



# Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.) Genotypes in Southwestern Ethiopia

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## ABSTRACT

Forty-nine bread wheat genotypes were studied under rainfed conditions at three locations namely, Chena, Masha and Shey Bench, each of varied agroecologies in southwestern Ethiopia during 2017 and 2018 with the objective of estimating their genetic variability, heritability and genetic advance using 7x7 simple lattice design. Data were collected for 12 agronomic characters. The analyses of variance showed highly significant differences ( $p < 0.01$ ) among wheat genotypes for all traits studied in all the locations except for the number of effective tillers per plant at Chena and biomass yield at Masha wherein genotypes had significant differences only at  $p < 0.05$  level and the number of spikelets per spike at Shey Bench wherein genotypes had expressed a non-significant difference. The phenotypic coefficients of variation (PCV) were relatively greater than those of genotypic coefficients of variation (GCV) for most of the characters studied at all the three locations; however, the magnitudes of the differences were relatively high for the number of tillers, number of kernels per spike, biomass yield and grain yield. High heritability coupled with moderate genetic advance (as percent of mean) were observed for days to heading, days to maturity, spike length and grain filling period at all locations. Therefore, any improvement of these characters would result in a substantial increment in grain yield in regions of southwestern Ethiopia which are otherwise rich in natural resources but poor in their efficient utilization.

**Keywords:** Bread wheat, GCV, genetic advance, heritability, PCV, variability

## Introduction

Bread wheat (*Triticum aestivum* L.), a self-pollinating annual plant, is the largest cereal crop extensively grown as staple food sources in the world (Mollasadeghi *et al.*, 2011) which accounts for 20% of nutritional sources of the people (Khabiri *et al.*, 2012). It provides nearly 55% of carbohydrates, 20% of the daily protein and 21% calories for about 40% of the global population (Khan and Naqvi, 2012). An estimated 1.2 billion poor people depend on wheat, a crop that is particularly vulnerable to climate change (USDA, 2017). To meet this demand, it was estimated that global wheat grain production must increase by 2% annually till 2050 (Rosegrant and Agcoili, 2010). However, the current trend shows lower rates of wheat yield increases (0.9% per year) which may result in no change to the per capita wheat harvest by 2050. World wheat production in 2017 was 743.2 million tons with average yield of 3.34 t ha<sup>-1</sup> accounting for nearly 30% of global cereal production (FAO, 2017a,b).

Ethiopia is the second largest wheat producer in sub-Saharan Africa and it is cultivated on 1.7 million hectares of land with the production of 4.54 million tons and productivity of only 2.67 t ha<sup>-1</sup> (CSA, 2017) as compared to the world average yield of 3.34 t ha<sup>-1</sup> (FAO, 2017a,b). Wheat production self-sufficiency is only 75% and the remaining 25% of wheat is imported and also obtained through food aid. However, cereal consumption has been increasing by 20% in recent years, making it the second most consumed cereal in Ethiopia after corn (USDA, 2017). Although the productivity of wheat has increased in the last few years in Ethiopia, it is still very low as compared to other wheat producing countries. The low yield productivity is attributed to many factors, such as unavailability of quality seed of varieties that are high yielding as well as adapted to wide range of agro-ecologies of the country. Hence, the first step in the development of varieties is assessing the genetic variability of available genotypes for the characters of agronomic interest (Rahman *et al.*, 2016).

The knowledge of genetic variability and the extent of variations among genotypes in a population are essential not only for selection of better genotypes but they also help in designing crop improvement through combination breeding. In addition, genetic improvement to develop varieties with high yield potential and tolerance to abiotic and biotic stresses, with acceptable end use quality, is the viable and environmentally-friendly option to sustainable increase in

wheat yield. Despite Bench Shako, Kaffa and Sheka Zones being potential wheat-producing areas in southwestern Ethiopia, the potential of the area for wheat crop is not exploited due to the lack of improved varieties and detailed information on the extent of adaptability and production status of the improved bread wheat varieties in the area (CSA, 2012). The present study was, therefore, conducted with the objectives of quantifying the variability, estimating heritability and genetic advance among genotypes of bread wheat for yield and yield-contributing characters.

