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Research Article
Study of Genetic Variability in Some Bread Wheat Accessions (*Triticum aestivum* L.) in Gurage Zone, Ethiopia

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Abstract

Background and Objective: Bread wheat (*Triticum aestivum* L.) is one of the most important and strategic cereal crop which contributes food supply worldwide and ensures food security. Developing desirable genotypes with high yield potential is the main concern of any breeders. So, the main objective of this study was performance evaluation of some bread wheat accessions at Gurage zone, Ethiopia to evaluate its genetic variability. **Materials and Methods:** A field experiment was conducted to study the genetic variability and association of characters among yield and yield-related traits in bread wheat accessions at Fereziye and Kotergedira during the main season of 2018. The experiment was conducted by using augmented design with 6 blocks and a total of 60 accessions and 4 checks were evaluated. **Results:** Analysis of variance revealed that there was highly significant difference among the samples for most of the characters studied. High heritability was estimated for tillers/plant, plant height, above ground biomass, spike length, days to heading and spikelet per spike at Fereziye and characters that showed high heritability at Kotergedira were also tillers/plant, plant height, above ground biomass, days to heading, spikes per plant and spikelet per spike. **Conclusion:** This indicated that these characters could be improved through selection relatively with simple way. For all traits, phenotypic coefficient of variation was highly higher than genotypic coefficient of variation this indicating that there was environmental influence on these traits.

Key words: Accessions, bread wheat, heritability, genetic variability, genotypic coefficient, phenotypic coefficient

INTRODUCTION

Bread wheat *(Triticum aestivum* L.) is a hexaploid plant with the chromosome number of 2, n = 42, which belongs to family poaceae. It is the most important and strategic cereal crop for the majority of world's populations. It is also an important staple food crop in Ethiopia, which ranks fourth in total area coverage next to teff, maize and sorghum. It is considered as precious gift by farmers in top producing areas just like Oromia, Amhara, Southern Nations Nationalities and People's Region (SNNP) and Tigray. In Ethiopia the production of wheat depends on an altitude which ranges from 1500-3000 masl, between 6-16°N latitude and 35-42°E longitude. But, the most suitable agro-ecological condition seems to be in the range of 1900-2700 masl[1]. Its production status is 4th in total next to maize, teff and sorghum. Four point 2.3 million t (4.23) of wheat is produced on an area of 1.7 million ha and about 4.6 million farmers were involved. Oromia, Amhara, SNNP and Tigray are the major wheat producing regions in the country with area coverage of 875641.45, 529609.63, 137294.72 and 108865.39 ha, respectively. Specifically when considered Gurage zone, 47259 farmers were involved with unestimated area coverage in 2015 main production season[2].

Plant breeding requires genetic variation of useful traits for crop improvement. Breeding for improved plant cultivars is based on two principles: genetic variation and selection. Genetic diversity study in plant is the key point and gives golden opportunity for plant breeders to develop new and improved cultivars with desirable characteristics for the benefit of the society[3]. Thus, to understand the most important desirable varieties, the study of statistical parameters that indicates the way forward in plant breeding are phenotypic coefficient of variation, genotypic coefficient of variation, environmental coefficient of variation, heritability and genetic advance which are crucial to evaluate the genetic stability and performance of any particular genotype. It is also helpful to determine the effectiveness of selection for a particular trait in that genotype to get superior cultivars. High genetic advance in conjugation with high heritability value indicated the most effective condition for selection[4]. Therefore, a good understanding of heritability and genetic advance present in different yield contributing character is the first option for improvement in bread wheat genotypes. Plant breeding with the help of the knowledge of quantitative genetics is considered as an effective programme and selection is on the right track when it depends on the presence of genetic variation of the breeding materials.

