

# Assessment of genetic variability among bread wheat genotypes for agronomic and morphological traits under optimum and stress condition

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## Research Article

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## Abstract

**Background:** Bread wheat is one of the most important cereal crops produced in almost all agro-ecologies of Ethiopia. Assessment of genetic variability in crop species is one of the major activities of plant breeding which helps to design breeding methods for further evaluation to meet the diversified goals.

**Methods:** The experiment was laid out in 8x8 simple lattice design under both optimum and stress conditions at middle Awash during 2019/20 growing season. Water stressed treatment was imposed by withholding three irrigation from 50% flowering up to physiological maturity. In the non-stressed water regime, plants were watered at every 10 days interval using furrow irrigation method. In order to avoid water leakage between treatments, the non-stressed water regime plots were established four meters away from the water stressed regime plots.

**Results:** Analysis of variance revealed highly significant ( $p \leq 0.01$ ) variation for all studied traits under both conditions. The variation observed for grain yield varied from 2.30-6.0 t ha<sup>-1</sup> and 1.01-4.36 t ha<sup>-1</sup> under optimum and stress conditions respectively. Genotypic and phenotypic coefficient of variation ranged from 3.88(days to maturity) to 20.84% (grain yield) and 4.76(days to maturity) to 24.73% (fertile tiller plant<sup>-1</sup>) under optimum condition respectively. Under stress condition GCV and PCV ranged from 4.30(days to maturity) to 18.41% (fertile tiller plant<sup>-1</sup>) and 5.19 (days to maturity) to 22.27% (fertile tiller plant<sup>-1</sup>) respectively. Broad sense heritability and genetic advance as a percentage of mean ranged from 43(spike length) to 89% (biomass yield) and 6.51(days to maturity) to 40.33% (grain yield) under optimum condition respectively, whereas under stress condition it ranged from 23.40 (harvest index) to 86.1% (days to heading) and 5.69% (harvest index) to 33.34% (biomass yield) respectively. High heritability coupled with high genetic advance as a percentage of mean was recorded for biomass yield and grain yield under optimum condition, whereas for biomass yield and fertile tiller plant<sup>-1</sup> under stress condition.

**Conclusions:** According to the mean performance of genotypes G3, G24, G26, G24 and G45 had yield advantage over checks under both conditions. Generally, the variation observed among the tested genotypes confirmed the possibility of improvement through selection and hybridization for the study area.

Keywords: Drought tolerance, Heritability, Variability, Wheat, Yield

## Background

Bread wheat (*Triticum aestivum* L.) is one of the important cereal crops produced worldwide serving as an important export and strategic commodity (Kumar 2013). The report on wheat production reveals that world production was 765.4 million metric tons with average yield of 3.48 t ha<sup>-1</sup> and it accounts for nearly 30% of global cereal production (FAO 2019). In Ethiopia, bread wheat is one of the most important cereal crops in terms of production and consumption (Kaleb 2017). The national average productivity of wheat in Ethiopia is

estimated to 2.76 t ha<sup>-1</sup>. It is cultivated on 1.7 million hectares of land and has the total production of 4.83 million tons with remain low productivity in the country as compared to the world average yield (CSA 2019). Wheat grain is used in Ethiopia in the preparation of wide range of traditional products like; staple pancake (“*injera*”), bread (“*dabo*”), local beer (“*tella*”), and several other local food items (Akililu et al. 2015).

Drought tolerance is a complex quantitative trait controlled by many genes with minor effect and is one of the most difficult traits to study (Maazou et al. 2016). Due to its polygenic nature and genotype by environment interaction, drought tolerance has low heritability (Blum 2011; Khakwani et al. 2012). A further problem is that the heritability of yield is reduced under the conditions where yield is reduced due to small genotypic variance or large genotype by environment interaction variances (Ludlow and Muchow 1990). Breeding for drought tolerance is affected by several factors, such as inheritance nature of drought tolerance (Blum 2011), availability of suitable genetic resources, a well-suited stress screening environment and high throughput selection methods (Araus and Cairns 2014). Grain yield is the principal selection criteria used under drought stress condition. However, the yield is a complex polygenic trait which gene is located differently from those controlling drought (Blum 1998). Thus, the selection efficiency could be improved if particular physiological and morphological attributes related to yield under a stress environment could be identified as selection criteria (Acevedo 1991).

The success of breeding for developing drought tolerant varieties depends on precise estimates of genetic variance components that consist of additive, dominant and epistasis genetic effects (Nouri et al. 2011). It also requires searching for possible correlation between agronomic, morphologic traits with grain yield (Jatoi et al. 2011). Generating information about the genetic variability, correlations and mechanisms of inheritance of the genetic traits involved is the key task in genetic improvement of any crop (Naik et al. 2015). Development of high yielding varieties requires detailed knowledge of variation among the traits and the association among yield components (Mary and Gopalan 2006). Selection of drought tolerant wheat varieties and subsequent development of candidate genotypes at target growing environments are the ultimate means of minimizing yield loss under drought environments (Alghabari et al. 2014; Mwadzingeni et al. 2016).

The lowland irrigated areas of Ethiopia are potential area for wheat production; but the country yearly imports wheat in order to meet the demand. Currently, the government has

embarked massive production of wheat in irrigated schemes to meet the growing demand through local production. However, the number of genotypes that fit into the drought/heat stress growing environments are limited. Encouraging research work have been undertaken for bread wheat under drought stress condition in Ethiopia (Desalegn et al. 2001; Habtamu et al. 2016; Assefa et al. 2019; Yared et al. 2020) but, few genotypes were released for lowland areas of the country and most of them are not under production currently. Hence, there is a need of conducting genetic variability to generate information for further breeding work to develop varieties for the area. In view of this, the study was conducted at middle Awash, North-eastern Ethiopia; where bread wheat is currently given due attention to investigate extent genetic variability among selected bread wheat genotypes for drought tolerance.

