yield related traits like number of fertile tiller per m<sup>2</sup>, plant height, thousand-kernel weight, kernel number per spike and harvest index. Berhanu *et al.* (2017) also reported similar findings as high heritability is coupled with moderate genetic advance as percent of mean for days to heading and days to maturity in bread wheat genotypes. This finding is in part similar with those reported by Gezahegn *et al.* (2015). Rehman *et al.* (2015) report explained that high heritability coupled with high genetic advance indicate that there could be predominance of additive gene action and might not much prejudiced by environmental fluctuations.

Contrasting results as compared to the present investigation, high heritability associated with high genetic advance noticed for days to heading, grain filling period, fertile productive tillers, spikelet per spike, spike length, kernel per spike, thousand grain weight and biomass yield per plot respectively by Dergicho *et al.* (2015); for moderate heritability coupled with high genetic advance observed for grain yield (41.71%, 63.05%) whereas high heritability couple with moderate genetic advance as percent of mean was observed for 1000 kernel weight (74.28%, 20.13%), and plant height (69.43%, 10.27%) respectively (Gezahegn *et al.*, 2015).

**Table 5. Estimates for variability components for twelve characters of thirty six bread wheat genotypes evaluated at Mehoni in 2017**

Trait	Range	Mean+ SE	PCV (%)	GCV (%)	H <sup>2</sup> b (%)	GA	GAM (%)
Plant height (cm)	74-97	85.7±3.18	7.74	5.67	53.60	7.34	8.56
Days to heading (days)	58-81	71.7±3.69	9.29	8.76	89.08	12.21	17.07
Grain filling period(days)	21-33	28.93±1.75	12.45	9.31	55.99	4.16	14.38
Days to maturity (days)	89-115	100.5±3.84	7.06	6.46	82.02	12.00	11.94
No. of fertile tillers/plant	1.4-2.9	2.18±0.2	19.08	14.74	59.61	0.51	23.47
Spike length (cm)	7.6-11.4	9.46±0.49	9.93	8.48	72.83	1.41	14.92
No. of spikelets/spike	15-22	18.38±0.85	9.12	7.37	65.16	2.25	12.27
No. of kernels/ spike	35-59	46.10±2.49	11.94	7.81	42.82	4.86	10.55
1000-kernel weight (g)	27-44	35.79±2.43	14.31	10.28	51.61	5.45	15.22
Grain yield (t/ha)	2.9-5.3	4.18±0.33	14.75	12.88	76.31	0.97	23.22
Biomass yield (kg/plot)	2.1-3.5	3.05±0.17	12.12	7.80	41.46	0.31	10.37
Harvest index (%)	21.9-42.1	34.61±2.87	15.81	13.59	73.85	8.34	24.09

PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H<sup>2</sup>b= Broad sense heritability  
GA=Genetic advance and GAM= Genetic advance as % of mean

## 5. SUMMARY AND CONCLUSIONS

The analysis of variance revealed highly significant differences among the genotypes for all characters. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all

characters studied, implying the influence of growing environment. Moderate GCV coupled with moderate PCV (10 to 20%) was observed for number of productive tillers per plant, thousand-kernel weight, grain yield, and harvest index, indicating the effectiveness of selection based on the phenotypic performance of the genotypes.

High heritability values were observed for days to heading, days to maturity, harvest index, grain yield, number of spikelets per spike and spike length. Genetic progress as a percentage of the mean was high for harvest index, grain yield and number of fertile tillers per plant, and it was moderate for spike length, number of spikelets per spike, days to heading, days to maturity, grain filling period, thousand-kernel weight, number of kernels per spike and biomass yield were showed moderate genetic advance as percent of mean. High heritability coupled with high genetic advance as percent of mean were found for grain yield and harvest index; while high heritability coupled with moderate genetic advance as percent of mean were observed days to heading, days to maturity, number of spikelets per spike and spike length. Moderate heritability coupled with high genetic advance was observed for number of fertile tillers per plant, whereas moderate heritability coupled with moderate genetic advance as percent of mean was observed for grain filling period, number of kernels per spike, thousand-kernel weight and biomass yield. This implies that the variation observed was mainly under genetic control and the possibility of progress from selection. In general, in the context of plant breeding, traits that exhibited medium GCV,  $H^2_b$  and GAM would be useful criteria for selection; as a result, number of productive tillers per plant, thousand-kernel weight, grain yield, and harvest index, were identified as the major contributors. Therefore, depending on the mean performances, genotypes such as QAFZAH-2/FERRIUG-2 (5.33 t ha<sup>-1</sup>), KAUZ'S/FLORKWA1//GOUNMRIA-3 (5.16 t ha<sup>-1</sup>), SERI 82/SHUHA'S//PASTOR-2 (5.15 t ha<sup>-1</sup>) and ETBW5957HUBARA-3\*2/SHUHA-4 (5.11 t ha<sup>-1</sup>) had mean performances higher than the highest performing check variety (Gambo=4.75 t ha<sup>-1</sup>) for grain yield (t ha<sup>-1</sup>) to improve the next bread wheat breeding programme to increase the farmer's productivity. However, since this is a one-year result, it is necessary to repeat the field experiment and evaluate the genotypes over several locations and years in order to make conclusive and comprehensive conclusions and recommendations.

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