When the evolution of novel genotypes in the population is highly depends on genetic cause with least environmental influence, the chance of getting superior genotypes is high. The evidence for this idea is that, the 2 important source of evolution are genetic variation and mutation. So, the formation of new species is impossible without genetic variation. That is why breeders are interested to perform experiments on different locations with different samples. However, what is difficult in the study of phenotypic variability is that, it is an ambiguous to distinguish what proportion of the observed variability is heritable and what proportion is non-heritable, because of epistasis and pleiotropic nature of a certain characters which is controlled by polygenic system. For that matter, selection of good quality seed and the progress of breeding in such a population are primarily determined by the magnitude, nature and interrelation of genotypic and environmental variation for various plant characters including bread wheat[5]. The transmission of genetic material from parent to off spring of a trait thus, guides a plant breeder to predict the nature of each subsequent generation and enables them to select desirable genotypes. It is therefore, useful for breeders to know the genetic background of the breeding material and variety[6]. Generally, to improve the yield through selection of better varieties, knowledge of the nature of association of bread wheat yield with yield contributing characters is very essential. The present information is undertaken to study genetic parameters for important traits. Even though bread wheat is the most important food for the majority of world population, increasing its consumption even hand to mouth is still under expectation in developing countries including Ethiopia. Doing something non-significant for the society is not better than doing nothing, because food security does not exist in proportional to population growth. Researchers should engage their full time with the help of genetics to facilitate the improvement of crops for enhanced yield and quality.

Even though genetics and biotechnology were performed for a long period of time working in collaboration with farmers and give tireless information is not satisfactory enough. That is why agriculture is facing many challenges to produce more output with less input beyond the energy have lost in developing countries. Genetic crop improvement can contribute towards solving this complex problem. Therefore, Ethiopia in general and Wolkite University in particular should have taken responsibilities to solve this problem. Considering the importance of genetic variability as a basic breeding tool for improvement, the present study would be conducted to evaluate the genetic advance and selection of suitable diverse parents for yield and related traits in future breeding program.

MATERIALS AND METHODS

Description of the study area: The study were conducted at Fereziye and Kotergedra during rainy season from October, 2017-January, 2018, which is the agricultural research site of Wolkite University, situated in Cheha and Ezha Weredas, Gurage zone, respectively (Table 1).

Experimental material: For this study, 60 accessions and 4 released verities as a standard check, which were collected from Ethiopian Biodiversity Institute and Kulumsa Agricultural Research Center, respectively would be sown in Fereziye and Kotergedra agricultural research site of Wolkite University (Table 2).

Experimental design: Augmented design with 6 blocks was used for the experiment. Those collected accessions from Ethiopian Biodiversity Institute would be sown on well prepared plots. Each experiment would have 6 rows and

20 cm spacing between row having plot area of 3 m² (1.2×2.5 m). Spacing between plots would be 0.50 m and the distances between replications would be 1 m. About 100 kg ha⁻¹ NPS fertilizer would be applied at the time of planting and tillering. Seedling was done at the rate of 125 kg ha⁻¹. Seed and fertilizer would drill uniformly by hand. Weeding and other agronomic practice were carried out as per recommendations of the respective sites.

Data collection: Data was collected based on an average of 10 randomly selected plants and plot basis. Ten representative plants per plot were randomly selected from the central rows excluding the 2 border rows and tag for observations. Data was collected based on the following parameters:

Tillers/plant (TPP), Plant Height (PH), Kernels Per Spike (KPS), Spikelet Per Spike (SkPS), Spike Length (SL), Spikes Per Plant (SPP), Days To Heading (DTH), Days To Maturity (DTM), Grain Filling Period (GFP), Grain Yield (GY), Above Ground Biomass (AGB), Harvest Index (HI).

Table 1: Location and descriptions of weather conditions for the 2 testing sites

Sites	Annual temperature (°C) max	min	Annual rainfall (mm)	Location	Altitude (masl)
Yefereziye	24.37	10.2	1336.8	8.2°N and 37.9°E	1980
Kotergedra	23	8	1450.0	8.05°N and 37.5°E	2600

Table 2: Passport data of *Triticum aestivum*

Entry No.	Accession No.	Obtained from	Entry No.	Accession No.	Obtained from	Entry No.	Accession No.	Obtained from
1	5011	EBI	23	7028	EBI	45	7285	EBI
2	5241	EBI	24	7033	EBI	46	7292	EBI
3	5261	EBI	25	7037	EBI	47	7298	EBI
4	5377	EBI	26	7038	EBI	48	7339	EBI
5	5380	EBI	27	7049	EBI	49	7341	EBI
6	5418	EBI	28	7139	EBI	50	7407	EBI
7	5435	EBI	29	7143	EBI	51	7451	EBI
8	5548	EBI	30	7145	EBI	52	7453	EBI
9	5670	EBI	31	7146	EBI	53	7459	EBI
10	5673	EBI	32	7177	EBI	54	7565	EBI
11	5694	EBI	33	7221	EBI	55	7646	EBI
12	5721	EBI	34	7231	EBI	56	7946	EBI
13	5747	EBI	35	7248	EBI	57	7981	EBI
14	5774	EBI	36	7251	EBI	58	7991	EBI
15	6089	EBI	37	7253	EBI	59	8285	EBI
16	6105	EBI	38	7257	EBI	60	8313	MARC
17	6859	EBI	39	7259	EBI	61	Hidase	kulumsa
18	6883	EBI	40	7275	EBI	62	Lemu	kulumsa
19	6884	EBI	41	7276	EBI	63	King bird	kulumsa
20	6934	EBI	42	7279	EBI	64	Alidoro	kulumsa
21	6991	EBI	43	7281	EBI			
22	7010	EBI	44	7284	EBI			

