ISSN 1819-1894

Asian Journal of Agricultural Research

http://knowledgiascientific.com

Knowledgia
SCIENTIFIC
A Place to Publish Outstanding Research

OPEN ACCESS Asian Journal of Agricultural Research

ISSN 1819-1894
DOI: 10.3923/ajar.2020.1.12

Research Article

Assessment of Genetic Variability among Agronomic Traits and Grain Protein Content of Elite Bread Wheat (*Triticum aestivum* L.) Genotypes in the Central Highlands of Ethiopia

Nesru Muhder, Mesfin Kebede Gessese and Zemach Sorsa

Wolaita Sodo University, P.O. Box 138, Wolaita Sodo, Southern Nations, Nationalities and People Region, Ethiopia

Abstract

Background and Objectives: The productivity of wheat in national and central part of the country is very low as a result of inaccessibility of improved varieties and prevalence of important diseases for wheat. In view of this the present study was initiated to assess the extent of genetic variation for grain yield and other agronomic traits. **Materials and Methods:** The field experiment was conducted using 5×5 simple lattice design across two locations during the 2017 main cropping season. Data collected on 14 quantitative characters and grain protein content. Analysis of variance computed for each location and over locations. The results of pooled ANOVA revealed presence of significant variations among genotypes for all traits except number of productive tillers/plant. **Results:** The mean square for genotype×location was significant for most of the traits suggested the differential performance of genotypes at different locations. The highest grain yield was registered by ETBW9551. The genotype, ETBW 9549 had the highest grain protein content over locations. The highest PCV and GCV values were computed for number of productive tillers m^{-2}. The highest broad sense heritability (h^2_b) was recorded from number of productive tillers/plant while genetic advance percent mean (GAM) ranged from 1.81% for number of productive tillers/plant to 13.32% for days to heading. **Conclusion:** It can be concluded that the variability observed among genotypes for desirable traits including grain yield and grain protein content could be exploited in bread wheat breeding in the test locations and similar agro ecologies.

Key words: Heritability, genetic advance, grain yield, genetic variation, genotype

Citation: Nesru Muhder, Mesfin Kebede Gessese and Zemach Sorsa, 2020. Assessment of genetic variability among agronomic traits and grain protein content of elite bread wheat (*Triticum aestivum* L.) genotypes in the central highlands of Ethiopia. Asian J. Agric. Res., 14: 1-12.

Corresponding Author: Mesfin Kebede Gessese, Wolaita Sodo University, P.O. Box 138, Wolaita Sodo, Southern Nations, Nationalities and People Region, Ethiopia

Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Wheat is the 2nd most imperative crop next to rice which offers 21% of the entire food calories and 20% of the protein for more than 4.5 billion people in 94 developing countries[1]. It accounts for nearly 30% of worldwide cereal production, covering an area of 222.42 million hectares with overall production[2] of 725.12 million t. Wheat is a temperate crop; however, it is also becoming one of the most important cereals grown on a large scale in the tropical and subtropical regions of the world[3]. Wheat is grown under diverse environmental situations around the world[4]. The phenomena of wheat to adapt wide range of environmental conditions are mainly due to the complex nature of its genome, which is providing great flexibility to the crop[5].

In Ethiopia, wheat is mostly grown in the highlands, with altitudes ranging from 1500-3000 m above sea level. The most appropriate altitudinal zones of wheat in Ethiopia fall between 1900-2700 m above sea level[6]. Wheat is the fourth important cereal crop in terms of area and production, next to teff (*Eragrostis tef* (Zucc.) trotter), maize and sorghum respectively[7]. The total land area covered by grain crops were about 12.57 million ha and grain production estimated about 29.04 million t/annum. Among the grain crops, cereals are the major food crops that covered about 81.27% (10.2 million ha) and contributed 87.42% of grain production which is equivalent to 25.39 million t. From the total grain crops area and production, wheat shared about 13.49 and 15.63% of grain production, respectively[8]. The most cultivated wheat species are durum (*Triticum turgidum* L. var durum) and bread wheat (*Triticum aestivum* L.); in addition, other species are cultivated to a smaller amount[9]. Ethiopia is considered to be one of the centers of genetic diversity to durum wheat while bread wheat has been introduced relatively recently[10]. Previously durum wheat accounted for 65-70% of the entire area, whereas bread wheat occupied the remaining 30-35%. However, recent studies showed the area under bread wheat has exceeded that of durum wheat; which is due to its implication as cash crop, high level of production per unit area and its major role in providing the nutritional necessities of the society[11].

The national average yield of wheat production (2.67 t ha^{-1}) is very low compared with other major wheat producing countries in the world like Germany (7.64 t ha^{-1}), Denmark (7.2 t ha^{-1}), Egypt (6.58 t ha^{-1}), China (5.4 t ha^{-1}), France (5.3 t ha^{-1}), India (3.09 t ha^{-1})[12]. In East Shewa zone of Oromia region, where the experiment has been conducted wheat stands third both in area and amount of production next to teff and maize. The production of wheat in east Shewa zone of Oromia region has declined by 14.94% as compared to 2015/16 cropping season and annual average yield ha^{-1} was 2.94 t ha^{-1}. A wide gap in the yield was attributed mainly due to shortage of improved varieties for different agro ecological zones of the country. In addition, poor agronomic practices, drought, poor soil fertility, diseases and insect pests, etc. are the major constraints of wheat production in Ethiopia[13]. Therefore, it is necessary to generate information on phenotypic and genotypic variances as well as heritability and genetic advance among bread wheat varieties as one of the approaches to alleviate these limitations. Precise knowledge about germplasm variability and genetic relationship among breeding materials is a pre requisite for crop improvement programs since it helps in the development of superior recombinants[14]. Therefore, precise information on the nature and degree of genetic variability present in wheat would help to select parents for evolving superior varieties. For an effective breeding program, the occurrence of genetic variability plays a great role because the more diverse the plants, the greater chance of exploiting to generate productive recombinants and broad variability in segregating generations during genetic improvement[15].

For wheat yield improvement, selection made on the basis of phenotypic variation cannot be efficient unless it relied on the evaluation and utilization of genetic variability. Consequently, in bread wheat breeding programs, information on the extent and pattern of genetic variability present in a population and the relationship between various characters and their contribution to yield is principal to raise bread wheat production in the region as well as in a country. Several studies conducted at different locations of Ethiopia assessed the existence of genetic variability among the previously released bread wheat genotypes through estimating components of variance, association between grain yield and its components, direct and indirect effects of yield components on grain yield[9,16-19]. Since, the average life span of wheat cultivars is very short due to occurrence of diseases (such as rusts and septoria) and introduction of elite genotypes and new varieties is very common to replace the susceptible and low yielding cultivars, assessment of genetic variability is useful to maintain the genetic variability of wheat varieties grown in the country. It is also known that plant breeding activities in most self pollinated crops narrow the genetic diversity of the crop species; hence we need to check the variability of the available germplasm now and then to modify our breeding strategy. Due to these reasons, the present study was conceived to estimate the genetic variability of Ethiopian common wheat germplasm composed of recently released commercial cultivars and promising elite genotypes that were under competitive field performance trials.

MATERIALS AND METHODS

Descriptions of the study area: Field experiments were carried out at the two testing locations (Debre Zeit and Chefe Donsa) during 2017, main cropping season. Debre Zeit Agricultural Research Center (DZARC) is located at geographic coordinates of 8°44'N latitude and 38°58'E longitude with an altitude of 1900 m above sea level. This location receives mean annual rainfall of 851 mm. The mean annual minimum and maximum temperatures are 11.23 and 25.19°C, respectively, with mean annual temperature of 19°C. The dominant soil types are vertisol, mollisol and alfisols. The second trial site, Chefe Donsa, is 37 km away from Debre Zeit. Chefe Donsa is one of the sub research centers of DZARC, which is located at geographic coordinates of 08°57'15"N latitude and 39°06'04"E longitude with an altitude of 2450 m above sea level and has hot to warm sub-humid climate. This location receives annual precipitation of 909 mm with uniform and erratic rain fall distribution.

Agronomic practices: Sowing was done by hand drilling and covered lightly with soil. The seed and fertilizer rate were 150 kg ha^{-1}. All other agronomic practices were applied as recommended for wheat production by DZARC to the specific area.

Plant materials and experimental design: The experimental materials comprised of 21 advanced bread wheat genotypes along with four released bread wheat varieties; namely, Honqolo, Bika, Lemu and Wane that were evaluated for their genetic variability and association for agronomic traits. The description of bread wheat genotypes used for the study is presented in Table 1. The treatments were laid out in Simple Lattice Design (5×5) with 2 replications of 5 blocks/replications and 5 treatments/block. Each plot consisted of 6 rows of 2.5 m lengths with spacing of 20 cm between rows. The space between plots within a block was 1 m and (broad bed furrow = 0.6 m) between blocks within each replication was also 1 m. Sowing was done in July, 2017 main cropping season under rain fed condition.

