

Genetic Variation of Bread Wheat (*Triticum aestivum* L.) Varieties Based on Phenological, Morphological and Quality Traits at Guay Kebele in Debre Elias District, East Gojjam Zone, Northwestern Ethiopia

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Abstract

Genetic variation study was conducted at Guay Kebele, D/Elias district in 2018/19, to select superior varieties of bread wheat on farmer's field. Ten alternative bread wheat varieties including standard check were evaluated under rain fed conditions using a randomized complete block design with three replications. The analysis of variance (ANOVA) of phenological, agronomic and quality traits indicated the presence of significant ($P < 0.05$) variation in protein content and harvest index while, days to 50% emergence, days to 75% heading, days to maturity, plant height, effective tiller, spikelet per spike, spike length, grain per spike, biomass yield, grain yield, 1000 kernel weight, hectoliter weight showed highly significant ($P < 0.01$) difference. Abola ($3.99\text{ton}\cdot\text{ha}^{-1}$) and Ogoloncho ($3.87\text{ton}\cdot\text{ha}^{-1}$) were the higher yielders over the standard check (Kekeba= $3.18\text{ton}\cdot\text{ha}^{-1}$) and to the other varieties tested. Grain yield revealed strong, positive and highly significant correlation with harvest index ($r=0.88^{**}$), plant height ($r=0.67^{**}$), number of effective tillers ($r=0.73^{**}$), spike length ($r=0.74^{**}$), spikelet per spike ($r=0.70^{**}$), number of grain per spike ($r=0.80^{**}$), biomass yield ($r=0.85^{**}$), 1000 seed weight ($r=0.76^{**}$) and hectoliter weight ($r=0.83^{**}$). The higher genotypic coefficient of variation was observed from thousand kernel weight (79.27%) and the higher phenotypic coefficient of variance was also observed from thousand kernel weight (88.25) and effective tiler weight (26.94%). Spikelet per spike (92.42%), grain yield (80.39%), hectoliter weight (96.6%), plant height (85.49%) and days to physiological maturity (95.7%) had higher heritability with moderate and low genetic advances. Therefore, based on the results of this there were variability among the tested varieties and then Abola and Ogoloncho are recommended for any genetic improvement as well as for production in the study area.

Keywords: Bread wheat, coefficient of variation, correlation, heritability, standard check

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1. INTRODUCTION

Bread wheat (*Triticum aestivum* L. $2n=6x=42$), is allopolyploid, a self-pollinating annual plant in the true grass family Gramineae (*Poaceae*) and it is largest cereal crop extensively grown as staple food sources in the world (Mollasadeghi *et al.*, 2012). Wheat provides more nourishment for the people of the world than any other crop, and provides the nutrition for the greater part of the world population. The world wheat production is 728.3 million tons and East Africa produced 5.7 million tons, from this Ethiopia had a share of 4.6 million tons (FAO, 2019).

Wheat is grown at an altitude ranging from 1500 to 3000 meters above sea level, between 6-160 N latitude and 35-420 E longitude but its suitable agro-ecological zones, fall between 1900 and 2700 m a.s.l. (Kifle *et al.*, 2016). Wheat is the third most important small cereal crops in Ethiopia in terms of cultivated land, food value and number of smallholders engaged in production after Tef (*Eragrostis tef* L.) and Maize (*Zea mays* L.) (Birhanu *et al.*, 2016).

The total wheat area coverage and production in the Amhara region was 554,661.74 ha (32.7% of the countries coverage) and 1319197.1 tons respectively with the productivity of 25.33qt/ha in 2016/17 Meher season (CSA, 2017). In Amhara region administrative Zones, East Gojjam zone Ranks first in area coverage and productivity which is 127,469.49ha with 25.05qt/ha followed by South Wollo 99,702.51ha with 22.98qt/ha, and North Shoa 83,238.27ha with 25.96qt/ha respectively (CSA, 2017). The productivity of wheat in this administrative zone (25.09qt/ha) is relatively better than regional productivity (23.80qt/ha) but, lower than the national average (26.75qt/ha) (CSA, 2017).

However, wheat production is limited with disease, low productivity, limited availability of varieties especially using of old improved and sole variety Kekeba in the study area. Hence, to make an effective selection for grain yield, understanding the genetic variability, heritability and genetic advance as percent of mean as well as the association of grain yield with yield contributing characters is important (Birhanu *et al.*, 2016). According to Abhilasha *et al.* (2018), the availability of a wide variability provides the breeder with a greater chance of selecting desired material. In addition, to evolve superior genotype for further hybridization and selection it is important to get precise information on the nature and degree of genetic diversity present in wheat collections from principal areas of cultivation. Existence of genetic diversity is very essential to meet the present and future crop breeding challenges. It is a prerequisite for the development of improved cultivars with wider adaptability and

broad genetic base (Hailu, 2011).

Therefore, genetic variation of bread wheat varieties based on phenological, growth and quality traits selection was conducted to evaluate and identify high yielding and good quality of bread wheat based on the difference in the genetic makeup of the varieties at Guay Kebele in Debre Elias district.