EBI: Ethiopian biodiversity institute

Table 3: Analysis of variance (ANOVA)

Source of variation	Degree of freedom	Mean of square	Expected mean
Replication	r-1	MSr (M1)	$\sigma^2e+r\,\sigma^2g$
Genotype	g-1	MSg (M2)	$\sigma^2e+\sigma^2g$
Error	(r-1) (g-1)	MSe (M3)	σ^2e
Total	(rg-1)		

R: Number of replications, g: Number of genotypes, MSr: Mean of squares due to replication, MSg: Mean of squares due to genotypes, MSe: Mean of squares due to error, σ^2e: Error variance, σ^2g: Genotypic variance

Estimation of genetic parameters: The phenotypic and genotypic coefficients of variation were estimated according to the following method[7]:

- Environmental variance $(\sigma\,2e)$ = Mse (mean square)
- Genotypic variance (σ^2g) = MSg -MSe
- Phenotypic variance (σ^2p) = $\sigma^2g+\sigma^2e$:

$$PCV\,(\%) = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Population mean for the character}} \times 100$$

$$GCV\,(\%) = \frac{\sqrt{\text{Genotypic variance of genotypes}}}{\text{Population mean for the character}} \times 100$$

Broad-sense heritability: Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance $(g\sigma^2)$ to the phenotypic variance (σ^2p) and was estimated on genotype mean[8]:

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

Where:

H (h^2) = Heritability in board sense
σ^2p = Phenotypic variance
σ^2g = Genotypic variance

Genetic Advance under selection (GA): Expected genetic advance for each character at 5% selection intensity will be calculated by the formula [9]:

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

Where:

h^2 = Heritability in broad sense
σ_p = Phenotypic standard deviation of the trait
K = Standard selection differential which is 2.056 at 5%

Selection intensity: Genetic advance as percent mean (GAM) will be calculated to compare the extent of predicted advances of different traits under selection by the formula:

$$GA\,(\%) = \frac{\text{Genetic advance}}{\text{Population mean for the character}} \times 100$$

Statistical analysis: The plot mean values were subjected to statistical analysis as augmented design and under taken separately for each character[10]. That is the SAS system of statistical software was employed for the analysis of variance. (Table 3).

RESULTS

Estimates of genetic parameters
Estimates of variance components, phenotypic and genotypic coefficient of variation: Those values obtained from the analysis of variance of 13 quantitative traits grown at Fereziye indicated that, the mean square due to accession were highly significant which includes among treatments and among test (p<0.01) for traits tillers/plant, plant height, spikelet per spike, spike length, spikes per plant, days to heading, days to maturity, above ground biomass and grain yield (p<0.05) among treatments (Table 4). The mean square was non-significant for all other traits. The results of the analysis of variance of 13 quantitative traits at kotergedra indicated that, the mean square due to accession were significant (p<0.01) for most of the traits like; tillers/plant, plant height, kernels per spike, spikelet per spike, days to maturity, spikes per plant, days to heading, days to maturity, above ground biomass (Table 5) indicated sufficient genetic variability for these traits.

Estimates of genotypic variance (σ^2g), phenotypic variance (σ^2p), environmental variance (σ^2e), Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability (H%), Genetic Advance (GA) and Genetic Advance as percent Mean (GAM) is shown on Table 6. The highest genotypic variance 24737.7 and 651.9, phenotypic variance 34623.7 and 1385.5 as presented in Table 6, environmental variance (9886) and (733.6) were recorded for above ground biomass and grain yield, respectively as presented in Table 4.