Table 1: Description of bread wheat genotypes used in the field experiment

Entries	Genotypes	Pedigree	Origin	Released by	Year of release
1	HONQOLO (ETBW 5879)	SAMAR-12/DOLLARBIRD	ICARDA	KARC	2014
2	BIKA	PASTOR//MXL7573/2*BAU/3/SOKOLL/WBLL1	CIMMYT	KARC	2014
3	LEMU (ETBW6861)	WAXWING*2/HEILO	CIMMYT	KARC	2016
4	WANE (6130)	SOKOLL/EXCALIBUR	CIMMYT	KARC	2016
5	ETBW 8751	SUP152//ND643/2*WBLL1	-	-	-
6	ETBW 8858	SWSR22T.B./2*BLOUK#1//WBLL1*2/KURUKU	-	-	-
7	ETBW 8870	WAXWING*2/TUKURU//KISKADEE#1/3/FRNCLN	-	-	-
8	ETBW 8802	CHAM-4/SHUHA S/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB/4/BOW'S"	-	-	-
9	ETBW 8991	SUP152//ND643/2*WBLL1	-	-	-
10	ETBW 8862	C80.1/3*BATAVIA//2*WBLL1/3/C80.1/3*QT4522//2*PASTOR/4/WHEAR/SOKOLL	-	-	-
11	ETBW 8804	TURACO/CHIL/6/SERI82/5/ALD'S'/4/BB/GLL//CNO67/7C/3/KVZ/TI	-	-	-
12	ETBW 8996	FALCIN/AE.SQUARROSA(312)/3/THB/CEP7780//SHA4/LIRA/4/FRET2/5DANPHE#1 /11/CROC-1/AE.SQUARROSA(213)//PGO/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA	-	-	-
13	ETBW 8583	MINO/898.97/4/PFAU/SERI.1B//AMAD/3/KRONSTADF20	-	-	-
14	ETBW 8668	BAVIS*2/3/ATTILA/BAV92//PASTOR	-	-	-
15	ETBW 8595	BAVIS*2/3/ATTILA/BAV92//PASTOR	-	-	-
16	ETBW 8684	PASTOR//HXL7573/2*BAU/3/WBLL1/4/1447/PASTOR//KRICHAUFF	-	-	-
17	ETBW 9486	FRANCOLIN#1/3/PBW343*2/KUKUNA*2//YANAC/4/KINBIRD#1//INQALAB91*2/TUKURU	-	-	-
18	ETBW 9547	MUTUS*2/AKURI//MUTUS*2/TECUE#1	-	-	-
19	ETBW 9548	REEDLING#1//KFA/2*KACHU	-	-	-
20	ETBW 9549	KFA/2*KACHU/3/KINGBIRD#1//INQALAB91*2/TUKURU/4/KFA/2*KACH	-	-	-
21	ETBW 9550	KFA/2*KACHU*2//WAXB	-	-	-
22	ETBW 9551	KFA/2*KACHU/4/KACHU#1//PI610750/SASIA/3/KACHU/5/KFA/2*KACH	-	-	-
23	ETBW 9553	MURGA/KRONSTADF2004/3/KINGBIRD#1//INQALAB91*2/TUKURU	-	-	-
24	ETBW 9554	SAUAL/MUTU/6/CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7/7/CNO79//PF70354/MUS/3/PASTOR/4BAV92*2/5/FH6-1-7	-	-	-
25	ETBW 9556	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR	-	-	-

Source center for cultivars Bika Lemu and Wane is CIMMYT, while ICARDA is for all other genotypes, CIMMYT: International maize and wheat improvement center, ICARDA: International center for agricultural research in the dry areas, KARC: Kulumsa agricultural research center

Data collection for agronomic traits: Data was collected on plot and plant basis from the 4 central rows for all parameters. The yield and yield component data that were collected on plant and plot basis for both locations. The observations were recorded from ten randomly selected plants for all characters on plant basis viz., number of productive tillers/plant, plant height (cm), number of kernels/spike, number of spikelets/spike, peduncle length (cm) and spike length (cm). While the data for days to heading (75%) and days to maturity (90%), grain filling period, number of productive tillers m^{-2}, thousand-kernels weight (g), aboveground biomass (kg m^{-2}), grain yield (t ha^{-1}) and harvest index (%) were collected on plot basis.

Data on quality parameter: Wheat grain protein content (GPC %) of each experimental unit was estimated by using Inframatic 8800 by taking about 200 g grain sample[20].

Data on disease parameter: Disease data was recorded for stem rust, leaf rust and septorial blotch when the disease incidence and severity was observed in the field. The data was recorded every week until the susceptible plants showed 100% susceptibility. The 1-9 scoring scale was adopted to record the data[21].

Data analysis

Analysis of variance: The genetic and environmental variances are generally confused in lattice design[22]. Therefore, an estimation of various genetic parameters is easier and standardized in RCBD and simple lattice being flexible[23]. Further, analysis of the data was based on the RCBD only as shown in Table 2 and 3. All collected data were subjected to analysis of variance (ANOVA) using procedure of general linear model of SAS software[24] version 9.0 and treatment means were tested as significant at 5% probability level and as highly significant at 1% probability level. Mean comparison among genotypes were carried out using LSD at 5% probability levels.

Phenotypic and genotypic variability: The phenotypic and genotypic coefficient of variation were estimated according to the methods suggested by Burton and Devane[25]:

$$\sigma^2_g = \frac{MSg - MSe}{r}$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Table 2: Analysis of variance (ANOVA) for individual location

Source of variation	Degree of freedom	Mean square	F-value
Replication	r-1	MSr	
Genotype	g-1	MSg	MSg/MSe
Error	(r-1) (g-1)	MSe	
Total	rg-1		

r: Number of replication, g: Genotype, MSr: Mean squares due to replication, MSg: Mean square due to genotype, MSe: Mean square for error

Table 3: Combined analysis of variance (ANOVA) for both locations

Source of variation	Degree of freedom	Mean square	F-value
Location	l-1	MSl	
Replication	l (r-1)	MSr	
Genotype	g-1	MSg	MSg/MSe
G×E	g-1	MSg×e	MSg×e/MSe
Error	l (r-1) (g-1)	MSe	
Total	lrg-1		

r: Number of replication, g: Genotype, l: Location, MSr: Mean square of replication, MSg: Mean square of due to genotypes, MSe: Mean square of error, MSl: Mean square of location and MSg×e: Mean square due to genotype by environment interaction

Where:

σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance
MSg = Mean squares of genotypes
MSe = Mean square due to error
r = Number of replications

$$PCV = \frac{\sqrt{\sigma^2 p}}{X} \times 100$$

$$GCV = \frac{\sqrt{\sigma^2 g}}{X} \times 100$$

Where:

PCV = Phenotypic coefficient of variation
GCV = Genotypic coefficient of variation
X = Grand mean value of the trait

Estimation of heritability: Heritability in broad sense (h^2_b) for all characters was computed using the formula adopted by Allard[26]:

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where:

h^2_b = Heritability in broad sense
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

Estimation of genetic advance: Genetic advance was computed using the equation adopted from Johnson *et al.*[27] and Allard[26]:

$$GA = (k)\,(\sigma_p)\times(h^2_b)$$

Where:

GA = Genetic advance

K = Selection intensity (K = 2.06 at 5% selection intensity)

σ_p = Phenotypic standard deviation

h^2_b = Heritability in broad sense

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

Where:

GAM = Genetic advance percent of mean

GA = Genetic advance

X = Mean value of the trait

Genetic variance components of over locations were computed in a similar approach as for individual locations by using the following equation adopted from Allard[26]:

$$\text{Environmental variance } (\sigma^2 e) = \text{Mse}$$

$$\text{Genotype variance } (\sigma^2 g) = \frac{\text{MSg} - \text{MSe}}{\text{lr}}$$

$$\text{Genotype by location interaction variance } (\sigma^2 gl) = \frac{\text{Mgl} - \text{MSe}}{\text{r}}$$

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

Where:

MSe = Error mean square

MSgl = Mean square of genotype by location interaction

MSg = Mean square of genotype

r = Replication

l = Location

RESULTS

Analysis of variance: The analysis of variance showed that significant ($p<0.05$) and highly significant ($p<0.01$) differences among genotypes for the characters, days to heading, days to maturity, grain filling period, plant height, peduncle length, number of kernels/spike, aboveground biomass/plot, thousand kernels weight, harvest index, grain protein content and grain yield ha^{-1} at both locations (Appendix Table 1 and 2). Three of the traits; number of productive tillers/plant at both locations and number of productive tillers m^{-2} and number of spikelets/spike were non-significant at Chefe Donsa. This study demonstrated the existence of considerable differences among genotypes for many of the traits investigated.