## Materials and Methods

### *Experimental materials*

Experimental materials comprised forty-nine bread wheat genotypes released from different agricultural research centers of the country (Table 1).

### *Description of the study area*

The experiments were conducted in Chena, Masha and Shey Bench woredas (districts) of Bench Bonga, Sheka and Shako zones, respectively (Table 2).

### *Experimental design and management*

The experiment was laidout in 7x7 simple lattice design. Each genotype was planted in a plot consisting of six rows of 2.5 m long and 1.2 m wide with spacing of 20 cm between rows. The distances between plots, blocks and replications were 0.5, 0.5 and 1.5 m, respectively. A seed rate of 150 kg ha<sup>-1</sup> and fertilizer rate of 100 kg ha<sup>-1</sup> containing NPS were used. Weeding and other agronomic practices were carried out as per recommendations of the respective sites.

### *Data collection*

Ten randomly selected plants from the four central rows of each plot were used for data collection. Data on days to 50% heading, days to physiological maturity, plant height, productive tillers per plant, number of kernels per spike, number of spikelets per spike, spike length, grain yield, biomass yield and harvest index were collected.

### *Statistical analysis*

The mean values of the genotypes were subjected to analysis of variance based on triple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS 9.3 (SAS, 2011) after testing the ANOVA assumptions. Mean separations were estimated using least significant difference (LSD) test at 5% and 1% levels of significance.

### *Estimation of variance components and associations*

Genotypic and phenotypic coefficients of variability were computed according to Burton and Devane (1953) :

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

$$\text{Environmental coefficient of variability (ECV)} = \frac{\sqrt{\sigma^2_e}}{\bar{x}} \times 100$$

Where,  $\sigma^2_g$  = Genotypic variance,  $\sigma^2_p$  = Phenotypic variance,  $\sigma^2_e$  = Environmental variance and  $\bar{x}$  = General mean of character.

Heritability (broad-sense heritability) was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Falconer and Mackay, 1996) :

$$h^2_B = \frac{V_g}{V_p} \times 100$$

Where,  $h^2_B$  = Heritability,  $V_g$  = Genotypic variance,  $V_p$  = Phenotypic variance

Genetic advance (GA) in absolute unit and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated according to Johnson *et al.* (1955) :

$$GA = K \sigma_p h^2$$

$$GAM = (GA / \bar{x}) \times 100$$

Where, K= Intensity of selection at 5% (K= 2.06, K is selection differential),  $\sigma_p$ = Phenotypic standard deviation,  $h^2$ = Heritability,  $\bar{x}$ = General mean of the character.

Table 1. Wheat genotypes used in the study.