2. MATERIALS AND METHODS

2.1. Description of Experimental site

Genetic variation of bread wheat trial was conducted at Guay Kebele in Debre Elias district, East Gojjam Zone in 2018/2019 main cropping season. The study area (Debre Elias) is located around 335 km northwest from Addis Ababa and 42kms from Debre Markos city. Debre Elias is one of the districts of Amhara region in E/Gojjam Zone. It is bordered on the south and west by Abay river which separates it from Oromia region, on the northwest by west Gojjam zone, on the north by Machakel district and on the east by Gozamin district. The district town is called Elias. The mean annual temperature of the district ranges from 18-27°C and receives mean annual rainfall of 1150 mm and red soils are the dominant soil type and it is moderately fertile (Achenef and Admas, 2012). The district comprises altitudes ranging between 800 and 2600 m.a.s.l and about 99% of the district is mid altitude. The area mainly consists of plain topography (85%) while the rest (15%) is undulating topography. Debre Elias has an area of about 94,000 ha and its population size is 102,000. The average land holding of the district is 1.93 ha per household and its average family size is six. The most important crops grown in the district are Wheat, Tef, Maize, Faba bean, Barley, Niger seed and linseed (Debre-Elias District Agriculture and Rural Development Office, 2005). In this area, agriculture is predominantly rain fed.

a. Experimental materials

The experimental materials used for the study include Tsehay, Shorima, Danda'a, Wane, Ogoloncho, Kekeba, King bird, Lemu, Tay and Abola Bread wheat varieties Those varieties were developed by different research institutes. They have chosen based on superiority in grain yield performance (high yielding), disease resistance, stability and wide adaptation.

Table 1. List of Varieties tested at Guay and Tijagotir in 2018/2019.

Treatment no	Variety Name	Source/ Releaser	Year of Release	Adaptation Zone		Productivity (Q/ha)
				Altitude (M a.s.l)	Rain fall (mm)	
1	Ogoloncho	Kulmsa	2012	1600-2100	400-500	33-50
2	Tsehay (HAR-3837)	Kulmsa	2014	2600-3100	>900	38
3.	Shorima(ETBW5483)	Kulmsa	2011	1900-2600	600-900	44-63
4.	Kekeba	Kulmsa	2010	1500-2000	500-800	33-52
5.	Danda'a	Kulmsa	2010	2000-2600	>600	35-55
6.	Tay	Adet	2005	1900-2800	>700	25-61
7.	King Bird	Kulmsa	2015	1500 -2200	500 - 850	46.5- 63.1
8	Lemu	Kulumsa	2016	>2200	800-1100	55-65
9	Wane	Sinana	2016	2100-2700	700-1000	50-60
10	Abola(HAR-1522)	D/Birhan ARC	1997	2200-2700	>600	40-65

2.2. Experimental Design and Trial Management

The mother trial experiment was laid out by RCBD with three replications in Guay FTC having full set up while the baby trial was also laid out in RCBD method with locations/sites as replications. The varieties were randomized in each field and each of them was planted on the plot of 7.5m² (2.5mx3m) having 1m and 0.5m spacing between blocks and plots respectively. During sowing, the seeds were manually drilled into three meters long in 10 rows and plots were spaced 25cm apart.

2.3. Data Collected

Data collected on plant basis was (plant height, spike length, spikelet per spike, fertile tiller per plant kernels per spike, yellow rust, leaf rust and stem rust) and plot basis (days to 50% emergence, days to heading, days to 90% maturity, above ground biomass, grain yield, harvest index, hectoliter weight and protein content). For data collection on plant bases, ten plants were randomly taken from the six middle rows of each plot excluding the four rows from both sides of each plot which were considered as border and the mean value of these ten plants was calculated using Micro soft Excel and used as plot data for analysis. Yield data was also taken from the plot net area which was (3m²) and then, converted to ton-ha⁻¹. The study data were recorded on the phenological, growth, yield and yield related trait and quality traits.

2.4. Statistical Analysis

(i) Analysis of Variance (ANOVA)

The data collected for each quantitative trait subjected to Proc GLM procedures of SAS software version 9.4 (SAS, 2013) with treatment and replications as the class variables and the response variables were the traits on which data was collected.

(ii) Analysis of genetic parameters/ Variance components

a. Estimation of phenotypic and genotypic coefficient of variance

The genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability were estimated according to the method suggested by Burton and Devane (1953)

- ✓ Genotypic coefficient of variability (GCV) = $\frac{\sqrt{\sigma^2g} \times 100}{\bar{X}}$
- ✓ Phenotypic coefficient of variability (PCV) = $\frac{\sqrt{\sigma^2p} \times 100}{\bar{X}}$
- ✓ Environmental coefficient of variation (ECV) = $\frac{\sqrt{\sigma^2e} \times 100}{\bar{X}}$

Where σ^2g = Genotypic variance, σ^2p = phenotypic variance, σ^2e = environmental variation and \bar{x} = Grand mean of a character. Genetic improvement of any character is difficult without having sufficient genetic variability. Therefore, the existence of genetic variability in population is pre-requisite for any crop improvement programme. Fisher (1918) interprets quantitative characters in terms of Mendelian genetics and subsequently the estimates of genotypic and phenotypic variations were used to predict the expected genetic response. The coefficient of variability is used to assess the extent of variability between two diverse characteristics. The variance component is used to compute the genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) and expected genetic advance.

b. Estimation of heritability in broad sense and Genetic advance

Heritability is difference due to the environment and inheritance. The greater the proportion of the total variability that is due to the environment, the more difficult it would be to select for inherent differences. On the other hand, if environmental variability is small in relation to genotypic differences, selection will be efficient, because the selected character will be transmitted to the progeny. The inherent portion of the variability is termed as heritability (Allard, 1960). Heritability (H): heritability in broad sense for all characters was computed using the formula given by Falconer, (1997) and Hanson *et al.*, (1956).

$$\text{Heritability (h}^2\text{b)} = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where: H= heritability in broad sense, σ^2p = Phenotypic variance, σ^2g = Genotypic variance.