Before pooling of the data across environments, test of heterogeneity for error variance was done. All the characters, except harvest index, showed homogeneity in the tested environments. As the test of homogeneity of variance showed uniformity, the data were pooled across environments and analyzed. The result of the combined analysis of variance across the 2 locations is presented in Table 4. Combined analysis of variance over locations showed that the effects of genotypes were highly significant ($p<0.01$) and significant ($p<0.05$) for days to heading, days to maturity, grain filling period, plant height, pedicle length, spike length, number

Table 4: Mean squares of combined analysis of variance of the 15 traits of 25 bread wheat genotypes tested at debre zeit and chefe donsa

Traits	Loc. (df = 1)	Rep (loc.) (df = 2)	Gen. (df = 24)	Loc. Gen. (df = 24)	Error (df = 48)	Total (df = 99)	CV (%)
Days to heading	864.36**	59.68	98.83**	12.94**	1.49	37.76	1.82
Days to maturity	3058.09**	34.85	66.69**	24.63**	2.68	55.03	1.41
Grain filling period	670.81**	8.45	11.28**	9.2**	2.05	12.91	2.93
Productive tillers/plant	41.60**	2.43	0.41^{ns}	0.43^{ns}	0.33	0.83	15.99
Productive tillers m^{-2}	187922.25**	15159.25	14120.83*	10987.87^{ns}	6964.98	11668.37	20.80
Plant height	898.80**	36.06	65.36**	12.73^{ns}	8.88	33.04	3.47
Pedicle length	6.29^{ns}	0.63	28.92**	2.10^{ns}	3.36	9.23	5.36
Spike length	6.52**	0.15	1.18**	0.49**	0.17	0.56	5.36
Spikelets/spike	0.09^{ns}	0.81	3.36**	1.97**	0.71	1.65	4.98
Kernels/spike	69.06*	8.97	49.26**	27.21**	11.16	24.83	7.01
Aboveground biomass	0.45*	0.37	0.4**	0.31**	0.09	0.23	9.60
Thousand kernels weight	3066.39**	5.24	48.51**	18.33**	2.97	48.72	4.49
Harvest index	0.0034*	0.0007	0.003**	0.0014**	0.00057	0.0014	7.09
Grain protein content	250.91**	1.85	2.74**	0.35^{ns}	0.33	3.48	4.59
Grain yield	2.05^{ns}	150.6302	103.18**	137.30**	21.98	72.02	8.79

^{ns}Non-significant, **Highly significant at 1%, *Significant at 5% probability levels, Gen.: Genotype, Rep.: Replication, Loc.: Location, CV (%): Coefficient of variations, df: Degree of freedom

Appendix Table 1: Mean squares for the different sources of variation and their corresponding CV for the 15 traits of 25 bread wheat genotypes tested at Debre Zeit

Traits	Replication (df = 1)	Treatments (df = 24)	Error (df = 24)	Total (df = 49)	CV (%)
Days to heading	103.68	82.83**	1.35	43.35	1.81
Days to maturity	69.62	80.10**	2.16	41.71	1.33
Grain filling period	3.38	12.03**	2.30	7.09	3.27
Productive tillers/plant	4.81	0.53^{ns}	0.47	0.59	16.13
Productive tillers m^{-2}	30258.00	14377.79*	6048.63	10622.00	17.49
Plant height	71.07	42.47**	9.96	27.13	3.56
Pedicle length	0.81	15.12**	4.50	9.63	6.25
Spike length	0.01	0.98**	0.19	0.57	5.41
Spikelets/spike	0.01	4.07**	0.68	2.33	4.85
Kernels/spike	2.93	40.36**	10.27	24.86	6.85
Aboveground biomass	0.67	0.39**	0.096	0.25	9.55
Thousand kernels weight	10.49	38.42**	2.32	20.17	4.64
Harvest index	0.0006	0.0032**	0.00093	0.0021	9.24
Grain protein content	3.28	1.37**	0.37	0.92	4.31
Grain yield	300.27	147.35**	16.38	86.32	7.56

*Significant at p = 0.05, **Highly significant at p = 0.01, df: Degree of freedom, CV (%): Coefficient of variation, ^{ns}Non-significant

Appendix Table 2: Mean squares for the different sources of variation and their corresponding CV for the 15 traits of 25 bread wheat genotypes tested at Chefe Donsa

Traits	Replication (df = 1)	Treatments (df = 24)	Error (df = 24)	Total (df = 49)	CV (%)
Days to heading	15.68	28.95**	1.64	15.30	1.83
Days to maturity	0.08	11.22**	3.21	7.07	1.47
Grain filling period	13.52	8.48**	1.81	5.32	2.61
Productive tillers/plant	0.05	0.31^{ns}	0.19	0.25	14.90
Productive tillers m^{-2}	60.50	10730.92^{ns}	7881.33	9117.44	24.80
Plant height	1.06	35.62**	7.79	21.28	3.37
Pedicle length	0.45	15.91**	2.22	8.89	4.33
Spike length	0.29	0.70**	0.16	0.43	5.31
Spikelets/spike	1.62	1.25^{ns}	0.74	1.01	5.10
Kernels/spike	15.02	36.11**	12.05	23.89	7.16
Aboveground biomass	0.07	0.32**	0.09	0.20	9.65
Thousand kernels weight	0.0002	28.43**	3.62	15.69	4.33
Harvest index	0.0007	0.0011**	0.0002	0.0007	4.20
Grain protein content	0.42	1.72**	0.29	0.99	4.93
Grain yield	0.99	93.13**	27.59	59.15	9.87

*Significant at p = 0.05, **Highly significant at p = 0.01, DF: Degree of freedom, CV (%): Coefficient of variation, ^{ns}Non-significant

of kernels/spike, aboveground biomass, thousand kernels weight, harvest index, grain protein content, grain yield ha^{-1} and number of productive tillers m^{-2}, whereas number of productive tillers/plant was non-significant. Location effect was significant for all studied traits except pedicle length, spikelets/spike and grain yield ha^{-1}.

Mean performance of genotypes: Estimated range and mean performance of the 25 genotypes for the 15 characters are presented in Appendix Table 3 and 4 for Debre Zeit and Chefe Donsa, respectively. The result showed presence of significant differences for all traits studied at both locations at 5% probability level that further confirmed by mean comparison tests using the respective LSD values. The mean data indicated that days to heading of bread wheat genotypes was late at Chefe Donsa as compared to Debre Zeit, which could be the difference in degree days between the 2 environments as there was variations in rain fall amount and distribution, average day and night temperatures, light intensity etc. Days to maturity ranged from 99-121 at Debre Zeit and 118-127 at Chefe Donsa, respectively.

The genotypes grouped as early and late heading genotypes corresponded with the respective early and late maturity characteristics of each location. In other words, early heading genotypes matched with early matured genotypes location wise and the vice versa. Similarly, data on plant height indicated that average height of genotypes at Chefe Donsa was shorter compared to Debre Zeit that could further magnify the influence of environmental factors on the performance of the genotypes for plant height. On the other hand, genotypes at Chefe Donsa produced highest number of kernel/spike as compared to Debre Zeit. Similarly mean performance of thousand kernel weight were higher in Chefe Donsa compared to Debre Zeit. However, mean performance of aboveground biomass at Debre Zeit was superior to Chefe Donsa. With regard to grain protein content, higher average values were obtained in Debre Zeit compared to Chefe Donsa. In the same manner, higher performance of genotypes for grain yield (6.67 t ha^{-1}) for all genotypes was recorded at Debre Zeit compared to (5.35 t ha^{-1}) Chefe Donsa.