## **Methods**

### **Description of the study area**

The study was conducted during the off season (November to February) during 2019/20 at Werer Agricultural Research Center (WARC) experimental field. Werer is located 9°27' N and 40°15' E in Northeastern part of Ethiopia. The altitude of Werer is 740 m.a.s.l. The average maximum and minimum temperature of the area is 34°C and 19°C, respectively, and the annual total rainfall in the area is about 571 mm annually. The soil type in the experimental site is Vertisol with the porosity and bulk density (0-25 cm depth) of 49.06% and 1.35 g/cm<sup>3</sup>, respectively (Wondemagegn and Abera 2012).

### **Experimental materials**

The experimental materials comprised 62 diverse bread wheat genotypes from elite spring bread wheat yield trial (ESBWYT) obtained from International Center of Agricultural Research for Dry Areas (ICARDA) and two released check varieties from national wheat breeding program (Table 1).

### **Experimental design and procedures**

The experiment was laid out in 8\*8 simple lattice design consisted of 64 bread wheat genotypes. The plot size was 4.5 m<sup>2</sup> (1.8 m x 3 m) and it consisted of six rows at 0.3 m interval on 0.6m ridge having two rows each. Seeds were sown on rows with manual drilling at a rate of 100 kg ha<sup>-1</sup> basis. The fertilizer application were at a rate of 50 kg ha<sup>-1</sup> DAP and 100kg ha<sup>-1</sup> of Urea. Di ammonium phosphate (DAP) was applied once at sowing time and

Urea was applied in split half at seedling stage and the remaining 50% at booting /spike initiation growth stage. Water stressed treatment was imposed by withholding three irrigation from 50% flowering up to physiological maturity. In the non-stressed water regime, plants were watered at every 10 days interval using furrow irrigation method. In order to avoid water leakage between treatments, the non-stressed water regime plots were established four meters away from the water stressed regime plots.

### **Data collection**

Data like days to heading, days to maturity, days to grain filling period, biomass yield, grain yield, 1000 kernel weight, harvest index, fertile tiller per plant, plant height, spikelets spike, spike length and number of kernels spike were collected as per descriptor for wheat (IPGR 1985).

### **Data analysis**

The data were subjected to analysis of variance using PROC GLM procedure in SAS v9.2 (SAS 2008) statistical software. The mean comparison of genotypes was done following the significance of mean squares using Duncan Multiple Range Test (DMRT).

### **Estimates of variance components**

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:

$$\text{Genotypic variance, } (\sigma^2 g) = \frac{MS_g - MS_e}{r}$$

$$\text{Phenotypic variance, } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Where,  $\sigma^2 g$  = genotypic variance  $MS_g$  = mean square of genotype  $MS_e$  = mean square of error  $r$  = number of replications  $\sigma^2 e$  = Environmental variance,  $\sigma^2 p$  = phenotypic variance and  $r$  = replication.

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

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

Where, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation and  $\bar{X}$  = population mean of the character being evaluated. PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high (>20%) as indicated by Sivasubramaniah and Menon (1973).

### **Heritability and genetic advance**

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

$$H^2 = \left( \frac{\sigma^2_g}{\sigma^2_p} \right) \times 100$$

The heritability percentage was categorized as low (0 - 30%), moderate (30-60%) and high (> 60%) as suggested by Johnson et al. (1955).

### **Expected genetic advance under selection (GA)**

Genetic advance in absolute unit (GA) and as percentage 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).

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

### **Genetic advance as percentage of mean (GAM)**

Genetic advance as percentage of mean was estimated as follows:

$$GAM = \frac{GA}{\bar{x}} * 100$$

Where, GAM = Genetic advance as percentage of mean GA = Genetic advance. The GA as percentage of mean was categorized as low (0 - 10%), moderate (10-20%) and high (>20%) as suggested by Johnson et al. (1955).

## **Results and discussion**

Separate analyses of variance showed highly significant variation among bread wheat genotypes for twelve traits studied under optimum and moisture stress conditions (Table 2 and 3). Under optimum condition, the tested genotypes exhibited highly significant ( $P \leq 0.01$ ) variation for days to heading, days to maturity, grain filling period, biomass yield, grain yield, harvest index, thousand kernel weight, plant height, fertile tiller plant<sup>-1</sup>, spike length, number of spikelet spike<sup>-1</sup> and number of kernels spike<sup>-1</sup>. Many authors previously reported highly significant variation in bread wheat for most of the traits reported herein (Obsa 2014; Dargicho *et al.* 2015b; Birhanu *et al.* 2016; Ashebir *et al.* 2020).

Under stress condition the tested genotypes exhibited highly significant ( $P \leq 0.01$ ) variation for all traits studied. Several types of research have been conducted on bread wheat under drought condition and found highly significant variation for the traits reported herein our study (Rehman *et al.* 2015; Mwadzingeni *et al.* 2017; Abd-Allah *et al.* 2018; Pour-Aboughadareh *et al.* 2020). In contrary to the present result non-significant variation was reported for biomass yield and harvest index (Sahar *et al.* 2016) in wheat under drought condition.

The result indicated that there was sufficient variability present in the studied genotypes under both optimum and stress conditions, which could be utilized for the further breeding program. Such a considerable range of variations would provide a good opportunity for yield improvement. The results also justify carrying out further genetic analyses by considering the agro-morphological traits that showed significant variation from general ANOVA.