The broad sense heritability estimates were classified as low, moderate and high as follows: 0-40 % = Low, 40-80 % = Moderate, and > 80 % = High (Singh *et al.*, 2001).

c. Genetic advance expected

Genetic advance is also considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.*, 2003). High genetic advance coupled with high heritability estimates offers the most effective condition for selection (Larik *et al.*, 2000). Heritability measures the degree to which the variability of a character is transmitted to the progeny, serves as a guide to the reliability of phenotypic variability in the selection programme and hence determines its success (Dawit *et al.*, 2012). However, Johnson *et al.* (1955) stated that heritability estimates together with genetic advance are more important than heritability alone to predict the resulting effect of selecting the best individuals. Genetic advance was computed using the formula suggested by Allard (1960) and Johnson *et al.*, (1955). $GA = (k) (\sigma_p) (h^2)$ or $(k) (\sqrt{P_v}) (h^2b)$. Where, k = selection differential (at 5% selection intensity = 2.06), σ_p = phenotypic standard deviation ($\sqrt{P_v}$ = expressed the phenotypic standard deviation), h^2b = broad sense heritability. The GA was categorized as, <10 % = Low, 10-20 % = Moderate, and, >20 % = High

3. RESULT AND DISCUSSION

3.1. Analysis of Variance (ANOVA)

Mean squares of the 14 characters from analysis of variance (ANOVA) are presented in (Table 2). Highly significant differences among varieties ($P < 0.01$) were observed for Twelve characters (days to emergence, days to heading, days to maturity, plant height, effective tillers per plant, spike length, spikelets per spike, grain per spike, 1000 kernel weight, biomass yield, grain yield and hectoliter weight), significant at ($p < 0.05$) for the rest two characters; namely, harvest index and protein content. This result indicating that there is variability among the genotypes studied and would respond positively to selection.

Table 2. Analysis of variance (ANOVA) for the 14 characters of 10 bread wheat varieties grown at Guay (2018/19)

Traits	MSt	MSr	Mse	CV(%)
DE	3.05**	0.90*	0.19	6.15
DH	60.40**	12.70*	2.95	2.57
DM	213.41**	3.90	3.12	1.61
PH	172.35**	10.13	9.23	3.60
ETL	1.53**	0.18	0.60	7.46
SPL	2.37**	0.54*	0.11	4.47
SPS	5.66**	3.60**	0.15	2.27
NGS	110.81**	140.40**	13.36	7.76
BY	4.00**	1.87	0.65	8.40
GY	1.35**	0.19	0.12	12.11
TKW	16.44**	3.79*	1.01	2.81
HI	38.82*	4.59	10.88	11.17
HLW	25.08**	6.84**	0.29	1.79
PC	0.99*	8.71*	0.71	6.49

Where, MSt= mean square due to treatments, MSr= mean square due to replication, MSe= mean square due to error, CV = coefficient of variation, ns = non-significant, DE = days to 50% emergence, DH= days to 75% flowering, DM =, days to 90% maturity, PH= plant height, ETN= effective tiller number, SPS= spikelet per spike, SPL= spike length, *= significant, **= highly significant, NGS= number of grains per spike, BY= biomass yield, TKW= thousand kernel weight, HI= harvest index in %, HLW= hectoliter weight, PC= protein content.

3.2. Comparison of bread wheat varieties in phenological, growth and quality traits

The analysis of variance (ANOVA) of phenological, growth and quality traits revealed the presence of highly significant variance ($P < 0.01$) among the tested varieties for 12 characters studied while significant variance ($P < 0.05$) for harvest index and protein content (Table 2). In contrast to the present study, non-significant difference was observed among the varieties for, spike length, number of fertile tillers per plant, number of spikelet per spike and number of kernels per spike (Obsa *et al.*, 2018). Mean values for phenological, growth and quality traits are presented in mean separation table (Table 3).

a. Phenological traits:

Days to 50% emergence; Variety Kekeba (5.66 days), Tsehay (6.33 days), Wane (6.33 days) and Kingbird (7.33 days) emerged earlier than other varieties while Abola (8.33 days) and Tay (8.00 days) were emerged lately than the rest tested varieties. The variations of varieties in days to 50% emergence indicate that the existence of variation in genetic makeup. This could be used in the selection program due to its direct effect on days to heading and maturity. In areas where rainfall scarcity and fluctuation, early maturing varieties might have vital role in escaping the season of moisture stress.

Days to 75% heading: With respect to days to 75% heading, shortest day to heading was recorded for variety Kekeba (58 days) and longest day to heading was revealed by variety Lemu (75 days). This indicates that from the tested varieties Kekeba took short period of time to reach heading stage whereas Abola, Lemu, Tay and Danda'a took prolonged period of time. This result agrees with the findings of (Kifle *et al.*, 2017) who reported that there was highly significant variation among the tested varieties. This also in line with Assaye *et al.* (2013) who reported significant difference among the tested varieties at Wonberma district.

Days to 90% physiological maturity: Kekeba was early maturing variety (92 days) followed by Shorima (98 days) whereas, Abola, Tay, and Ogoloncho was late maturing varieties with 118, 116 and 115.66 days respectively (Table 4.6). Likewise, Astawus Esatu, (2016) reported that varieties Kekeba (58.7 days) and Kingbird (61 days) headed early and Kekeba (105 days) was matured early than Kingbird. This could be the fact that early matured varieties require shorter period to reach physiological maturity and lately headed varieties also require longer period to mature. Kifle *et al.* (2017) reported comparative result of 112.67 days to maturity for variety Mekele 01 and 109 days to maturity for variety Mekele 02.

b. Growth and agronomic traits:

Plant height; Abola (94.54 cm), Tay (94.50) and Danda'a (89.83 cm) were the tallest varieties while Wane (71.88 cm) and Lemu (76.37cm) was the shortest varieties (Table 3). Astawus Esatu, (2016) reported that TAY (102.9 cm) and Danda'a (98.6 cm) had the highest plant height while Kingbird (77.9cm) and Kekeba (80.3 cm) were the shortest varieties. The varieties which had the highest plant height in both trials resulted higher above ground biomass and grain yield. This might be due to the direct effect of plant height i.e. when plant height increases, spike length, number of grain per spike and spikelets per spike could increase and as result it may have attributed to increase in biomass and grain yield. Significant variation among bread wheat genotypes for plant height was also reported by many authors including by (Assaye *et al.*, 2013, Asefa *et al.*, 2014, Obsa and Yared, 2017). In contrast, non-significant variation in plant height among bread wheat varieties was reported by Fano and Tadeos,

(2017).