Appendix Table 3: Mean performance of 25 bread wheat genotypes and their studied traits tested at Debre Zeit

Entries	Genotypes	DH	DM	GFP	PTPP	PTPM2	PH	PL	SL	SKPS	KPS	ABM	TKW	HI	GPC	GY
1	HONQOLO	72.0^{bc}	114.5^{d-f}	42.5^{h}	3.70^{f-h}	670.00^{a}	82.98^{kl}	35.24^{a-e}	7.41^{f-j}	16.65^{e-h}	41.85^{g-i}	3.25^{d-h}	28.8^{h-j}	0.31^{e-h}	12.75^{i}	5.00^{ef}
2	ETBW8751	61.0^{j-m}	107.5^{j-l}	46.5^{c-g}	4.55^{a-e}	345.00^{f}	90.58^{b-i}	32.48^{e-g}	8.63^{ab}	17.55^{a-f}	51.2^{a-d}	3.35^{b-h}	33.6^{c-g}	0.34^{b-f}	13.6^{d-h}	5.73^{a-e}
3	ETBW8858	63.0^{h-k}	106.5^{l-n}	43.5^{gh}	3.45^{gh}	410.00^{c-f}	92.23^{b-g}	33.13^{d-g}	9.03^{a}	17.85^{a-e}	51.4^{a-c}	3.15^{e-i}	34.6^{b-e}	0.35^{b-e}	14.35^{cd}	5.43^{c-e}
4	ETBW8870	64.0^{f-i}	111.5^{f-i}	47.5^{c-e}	4.55^{a-e}	417.5^{c-f}	95.37^{a-c}	34.84^{c-f}	8.98^{a}	18.15^{a-e}	51.7^{a-c}	3.55^{b-f}	32.2^{d-h}	0.33^{d-g}	14.00^{c-g}	5.84^{a-e}
5	ETBW8802	67.5^{de}	119.5^{ab}	52.00^{a}	4.00^{d-h}	427.5^{c-f}	90.5^{b-i}	33.7^{c-f}	7.49^{f-j}	16.9^{d-g}	46.6^{c-g}	2.65^{i-k}	23.4^{l}	0.25^{j}	13.35^{g-i}	3.19^{i}
6	ETBW8991	60.0^{l-n}	104.0^{m-o}	$44.0f^{gh}$	4.50^{a-f}	425.00^{c-f}	87.15^{f-k}	30.29^{gh}	7.76^{d-h}	17.1^{c-f}	47.4^{b-f}	2.8^{h-k}	34.2^{b-f}	0.36^{b-e}	13.05^{hi}	4.94^{e-g}
7	ETBW8862	55.5^{pq}	107.0^{k-m}	51.5^{ab}	4.25^{b-g}	632.5^{ab}	98.05^{a}	38.63^{a}	8.61^{ab}	18.1^{a-e}	52.85^{a}	3.15^{e-i}	34.4^{b-f}	0.36^{b-d}	14.05^{c-g}	5.61^{b-e}
8	ETBW8804	54.5^{q}	99.0^{p}	44.5^{e-h}	4.95^{a-c}	525.00^{a-e}	78.5^{l}	34.21^{c-f}	7.84^{c-g}	15.3^{g-h}	37.95^{i}	2.45^{k}	28.4^{ij}	0.31^{e-h}	14.35^{cd}	3.78^{hi}
9	ETBW8996	56.5^{o-q}	102.5^{o}	46.0^{c-g}	4.50^{a-f}	380.00^{ef}	89.25^{d-j}	36.74^{a-c}	7.89^{b-g}	15.25^{hi}	47.15^{b-g}	2.9^{g-k}	33.7^{c-g}	0.38^{a-c}	14.25^{c-e}	5.40^{c-e}
10	ETBW8583	63.5^{g-j}	110.0^{i-k}	46.5^{c-g}	3.75^{e-h}	375.00^{ef}	85.93^{i-k}	31.73^{fg}	7.88^{b-g}	17.4^{b-f}	49.65^{a-f}	3.05^{f-j}	31.8^{d-i}	0.33^{c-g}	13.3^{g-i}	4.97^{e-g}
11	ETBW8668	56.0^{o-q}	101.5^{op}	45.5^{d-h}	4.30^{b-f}	562.5^{a-c}	86.73^{g-k}	36.24^{a-d}	7.00^{ij}	14.7^{i}	38.5^{i}	3.05^{f-j}	39.8^{a}	0.37^{b-d}	13.10^{hi}	5.51^{b-e}
12	ETBW8595	57.0^{o-q}	104.0^{m-o}	47.0^{c-f}	4.20^{c-g}	520.00^{a-e}	93.06^{a-e}	36.37^{a-d}	7.15^{g-j}	14.7^{i}	38.95^{i}	3.25^{d-h}	40.00^{a}	0.38^{ab}	13.35^{g-i}	6.22^{a-d}
13	ETBW8684	58.0^{n-p}	104.0^{m-o}	46.0^{c-g}	4.40^{a-f}	425.00^{c-f}	86.3^{h-k}	33.09^{d-g}	6.78^{j}	14.95^{i}	45.85^{e-h}	3.05^{f-j}	32.8^{c-g}	0.37^{b-d}	13.60^{d-h}	5.55^{b-e}
14	ETBW9486	61.5^{i-l}	110.5^{h-j}	49.0^{a-c}	4.95^{a-c}	482.5^{b-f}	84.62^{jk}	35.18^{b-e}	9.11^{a}	18.05^{a-e}	51.4^{a-c}	3.6^{b-f}	37.6^{ab}	0.36^{b-d}	15.80^{a}	6.48^{ab}
15	ETBW9547	77.5^{a}	120.0^{ab}	42.5^{h}	4.05^{d-g}	427.5^{c-f}	84.63^{jk}	27.87^{h}	8.39^{a-e}	18.3^{a-d}	45.85^{e-h}	3.85^{a-c}	39.8^{a}	0.32^{d-h}	14.05^{c-g}	6.2^{a-d}
16	ETBW9548	70.0^{cd}	114.0^{d-g}	44.0^{fgh}	4.60^{a-d}	365.00^{ef}	85.03^{i-k}	27.61^{h}	7.97^{b-f}	18.35^{a-d}	51.2^{a-d}	2.55^{jk}	35.00^{b-d}	0.42^{a}	15.25^{ab}	5.15^{ef}
17	ETBW9549	72.0^{bc}	121.0^{a}	49.0^{a-c}	4.65^{a-d}	410.00^{c-f}	92.48^{a-f}	33.45^{c-g}	8.54^{a-c}	19.1^{a}	51.00^{a-e}	4.25^{a}	34.4^{b-f}	0.3^{f-i}	15.65^{a}	6.34^{a-c}
18	ETB9550	66.5^{ef}	114.0^{d-g}	47.5^{c-e}	3.75^{e-h}	412.5^{c-f}	87.98^{e-k}	31.45^{fg}	7.54^{f-i}	16.9^{d-g}	48.55^{a-f}	3.9^{ab}	31.1^{f-j}	0.33^{d-g}	15.60^{a}	6.31^{a-c}
19	ETBW9551	65.0^{e-h}	113.5^{e-h}	48.5^{b-d}	3.20^{h}	412.5^{c-f}	91.79^{b-h}	34.21^{c-f}	8.15^{b-f}	17.2^{b-f}	46.45^{c-g}	3.8^{a-d}	35.8^{bc}	0.35^{b-e}	14.50^{bc}	6.70^{a}
20	LEMU	70.5^{c}	116.0^{c-e}	45.5^{d-h}	3.70^{f-h}	380.00^{ef}	86.5^{h-k}	36.24^{a-d}	8.98^{a}	17.85^{a-e}	46.00^{d-h}	2.9^{g-k}	24.6^{kl}	0.28^{h-j}	14.45^{c}	3.99^{g-i}
21	ETBW9553	73.5^{b}	118.5^{a-c}	45.0^{e-h}	3.90^{d-h}	362.5^{ef}	89.73^{c-j}	33.07^{d-g}	8.94^{a}	18.8^{ab}	52.35^{ab}	3.55^{b-f}	28.8^{h-j}	0.31^{e-h}	13.45^{f-i}	5.52^{b-e}
22	ETBW9554	71.0^{bc}	117.0^{b-d}	46.0^{c-g}	4.25^{b-g}	407.5^{c-f}	95.73^{ab}	33.46^{c-g}	8.52^{a-d}	18.55^{a-c}	44.55^{f-h}	3.65^{b-e}	31.4^{e-i}	0.29^{g-j}	13.55^{e-h}	5.26^{de}
23	BIKA	60.5^{k-n}	109.0^{i-l}	48.5^{b-d}	3.85^{d-h}	385.00^{d-f}	87.00^{f-k}	36.25^{a-d}	7.81^{c-g}	14.93^{i}	40.7^{hi}	3.1^{e-j}	27.95^{jk}	0.32^{d-h}	14.45^{c}	5.01^{ef}
24	ETBW9556	66.0^{e-g}	111.0^{g-i}	45.0^{e-h}	5.05^{ab}	410.00^{c-f}	93.68^{a-d}	34.15^{c-f}	7.72^{e-i}	16.1^{f-i}	45.4^{f-h}	3.3^{c-h}	37.4^{ab}	0.33^{d-g}	14.20^{c-f}	5.41^{c-e}
25	WANE	58.5^{m-o}	103.5^{no}	45.0^{e-h}	5.20^{a}	545.00^{a-d}	83.33^{kl}	38.37^{ab}	7.03^{h-j}	15.05^{hi}	45.25^{f-h}	3.4^{b-g}	30.6^{g-j}	0.26^{ij}	14.45^{c}	4.27^{f-h}
	Mean	64.04	110.38	46.34	4.25	444.60	88.76	33.92	8.04	16.95	46.79	3.26	32.89	0.33	14.10	5.35
	LSD 5%	2.6114	3.1138	3.3802	0.8413	163.71	5.6853	3.3931	0.7595	1.6279	5.3338	0.5899	3.4241	0.0499	0.7993	0.98899