### **Mean performance of genotypes**

#### **Phenology and growth character**

Under optimum condition the mean performance of genotypes for days to heading, days to maturity and grain filling periods ranged from 45.5 to 58.5, 82 to 98.5 and 30 to 46 days with mean values of 51.51, 87.93 and 36.42 days respectively. The highest days to heading was recorded for G12 (58.5 days) followed by G55 (56.5 days), G1(56.0 days) and G38 (56.0 days), whereas the lowest days to heading was recorded for G62 (45.5 days) followed by G10 (45.5 days), G32 (48.5 days), G44 (48.5 days) and G20 (48.5 days) (Appendix Table 1). The

highest days to maturity was recorded for G24 (98.0 days) followed by G52 (97.0 days), G57 (96.5 days) and G42 (96.0 days). Genotypes G33 (82.0 days), G63 (83.0 days) 62 (83.0 days) and G43 (83.0 days) had lowest days to maturity and were early maturing genotypes. Grain filling is also an important trait that eventually affects the overall grain yield by increasing grain weight. Long grain filling period was recorded for G23 (46.0 days) followed by G42 (45.0 days), G57 (42.0 days) and G52 (42.0 days), whereas the short grain filling duration was recorded for G12 (30.0 days), G63 (30.5 days), G43 (32.0 days) and G2 (32.5 days). Twenty five genotypes had mean performance lower than standard check (kingbird) for days heading whereas, Twenty five and nineteen genotypes had mean performance lower than standard check (kingbird) for days to maturity and grain filling period respectively. In this study, the genotypes with early heading also showed early maturity and late maturing ones exhibited similarly late days to heading. Several authors previously reported similar ranges and means for days to heading, days to maturity and grain filling period in bread wheat (Tadiyos *et al.* 2019; Mihratu *et al.* 2020).

The mean performance under optimum condition, for plant height and fertile tiller plant<sup>-1</sup> ranged from 53.33 to 76.66 cm and 1.25 to 5.75 with mean values of 64.54 cm and 3.76 respectively (Appendix Table 1). Genotypes G30 (76.66 cm) followed by G14 (76 cm), G16 (74.33 cm) and G26 (74.17 cm) were the tallest whereas, G13 (53.33 cm) followed by G7 (54.16 cm), G11 (56.0 cm), G10 (56.5 cm) and G40 (56.66 cm) were the shortest genotypes. The highest number of fertile tiller plant<sup>-1</sup> was recorded for G33 (5.75) followed by G10 (5.5), G29 (5.25), G57 (4.83) and G41 (4.75), whereas the lowest was recorded for G2 (1.25), G7 (1.75), G12 (2.0) and G15 (2.0). Fourteen genotypes showed mean performance superior to standard check (Kingbird) for plant height. Forty five genotypes had mean value shorter than check (Fentalle-2) for plant height and nineteen genotypes had low number fertile tiller plant<sup>-1</sup> than standard check (kingbird). Girma (2018), Alemu *et al.* (2019) and Mihratu *et al.* (2020) reported similar ranges and means in their study for plant height and fertile tiller plant<sup>-1</sup>.

Under stress condition the mean performance of genotypes for days to heading, days to maturity and grain filling periods ranged from 43 to 59.5, 75 to 94 and 26 to 36 days with mean values of 51.0, 83.71 and 32.75 days respectively (Appendix Table 2). The highest mean value for days to heading was recorded for G7 (59.5 days) followed by G12 (59.5 days), G1 (59 days) and G14 (59 days), whereas the shortest days to heading was observed

for G10 (43.0 days) followed by G43 (46.0 days) and G32 (49 days). Genotypes, G23 (94 days), G12 (92 days), G14 (91.5 days) and G1 (90 days) were late maturing whereas G62 (75 days), G10 (75 days), 29 (76.5 days) and G39 (77.5 days) were early maturing genotypes. The longest duration for grain filling period was recorded for G49, G50, G40, G45, G26, G6, G26 and G38 having mean value of 36 days, while lowest grain filling duration was observed for G62 (26 days) followed by G7 (27 days), G29 (27.5 days) and G11 (28 days). Twenty three and fourteen genotypes had mean performance lower than check (Fentalle-2) for days to heading and days to maturity whereas thirteen genotypes had mean value of lower than standard check (Kingbird) for grain filling period. Drought significantly reduced days to maturity and grain filling period by 5% and 10%, respectively. Among tested genotypes 35.93%, 21.8% and 20.3% exhibited low mean value of days to heading, days to maturity and grain filling period respectively. This suggests that high probability of selecting early maturing genotypes those can escape terminal drought stress.

Water deficit causes early flowering and maturity in wheat genotypes compared with optimum condition. Early flowering and early maturity helps the crop to complete the life cycle before onset of the stress. Therefore, earliness could be reflected as an escape approach and resilient adaptation under drought stress (Shavrukov *et al.* 2017). Similar ranges and means were reported by Tadiyos *et al.* (2019) for days to heading, days to maturity and grain filling period at middle awash under stress condition. The variation reported in this experiment was lower for days to heading and days to maturity in comparison to report of Abd-Allah *et al.* (2018) who reported range of variation for days to heading (64.3 to 81.8 days) and days to maturity (106.5 to 115.5 days) in bread wheat under drought condition. The differences of reports by different authors might be due to the differences in the genetic material carried by the genotypes, growing seasons and environments where the genotypes evaluated.