Effective tillers per plant: The number of effective tiller per plant ranged from 2.68 to 4.86 as shown in (Table 3). Ogoloncho (4.86) and Abola (4.55) had higher number of effective tillers per plant over the standard check and Tay, Shorima, Tsehay, Kingbird, Wane and Lemu. The higher effective tiller per plant, the higher could be grain yield. This is due to; effective tillers might have few to several grains which could directly related to yield. This is in agreement with the finding of Astawus *et al.* (2018) who reported significant variation for effective tillers per plant among the tested varieties. Further, Kifle *et al.* (2018) also reported significant variation among the tested varieties for the trait of effective tillers per plant.

Spike length (cm): Abola (9.17 cm) had longer spike length followed by Tay (8.75cm) while Lemu (6.25cm) had the shortest spike length. Spike length mean values ranged from 6.25cm to 9.17cm. The reason for this much spike length difference might be due to the presence of genetic difference among varieties. The varieties which had longest spike length attributed to higher grain yield, number of grains per spike and spikelets per spike. This might be due to the reason that the positive association of spike length with those traits or a direct influence on the increase or decrease of yield components. This result is in agreement with the finding of (Assaye *et al.*, 2013), who studied participatory varietal selection on wheat and he stated that the spike length difference ranged from 9.8 cm for variety ETBW5526 and 7.8 cm for Millennium variety.

Number of spikelet per spike: Abola (19.58) and Tay (19.08) followed by Ogoloncho (18.21) showed higher number of spikelet per spike while Lemu (15.5) and Wane (15.83) had few number of spikelet per spike. This is due to the fact that, when the length of spike increases, number of spikelets per spike increased, the number of grains per spike may increase and as a result the grain yield can increase. Similarly, the present result is supported by Kifle *et al.* (2018) and Assaye *et al.* (2013) who reported that larger spike length has a direct effect or contribution for higher number of spikelets. On other hand, non-significant variations among the tested bread varieties for spikelets per spike was reported by (Obsa *et al.*, 2018).

Number of grain per spike: The highest number of grain per spike was recorded for Abola (57) followed by Tay (55) and Ogoloncho (49.33) while the lowest number of kernels was recorded for Lemu (37.33) (Table 3). In line with the present result, Mitiku and Regassa, (2019) reported that highest numbers of grains per spike were counted for Ogoloncho (37.3) over the other varieties under study.

Above ground dry biomass yield (ton ha⁻¹): The mean values of biomass yield ranged from 7.6 to 11.3-ton ha⁻¹. Abola (11.27-ton ha⁻¹) and Ogoloncho (11.08-ton ha⁻¹) recorded higher above ground biomass followed by Tay (10.50-ton ha⁻¹) and Shorima (10.11-ton ha⁻¹) whereas Lemu (7.66-ton ha⁻¹) followed by Wane (8.29-ton ha⁻¹) recorded lower biomass yield among the varieties (Table 3). Abola and Ogoloncho had best performance while Lemu and Wane showed low and least performance for above ground biomass yield. This could be due to their stiff and hard stalks, large spikes, higher number of grains per spike and could result higher biomass yield. Similarly, higher biomass of Abola and Ogoloncho could be due to, they had longest plant height, higher tiller, large spike length and those traits could be contributed for higher biomass yield. Accordingly, varieties which showed lower biomass yield also had short plant height, fewer tiller, short spike length and resulted lower biomass. Therefore, biomass yield was significantly influenced by plant height, tiller number and spike length. Likewise, Yetsedaw *et al.* (2013), reported that, there was highly significant difference ($p < 0.01$) in biomass yield on malt barley genotypes. According to his result the tasted genotypes mean value of biomass yield ranged from 3.1 to 5.8 t/ha.

Thousand kernel weight (gram): highest thousand seed weight was (38.95g) for Abola followed by Ogoloncho (38.80g) and Tay (37.00g) but, a lowest was Lemu (32.31g). Even though, variety Abola and Ogoloncho had better thousand seed weight in the study area, they are still under mean weight of thousand seeds for bread Wheat studied in India which was 46.18g with a standard error of ($\pm 0.36g$) (Deivasigamani and Swaminathan, 2018).

Grain yield (ton ha⁻¹): Abola (3.99ton ha⁻¹) followed by Ogoloncho (3.87ton ha⁻¹) was higher grain yielder while Wane (1.93ton ha⁻¹) was the lower grain yielder. Astawus *et al.* (2018) reported that higher grain yield was observed by the variety Abola (6.4ton/ha) and Shorima (6.3ton/ha) over 25 varieties of under study. In contrary, Assefa *et al.* (2014) and Mitiku and Regassa (2019) reported that Picaflour/Kekeba gave very significantly higher grain yields than the check as well as the other varieties tested in the study. Likewise, Mitiku and Regassa, (2019) reported that maximum grain yield was recorded on improved bread wheat variety of Ogoloncho with productivity of (2746 Kg/ha) in Madda Walabu District Bale Zone of South Eastern Ethiopia.