S.N	Entry / variety	Source center	Year of release
1	Ogolcho	Kulumsa	2012
2	Hoggana	Kulumsa	2011
3	Hulluka	Kulumsa	2012
4	Mekelle-3	Mekelle	2012
5	Mekelle-4	Mekelle	2013
6	Shorima	Kulumsa	2011
7	Mekelle-1	Mekelle	2012
8	Mekelle-2	Mekelle	2011
9	Ga'ambo	Werer	2011
10	Kekeba	Kulumsa	2010
11	Danda'a	Kulumsa	2010
12	Gassay	Adet	2007
13	Alidoro	Holleta	2007
14	Dagelu	Kulumsa	2005
15	Tay	Adet	2005
16	Sofumar	Sinana	1999
17	Mada-Wolabu	Sinana	1999
18	Pavon-76	Kulumsa	1982
19	Jefferson	Kulumsa	2012
20	King Bird	Kulumsa	2014
21	Enkoy	Holeta	1974
22	DERESELGNE	Deberzeit	1974
23	K6290-Bulk	Kulumsa	1977
24	K6290-Bulk	Kulumsa	1980
25	Et-13 A2	Holetta	1981
26	Dashen	Holetta	1984
27	Mitike	Kulumsa	1993
28	Kubsa	Kulumsa	1994
29	Galama	Kulumsa	1995
30	Tusi	Kulumsa	1997
31	Katar	Kulumsa	1998
32	Hawi	Kulumsa	1999
33	Sirbo	Kulumsa	2001
34	Doddota	Kulumsa	2001
35	Bobicho	Kulumsa	2002
36	Meraro	Kulumsa	2005
37	Millinium	Kulumsa	2007
38	Honqolo	Kulumsa	2014
39	Mandoye	Sinana	2014
40	Sanate	Sinana	2014
41	Wane	Kulumsa	2016
42	Bollo	Kulumsa	2009
43	Menze	DaberBeran	2007
44	Dinkinesh	Sinana	2007
45	Kulkulu	Holetta	2009
46	Batu	Holetta	1984
47	KBG-01	Kulumsa	2001
48	Hidase	Kulumsa	2012
49	Biqa	Kulumsa	2014

Table 2. Description of testing locations.

Location	Altitude (m.a.s.l*)	Average rainfall (Min/Max)	Average temp. (Min/Max)	Global position	
				Latitude	Longitude
Shey Bench	1400-2485	1547-2000 mm	22-29°C	5 <sup>0</sup> 30' - 7 <sup>0</sup> 00''N	34 <sup>0</sup> 00'' - 36 <sup>0</sup> 00''E
Chena	500-3350	1600-2200 mm	18-21°C	6 <sup>0</sup> 24' - 7 <sup>0</sup> 70' N	35 <sup>0</sup> 69' - 36 <sup>0</sup> 78' E
Masha	1900-2750	1800-2200 mm	12-29 °C	7 <sup>0</sup> 24' - 7 <sup>0</sup> 52' N	35 <sup>0</sup> 13' - 35 <sup>0</sup> 35'E

\* m.a.s.l= Meter above sea level

## Results and Discussion

The analysis of variance showed highly significant differences ( $p < 0.01$ ) among wheat genotypes for all the traits studied in all locations except for the number of effective tillers at Chena, biomass yield at Masha wherein genotypes had significant differences only at  $p < 0.05$  level of significance and the genotypes had shown a non-significant difference for the number of spikelets per spike at Shey Bench (Table 3). Significant genetic variation among genotypes for the studied characters suggests that ample scope of selection for different quantitative characters exists for the improvement of wheat crop. By analogy, a number of workers have also reported significant differences among wheat genotypes for yield and yield-related traits for most of the characters studied in our experiment (Alemu, 2016; Kifle *et al.*, 2016a,b; Birhanu *et al.*, 2017a,b; Obsa *et al.*, 2017).

Table 3. Mean squares for 12 characters of 49 bread wheat genotypes at three experimental sites.

Trait	Locations											
	Chena				Masha				Shey Bench			
	MSG	MSE	Mean	CV	MSG	MSE	Mean	CV	MSG	MSE	Mean	CV
DH	114.78**	5.25	69.35	4.36	123.83**	4.09	71.62	3.75	129.25**	6.34	67.35	9.31
DM	156.48**	4.64	132.9	5.89	159.58**	7.69	135.2	5.28	162.5**	5.86	129.4	8.84
GFP	46.06**	5.12	61.65	3.57	47.24**	5.82	63.98	2.96	53.25**	6.28	59.36	6.52
PH	112.21**	1.52	92.5	6.37	92.85**	16.24	95.4	7.76	118.85**	19.32	96.18	8.32
NT	1.79*	0.78	2.32	11.03	2.28**	0.15	1.56	10.4	2.18**	0.09	1.21	13.98
NGS	79.14**	12.09	47.65	4.8	83.89**	23.44	45.33	4.19	53.89**	21.25	39.56	7.75
NSS	6.95**	0.92	15.62	8.92	3.92**	0.91	14.15	8.31	1.45 <sup>ns</sup>	0.98	13.25	8.87
SL	3.82**	0.45	10.25	5.14	2.27**	0.23	8.95	4.53	2.97**	0.19	7.25	8.09
TKW	61.84**	0.43	34.63	5.64	35.69**	7.02	34.1	5.03	29.63**	8.24	28.45	7.91
BMV	2.21**	0.762	9.86	14.96	1.77*	1.26	9.29	14.3	2.57**	1.18	7.62	16.59
HI	78.15**	0.51	45.62	10.26	61.62**	35.54	43.49	11.6	49.26**	6.91	38.95	13.21
GY	2.39**	0.21	3.85	12.75	2.27**	0.25	3.75	12.1	2.18**	0.12	2.86	15.7