The mean performance in stressed condition for plant height and fertile tiller plant<sup>-1</sup> ranged from 50 to 74.66 cm and 1.66 to 4.1 with mean values of 61.33 cm and 2.81 respectively. The longest genotypes were G53 (74.66 cm), G23 (71.67cm), G24 (71.83 cm), G57 (70.83 cm), G26 (70.67 cm) and G8 (70.33 cm), while G7 (50.0 cm), G48 (51.0 cm), G1 (52.5 cm), G40 (52.83 cm) and G55 (53.0 cm) were among the shortest. High number of fertile tiller plant<sup>-1</sup> was recorded G43 (4.1) followed by G63 (4.06), G47 (3.83) and G21 (3.75) whereas low number of fertile tiller plant<sup>-1</sup> was observed for G1 (1.66) followed by G58 (1.8), G60 (1.83),

and G31 (2.0). None of the new entry showed superior to the highest performing standard check (Kingbird) for plant height while thirty three genotypes had mean value of fertile tiller plant<sup>-1</sup> greater than standard check (Kingbird). Fifty one and three genotypes had mean value of lower than check (Fentalle-2) for plant height and number of fertile tiller plant<sup>-1</sup> respectively (Appendix Table 2). Growth character, fertile tiller plant<sup>-1</sup> and plant height reduced by 25% and 5% due to drought stress respectively. Different range and mean value was reported for plant height by Amiri *et al.* (2013) and Arya *et al.* (2013) and Chowdhury *et al.* (2018). Sahar *et al.* (2016) reported similar result for fertile tiller plant<sup>-1</sup> under drought condition.

### **Spike character, harvest index, biomass yield and grain yield**

Under optimum condition the mean performance observed for spike length, number of spikelets spike<sup>-1</sup>, number of kernels spike<sup>-1</sup> and thousand kernel weight were ranged from 4.83 to 8.83 cm, 13.0 to 18.25, 29.83 to 55.67 and 27.52 to 43.99 g with mean values of 6.97 cm, 15.98, 45.29 and 36.68 g respectively (Appendix Table 1). The longest spike length was observed for G27 (8.83 cm) followed by G45 (8.33 cm), G55 (8.33 cm) and G16 (8.17 cm), while shortest spike length was recorded for G15 (4.83 cm) followed by G56 (5.0 cm), G38 (5.0 cm), and G63 (5.1 cm). The highest number of spikelets spike<sup>-1</sup> was observed for G26 (18.25), G39 (17.75), G32 (17.67), G4 (17.66) and G28 (17.66), while lowest number of spikelet spike<sup>-1</sup> was recorded for G38 (13.0), G7 (13.0), G12 (13.33) and G63 (13.66). Genotypes, G13 (55.67) followed by G8 (55.33) and G24 (53.67) had highest number of kernels spike<sup>-1</sup>, while G17 (29.83), G44 (34.83), G9 (35.17) and G47 (36.5) had lowest number of kernels spike<sup>-1</sup>. The highest thousand kernel weight was recorded for G19 (43.99 g) followed by G47 (43.19 g), G24 (42.7 g), G42 (42.66 g) and G55 (42.61), while the lowest thousand kernel weight was recorded for G7 (27.52 g) followed G40 (30.35 g), G23 (31.06 g), G63 (31.5 g) and G2 (31.76 g). Eight genotypes had mean performance of superior to check (Fentalle-2) for number of spikelet spike<sup>-1</sup> and eleven genotypes had mean values higher than standard check (kingbird) for number of kernels spike<sup>-1</sup>. Twenty six genotypes had mean value of greater than check (Fentalle-2) for spike length. Fifty genotypes exhibited mean performance superior to check (Fentalle-2) for thousand kernel weight. Different authors reported similar range of variations for spike length, spikelet spike<sup>-1</sup>, number of kernels spike<sup>-1</sup> and thousand kernel weight in their study (Gezahegn *et al.* 2015; Dargicho *et al.* 2015b; Alemu *et al.* 2019; Ashebir *et al.* 2020).

The mean performance of genotypes under optimum condition for biomass yield and harvest index were ranged from 7.57 to 15.50 t ha<sup>-1</sup> and 25.41 to 41.32% with mean values of 11.81t ha<sup>-1</sup> and 34.09% respectively (Appendix Table 1). The highest biomass yield was recorded for G64 (15.5 t ha<sup>-1</sup>) followed by G10 (15.47 t ha<sup>-1</sup>), G24 (14.89 t ha<sup>-1</sup>), G55 (14.88 t ha<sup>-1</sup>) and G1 (14.78 t ha<sup>-1</sup> whereas, G38 (7.57 t ha<sup>-1</sup>), G7 (7.69 t ha<sup>-1</sup>), G15 (8.68 t ha<sup>-1</sup>) and G2 (8.83 t ha<sup>-1</sup>) had lowest mean value for biomass yield. The highest value of harvest index was recorded for G28 (41.32%) followed by G5 (40.66%), G4 (39.93%), G10 (38.85%) and G31 (38.84%) while lowest value was observed for G56 (25.41%), G12 (25.48%), G59 (28.08%) and G57 (28.71%). Twenty one genotypes exhibited mean performance greater than check (Fentalle-2) for above ground biomass, while nine genotypes had mean values lower than standard check (Kingbird) for biomass yield. Four genotypes had mean performance higher than check (Fentalle-2), while twenty nine genotypes had mean performance lower than standard check (Kingbird) for harvest index. Wide ranges of variations were reported for biomass yield and harvest index in bread wheat previously by Dargicho *et al.* (2015b), Girma (2018) and Alemu *et al.* (2019).