Means followed by the same letter are not significantly different (p = 0.05)

Appendix Table 4: Mean performance of 25 bread wheat genotypes and their studied traits, tested at Chefe Donsa

Entries	Genotypes	DH	DM	GFP	PTPP	PTPM2	PH	PL	SL	SKPS	KPS	ABM	TKW	HI	GPC	GY
1	HONQOLO	77.50^{a}	127.0^{a}	49.5^{d-f}	3.15^{bc}	322.5^{b-e}	79.23^{g-j}	36.08^{b-f}	6.63^{g}	16.05^{b-e}	43.65^{d-g}	3.75^{ab}	39.79^{j-l}	0.35^{c-f}	10.15^{f-j}	6.56^{a}
2	ETBW8751	67.5^{g-j}	121.0^{c-g}	53.5^{ab}	2.70^{c}	225.0^{e}	87.93^{a-c}	34.43^{e-h}	7.52^{b-f}	17.55^{a-c}	53.45^{ab}	3.1^{d-h}	41.27^{h-k}	0.41^{a}	9.90^{h-j}	6.29^{ab}
3	ETBW8858	68.5^{f-h}	120.0^{d-g}	51.5^{a-e}	2.70^{c}	375.0^{a-e}	82.43^{c-i}	31.7^{h-j}	7.92^{a-e}	17.65^{a-c}	55.8^{a}	2.7^{h-j}	40.04^{i-k}	0.34^{d-h}	11.45^{c-e}	4.53^{e-g}
4	ETBW8870	69.5^{e-g}	123.5^{a-d}	54.0^{a}	2.45^{c}	325.0^{b-e}	85.84^{a-f}	36.33^{b-e}	8.15^{a-d}	17.1^{a-d}	52.15^{a-c}	3.6^{a-d}	41.35^{g-k}	0.32^{hi}	10.40^{e-j}	5.79^{a-d}
5	ETBW8802	73.5^{cd}	123.5^{a-d}	50.0^{c-f}	2.80^{c}	415.0^{a-d}	83.03^{b-h}	33.88^{e-i}	7.00^{e-g}	17.00^{a-e}	46.7^{b-f}	2.9^{f-i}	35.93^{l}	0.32^{i}	11.05^{d-h}	4.61^{e-g}
6	ETBW8991	67.0^{h-j}	121.0^{c-g}	54.0^{a}	3.25^{a-c}	272.5^{de}	81.55^{e-i}	33.73^{e-i}	6.84^{fg}	15.75^{c-e}	42.00^{e-g}	3.05^{d-h}	38.03^{kl}	0.36^{b-d}	9.85^{ij}	5.49^{b-e}
7	ETBW8862	70.0^{ef}	123.0^{b-e}	53.0^{a-c}	3.25^{a-c}	295.0^{b-e}	89.15^{a}	40.8^{a}	8.2^{a-c}	17.9^{ab}	54.15^{ab}	3.2^{b-h}	43.94^{d-i}	0.33^{f-i}	11.30^{d-f}	5.27^{c-f}
8	ETBW8804	65.5^{jk}	120.0^{d-g}	54.5^{a}	3.85^{ab}	520.0^{a}	71.6^{k}	33.34^{e-i}	7.68^{a-f}	16.00^{b-e}	41.8^{fg}	2.9^{f-i}	40.48^{i-k}	0.34^{d-h}	10.90^{d-i}	4.96^{d-f}
9	ETBW8996	66.5^{h-j}	119.5^{e-g}	53.0^{a-c}	3.05^{bc}	355.0^{a-e}	87.48^{a-d}	37.69^{a-d}	7.39^{b-g}	15.05^{e}	38.5^{g}	2.75^{g-j}	41.29^{h-k}	0.38^{b}	10.90^{d-i}	5.23^{c-f}
10	ETBW8583	68.0^{f-i}	120.5^{d-g}	52.5^{a-d}	4.10^{a}	452.5^{a-d}	81.03^{f-i}	33.00^{f-j}	7.27^{c-g}	17.6^{a-c}	47.65^{b-f}	3.55^{a-e}	42.92^{f-j}	0.34^{d-h}	11.75^{b-d}	6.04^{a-c}
11	ETBW8668	63.5^{k}	118.0^{g}	54.5^{a}	2.55^{c}	372.5^{a-e}	85.2^{a-f}	35.83^{c-f}	8.33^{ab}	17.6^{a-c}	51.05^{a-d}	3.00^{e-i}	46.18^{a-f}	0.36^{c-e}	10.25^{f-j}	5.31^{c-f}
12	ETBW8595	66.5^{h-j}	120.0^{d-g}	53.5^{ab}	3.10^{bc}	320.0^{b-e}	84.03^{a-g}	35.48^{c-g}	8.11^{a-d}	17.15^{a-d}	47.95^{b-f}	3.35^{b-f}	50.01^{a}	0.36^{c-e}	9.25^{j}	6.00^{a-c}
13	ETBW8684	66.0^{ij}	119.0^{fg}	53.0^{a-c}	2.85^{c}	282.5^{c-e}	77.33^{ij}	34.23^{e-h}	6.59^{g}	15.35^{de}	47.3^{b-f}	2.45^{ij}	45.72^{b-f}	0.37^{bc}	10.15^{f-j}	4.44^{fg}
14	ETBW9486	68.0^{f-i}	121.0^{c-g}	53.0^{a-c}	3.00^{bc}	467.5^{ab}	78.00^{h-j}	33.9^{e-i}	7.61^{a-f}	16.7^{a-e}	49.15^{a-f}	2.25^{j}	44.49^{d-h}	0.35^{c-g}	12.80^{ab}	3.83^{g}
15	ETBW9547	75.0^{bc}	124.5^{a-c}	49.5^{d-f}	3.10^{bc}	320.0^{b-e}	82.1^{d-i}	28.15^{k}	7.7^{a-f}	16.55^{a-e}	45.00^{c-g}	3.00^{e-i}	49.23^{ab}	0.34^{d-h}	11.15^{d-g}	5.13^{c-f}
16	ETBW9548	71.5^{de}	120.5^{d-g}	49.0^{ef}	2.95^{bc}	302.5^{b-e}	82.60^{b-i}	29.85^{jk}	7.2^{d-g}	17.00^{a-e}	51.95^{a-c}	2.8^{f-j}	45.23^{c-h}	0.35^{c-g}	12.55^{a-c}	4.84^{d-f}
17	ETBW9549	73.0^{cd}	123.5^{a-d}	50.5^{b-f}	2.45^{c}	332.5^{b-e}	82.18^{d-i}	32.9^{f-j}	6.8^{fg}	16.45^{a-e}	44.9^{c-g}	3.2^{b-h}	46.29^{a-f}	0.34^{e-i}	13.00^{a}	5.35^{b-f}
18	ETBW9550	71.5^{de}	120.5^{d-g}	49.0^{ef}	2.65^{c}	287.5^{b-e}	75.28^{jk}	30.73^{i-k}	7.03^{e-g}	16.95^{a-e}	48.2^{a-f}	2.8^{f-j}	42.77^{f-j}	0.33^{g-i}	11.75^{b-d}	4.57^{e-g}
19	ETBW9551	71.5^{de}	120.0^{d-g}	48.5^{ef}	2.75^{c}	457.5^{a-c}	81.5^{e-i}	32.58^{g-j}	7.43^{b-g}	17.15^{a-d}	49.65^{a-e}	3.3^{b-g}	45.29^{b-g}	0.35^{c-g}	11.25^{d-f}	5.71^{a-d}
20	LEMU	77.0^{ab}	125.0^{ab}	48.0^{f}	3.35^{a-c}	385.0^{a-e}	86.88^{a-e}	39.25^{ab}	8.5^{a}	17.4^{a-c}	51.5^{a-c}	3.95^{a}	47.26^{a-e}	0.34^{e-i}	10.25^{f-j}	6.67^{a}
21	ETBW9553	76.0^{ab}	125.5^{ab}	49.5^{d-f}	2.85^{c}	355.0^{a-e}	84.88^{a-f}	33.45^{e-i}	7.63^{a-f}	16.75^{a-e}	46.9^{b-f}	3.7^{a-c}	47.78^{a-d}	0.28^{j}	10.05^{g-j}	5.21^{c-f}
22	ETBW9554	71.5^{de}	122.0^{b-f}	50.5^{b-f}	2.65^{c}	272.5^{de}	86.95^{a-e}	35.68^{c-g}	8.06^{a-d}	18.3^{a}	54.00^{ab}	3.25^{b-h}	49.90^{a}	0.33^{g-i}	10.75^{d-i}	5.24^{c-f}
23	BIKA	66.0^{ij}	118.5^{fg}	52.5^{a-d}	2.80^{c}	382.5^{a-e}	81.62^{e-i}	35.08^{c-g}	8.58^{a}	17.6^{a-c}	51.00^{a-d}	3.1^{d-h}	43.44^{e-j}	0.34^{d-h}	10.7^{d-i}	5.26^{c-f}
24	ETBW9556	70.0^{ef}	120.0^{d-g}	50.0^{c-f}	2.75^{c}	400.0^{a-e}	88.03^{ab}	34.47^{d-h}	7.47^{b-g}	17.1^{a-d}	48.9^{a-f}	3.15^{c-h}	48.91^{a-c}	0.32^{i}	10.95^{d-i}	4.95^{d-f}
25	WANE	67.5^{g-j}	119.0^{fg}	51.5^{a-e}	2.90^{c}	452.5^{a-d}	83.38^{b-h}	37.98^{a-c}	6.74^{fg}	16.6^{a-e}	48.00^{b-f}	3.35^{b-f}	41.56^{g-k}	0.35^{c-f}	10.8^{d-i}	5.81^{a-d}
	Mean	69.92	121.44	51.52	2.96	357.90	82.77	34.42	7.53	16.89	48.45	3.13	43.96	0.34	10.93	5.32
	LSD 5%	2.0444	3.743	3.769	0.9239	180.21	6.62	3.2206	0.9714	2.0478	7.6845	0.589	3.9902	0.0229	1.152	0.98398