Harvest index (%): Abola (35.44%) showed the highest harvest index followed by Ogoloncho (34.94%), Shorima (30.02) and Tay (30.44%) whereas Wane (23.22%) had the lowest harvest index. The probable reason for higher harvest index of Abola, Ogoloncho and Shorima could be due to their better performance to disease reaction and genetic makeup that enable the varieties to have higher harvest index. Similar results for harvest index was also obtained by several authors (Assaye *et al.*, 2013, Obsa and Yared, 2017 and Assefa *et al.*, 2014) who reported that higher harvest index was obtained from disease resistant and well performing varieties. According to the study conducted by Astawus *et al.* (2018), the highest ratio of grain to biomass (HI) was observed from variety

Kingbird (42.3%), Kekeba (42.1%) and Shorima (40.9%) over the other varieties studied.

c. Quality traits:

Analysis of variance (ANOVA) of quality traits of the varieties exhibited significant variation ($P < 0.05$) for hectoliter weight and protein content (Table 2). The mean separation table of hectoliter weight and protein content traits are presented on (Table 3).

Hectoliter weight (Kg/hl): Abola (78.16 kg/hl) followed by Ogoloncho (76.63 kg/hl) scored the highest hectoliter weight and Wane (69.43 kg/hl) and Lemu (69.46 kg/hl) both scored the lowest weight. In addition to inherent characteristics of the varieties, effects of disease incidence especially in grain filling period, could affect the weight of the seeds i.e. the bulk density of the wheat seed, especially for those susceptible varieties, and thus, they had showed lowest thousand seed weight and hectoliter weight of the varieties. Astawus Esatu (2016) reported also that hectoliter weight was highly significantly affected by the varieties and higher hectoliter weight was recorded from varieties Bika (75.51 kg/hl), Shorima (74.48 kg/hl), Mekelle-1 (73.98 kg/hl) and Jefferson, (73.97 kg/hl) in two districts of Arsi Zone Ethiopia.

Protein content (%): The highest protein content was found on Abola (14.46%). Proteins are important in determining the nutritional value of wheat, for both human and animal consumption, and are the main factors of baking quality. The protein content of wheat varies between 10 and 20%; wheat for bread has 10–15%, for pasta 11–17% (Uthaya *et al.* 1999). Bordes *et al.* (2008) reported similar results of a larger range of grain protein content of 10.9–19.2% among the varieties tested in different locations. Because grains were collected from plants grown under different conditions in field trait at each location during the same growing season, the influence of environmental factors and/or varietal variation could be the factors for such variation of the total grain protein.

Table 3. Mean separation of 14 different phenological, growth and quality traits for 10 alternative bread wheat varieties at Guay kebele, D/Elias district in 2018/19

Varieties	DE	DH	DM	PH (cm)	ETN	SL (cm)	SPS	GPS	BY (t-ha ⁻¹)	GY (t-ha ⁻¹)	TKW (g)	HI (%)	HLW (Kg/hl)	PC (%)
Ogoloncho	7.6bc	67.3bc	116ab	88.7bc	4.86a	8.2b	18.2b	49.3bc	11.1a	3.87a	38.8a	34.94a	38.5ab	15.4ab
Tsehay	6.3de	65.3bc	108.6c	81.8de	3.1cd	6.8c	16.3def	46.6cde	9.3bc	2.8bc	34cde	28.5bc	38.3ab	15.4ab
Shorima	7.6bc	66.6bc	98.0d	78.8ef	3.1cd	7.2c	17.0cd	47.6cd	10ab	2.9bc	34.3cd	30.0ab	38.0ab	15.2ab
Kekeba (Check)	5.6c	58.0e	92.0e	84.3cd	2.6d	7.2c	16.1efg	43def	9.2bc	2.6bcd	34.5cd	29.3b	35.9b	14.6b
Danda'a	8.6a	69.0b	114b	89.8ab	3.4c	7.3c	17.5c	48.3cd	9.3bc	2.6cd	35.4bc	27.2bc	37.3ab	15.1ab
Tay	8.0ab	68.0bc	115ab	94.5a	3.9b	8.7ab	19.1a	55.0ab	10.5ab	3.18b	37.0b	30.4ab	38.2ab	15.5ab
King bird	7.3de	66.6bc	107c	82.4de	3.4c	7.3c	17cde	44.6cde	9.2bc	2.6bcd	33.5de	28.7bc	37.9ab	15.2ab
Lemu	7.0cd	75.0a	114b	76.3fg	3.4c	6.2d	15.5g	37.33f	7.66d	2.1ed	32.31e	27.3bc	42.2ab	15.5ab
Wane	6.3de	62.0d	107.6c	71.8g	2.8d	7.2c	15.8fg	41.3ef	8.3cd	1.9e	33.0de	23.22c	35.5b	14.6b
Abola	8.3ab	69.0b	118a	94.5a	4.5a	9.2a	19.6a	57.66a	11.3a	4.0a	38.9a	35.44a	40.9ab	16.9a
Sig. diff.	**	**	**	**	**	**	**	**	**	**	**	*	*	*
SE±	0.38	1.40	1.44	2.48	0.24	0.27	0.32	2.98	0.66	0.28	0.82	2.69	2.63	0.87
CV	6.15	2.57	1.61	3.60	7.46	4.47	2.27	7.76	8.40	12.11	2.86	11.17	8.41	6.89

Where, DE = days to 50% emergence, DH= days to 75% heading/flowering, DM =, days to 90% maturity, PH= plant height, ETN= effective tiller number, SPS= spikelet per spike, SPL= spike length, NGS= number of grains per spike, BY= biomass yield, GY= Grain yield, TKW= thousand kernel weight, HI= harvest index, HLW= hectoliter weight, PC= protein content, CV=coefficient of variance, SE= standard error, *= significantly different ($P < 0.05$), **= highly significantly different ($P < 0.01$).