Grain yield is the prime goal of plant breeder in any crop improvement program. The mean performance of grain yield under optimum condition ranged from 2.3 to 6.0 t ha<sup>-1</sup>; with mean value of 4.05 t ha<sup>-1</sup> (Appendix Table 1). The highest grain yield was recorded for G10 (6.0 t ha<sup>-1</sup>), followed by G64 (5.89 t ha<sup>-1</sup>), G3 (5.56 t ha<sup>-1</sup>), G44 (5.4 t ha<sup>-1</sup>), G39 (5.31 t ha<sup>-1</sup>), G24 (5.3 t ha<sup>-1</sup>), G1 (5.13 t ha<sup>-1</sup>), G26 (5.06 t ha<sup>-1</sup>) and G14 (5.05 t ha<sup>-1</sup>), while lowest grain yield was recorded for G38 (2.3 t ha<sup>-1</sup>) followed by G12 (2.6 t ha<sup>-1</sup>), G63 (2.63 t ha<sup>-1</sup>), G7 (2.63 t ha<sup>-1</sup>), G2 (2.63 t ha<sup>-1</sup>) and G56 (2.72 t ha<sup>-1</sup>). Depending on the mean yield performance, twelve genotypes had mean value of greater than best performing check (Fentalle-2= 4.84 t ha<sup>-1</sup>) for grain yield. Nine genotypes had mean values lower than standard check (Kingbird=3.22 t ha<sup>-1</sup>) for grain yield. Similarly, several authors reported wide range of variation in bread wheat for grain yield (Dargicho *et al.* 2015b; Alemu *et al.* 2019; Sohail *et al.* 2019; Ashebir *et al.* 2020).

Under stress condition the mean performances for spike length, number of spikelet spike<sup>-1</sup>, number of kernels spike<sup>-1</sup> and thousand kernel weight were ranged from 5.33 to 8.33 cm, 13.0 to 18.33, 30.66-57.16 and 29.44 to 39.83 g with mean values of 6.71 cm, 15.53, 43.66 and 33.50 g respectively (Appendix Table 2). The longest spike length was observed for G55 (8.33 cm) followed by G45 (8.18 cm), G25 (7.83 cm), G13 (7.67 cm) and G12 (7.66 cm),

while the shortest was observed for G6 (5.33 cm) followed by G46 (5.33 cm), G1 (5.66 cm) and G51 (5.67 cm). The highest number of spikelets spike<sup>-1</sup> was observed for G28 (18.33) followed by G7 (18.0), G26 (18.0), G12 (17.67) and G53 (17.5), while the lowest number of spikelets spike<sup>-1</sup> was observed for G43 (13.0) followed by G22 (13.17), G44 (13.3), G14 (13.5) and G35 (13.5). Eight genotypes had mean performance superior to check (Fentalle-2) for spike length, whereas four genotypes had mean values higher than standard check (Kingbird) for number of spikelet spike<sup>-1</sup>. Fifteen genotypes had mean performance greater than best performing check (Kingbird) for number of kernels spike<sup>-1</sup>. Twenty three genotypes had mean values higher than best performing check (Kingbird) for thousand kernel weight.

The highest number of kernels spike<sup>-1</sup> was observed for G7 (57.16) followed by G25 (53.67), G52 (53.33), G46 (52.33) and G41 (51.5) whereas G48 (30.66) followed G44 (32.33), G9 (32.5), G53 (32.83) and G63 (33.0) had lowest number of kernels spike<sup>-1</sup>. Genotypes, G1 (39.83 g) followed by G64 (39.83 g), G46 (39.66 g), G45 (38.34 g) and G44 (38.48 g) had high thousand kernel weight, while G48 (29.44 g) followed by G6 (29.62 g), G7 (29.62 g), G13 (29.62 g), G61 (29.88 g), G52 (29.91 g) and G36 (29.95 g) had lowest thousand kernel weight. Among 64 genotypes 12.5%, 6.25%, 23.43% and 35.93% showed superior to standard check (Kingbird) for spike length, number of spikelet spike<sup>-1</sup>, number kernels spike<sup>-1</sup> and thousand kernels weight. Several authors previously reported similar ranges of variation in bread wheat for spike length, number of spikelets spike<sup>-1</sup>, number of kernels spike<sup>-1</sup> and thousand kernel weight (Arya *et al.* 2013; Bazzaz *et al.* 2018).

The mean performance under stressed condition for above ground biomass and harvest index were ranged from 5.01 to 12.61 t ha<sup>-1</sup> and 20.21 to 38.28% having mean values of 7.84 t ha<sup>-1</sup> and 33.72% respectively. Fourteen and fifteen genotypes had mean performance superior to standard check (Kingbird) for above ground biomass and harvest index respectively. The highest biomass yield was recorded for G28 (12.61 t ha<sup>-1</sup>) followed by G40 (10.46 t ha<sup>-1</sup>), G55 (10.41 t ha<sup>-1</sup>), G8 (10.16 t ha<sup>-1</sup>) and G19 (10.0 t ha<sup>-1</sup>), while G42 (5.01 t ha<sup>-1</sup>) followed by G35 (5.12 t ha<sup>-1</sup>), G52 (5.65 t ha<sup>-1</sup>), G38 (5.68 t ha<sup>-1</sup>), G34 (5.85 t ha<sup>-1</sup>) and G17 (5.89 t ha<sup>-1</sup>) had lowest biomass yield. Wide range of variation was reported for biomass yield previously by Arya *et al.* (2013), Sahar *et al.* (2016) and Pour-Aboughadareh *et al.* (2020). The highest harvest index was observed for G41 (38.28%) followed by G1 (38.08%), G60 (37.81%), G6 (37.62%) and G48 (37.29%) while G42 (20.21%), G7 (25.77%), G54 (27.1%) and G12 (27.2%) had low value of harvest index (Appendix Table 2). The result was

concurrent with the previous report of Arya *et al.* (2013) and Sahar *et al.* (2016) for harvest index. 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). Among 64 genotypes 21.87% and 23.43% showed superior to standard check (Kingbird) for biomass yield and harvest index.