In the present study, the estimation of heritability was higher (85.5%) for tillers/plant, plant height (88.4%), above ground biomass (71.4%), spike length (83.70%), days to heading (95%), spikes per plant (85.5) and spikelet per spike (77.3%) at Fereziye. In the case of Kotergedira, the highest

Table 4: Analysis of variance for the 13 characters of 64 bread wheat accession grown at Fereziye, 2018

Characters	Block (adj) (df = 5)	Error (df = 15)	Trt (adj) (df = 63)	Among controls (df = 3)	Among test (df = 59)	Test vs. control (df = 1)	CV (%)
TPP	1.91	2.97	20.5**	0.96	21.3**	20.19*	17.9
PH	21.5	49.02	422.4**	195.53*	405.92**	389.28*	7.8
KPS	77.23	52.13	96.04	52.06	94.96	23.53	14.7
SkPS	5.56	0.93	4.09**	2.84	4.22**	8.28**	5.2
SL	8.06	1.2	7.38**	0.39	7.66**	6.99*	10.2
SPP	1.91	2.97	20.54**	0.96	21.27**	21.22*	16.2
DTH	27.5	7.2	142.5**	130.26**	134.38**	32.58	3.4
DTM	174.8	67.8	81.2	119.89	76.16	0.19	6.7
GFP	193.97	77.3	88.97	3.53	73.09	34.39	19.7
GY	864.17	733.6	1385.5**	2594.12	1208.06	6954.14	10.49
TKW	0.05	0.045	0.06	0.009	0.063	0.089	6.2
AGB	15366.7	9886	34623.7**	8122.1	33412.7**	102001*	10.3
HI	0.0021	0.0013	0.002	0.0017	0.00118	0.00002	13.65

**Means highly significant, *Significant, Adj: Adjusted values, df: Degree of freedom, Trt: Treatment, TPP: Tillers/plant, PH: Plant height, KPS: Kernels per spike, SkPS: Spikelet per spike, SL: Spike length, SPP: Spikes per plant, DTH: Days to heading, DTM: Days to maturity, GFP: Grain filling period, GY: Grain yield, TKW: 1000-kernel weight, AGB: Above ground biomass, HI: Harvest index

Table 5: Analysis of variance for the 13 characters of 64 bread wheat accession grown at kotergedra, 2018

Characters	Block (adj) (df = 5)	Error (df = 15)	Trt (adj) (df = 63)	Among controls (df = 3)	Among test (df = 59)	Test vs. control (df = 1)	CV (%)
TPP	2.31	2.39	17.38**	0.12	15.97**	14.04**	17.6
PH	17.4	36.51	289.03**	132.03	280.8**	235.7*	7.5
KPS	55.12	50.8	70.12	3.46	73.2	60.99	15.8
SkPS	4.8	1.16	2.9*	5.4	2.8*	11.95**	6.4
SL	2.8	2.08	2.6**	2.8	2.6	0.02	13.4
SPP	2.32	2.4	15.5**	0.12	15.97**	23.8**	15.8
DTH	57.4	12.3	37.6**	2.2	39.98**	0.05	3.8
DTM	116.8	29.12	43.81	7	38.5	6.6	3.95
GFP	18.07	18.02	23.24	1.8	18.6	7.8	10.8
GY	1297.5	520.28	1248.15*	1029.2	1213.13*	142.24	12.52
TKW	0.012	0.031	0.034	0.02	0.03	0.006	5.2
AGB	14166.7	6111	22171.8**	8210.8	22537**	3629.5	11.5
HI	0.002	0.00086	0.00087	0.0002	0.0008	0.000005	10.84

TPP: Tillers/plant, PH: Plant height, KPS: Kernels per spike, SkPS: Spikelet per spike, SL: Spike length, SPP: Spikes per plant, DTH: Days to heading, DTM: Days to maturity, GFP: Grain filling period, GY: Grain yield, TKW: 1000-kernel weight, AGB: Above ground biomass, HI: Harvest index

Table 6: Estimates of genetic component of variance, heritability and genetic advance of 64 bread wheat accessions grown at Fereziye, 2018