3.3. Variability components and coefficient of variation

According to Burton and De Vane (1953), PCV and GCV values roughly more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. Based on this bench mark, genotypic coefficient of variance was maximum for hectoliter weight (79.27) and minimum for grain yield (1.82%). The highest genetic coefficient of variance (>20%) was estimated from hectoliter weight (79.27) and moderate genotypic coefficient of variance (10-20%) was obtained from harvest index (10.33%), biomass yield (11.02%), grain per spike (12.69%), spike length (11.67%), effective tiller (15.73%) and days to 50% emergence (13.53%). this suggesting that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. In line with the present result, Birhanu *et al.* (2016) reported moderate GCV of harvest index, biomass yield, grain per spike and effective tiller on bread wheat varieties. In contrary to this study, Gour *et al.*, (2017) reported high genotypic and phenotypic coefficient of variation for seed yield per plant, days to 50% flowering, biological yield per plant, spikelets/plant, harvest index, number of tillers/plant and plant height on rice

Lower genetic coefficient of variance (<10%) was obtained from days to heading, days to 90% maturity, plant height, spikelets per spike, grain yield, hectoliter weight and protein content (Table 4). High PCV was estimated from TKW (88.25) and ETN (26.94%) and moderate PCV was obtained from days to 50% maturity (14.83%), harvest index (15.21%), grain per spike (14.37%), biomass yield (13.85%) and from spike length (12.28%) but lower PCV (<10%) also estimated from days to 75% heading, days to 90% maturity, plant height, spikelets per spike, grain yield, hectoliter weight and protein content. Likewise, Ali *et al.* (2012) reported medium PCV and GCV for grain yield per plot in 20 bread wheat genotypes. Furthermore, Sentayehu *et al.* (2015) reported high PCV and GCV in traits of number of tillers plant-1, spike length, kernel per spike, thousand-grain weight, biomass yield per plot, harvest index, and grain yield per plot. The higher PCV and GCV values for most of the characters

could be evidence for the existence of a wide range of variation for such characters.

Phenotypic coefficient of variation for all the traits was relatively higher than the genotypic coefficient of variation (Table 4.) which indicates the presence of little influence of environment in the expression of these metric traits. In general, the PCV values for most characters were closer with the corresponding GCV values showing little environment effect on the expression of these characters but higher variation between GCV and PCV was observed on effective tiller (GCV=15.73%, PCV=26.94%) and thousand kernel weight (GCV=79.07%, PCV=88.25%) (Table 4). Similar results were also observed by Mohammed *et al.* (2011) and Subhashchandra *et al.* (2009), who reported that higher variation between phenotypic coefficient of variance and genotypic coefficient of variance was observed for effective tiller and thousand kernel weight traits. Therefore, selection of varieties based on a phenotypic basis for effective tiller and thousand kernel weight may not be effective in the genetic improvement of such traits due to influence of the environment or growing condition on the varieties.

The traits which showed lower PCV and GCV values implying the difficulty of improving these traits through simple selection. However, contradicting results were obtained from the works of Tazeen *et al.* (2009) who found that wide range between PCV and GCV for thousand seed weight in durum wheat. The high PCV and GCV value with little difference indicates that selection may be effective based on these traits.

High ECV was estimated from two traits thousand kernel weight (36.67%) and effective tiller (21.88%) out of fourteen traits and moderate ECV was also observed from single trait harvest index (11.17%) whereas all traits except effective tiller and thousand kernel weight had minimum ECV. From this trial there was great variability in the traits under the studied varieties of bread wheat. The traits which showed low ECV was not influenced by the environment i.e. the influence of environment on those characters was lower and phenotypic selection could be effective.

Table 4. Variance, genotypic and phenotypic coefficient of variability of 14 traits of bread wheat varieties tested at Guay Kebele (2018/19)

Traits	MSt	Mse	GM	GV	EV	PV	GCV (%)	PCV (%)	ECV (%)	h ² b %	GA
DE	3.05	0.19	7.20	0.95	0.19	1.14	13.53	14.83	6.05	83.33	1.83
DH	60.40	2.95	66.70	19.15	2.95	22.10	6.56	7.04	2.57	86.65	8.40
DM	213.41	3.12	109.10	70.09	3.12	73.21	7.66	7.84	1.62	95.74	16.87
PH	172.35	9.23	84.33	54.37	9.23	63.60	8.71	9.45	3.60	85.49	14.04
ETN	1.53	0.6	3.54	0.31	0.60	0.91	15.73	26.94	21.88	34.07	0.67
SPL	2.37	0.11	7.55	0.75	0.11	0.86	11.47	12.28	4.39	87.21	1.66
SPS	5.66	0.15	17.21	1.83	0.15	1.98	7.86	8.17	2.25	92.42	2.68
NGS	110.81	13.36	47.10	32.46	13.36	45.82	12.09	14.37	7.76	70.84	10.94
BY	4.00	0.65	9.60	1.12	0.65	1.77	11.02	13.85	8.39	63.28	1.73
GY	1.35	0.12	35.16	0.41	0.12	0.51	1.82	2.01	0.98	80.39	1.18
TKW	16.44	1.01	2.86	5.14	1.01	6.15	79.27	88.25	36.67	83.58	4.26
HI	38.82	10.88	29.53	9.31	10.88	20.19	10.33	15.21	11.17	46.11	4.27
HLW	25.08	0.29	73.27	8.26	0.29	8.55	3.92	3.99	0.73	96.61	5.82
PC	0.99	0.71	13.00	0.09	0.71	0.80	2.30	6.88	6.50	11.25	0.2

Where, DE = days to 50% emergence, DH= days to 75% heading/flowering, DM =, days to 90% maturity, PH= plant height, ETN= effective tiller number, SPS= spikelet per spike, SPL= spike length, NGS= number of grains per spike, BY= biomass yield, GY= Grain yield, TKW= thousand kernel weight, HI= harvest index, HLW= hectoliter weight, PC= protein content, h²b=broad sense heritability, GA=genetic advance, Mst= mean square due to treatment/genotype, Mse= mean square due to error, GM= grand mean, GV= genotypic variance, EV= environmental variance, PV= phenotypic variance, GCV= genotypic coefficient of variance, ECV= environmental coefficient of variance, PCV= phenotypic coefficient of variance.