The mean performance for grain yield in stressed condition ranged from 1.01 to 4.36 t ha<sup>-1</sup> with mean value of 2.65 t ha<sup>-1</sup> respectively. Fourteen genotypes showed superior to standard check (Kingbird=3.18t ha<sup>-1</sup>) for grain yield (Appendix Table 2). The highest grain yield was recorded for G28 (4.36 t ha<sup>-1</sup>) followed by G40 (3.56 t ha<sup>-1</sup>), G24 (3.56 t ha<sup>-1</sup>), G48 (3.48 t ha<sup>-1</sup>) and G8 (3.40 t ha<sup>-1</sup>), while the lowest grain yield was recorded for G42 (1.01 t ha<sup>-1</sup>) followed by G35 (1.57 t ha<sup>-1</sup>), G52 (1.67 t ha<sup>-1</sup>), G12 (1.7 t ha<sup>-1</sup>) and G17 (1.82 t ha<sup>-1</sup>). Similar range of variation was reported by Bazzaz *et al.* (2018) for grain yield under drought condition. Among 64 genotypes 21.87% showed superior to standard check (Kingbird) for grain yield. Drought reduced significantly the yield and yield components. Grain yield showed 34.5% of reduction under stress condition. Similar findings were reported under drought condition in bread wheat by Darzi-Ramandi *et al.* (2016) Sahar *et al.* (2016) and Assefa *et al.* (2019) who reported 49.9%, 42% and 30.6% of yield reduction respectively. Generally bread wheat genotypes performance reduced under drought stress, while some of them perform well indicating that presence of ample magnitude of genetic variability among selected bread wheat genotypes used for breeding program under drought stress condition.

## **Estimates of variance components**

### **Phenotypic and Genotypic coefficient of variation**

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are used to measure the variability that exists in a given population. Under optimum condition, genotype coefficient of variation (GCV) ranged from 3.88% for days to maturity to 20.84% for grain yield; while phenotypic coefficient of variation (PCV) ranged from 4.76% for days to maturity to 24.73 % for fertile tiller plant<sup>-1</sup> (Table 4). Sivasubramaniam and Menon (1973) suggested the values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (0-10), moderate (10-20) and high (>20). Accordingly, high GCV and PCV were recorded for grain yield. The result was in agreement

with the previous findings of Dargicho *et al.* (2015b) and Jamil *et al.* (2017) who reported high GCV and PCV values for grain yield per hectare. Berhanu *et al.* (2017) also reported high PCV value for fertile tiller plant<sup>-1</sup> which agrees to the present result.

Under optimum condition moderate GCV values were recorded for biomass yield and fertile tiller plant<sup>-1</sup> whereas, intermediate PCV values were recorded for biomass yield, number of kernels spike, spike length and thousand kernel weight (Table 4). Moderate GCV coupled with moderate PCV were observed for biomass yield indicating the effectiveness of selection based on the high mean performance for this trait in improving yield in bread wheat. Kolakar *et al.* (2012) and Berhanu *et al.* (2017) reported intermediate values of PCV for biomass yield, spike length, number of spikelets spike<sup>-1</sup>, number of kernels spike<sup>-1</sup> and 1000-grain weight. Adhiena *et al.* (2016) reported moderate GCV for biomass yield. The result is in contrary to the result of Dargicho *et al.* (2015b) who reported high GCV value for biomass yield and fertile tiller plant<sup>-1</sup>. Mitsiwa (2013) also reported low GCV and intermediate PCV values for fertile tiller plant<sup>-1</sup> which contradicts with the present result.

Low GCV coupled with low PCV values were noted for days to heading, days to maturity, grain filling period, harvest index, plant height and number of spikelets spike<sup>-1</sup> under optimum condition. The present result is in agreement with the finding of Alemu *et al.* (2019) who reported low GCV and PCV values for days to heading, days to maturity, Harvest index, plant height and spikelets spike<sup>-1</sup>. A low GCV value was recorded for number of kernels spike<sup>-1</sup> and thousand kernel weight (Table 4). The result is in line with the finding of Gezahegn *et al.* (2015) for characters days to maturity, number of spikelets spike<sup>-1</sup>. Mitsiwa (2013) also reported low PCV and GCV for grain filling period, days to maturity and kernels spike<sup>-1</sup>. Salman *et al.* (2014) reported moderate GCV for plant height, days to heading, and maturity, and high GCV for spike length, spikelets spike<sup>-1</sup>, 1000 kernel weight, and, which contradicts the current finding.

Under stress condition genotypic coefficient of variation (GCV) ranged from 4.30% for days to maturity to 18.41% for fertile tiller plant<sup>-1</sup>; while phenotypic coefficient of variation (PCV) ranged from 5.19% for days to maturity to 22.27% for fertile tiller plant<sup>-1</sup> (Table 5). High PCV values were recorded for fertile tiller plant<sup>-1</sup> and grain yield. Similarly, Naseri *et al.* (2012) and Rehman *et al.* (2015) reported high PCV value, for grain yield (t ha<sup>-1</sup>) under stress condition in wheat. Singh *et al.* (2014) reported high PCV value for fertile tiller plant<sup>-1</sup> under drought condition in bread wheat. Moderate GCV values were recorded for number of fertile

tiller plant<sup>-1</sup>, biomass yield, grain yield and number of kernels spike<sup>-1</sup>, whereas intermediate PCV values were recorded for biomass yield, harvest index, number of spikelet spike<sup>-1</sup>, spike length and plant height. Intermediate PCV were reported for spike length, harvest index and number of kernels spike<sup>-1</sup> (Singh *et al.* 2014). Rehman *et al.* (2015) also reported intermediate PCV value for spike length, plant height and number of spikelets spike<sup>-1</sup>, whereas intermediate GCV for grain yield was reported by the author which supports the present finding.