Characters	Range Mean	Min	Max	$\sigma^2 g$	$\sigma^2 p$	PCV (%)	GCV (%)	H^2	GA	GAM (%)
TPP	9.6	4.88	25.38	17.53	20.5	47.2	43.7	85.5	7.98	83.2
PH	90.12	68.59	142.64	373.38	422.4	22.8	21.4	88.4	37.42	41.5
KPS	49.08	18.71	68.24	43.91	96.04	19.97	13.5	45.7	9.23	18.8
SkPS	18.52	10.41	24.39	3.16	4.09	10.92	9.5	77.3	3.22	17.4
SL	10.71	7.1	17.63	6.18	7.38	25.4	23.2	83.7	4.7	43.8
SPP	10.65	5.88	26.38	17.57	20.54	42.6	39.4	85.5	7.98	75
DTH	78.7	62.46	97.21	135.3	142.5	15.2	14.7	94.95	23.35	29.7
DTM	123.6	97.54	144.54	13.4	81.2	7.2	2.9	16.5	3.06	2.5
GFP	44.65	25.08	68.83	11.67	88.97	21.12	7.6	13.1	2.55	5.7
GY	258.1	155.83	342.08	651.9	1385.5	14.4	9.9	47.05	36.03	13.96
HKW	34.3	30	3.88	0.015	0.06	7.14	3.6	25	0.12	3.67
AGB	966	689.58	1539.58	24737.7	34623.7	19.8	16	71.4	272	28.15
HI	0.27	0.16	0.32	0.0007	0.002	21.1	17.2	35	0.03	11.94

TPP: Tillers/plant, PH: Plant height, KPS: Kernels per spike, SkPS: Spikelet per spike, SL: Spike length, SPP: Spikes per plant, DTH: Days to heading, DTM: Days to maturity, GFP: Grain filling period, GY: Grain yield, TKW: 1000-kernel weight, AGB: Above ground biomass, HI: Harvest index

Table 7: Estimates of genetic component of variance, heritability and genetic advance of 64 bread wheat accessions grown at Kotergedira, 2018

Characters	Range			$\sigma^2 g$	$\sigma^2 p$	PCV (%)	GCV (%)	H²	GA	GAM (%)
	Mean	Min	Max							
TPP	8.8	2.65	21.68	14.99	17.38	47.7	43.9	86.24	7.4	84.1
PH	80.74	64.7	131.34	252.52	289.03	21.06	19.68	87.4	30.6	37.9
KPS	45.3	19.95	63.28	19.32	70.12	18.5	9.8	27.6	4.8	10.6
SkPS	16.9	12.23	22.32	1.74	2.9	10.05	7.8	60	2.1	12.4
SL	10.8	5.78	14.28	0.52	2.6	14.8	6.7	20	0.7	6.4
SPP	9.8	3.65	22.57	13.1	15.5	40.2	36.9	84.5	6.9	70.4
DTH	92.06	69.4	109.4	25.3	37.6	6.7	5.5	67.3	8.5	9.2
DTM	136.7	122.5	160.96	14.69	43.81	4.8	2.8	33.5	4.6	3.4
GFP	44.6	35.58	65.58	5.22	23.24	10.8	5.12	22.5	2.2	4.9
GY	182.2	122.5	290	727.87	1248.15	19.4	14.8	58.3	42.4	23.3
TKW	34	30.7	3.69	0.003	0.034	5.4	1.6	8.8	0.03	0.88
AGB	681.9	445.83	1245.83	16060.8	22171.8	21.8	18.6	72.4	222.2	32.6
HI	0.3	0.18	0.34	0.00001	0.00087	9.8	1.05	1.15	0.0007	0.23

TPP: Tillers/plant, PH: Plant height, KPS: Kernels per spike, SkPS: Spikelet per spike, SL: Spike length, SPP: Spikes per plant, DTH: Days to heading, DTM: Days to maturity, GFP: Grain filling period, GY: Grain yield, TKW: 1000-kernel weight, AGB: Above ground biomass, HI: Harvest index

Table 8: Combined analysis of estimates of error, mean square and variance components, phenotypic and genotypic coefficient of variation over 2 locations grown at Fereziye and Kotergedira, 2018