3.4. Heritability (H²) and Genetic Advance

The estimates of heritability and genetic advance for mother and baby trials presented in (Table 4). In the mother trial, the highest heritability of 93.93% was exhibited by biomass yield and the lowest heritability was exhibited by wet gluten (24.81%). According to Singh, (2001), if heritability of a character is (high, h²≥80%, moderate (40 to 80%), low if h²< 40%). Considering this benchmark, heritability estimate was high (>80%) for days to 50% emergence, days to heading, plant height, biomass yield, thousand kernel weight, spikelet per spike, harvest index, stem rust and leaf rust. For those traits which showed high heritability, selection could be easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype.

The heritability estimate ranged between 11.25% (protein content) and 96.61% (hectoliter weight). High heritability (>80%) estimate was observed from DE, DH, DM, PH, SPL, SPS, GY, TKW, HLW and moderate heritability (40-80%) was observed from HI, BY and NGS but low heritability (<40%) was showed from ETN and

PC. High heritability related to time to heading and thousand grain weight were obtained in the studies conducted previously (Tazeen *et al.*, 2009). Higher heritability of the most important trait i.e. grain yield, plant height, spikelet per spike, grain per spike, biomass yield, thousand grain weight and harvest index was high, this clearly indicating higher influence of genetic factors than the environment on the expression of this trait. Likewise, Khan *et al.* (2017), reported high heritability estimates for plant height, number of spikelets spike⁻¹, spike length, number of grains spike⁻¹, 1000 grain weight and yield. Further, this finding is supported by the findings of Kashif and Khaliq (2004) and Haq *et al.* (2008). Estimation of different genetic parameters has imperative advantage to study the genetic basis of different traits that can contribute to crop yield. The high heritability magnitude indicates the reliability with which the high chance of the genotype to be recognized by its phenotypic expression. The traits which showed low heritability ($\leq 40\%$) values suggesting, selection for these characters would not be effective due to predominant effects of non-additive genes in this population. Contradict results obtained by the previous studies i.e. low heritability for biological yield and grain yield were recorded in durum wheat genotypes that were evaluated previously (Kahrizi *et al.*, 2010).

Genetic advance (GA)

Estimates of GA for all studied traits of the bread wheat varieties presented in (Table 4). Moderate genetic advance was observed from days to 90% maturity, plant height and number of grains per spike while the rest traits showed low genetic advance ($<10\%$) (Table 4). In this trial, no trait showed higher genetic advance. However, those traits which showed moderate genetic advance together with traits which had higher heritability could be most important traits for selection in the breeding program. Kumar *et al.* (2014) also evaluated thirty genotypes of bread wheat and reported high genetic advance for plant height, biological yield per plant and moderate for harvest index, test weight and low genetic advance was observed for days to 50% flowering and spike length.

In contrary to the present study, Ferdous *et al.* (2010) reported that, grains spike⁻¹, grain yield, days to maturity, grains spike⁻¹, grain yield, effective tillers plant⁻¹, grains spike⁻¹, 100-grain weight and grain yield showed high genetic advance. High heritability and high genetic advance indicates that preponderance of additive gene effect, therefore, characters can be better exploited through selection (Harshwardhan *et al.*, 2016).

3.5. Correlation among traits

Grain yield revealed strong, positive and highly significant correlation with most important agronomic traits, harvest index (HI, $r=0.88^{**}$), plant height (PH, $r=0.67^{**}$), number of effective tillers (ETN, $r=0.73^{**}$), spike length (SL, $r=0.74^{**}$), spikelet per spike (SPS, $r=0.70^{**}$), number of grain per spike (NGS, $r=0.80^{**}$), biomass yield (BY, $r=0.85^{**}$), 1000 seed weight (TSW, $r=0.76^{**}$) and hectoliter weight (HLW, $r=0.83^{**}$). (Table 4.14). On the other hand, grain yield had weak, positive and significant correlation with days to 50% emergence (DE, $r=0.41^*$) while weak, positive and insignificant correlation with days to heading (DH, $r=0.10_{ns}$), days to maturity (DM, $r=0.34_{ns}$) and protein content (PC, $r=0.27_{ns}$) (Table 5).

The grain quality traits i.e. protein content showed positive and significant association with days to 75% heading while weak and non-significant correlation with days to 50% emergence, days to 90% maturity, biomass yield, thousand kernel weight, grain yield, harvest index and hectoliter weight. From previous literature, significant and positive correlations of yield with other agronomic traits were observed i.e. number of effective tillers per plant with 1000 grain weight (Rahman *et al.*, 2016) which was in agreement with this study in which the correlation analysis showed that positive correlation among agronomic traits such as effective tillers per plant, plant height, 1000-grain weight, spike length, spikelet per spike, biomass yield, harvest index, hectoliter weight and grains per spike.

The positive associations of those important agronomic traits with grain yield explained that varieties which had high number of tillers per plant, number of grains per spike, more effective tillers, large spike length, high hectoliter weight, more spikelet per spike, biomass yield, 1000-seed weight and harvest index resulted in high grain yield production. Likewise, this result is in agreement with the result obtained by (Assefa *et al.*, 2014). Similar result also reported by Astawus Esatu, (2016) who obtained positive, strong and highly significant correlation of grain yield with days to heading, days to maturity, plant height, number of fertile tillers, spikelet per spike and spike length. This also in agreement with the report of Khan *et al.*, (2007) i.e. positive significant correlation was found for spike length, number of spikelets spike⁻¹, grain yield plant⁻¹ and 1000-grain weight with yield (kg ha⁻¹).