Means followed by the same letter are not significantly different (p = 0.05)

Appendix Table 5: Estimated variance components, phenotypic (PCV) and genotypic (GCV) coefficients of variability, broad sense heritability (h^2_b), genetic advance (GA) and genetic advance as percentage of mean (GAM %) for 15 traits of bread wheat genotypes tested at Debre Zeit

Traits	Mean	σ^2_g	σ^2_p	σ^2_e	PCV	GCV	h^2_b	GA 5%	GAM 5%
Days to heading	64.04	40.74	42.09	1.35	10.13	9.97	0.97	12.94	20.20
Days to maturity	110.38	38.97	41.13	2.16	5.81	5.66	0.95	12.52	11.34
Grain filling period	46.34	4.87	7.17	2.30	5.78	4.76	0.68	3.74	8.08
Productive tillers/plant	4.25	0.03	0.50	0.47	16.64	4.08	0.06	0.09	2.06
Productive tillers m^{-2}	444.60	4164.58	10213.21	6048.63	22.73	14.51	0.41	84.89	19.09
Plant height	88.76	16.26	26.22	9.96	5.77	4.54	0.62	6.54	7.37
Pedicle length	33.92	5.31	9.81	4.50	9.23	6.79	0.54	3.49	10.30
Spike length	8.04	0.40	0.59	0.19	9.51	7.81	0.68	1.06	13.23
Spikelets/spike	16.95	1.70	2.38	0.68	9.09	7.68	0.71	2.27	13.37
Kernels/spike	46.79	15.05	25.32	10.27	10.75	8.29	0.59	6.16	13.16
Aboveground biomass	3.26	0.15	0.24	0.10	15.12	11.76	0.60	0.61	18.84
Thousand kernels weight	32.89	18.05	20.37	2.32	13.72	12.92	0.89	8.24	25.05
Harvest index	0.33	0.0011	0.0021	0.0009	13.78	10.22	0.55	0.05	15.60
Grain protein content	14.1	0.50	0.87	0.37	6.62	5.01	0.57	1.10	7.83
Grain yield	53.51	65.49	81.87	16.38	16.91	15.12	0.80	14.91	27.86

Appendix Table 6: Estimated variance components, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (h^2_b), genetic advance (GA) and genetic advance as percentage of mean (GAM %) for 15 traits of bread wheat genotypes tested at Chefe Donsa

Traits	Mean	σ^2_g	σ^2_p	σ^2_e	PCV	GCV	h^2_b	GA 5%	GAM5%
Days to heading	69.92	13.66	15.30	1.64	5.59	5.28	0.89	7.19	10.29
Days to maturity	121.44	4.01	7.22	3.21	2.21	1.65	0.56	3.07	2.53
Grain filling period	51.52	3.34	5.15	1.81	4.40	3.54	0.65	3.03	5.88
Productive tillers/plant	2.96	0.06	0.25	0.19	16.89	8.28	0.24	0.25	8.35
Productive tillers m^{-2}	357.90	1424.80	9306.13	7881.33	26.95	10.55	0.15	30.43	8.50
Plant height	82.77	13.92	21.71	7.79	5.63	4.51	0.64	6.15	7.43
Pedicle length	34.42	6.85	9.07	2.22	8.75	7.60	0.76	4.68	13.61
Spike length	7.53	0.27	0.43	0.16	8.71	6.90	0.63	0.85	11.26
Spikelets/spike	16.89	0.26	1.00	0.74	5.91	2.99	0.26	0.53	3.12
Kernels/spike	48.45	12.03	24.08	12.05	10.13	7.16	0.50	5.05	10.42
Aboveground biomass	3.13	0.12	0.21	0.09	14.48	10.85	0.56	0.52	16.74
Thousand kernels weight	43.96	12.41	16.03	3.62	9.11	8.01	0.77	6.38	14.52
Harvest index	0.34	0.0005	0.0007	0.0002	7.47	6.21	0.69	0.04	10.65
Grain protein content	10.93	0.72	1.01	0.29	9.17	7.73	0.71	1.47	13.44
Grain yield	53.23	32.77	60.36	27.59	14.60	10.76	0.54	8.69	16.32

Estimates of variance components: The results of estimated variance components, phenotypic (PCV) and genotypic coefficient of variation (GCV), broad sense heritability (h^2_b), genetic advance (GA) and genetic advance as percentage of mean (GAM %) were calculated for the 15 traits investigated using the ANOVA computed between the tested genotypes and presented in Appendix Table 5 and 6 for Debre Zeit and Chefe Donsa respectively.

Phenotypic and genotypic coefficients of variation: The PCV values computed for the 15 traits across locations ranged from 2.21 for days to maturity to 26.95 for number of productive tillers m^{-2} while GCV ranged from 1.65 for days to maturity to 15.12 for grain yield ha^{-1}. The value of phenotypic coefficients of variation were generally slightly higher than the corresponding value of genotypic coefficients of variation for all traits studied indicating that the influence of growing environments. High PCV was observed only for number of productive tillers m^{-2} along with moderate GCV value at both locations. Moderate PCV were observed for aboveground biomass, grain yield in t ha^{-1}, number of kernels/spike and number of productive tillers/plant at both locations. In addition, moderate PCV values were observed for days to heading, harvest index and thousand kernels weights at Debre Zeit.

Moderate GCV value was observed for aboveground biomass, number of productive tillers m^{-2} and grain yield t ha^{-1} over locations. Furthermore thousand kernels weight and harvest index exhibited moderate GCV value at Debre Zeit. On the other hand days to maturity, grain filling period, plant height, pedicle length, spike length, number of spikelets/spike and grain protein content exhibited low GCV and PCV values across locations (Appendix Table 5 and 6).