Under stress condition moderate GCV coupled with moderate PCV values were observed for biomass yield and number of kernels spike<sup>-1</sup>. The traits that had low GCV value were days to maturity, days to heading, spikelet spike<sup>-1</sup>, plant height, spike length, grain filling period, thousand kernel weight and harvest index, while low PCV values were recorded for days to maturity, days to heading, spikelet spike<sup>-1</sup>, grain filling period and thousand kernel weight (Table 5). Singh *et al.* (2014) reported low GCV and PCV values for days to maturity and plant height which agree with the present finding. Rehman *et al.* (2015) also reported low PCV and GCV values for days to heading.

### **Estimates of broad sense heritability, expected genetic advance and genetic advance as percentage of mean**

Under optimum condition, broad sense heritability ranged from 43 to 89% for spike length and biomass yield, respectively (Table 5). High heritability was observed for biomass yield, grain yield, thousand kernel weight, harvest index, days to heading and days to maturity. The result is in agreement with that of Dargicho *et al.* (2015b) indicating high heritability values for characters such as, days to heading, thousand-grain weight and days to maturity. In line with the current finding, Birhanu *et al.* (2016) also reported high heritability for days to heading, days to maturity, thousand kernel weight, grain yield and harvest index. Morketa (2017) reported high heritability values for biomass yield, grain yield, harvest index, thousand kernel weight, days to heading and days to maturity which agree with the current finding. In contrast to present result low heritability value was reported by Adhiena *et al.* (2016) for grain yield and biomass yield.

Under optimum condition moderate heritability value was noticed for fertile tiller plant<sup>-1</sup>, grain filling period, plant height, number of spikelets spike<sup>-1</sup>, spike length and number of kernels spike<sup>-1</sup> (Table 4). In line with the present finding Birhanu *et al.* (2017) reported

moderate heritability for grain filling period, number of kernels spike<sup>-1</sup> and plant height. Alemu *et al.* (2019) reported moderate heritability values for grain filling period, spikelets spike<sup>-1</sup> and fertile tillers plant<sup>-1</sup> indicating that the variation observed were mainly due to influence of the environment.

Under optimum condition genetic advance as percentage of mean was ranged from 6.51 to 40.33% for days to maturity and grain yield respectively (Table 4), indicating selection of the top 5% base population could results in an advance of 6.51% and 40.33% over respective population. According to Johnson *et al.* (1955), genetic advance as percentage of mean was classified as low (<10%), moderate (10-20%) and high (>20%). Accordingly, high genetic advance as percentage of mean was noted for biomass yield, grain yield and fertile tiller plant<sup>-1</sup>. Arati *et al.* (2015) reported high value of genetic advance as percentage of mean for grain yield. Dargicho *et al.* (2015b) reported high genetic advance as percentage of mean for grain yield and fertile tiller plant<sup>-1</sup>. Birhanu *et al.* (2017) reported high values of genetic advance as percentage of mean for biomass yield and grain yield. Moderate value of genetic advance as percentage of mean was noted for harvest index, grain filling period, thousand kernel weight and number of kernel spike<sup>-1</sup>. Alemu *et al.* (2019) reported moderate values of genetic advance as percentage of mean for thousand kernel weight and number of kernels spike<sup>-1</sup>. Berhanu *et al.* (2017) also reported moderate genetic advance as percentage of mean for grain filling period which support the present finding. Low genetic advance as percentage of mean was noted for days to heading, days to maturity, plant height, number of spikelets spike<sup>-1</sup> and spike length indicating selection for these characters would not be effective due to the predominant effects of non-additive genes. In line with the present result, low value of genetic advance as percentage of mean for days to maturity, plant height and number of spikelets spike<sup>-1</sup> was reported by Alemu *et al.* (2019). Berhanu *et al.* (2017) reported low genetic advance as percentage of mean for spike length.

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 percentage of mean was found for biomass yield and grain yield (Table 4). This indicates that there could be predominance of additive gene action and might not much prejudiced by environmental fluctuations. Kumar *et al.* (2017) reported high heritability coupled with high genetic advance for biomass yield and grain yield. Moderate heritability coupled with moderate genetic advance as percentage of mean was noted for

grain filling period and number of kernels spike<sup>-1</sup>. Similar to present result, Girma (2018) reported moderate heritability coupled with moderate genetic advance as percentage of mean for grain filling period and number of kernels spike<sup>-1</sup>. Therefore, these characters could be useful criteria for selection and may be effective in early generations for these traits.

Under stress condition, broad sense heritability ranged from 23.4 to 86.1% for harvest index and days to heading respectively (Table 5). High heritability value was noticed for biomass yield, thousand kernel weight, days to heading, days to maturity, plant height, fertile tiller plant<sup>-1</sup> and number of spikelets spike<sup>-1</sup>. High heritability value for these traits indicated that the variation observed was mainly under genetic control and was less influenced by environment. So, these traits may be used as a selection criterion under stress. High heritability value was reported for plant height, thousand kernel weight and fertile tiller plant<sup>-1</sup> by Singh *et al.* (2014). Abd-Allah *et al.* (2018) also found high heritability values for days to heading and thousand kernel weight under drought condition which agrees with the present finding.

Under stress condition moderate heritability value was noted for grain filling period, grain yield and spike length,. Similar to the present result, Rehman *et al.* (2015) reported moderate heritability value for spike length under drought condition in bread wheat. Grain yield is a polygenic trait that is highly influenced by the environment under stressed condition; thus moderate heritability was expected for this trait (Mwadingeni *et al.* 2017). The author also found moderate heritability value for grain yield under drought stress condition which support present finding. Low heritability value was observed for the trait harvest index. Harvest index is an indicator of plant efficiency in distributing photosynthetic materials towards the grain. Similarly, some authors have reported a low heritability for harvest index (Wang *et al.* 2002; Talebi and Fayyaz 2012) in bread wheat under drought stress condition.