Molla *et al.* (2011), also indicated that the number of grain per spike, 1000 kernel weight and biological yield had the most direct and positive effect on grain yield. Parallely, Shamsi *et al.* (2011) also showed that the most important yield component on grain yield is number of grains per spike followed by number of spikes per meter square and 1000 kernel weight. Budak (2000) and Yagdi and Sozen, (2009) also reported the high and positive correlation of grain yield with number of tillers per plant, thousand grain weight, biological yield and harvest index and recommended these traits as selection criteria in durum wheat.

Table 5. Pearson's correlation coefficient (r) for all traits of the tested bread wheat varieties in 2018/2019.

Traits	DE	DH	DM	PH	ETN	SL	SPS	NGS	BY	TKW	GY	HI	HLW	PC
DE	1.00													
DH	0.55**	1.00												
DM	0.56**	0.66**	1.00											
PH	0.53**	0.12ns	0.42*	1.00										
ETN	0.53**	0.43*	0.72**	0.61**	1.00									
SL	0.58**	0.32ns	0.48**	0.78**	-0.45**	1.00								
SPS	0.59**	0.24ns	0.47**	0.82**	0.72**	0.88**	1.00							
NGS	0.23ns	-0.14ns	0.23ns	0.46**	0.44*	0.55**	0.51**	1.00						
BY	0.29ns	0.01ns	0.30ns	0.65**	0.59**	0.67*	0.64*	0.57*	1.00					
TKW	0.48*	0.05ns	0.49**	0.80*	0.77*	0.74**	0.75**	0.64**	0.28*	1.00				
GY	0.41*	0.10ns	0.34ns	0.67**	0.73**	0.74**	0.70**	0.80**	0.85**	0.76**	1.00			
HI	0.38*	0.15ns	0.22ns	0.53*	0.62**	0.61**	0.57**	0.28*	0.53**	0.61**	0.88**	1.00		
HLW	0.29*	0.02ns	0.29ns	0.80*	0.70**	0.79**	0.77**	0.68**	0.75**	0.88**	0.83**	0.68**	1.00	
PC	0.23ns	0.08ns	0.22ns	0.14*	0.27ns	0.34ns	0.43*	0.40*	0.31ns	0.26ns	0.27ns	0.11ns	0.32ns	1.00

Where, DE = days to 50% emergence, DH= days to 75% heading, DM =, days to 90% maturity, PH= plant height, ETN= effective tiller number, SPS= spikelet per spike, SPL= spike length, NGS= grains per spike, BY= biomass yield, GY= Grain yield, TKW= thousand kernel weight, HI= harvest index, HLW= hectoliter weight, PC= protein content, **= highly significantly ($P<0.01$), *= significantly ($P<0.05$) correlated, ns= insignificant correlation and (-) = negative sign for correlation among traits.

4. CONCLUSION

This study generally indicated that there was genetic variability among the varieties tested in the study area. This genetic variability could result good condition to select the best performing varieties and also create a great opportunity in the improvement of bread wheat varieties. The analysis of variance showed highly significant differences among varieties ($P<0.01$) were observed for Twelve characters (days to emergence, days to heading, days to maturity, plant height, effective tillers per plant, spike length, spikelets per spike, grain per spike, 1000 kernel weight, biomass yield, grain yield and hectoliter weight), significant at ($p<0.05$) for the rest two characters; namely, harvest index and protein content. The highest grain yield was obtained from variety Abola (4.0ton ha^{-1}) followed by Ogoloncho (3.87ton ha^{-1}) while the lowest was recorded from Wane (1.9ton ha^{-1}) followed by Lemu (2.1ton ha^{-1}). Similarly, Abola recorded the highest protein content which was (16.9%) the lower protein content was recorded from Wane (14.6%) and Kekeba (14.6%).

The genotypic and phenotypic coefficient of variability for most traits was similar in magnitude and directions that enable the genotypes to express their genetic potential. the maximum genotypic coefficient of variance recorded for hectoliter weight (79.27) and minimum for grain yield (1.82%). Lower genetic coefficient of variance ($<10\%$) was obtained from days to heading, days to 90% maturity, plant height, spikelets per spike, grain yield, hectoliter weight and protein content and higher PCV was estimated from TKW (88.25) and ETN (26.94%) but, the other traits showed moderate genotypic coefficient of variance. Grain yield, plant height, spikelet per spike, grain per spike, biomass yield, thousand grain weight and harvest index had higher heritability, suggesting that higher influence of genetic factors than the environment on the expression of this trait. Lower genetic coefficient of variance ($<10\%$) was obtained from days to heading, days to 90% maturity, plant height, spikelets per spike, grain yield, hectoliter weight and protein content and higher PCV was estimated from TKW (88.25) and ETN (26.94%) but, the other traits showed moderate genotypic coefficient of variance. Grain yield, plant height, spikelet per spike, grain per spike, biomass yield, thousand grain weight and harvest index had higher heritability, suggesting that higher influence of genetic factors than the environment on the expression of this trait.

Grain yield revealed strong, positive and highly significant correlation with most important agronomic traits, harvest index (HI, $r=0.88^{**}$), plant height (PH, $r=0.67^{**}$), number of effective tillers (ETN, $r=0.73^{**}$), spike length (SL, $r=0.74^{**}$), spikelet per spike (SPS, $r=0.70^{**}$), number of grain per spike (NGS, $r=0.80^{**}$), biomass yield (BY, $r=0.85^{**}$), 1000 seed weight (TSW, $r=0.76^{**}$) and hectoliter weight (HLW, $r=0.83^{**}$).

Generally, the tested varieties indicated the presence of variability in almost important agronomic and quality traits. Therefore, Abola and Ogoloncho had superior performance over the standard check and other varieties and this indicates that they would be used in multiplication, production as well as genetic resource for any crop improvement.

Therefore, the information generated from this study needs to be used by breeders who are interested in different traits. However, the present result is only an indication and cannot reach a definite conclusion. Therefore, since the experiment was carried out at one location in one season, it is advisable to continue with this study over several years and locations

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