Characters	Block (adj) (df = 5)	Error (df = 15)	Trt (adj) (df = 63)	Loc (df = 1)	CV (%)	Range			$\sigma^2 g$	$\sigma^2 p$	PCV (%)	GCV (%)	H²	GA	GAM (%)
						Mean	Min	Max							
TPP	2.85	1.45	35.19	28.59	13.1	9.19	2.8	24.6	33.74	35.19	63.21	64.55	95.88	11.66	126.88
PH	30.73	25.49	693.79	3692.25	5.91	85.43	54	141.8	668.3	693.79	30.26	30.83	96.33	52.01	60.88
KPS	114.94	20.34	160.33	607.51	9.6	47.18	21.5	70.6	139.99	160.33	25.08	26.84	87.31	22.66	48.03
SkPS	10.11	0.85	6.27	107.3	5.19	17.72	12.5	24.5	5.42	6.27	13.13	14.13	86.44	4.44	25.06
SL	3.57	1.92	8.19	0.4	12.89	10.76	5.2	16.5	6.27	8.19	23.27	26.6	76.56	4.5	41.82
SPP	2.84	1.52	38.87	33.13	12.1	10.21	3.8	25.6	37.35	38.87	59.86	61.06	96.09	12.28	120.27
DTH	19.53	55.77	113.1	7493.36	8.75	85.38	60	111	57.33	113.1	8.87	12.46	50.67	11.05	12.94
DTM	236.85	50.65	74.54	7150.1	5.47	130.13	100	161	23.89	74.54	3.76	6.63	32.04	5.67	4.36
GFP	151.08	46.88	49.65	0.15	15.34	44.63	27	79	2.77	49.65	3.73	15.79	5.58	0.81	1.81
GY	367.08	1095.7	1555.4	242288	15.03	220.18	140	355	459.7	1555.4	9.74	17.91	29.56	239	108.55
TKW	0.04	0.02	0.07	0.2	4.16	3.4	3	4	0.05	0.07	6.58	7.78	71.43	0.38	11.18
AGB	10845.8	14866.1	42349.02	3390108	14.8	823.99	500	1450	27482.9	42349	20.12	24.97	64.9	273.8	33.23
HI	0.0024	0.00099	0.0018	0.00041	11.7	0.27	0	0.38	0.00081	0.0018	10.54	15.71	45	0.04	14.81

Loc: Location, Trt: Treatment, CV: Coefficient of variation, TPP: Tillers/plant, PH: Plant height, KPS: Kernels per spike, SkPS: Spikelet per spike, SL: Spike length, SPP: Spikes per plant, DTH: Days to heading, DTM: Days to maturity, GFP: Grain filling period, GY: Grain yield, TKW: 1000-kernel weight, AGB: Above ground biomass, HI: Harvest index

heritability was recorded from plant height (87.4), tillers/plant (86.24), spikes per plant (84.5), days to heading (67.3) and above ground biomass (72.4) (Table 7).

Combined analysis of estimates of variance components, phenotypic and genotypic coefficient of variation over 2 locations: The highest phenotypic variance 42349 and 1555.4, environmental variance 14866.1 and 1095.7 were observed from above ground biomass and grain yield, respectively (Table 5). The difference was visible on genotypic variance and the phenotypic variance of characters like days to heading (57.33,113.1), days to maturity (23.89,74.54), grain filling period (2.77, 49.65), grain yield (459.7, 1555.4) and above ground biomass (27482.9,42349), respectively. This true for phenotypic and genotypic coefficient of variation again, days to heading (12.46, 8.87), days to maturity (6.63, 3.76) and grain yield (17.91, 9.74), above ground biomass (24.97, 20.12) and grain filling period (15.79, 3.73), respectively as compared to other characters. This combined analysis over 2 location results for better heritability values on characters like tillers/plant(95.88%), plant height (96.33%), kernels per plant(87.31%) spikes per plant (96.09%) and spikelet per spike (86.44%) (Table 8).

DISCUSSION

The positive and significant values of analysis of variance at both locations explain the presence of adequate genetic variability for those traits. Genotypic covariance, phenotypic covariance and environmental covariance is considered as baseline for explanation of a certain trait expression among yield and yield related traits. So, covariance is the differences visible between 2 characters which implied that whether 2 related characters tend to vary together or variation occurring simultaneously in 2 variables in the case of quantitative traits in bread wheat. Analysis of variance for this finding was in agreement with the study of Arya *et al.*[11] for tillers/plant, plant height, spikelet per spike, spike length, spikes per plant, days to heading, grain yield and above ground biomass.

The highest values of environmental and phenotypic variances were recorded from above ground biomass and grain yield in both locations and indicated that these traits are more influenced by environmental factors. This result was supported by Fikre *et al.*[12]. The previous authors reported that the highest genotypic variance 254880.20 and 205431.80 and phenotypic variance 1396847.80 and 492513.68, environmental variance 2283935.0 and 574163.7 were recorded for above ground biomass and grain yield,

respectively. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation in all characters since phenotypic coefficient of variation is a product of environmental and genetic variability. Non-significant difference between genotypic coefficient of variation and phenotypic coefficient of variation for tillers/plant, plant height, spike length and days to heading indicated that the environmental effect was small for the expression of this trait. The result in this study was in agreement with the study of Kumar *et al.*[13]. They recorded that PCV (7.45) and GCV (7.38) for days to heading, PCV (14.85) and (14.78) for plant height, PCV (20.6) and GCV (19.03) for tillers/plant as well as PCV (13.2) and GCV (11.93) for spike length.