Under stress condition estimates of genetic advance as percentage of mean ranged from 5.69 to 33.34% for harvest index and biomass yield (Table 5), indicating selection of the top 5% base population could result in an advance of 4.51% and 33.34% over respective population. High genetic advance as percentage of mean was recorded for biomass yield, fertile tiller plant<sup>-1</sup> and grain yield. Arya *et al.* (2013) found high genetic advance as percentage of mean for biomass yield, fertile tiller plant<sup>-1</sup> and grain yield which agree with the present finding. Singh *et al.* (2014) found high genetic advance as percentage of mean for number of tiller plant<sup>-1</sup> and grain yield. Moderate genetic advance as percentage of mean was noted for days

to heading, grain filling period, plant height, spike length, number of kernels spike<sup>-1</sup> and number of spikelets spike<sup>-1</sup>. Singh *et al.* (2014) found moderate genetic advance as percentage of mean for plant height, spike length and number of kernels spike<sup>-1</sup> which support the present finding. Low genetic advance as percentage of mean was reported for days to maturity by Singh *et al.* (2014) and Elahi *et al.* (2020).

Heritability estimates are useful in deciding the character to be considered while making selection, but selection based on this factor alone may limit the progress, as it is prone for changes with environment (Johnson *et al.* 1955). Accordingly, high heritability values coupled with high genetic advance as percentage of mean were noted for biomass yield and fertile tiller plant<sup>-1</sup> under stress condition. Hence, direct selection can be done through these characters for genetic improvement under drought condition. In agreement with the present finding, Arya *et al.* (2013) found high heritability coupled with high genetic advance as percentage of mean for number of tiller plant<sup>-1</sup> and biomass yield. High heritability coupled with high genetic advance as percentage of mean was also reported for number of tiller plant<sup>-1</sup> in bread wheat (Singh *et al.* 2014) and for above ground biomass in durum wheat (Alemayehu *et al.* 2019) under drought condition.

Under stress condition high heritability coupled with moderate genetic advance as percentage of mean were noted for days to heading, thousand kernel weight, plant height and number of spikelets spike<sup>-1</sup> (Table 5). The result was in accordance with the result of Arya *et al.* (2013) and Singh *et al.* (2014) for thousand kernel weight and plant height respectively. Moderate heritability coupled with moderate genetic advance as percentage mean were noted for spike length, number of kernel spike<sup>-1</sup> and grain filling period. Eid (2009) found moderate heritability coupled with moderate genetic advance as percentage of mean for spike length. Low heritability coupled with low genetic advance as percentage of mean was observed for harvest index. Chowdhury *et al.* (2018) reported low heritability value coupled with low genetic advance as percentage of mean for number of kernel spike<sup>-1</sup> which contradicts with the present finding.

## **Conclusion**

Analysis of variance revealed highly significant variation ( $p \leq 0.01$ ) for studied traits under both optimum and stress conditions. This indicated presence significant genetic variation among the tested genotypes for further breeding program. Highly significant variation was

observed for grain yield which ranged from 2.30-6.0 t ha<sup>-1</sup> and 1.01-4.36 t ha<sup>-1</sup> for optimum and stress condition respectively. Depending on the mean performance twelve genotypes had mean value of greater than best performing check (Fentalle-2= 4.84 t ha<sup>-1</sup>) for grain yield under optimum condition, whereas fourteen genotypes showed superior to standard check (Kingbird=3.18 t ha<sup>-1</sup>) for grain yield under stress condition.

Under optimum condition high GCV and PCV were observed for grain yield, whereas high PCV was noted for grain yield and fertile tiller plant<sup>-1</sup> under stress condition. Moderate GCV coupled with moderate PCV was observed for biomass yield under both conditions whereas, number of kernels spike<sup>-1</sup> showed moderate values of GCV and PCV under stress condition. High GCV and PCV indicate effectiveness of selection based phenotypic performance for these traits. Low GCV and PCV values were noted for days to heading, days to maturity, grain filling period, plant height, number of spikelets spike<sup>-1</sup> and number of kernels spike<sup>-1</sup>. Under stress condition low GCV and PCV values were observed for days to heading, days to maturity, grain filling period, thousand kernel weight and number spikelets spike<sup>-1</sup> indicating ineffectiveness of selection based on phenotypic performance for these traits. High heritability value was recorded for days to heading, days to maturity, biomass yield, grain yield, thousand kernel weight and harvest index under optimum condition. Days to heading, days to maturity, biomass yield, thousand kernel weight, plant height, fertile tiller plant<sup>-1</sup> and number of spikelets spike<sup>-1</sup> showed high heritability value under stress condition.

Genetic advance as percentage of mean was high for grain yield, biomass yield and fertile tiller plant<sup>-1</sup> under both conditions. High heritability value coupled with high genetic advance as percentage of mean were noted for biomass yield and grain yield under optimum condition, whereas biomass yield and number of fertile tiller plant<sup>-1</sup> showed high heritability coupled with high genetic advance as percentage of mean under stress condition. High heritability coupled with moderate genetic advance were observed for thousand kernel weight and harvest index under optimum condition; and days to heading, thousand kernel weight, plant height and number of spikelets spike<sup>-1</sup> showed high heritability coupled with moderate genetic advance as percentage of mean under stress condition. This indicated that the variation observed was under genetic control and possibility of undergoing selection for further evaluation. Generally, the tested genotypes exhibited sufficient genetic variation to be exploited in the breeding program. Based on the mean performance of genotypes, G3, G24,

G26, G28 and G45 had yield advantage over checks under both conditions and would be recommended for verification trial across lowland areas of the country.

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