Table 5: Estimated variance components, genotype by location interaction variance (σ^2gl), phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (h^2_b), genetic advance (GA) and genetic advance as percentage of mean (GAM %) for 15 traits of bread wheat genotypes tested at Debre Zeit and Chefe Donsa

Traits	Mean	σ^2gl	σ^2g	σ^2p	σ^2e	GCV	PCV	h^2_b	GA 5%	GAM 5%
Days to heading	66.98	5.73	24.34	31.55	1.49	7.36	8.39	0.77	8.92	13.32
Days to maturity	115.91	10.98	16.00	29.66	2.68	3.45	4.70	0.54	6.05	5.22
Grain filling period	48.93	3.58	2.31	7.93	2.05	3.10	5.76	0.29	1.69	3.45
Productive tillers/plant	3.61	0.05	0.02	0.40	0.33	3.92	17.54	0.05	0.07	1.81
Productive tillers m^{-2}	401.25	2011.45	1788.96	10765.39	6964.98	10.54	25.86	0.17	35.52	8.85
Plant height	85.76	1.93	14.12	24.93	8.88	4.38	5.82	0.57	5.83	6.79
Pedicle length	34.17	-0.63	6.39	9.12	3.36	7.40	8.84	0.70	4.36	12.76
Spike length	7.79	0.16	0.25	0.58	0.17	6.45	9.80	0.43	0.68	8.75
Spikelets/spike	16.92	0.63	0.66	2.00	0.71	4.81	8.36	0.33	0.96	5.70
Kernels/spike	47.62	8.03	9.53	28.71	11.16	6.48	11.25	0.33	3.66	7.69
Aboveground biomass	3.19	0.11	0.08	0.28	0.09	8.72	16.50	0.28	0.30	9.49
Thousand kernels weight	38.42	7.68	11.39	22.04	2.97	8.78	12.22	0.52	5.00	13.00
Harvest index	0.34	0.00	0.00	0.00	0.00057	7.34	11.89	0.38	0.03	9.34
Grain protein content	12.52	0.01	0.60	0.94	0.33	6.20	7.76	0.64	1.28	10.21
Grain yield	53.37	57.66	20.30	99.94	21.98	8.44	18.73	0.20	4.18	7.84

Heritability in broad sense: Broad sense heritability (h^2_b), which is an estimate of the total contribution of the genetic variance to the total phenotypic variance ranged from 0.06 (number of productive tillers/plant) to 0.97 (days to heading) at both location. The heritability was moderate to high for most of the traits at both locations, which might be due to smaller phenotypic variances and environmental influence on expression of traits. High heritability estimate was observed for days to heading, grain filling period, plant height, spike length and thousand kernels weight at both locations (Appendix Table 5 and 6). Heritability in broad sense for the combined ANOVA of the two locations revealed that greater than half characters exhibited moderate to high heritability ranges. High heritability were observed for days to heading, pedicle length and grain protein content whereas moderate heritability was observed for number of kernels/spike, thousand kernels weight, spike length, plant height, days to maturity and harvest index. The rest traits exhibited low heritability (Table 5).

Genetic advance: The genetic advance percent of means (GAM) expressed ranged from 2.06% for number of tillers/plant to 27.86% for gain yield at both locations. This refers to the improvement of the characters in genotypic value for the new population compared with the base population in one cycle of selection is within the range of 2.06-27.86% at 5% selection intensity. High GAM was observed at Debre Zeit for grain yield (27.86%) and for thousand kernels weight (25.05%) and for days to heading (20.2%).

At Chefe Donsa none of the traits had highest genetic advance percentage of the mean. However, moderate GAM was observed for days to heading (10.29%), spike length (11.26%), number of kernels/spike (10.42%), pedicle length (13.61%), aboveground biomass (16.74%), thousand kernels weight (14.52%), harvest index (10.65%) grain protein content (13.44%) and grain yield (16.32%).

DISCUSSION

The national average productivity of wheat is still very low as compared to other major wheat producing countries in the world. This is mainly due to insufficient improved bread wheat varieties, disease and other environmental factors hampering the productivity of the crop. In view of this, the present study accounted to evaluate the extent and pattern of genetic variance present in the common wheat elite germplasm of Ethiopia. The result of the experiments showed presence of significant and highly significant differences among genotypes for all characters except number of productive tillers/plant at both locations and number of productive tillers m^{-2} and number of spikelets/spike that were non-significant at Chefe Donsa. These implied that the presence of considerable variation among genotypes at both locations. The homogeneity of error variances were evident for all traits except harvest index that justify the comparison of genotypes performance on pooled mean values and pooled analysis of variance[28]. The results of pooled ANOVA revealed significance of mean squares of genotype for all traits except number of productive tillers/plant. The mean square for genotype × location was significant for most of the traits suggested the differential performance of genotypes at different locations.

These findings inspire carrying out further genetic studies to improve the cultivars through hybridization and selection programs. Similar findings in wheat has been reported by Kahn[29] who evaluated twenty one wheat genotypes for genetic variability at Khyber Pakhtunkhwa Agricultural University who found non-significant differences for number of fertile tillers/plant, number of spikelets/spike, number of kernels/spike and grain yield. On other hand, Majumder *et al*.[30] reported that bread wheat exhibited significant differences for days to maturity, days to 50% flowering, days to heading, plant height, spike length, spikes/plant, number of grains/spike, 1000 grain weight, harvest index and grain yield/plant.

With regard to time of heading and maturity of genotypes, the study showed almost all early and late heading genotypes corresponded with the respective early and late maturity characteristics of each location. In other words, early heading genotypes matched with early matured genotypes location wise and the vice versa. These findings are in line with the findings of Mollasadeghi *et al*.[31] who reported that days to heading and maturity corresponded with each other. The result of grain protein content analysis of genotypes revealed that all genotypes at Debre Zeit produced higher grain protein content relative to Chefe Donsa; which could be linked to the availability of nitrogen as a soil nutrient that could be influenced by higher rain fall distribution and daily temperature variations and leaching of more N in Chefe Donsa than Debre Zeit. Carson and Edwards[32] reported grain protein content and availability of N in the soil as affected by altitudinal variations, soil fertility, fertilizer inputs particularly nitrogen and temperature during the season, these authors further reported that additional nitrogen application resulted in increased vegetative growth rather than increasing the expected higher grain protein content.

The PCV values computed for the 15 traits across locations ranged from 2.21 for days to maturity to 26.95 for number of productive tillers m^{-2} while GCV ranged from 1.65 for days to maturity to 15.12 for grain yield t ha^{-1}. The broad sense heritability (h^2_b) ranged from 0.06-0.97 for number of productive tillers/plant and days to heading respectively. The GAM value ranged from 2.06% (PTPP) to 27.86% (GY), respectively. In general, high heritability coupled with high GAM was observed only for GY, DH and TKW at Debre Zeit. This has indicated that most probably the heritability is due to additive gene effects and selection may be effective in early generations for these traits. The present finding coincided with Ali and Shakor[33] who reported medium PCV and GCV for grain yield/plot in 20 bread wheat genotypes.

Combined ANOVA of the 15 quantitative traits showed that genotypic coefficient of variability ranged from 3.1% (Grain filling period) to 10.54% (number of productive tillers m^{-2}). Phenotypic coefficient of variability ranged from 4.7% (days to maturity) to 25.86% (number of productive tillers m^{-2}). As explained above, the PCV values were relatively greater than GCV for all traits, however, the magnitude of the difference between PCV and GCV was relatively low for days to heading, days to maturity, plant height, grain protein content, pedicle length and grain filling period, spike length, thousand kernels weight, number of spikelets/spike and harvest index. This suggested that the marked influence of environmental factors for the phenotypic expression of genotypes was low; hence, there is higher chance of improvement of these traits through selection based on the phenotypic values of the traits. Similar results were reported by Mesele[34] for days to heading, days to maturity, grain filling period, thousand kernel weight and harvest index. On the other hand, the difference in magnitudes between PCV and GCV values were relatively high for grain yield ha^{-1} (10.29) number of productive tillers m^{-2} (15.32), aboveground biomass (7.78), number of productive tillers/plant (13.62) and number of kernels/spike (4.77) (Table 5). This result was in close agreement with the findings of Demelash[18] who reported relatively high environmental variance than genotypic variance for number of tillers/plant, number of kernels/spike, biomass yield and grain yield.

High heritability estimate was observed for days to heading, grain filling period, plant height, spike length and thousand kernels weight at both locations (Appendix Table 5 and 6). High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. This may be attributed partly due to uniform environmental conditions during the commencement of the experiment. Degewione *et al*.[35] reported heritability estimates were very high for days to heading (89.08%) and grain yield/plot (84.64%), indicating the possibility of higher success rate in selection; while high heritability values for grain filling period (62.72%), days to maturity (76.17%), plant height (74.04%), number of grains/spike (68.34%) and thousand grain weight (60.23%). Sachan and Singh[36] also reported high heritability estimates for grain yield, number of spikelets/spike, number of seeds/spike, plant height and thousand seed weight which support the present findings.

The estimation of genetic advance support to explain the type of gene action involved in the expression of various polygenic characters. High values of genetic advance indicate the involvement of additive gene action whereas low values entail the presence of non-additive gene action[37]. Johnson *et al*.[27] reported that heritability estimates along with genetic gain would be more satisfying than heritability solitary in predicting the consequential effect of selection to choose the best individual. In general, high heritability along with high genetic advance in terms of mean was observed for grain yield, thousand kernels weight and days to heading at Debre Zeit. These indicate that most probably the heritability is due to additive gene effects and selection may be effective in early generations for these traits. The present result partially agree with Sabit *et al.*[38] who reported high heritability along with high GAM for number of grains/spike (89.63 and 23.19%), thousand kernels weight (86.26 and 26.27%), biological yield (80.95 and 37.92%) and harvest index (55.85 and 11.93%), respectively.