The key point for plant breeder during the choice of good quality crop from the given diversity is that heredity of the trait. However, traits cannot inherit directly from parent to offspring instead the gene that determines the trait can be inherited. Therefore, estimates of heritability helps for plant breeders to screen out superior genotypes from diverse genetic population and also gives good direction to know heredity of the given genetic materials. According to researchers, the value of heritability of a trait and selection for such traits has direct relationship[14]. It is to mean that if the heritability of a trait is high selection is simple and the reverse is true if heritability is low due to the effect of environmental influence. The high heritability along with high genetic advance suggested that the genotypic variation for the trait is probably attributed to high additive genetic effects[15] and such trait is least influenced by environmental effect. Besides this, the association of heritability with genetic advance would be more reliable than heritability alone for the selection of good quality seed in plant breeding, that why breeding is an art. In genetics, heritability is the proportion of phenotypic variation in a population that is due to differences among organisms. Variation among individuals may be due to genetic and/or environmental factors. According to Johnson *et al.*[9], effectiveness of selection depends not only on heritability but also on Genetic Advance (GA).

Generally, the expression of a character for each component depends on a sum of gene and environment. This contributed for the variation of each character from each other. Heritability can be classified as low, moderate and high according to Johnson *et al.*[16]. The 0-30%:Low 30-60%:Moderate 60% and above:High. However, heritability can be 2 types. These are broad sense and narrow sense. Heritability in "broad sense "refers to the ratio of genotypic variance to the total phenotypic variance. The "narrow-sense" heritability (h^2) is a technical statistical parameter. Instead of

including all genetic variation, it only includes additive genetic variation. Those traits with high heritability as indicated in the result part implies that these traits are mainly controlled by additive type of genes and direct selection for these traits could be effective. It also indicated that selection for these traits would be fairly easily[16]. They were reported that high heritability for spikelet per spike (86%), days to heading (84%), plant height (84.5%), above ground biomass (93%) and also they reported that nearly similar low heritability results for days to maturity (17) and (16%) in this case. The author reported exactly similar and higher heritability result of plant height (88.43%) which supported result of this study which was recorded as 88.4% for plant height[17]. The highest heritability of tillers/plant (85.6) was exactly similar with the study of which recorded values of tillers/plant (85.5) in their study[18].

The explanation of quantitative character which is the main concern for yield and yield related traits depends on the cause of the formation of new species and heredity of the trait. Estimation of genetic variability in crop improvement is considered as effective if the heritability of expected genotype is high. Characters which have got acceptable genetic variability in collaboration with environmental variation is the main target for the concept of heritability and it is necessary to identify the components that create the phenotypic variation in order to estimate the genetic variability and heritability based on that variation. Heritability estimated provide an indication of the expected response to selection in a segregating population and they are useful tools in designing an effective breeding program[7]. If heritability of a trait is very high, selection for such traits could be fairly easy. But, for traits with low heritability, selection may be considerably difficult due to the masking effect of the environment. The high heritability along with high genetic advance suggested that the genotypic variation for the trait is probably attributed to high additive genetic effects[15] and such trait is least influenced by environmental effect. Plant breeder can be confident enough when selection is performed based on heritability in conjunction with genetic advance. High heritability which is supported by moderate and high genetic advance indicated that most likely the heritability of these characters is due to additive gene effects and selection might be effective for these characters. The highest heritability of tillers/plant (86.24) and plant height (87.4) in this study was in harmony with those obtained by researchers with values tillers/plant (85.6) which is nearly similar and plant height (96) categorized as the highest just like the values (87.4) in this study[19].

Those characters that had greater values of phenotypic variance and phenotypic co coefficient of variation in the result part tell us environmental influence were high on that trait. So, attention shifted to the rest traits with almost similar values of genotypic variation and phenotypic variation. From the result of combined analysis mean square due to error is reduced as compared to those single locations. Higher values of heritability above 90 and better than the single location were observed from combined analysis over 2 locations. This reality speaks about phenotypic variability works become sufficient when it is performed more than one location. The lowest heritability values on grain yield and grain filling period explains that since those traits are controlled by polygenic inheritance its diminished value is not surprising.