\*, \*\* Significant at  $p \leq 0.05$  and  $p \leq 0.01$  probability levels, respectively and ns= non-significant, MSG= Mean squares of genotypes, MSE= Mean squares of error, CV= Coefficient of variation, DH= Days to heading, DM= Days to maturity, GFP= Grain filling period, PH= Plant height, NT= Number of productive tillers per plant, NGS= Number of grains per spike, NSS= Number of spikelets per spike, SL= Spike length, TKW= Thousand-kernels weight, BMV= Biomass yield, HI= Harvest index, GY= Grain yield ( $t ha^{-1}$ ).

Further, the genotypes showed a considerable mean and range variations for each studied characters across locations. The mean grain yield of the genotypes ranged from 2.69-4.18 t ha<sup>-1</sup>, 2.94-4.93 t ha<sup>-1</sup>, and 2.19-4.23 t ha<sup>-1</sup> with a mean value of 4.01 t ha<sup>-1</sup>, 3.95 t ha<sup>-1</sup> and 3.06 t ha<sup>-1</sup> at Chena, Masha and Shey Bench, respectively (Table 4; top, middle, bottom). The range and mean values suggest the existence of sufficient variability among the tested genotypes for the majority of the characters providing ample scope for selecting superior and desired genotypes for further improvement of bread wheat in the study areas.

### ***Estimates of variance components***

The results of statistical analyses for the studied characters have been presented in Table 4. Phenotypic coefficients of variation (PCV) ranged from 6.75% for days to maturity to 28.97 % for grain yield and genotypic coefficient of variability (GCV) ranged from 6.55 % to 25.43% for the same character, respectively at Chena. At Masha, PCV value ranged from 6.75% for days to physiological maturity to 26.54%, for the number of productive tillers/plant and GCV ranged from 5.44% for biomass yield to 21.28 % for grain yield. At Shey Bench, PCV ranged from 7.08% for days to physiological maturity to 36.67% for the number of productive tillers/plant, while GCV ranged from 3.66% for the number of spikelets per spike and 26.85% for the number of productive tillers/plant.

Among the characters under study the lowest PCV (6.76%, 6.76% and 7.09%) and GCV (6.75%, 6.45% and 6.84%) values were recorded for days to maturity and, plant height (8.16%, 7.74% and 8.64) and (8.05%, 6.49% and 7.33%) and grain filling period (8.21%, 8.11% and 9.19%) and (7.34%, 7.17% and 8.16%) at Chena, Masha and Shey Bench, respectively. In addition, biomass yield at Chena and Masha and the number of spikelets per spike at Masha and Shey Bench exhibited low GCV and PCV values. The results indicate that the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for improvement of these characters by direct selection of high performing genotypes. This is in agreement with the reports of Kifle *et al.* (2016a,b) and Berhanu *et al.* (2017a,b).