CONCLUSION

The study highlighted presence of significant genetic variations for agronomically important traits (such as grain yield and grain protein content) among Ethiopian bread wheat genotypes. The promising genotypes ETBW9551, ETBW8595 and ETBW8751 exhibited significantly higher grain yield than the standard checks included in the study. Hence, these genotypes can be considered as candidates for multi-environmental variety verification trials for possible registration and release as new commercial cultivars for similar agro-ecologies with the study area.

ACKNOWLEDGMENT

The first author thanks Ministry of Education, Federal Government of Ethiopia for sponsoring his postgraduate study scholarship and Debre-Zeit agricultural Research Center for hosting the field experiments. We thank Habte Mariam Zegeye, Mr. Wassihun and Mr. Ashenafi of Ethiopian agricultural research institute for providing seeds of bread wheat genotypes.

SIGNIFICANCE STATEMENT

This study discovered the presence of significant genetic variation among the tested genotypes for the 15 traits considered. The study also highlighted specific adaptation of wheat genotypes unusual to the characteristics of bread wheat cultivars known for its wider adaptation in most wheat growing regions.

REFERENCES

1. Braun, H.J., G. Atlin and T. Payne, 2010. Multi-Location Testing as a Tool to Identify Plant Response to Global Climate Change. In: Climate Change and Crop Production, Reynolds, M.P. (Ed.). Chapter 7, CABI, Surrey, UK., ISBN-13: 9781845936341, pp: 115-138.
2. FAO., 2015. News archive 2015. Food and Agriculture Organization of the United Nations. http://www.fao.org/news/archive/news-by-date/2015/en/
3. Onwueme, I.C. and T.D. Sinha, 1999. Field Crops Production in Tropical Africa. CTA Publications, Wageningen, pp: 250-266.
4. Kamali, M., 2008. Review on wheat status in the past, present and future. Proceedings of the 10th Conference on Sciences of Breeding, (CSB'08), Iran, pp: 23-45.
5. Acevedo, E., P. Silva and H. Silva, 2002. Wheat Growth and Physiology. In: Bread Wheat: Improvement and Production, Curtis, B.C., S. Rajaram and H.G. Macpherson (Eds.)., FAO Plant Production and Protection Series No. 30, Food and Agriculture Organization of the United Nations, Rome.
6. Hailu, F., A. Merker, H. Singh, G. Belay and E. Johansson, 2006. Multivariate analysis of diversity of tetraploid wheat germplasm from Ethiopia. Genet. Resour. Crop Evol., 53: 1089-1098.
7. CSA., 2015. Agricultural sample survey. Report on Area, Production and Yield of Meher Season Crops for Private Peasant Holdings. Statistical Bulletin No. 578, Central Statistical Agency, Addis Ababa, Ethiopia.
8. CSA., 2017. Crop production forecast sample survey, 2017. Report on Area and Crop Production forecast for Major Crops (for Private Peasant Holdings 'Meher' season). Central Statistical Agency, Addis Ababa, Ethiopia.
9. Amsal, T., 2001. Studies on genotypic variability and inheritance of water logging tolerance in wheat. Ph.D. Thesis, University of the Free State, Bloemfontein, South Africa.
10. Tesema, T., 1987. Durum wheat breeding in Ethiopia. Proceedings of the 5th Regional Wheat Workshop for Eastern, Central and Southern Africa and Indian Ocean, Antsirabe, Madagascar, October 5-10, 1987, CIMMYT., Mexico, D.F., pp: 18-22.
11. Taffesse, A.S., P. Dorosh and S. Asrat, 2011. Crop production in Ethiopia: Regional patterns and trends. ESSP II Working Paper No. 16, Development Strategy and Governance Division, International Food Policy Research Institute, Ethiopia Strategy Support Program II, Ethiopia, March 2011, pp: 1-27.
12. FAO., 2016. FAOSTAT data. Food and Agriculture Organization of the United Nations. http://faostat.fao.org/site/339/default.aspx
13. Fikre, G., A. Sentayehu and T. Zerihun, 2015. Genetic variability studies in bread wheat (Triticum aestivum L.) genotypes at kulumsa agricultural research center, South East Ethiopia. J. Biol. Agric. Healthcare, 5: 89-97.
14. Rauf, S., S.A. Tariq and S.W. Hassan, 2012. Estimation of pedigree based diversity in Pakistani wheat (*Triticum aestvium* L.) germplasm. Commun. Biometry Crop Sci., 7: 14-22.
15. Mohammadi, S.A. and B.M. Prasanna, 2003. Analysis of genetic diversity in crop plants-salient statistical tools and considerations. Crop Sci., 43: 1235-1248.

16. Balcha, Y., 2002. Assessment of stability and character association in bread wheat (*Triticum aestivum* L. em. Thell) genotype. M.Sc. Thesis, School of Graduate Studies of Haramaya University, Ethiopia.
17. Mamo, B., 2004. Genetic variability and character associations in bread wheat (*Triticum aestivum* L.) genotypes developed for semiarid areas. M.Sc. Thesis, School of Graduate Studies of Alemaya University, Ethiopia.
18. Demelash, L.A., T. Desalegn and G. Alemayehu, 2013. Genetic variation of bread wheat (*Triticumaestivum* L.) genotypes based on number of phonological and morphological traits at Marwold Kebele, Womberma Woreda, West Gojam. Wudpecker J. Agric. Res, 2: 160-166.
19. Degewione, A., T. Dejene and M. Sharif, 2013. Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. Int. Res. J. Agric. Sci., 1: 19-29.
20. AACC., 2000. Approved Methods of the American Association of Cereal Chemists. 10th Edn., American Association of Cereal Chemists Press, St. Paul, MN., USA.
21. Bariana, H.S., H. Miah, G.N. Brown, N. Willey and A. Lehmensiek, 2007. Molecular Mapping of Durable Rust Resistance in Wheat and Its Implication in Breeding. In: Wheat Production in Stressed Environments, Developments in Plant Breeding, Vol, 12, Buck, H.T., J.E. Nisi and N. Salomón (Eds.)., Springer, Dordrecht, pp: 723-728.
22. Dabholkar, 1999. Elements of Biometrical Genetics. Concept Publishing Company, New Delhi.
23. Cochran, W.G. and G.M. Cox, 1957. Experimental Designs. 2nd Edn., John Wiley and Sons, New York, Pages: 630.
24. SAS., 2004. SAS/STAT User's Guide. Version 9.0, 4th Edn., Statistical Analysis Institute Inc., Cary North Carolina.
25. Burton, W.G. and E.H. Devane, 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J., 45: 478-481.
26. Allard, R.W., 1960. Principle of Plant Breeding. John Wiley and Sons Inc., New York, USA.
27. Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Genotypic and phenotypic correlations and their implication in selection. Agron. J., 47: 477-483.
28. Gomez, K.A. and A.A. Gomez, 1984. Statistical Procedures for Agricultural Research. 2nd Edn., John Wiley Sons, New York, USA., ISBN: 978-0-471-87092-0, Pages: 704.
29. Kahn, S.A., 2013. Genetic variability and heritability estimates in F2 wheat genotypes. Int. J. Agric. Crop Sci., 5: 983-986.
30. Majumder, D.A.N., A.K.M. Shamsuddin, M.A. Kabir and L. Hassan, 2008. Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. J. Bangladesh Agril. Univ., 6: 227-234.
31. Mollasadeghi, V., S. Elyasi and B. Mirzamasoumzadeh, 2012. Genetic variation of 12 bread wheat genotypes based on number of phonological and morphological traits. Ann. Biol. Res., 3: 4734-4740.
32. Carson, G.R. and N.M. Edwards, 2009. Criteria of Wheat and Flour Quality. In: Wheat: Chemistry and Technology, 4th Edn., Khan, K. and P.R. Shewry (Eds.)., AACC International, USA., pp: 97-118.
33. Ali, I.H. and E.F. Shakor, 2012. Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. Mesopotamia J. Agric., 40: 27-39.
34. Mesele, A., 2015. Genetic variability and association among seed yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes at Ofla district, Northern Ethiopia. M.Sc. Thesis, Haramaya University, Ethiopia.
35. Degewione, A., T. Dejene and M. Sharif, 2013. Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. Int. Res. J. Agric. Sci., 1: 19-29.
36. Sachan, M.S. and S.P. Singh, 2003. Genetics of yield and its components in durum wheat (*Triticum durum* Desf.). J. Interacademicia, 7: 140-143.
37. Singh, P. and S.S. Narayanan, 1993. Biometrical Techniques in Plant Breeding. 1st Edn., Kalayani Publishers, New Dehli, India.
38. Sabit, Z., B. Yadav and P.K. Rai, 2017. Genetic variability, correlation and path analysis for yield and its components in f5 generation of bread wheat (*Triticum aestivum* L.). J. Pharmacogn. Phytochem., 6: 680-687.