CONCLUSION

The range and mean of agronomic traits obtained in this study indicated that there is sufficient variability in bread wheat accessions. The combined analysis over two locations assures that multiple locations were preferable in genetic variability works. The analysis of variance also revealed that there is sufficient variability among the 64 samples. The heights heritability coupled with heights, genetic advance and genetic advance as present of mean were obtained from tillers/plant, plant height, spikes per plant and above ground biomass at both locations. Hence, selection for these traits may be relatively safe and great emphasis should be given to this traits. Based on this study it could be more appropriate if the study is repeated in different seasons and more locations. It should be again in doing by using molecular markers.

SIGNIFICANCE STATEMENT

The study provides ground information about genetic variability of Ethiopian bread wheat accessions within yield and yield related traits collected from different bread wheat growing regions of Ethiopia for performance of good quality seed. It is also vital for further research as a base line in the study area.

REFERENCES

1. Tefera, A., 2012. Grain and feed annual report. Grain Report No. ET1201, April 18, 2012. Addis Ababa, Ethiopia.
2. CSA., 2012. Agricultural sample survey. Report on Area, Production and Yield of Meher Season Crops for Private Peasant Holdings. Statistical Bulletin 578, Central Statistical Agency, Addis Ababa, Ethiopia.

3. Govindaraj, M., M. Vetriventhan and M. Srinivasan, 2015. Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. Genet. Res. Int., Vol. 2015. 10.1155/2015/431487.

4. Larik, A.S, A.A. Kakar, M.A. Naz and M.A. Shaikh, 1999. Estimating genetic parameters in bread wheat (*Triticum aestivum* L.) crosses. Sarhad J. Agric., 15: 230-204.

5. Ferdous, M.F., A.K.M. Shamsuddin, D. Hasna and M.M.R. Bhuiyan, 2010. Performance and variability for yield and yield contributing characters in spring wheat. J. Bangladesh Agric. Univ., 8: 195-197.

6. Yasmin, S., M.S. Islam, K.M. Nasiruddin and M.S. Alam, 2006. Molecular characterization of potato germplasm by random amplified polymorphic DNA markers. Biotechnology, 5: 27-31.

7. Burton, W.G. and E.H. Devane, 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J., 45: 478-481.

8. Allard, R.W. and P.E. Hansche, 1964. Some parameters of population variability and their implications in plant breeding. Adv. Agron., 16: 281-325.

9. Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Genotypic and phenotypic correlations in soybeans and their implications in selection. Agron. J., 47: 477-483.

10. Gomez, K.A. and A.A. Gomez, 1984. Statistical Procedures for Agricultural Research. 2nd Edn., John Wiley and Sons, New York, ISBN: 0-471-87931-2, pp: 680.

11. Arya, V.K., J. Singh, L. Kumar, R. Kumar, P. Kumar and P. Chand, 2017. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). Indian J. Agric. Res., 51: 128-134.

12. 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.

13. Kumar, B., G.M. Lal, Ruchi and A. Upadhyay, 2009. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). Asian J. Agric. Sci., 1: 4-6.

14. Singh, T.P. and K.B. Singh, 1973. Association of grain yield and its components in segregating populations of green-gram. Indian J. Genet., 33: 112-117.

15. Panse, V.G., 1957. Genetics of quantitative characters in relation to plant breeding. Indian J. Genet., 17: 318-328.

16. Johnson, H.W., R.F. Comstock and P.H. Harvey, 1951. Genotypic and phenotypic correlations in corn and their implications in selection. Agron. J., 43: 282-287.

17. Rahman, M.A., M.L. Kabir, M. Hasanuzzaman, R.H. Rumi and M.T. Afrose, 2016. Study of variability in bread wheat (*Triticum aestivum* L.). Int. J. Agric. Res., 8: 66-76.

18. Bhuri, S. and P.K. Upadhyay, 2013. Genetic variability, correlation and path analysis in wheat (*Triticum aestivum* L.). Int. J. Plant Sci., 8: 230-235.

19. Kalimullah, S.J. Khan, M. Irfaq and H.U. Rehman, 2012. Gentetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. J. Anim. Plant Sci., 22: 330-333.