In general, the PCV were relatively greater than those of GCV for most of the characters at all the locations, however, the magnitudes of the difference were small for days to heading, days to maturity, grain filling period, spike length, thousand-seed weight, plant height and harvest index (Table 4). This suggests that the marked influence of



environmental factors for the phenotype expression of genotypes was low and the chances of improvement of these traits through selection of genotypes based on the phenotype would be higher. The magnitude of difference between PCV and GCV was relatively high for the number of tillers, number of kernels per spike and biomass yield. This implies greater influence of environmental factors for the phenotypic expression of these characters that makes difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the characters. These results are in close agreement with the findings of several workers (Desalegn and Kumar, 2016; Kifle *et al.*, 2016a,b; Berhanu *et al.* 2017a,b). The results obtained also revealed moderate GCV and PCV indicating that there is still some possibility for the improvement of the characters.

Table 4. Estimates of ranges, mean, phenotypic and genotypic variances, phenotypic and genotypic coefficients of variations (PCV and GCV), heritability (broad-sense heritability) and genetic advance for 12 characters of 49 bread wheat genotypes tested at three locations.

Chena site										
Traits	Range	Mean	$\sigma^2_e$	$\sigma^2_g$	$\sigma^2_{ph}$	PCV(%)	GCV(%)	H <sup>2</sup> (%)	GA	GAM(%)
DH	54.5-81.5	69.35	5.25	54.77	60.02	11.17	10.67	91.25	14.56	21.00
DM	108-143	132.85	4.64	75.92	80.56	6.76	6.56	94.24	17.42	13.12
GFP	57.85-74.65	61.65	5.12	20.47	25.59	8.21	7.34	80.00	8.34	13.52
PH	83.5-120.35	92.45	1.52	55.35	56.87	8.16	8.05	97.33	15.12	16.35
NT	2.3-5.9	4.26	0.92	0.45	1.36	27.32	15.48	32.10	0.77	18.07
NGS	44.75-59.25	47.65	12.09	33.53	45.62	14.17	12.15	73.50	10.23	21.46
NSS	13-18	15.62	0.92	3.02	3.94	12.70	11.12	76.62	3.13	20.04
SL	7.6-13.56	10.25	0.45	1.69	2.14	14.26	12.66	78.92	2.38	23.18
TKW	28.02-48.08	34.63	0.43	30.71	31.14	16.11	16.00	98.62	11.34	32.73
BMV	6.56-11.58	9.86	0.76	0.72	1.49	12.36	8.63	48.72	1.22	12.41
HI	27.68-61.49	45.62	0.51	38.82	39.33	13.75	13.66	98.70	12.75	27.95
GY	2.69-4.18	4.01	0.21	1.04	1.35	28.97	25.43	77.04	1.84	45.98

  

Masha site										
Traits	Range	Mean	$\sigma^2_e$	$\sigma^2_g$	$\sigma^2_{ph}$	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GA	GAM(%)
DH	55.25-82.5	71.62	4.09	59.87	63.96	11.17	10.80	93.61	15.42	21.53
DM	108.75-144	135.2	7.69	75.95	83.64	6.76	6.45	90.81	17.11	12.65
GFP	58.6-76	63.5	5.82	20.71	26.53	8.11	7.17	78.06	8.28	13.04
PH	84.25-123.25	95.4	16.24	38.31	54.55	7.74	6.49	70.23	10.68	11.20
NT	2.05-5.65	4.56	0.65	0.82	1.47	26.54	19.80	55.63	1.39	30.42
NGS	39.5-60	45.33	23.44	30.23	53.67	16.16	12.13	56.32	8.50	18.75
NSS	13.75-18.75	14.15	0.91	1.51	2.42	10.98	8.67	62.32	2.00	14.10
SL	8.35-14.30	8.95	0.23	1.22	1.45	13.45	12.34	84.14	2.09	23.32
TKW	28.77-48.85	34.1	7.02	14.34	21.36	13.55	11.10	67.13	6.39	18.74
BMV	7.31-12.45	9.29	1.26	0.26	1.52	13.25	5.44	16.83	0.43	4.59
HI	28.43-62.24	43.49	3.54	29.04	32.58	13.12	12.39	89.13	10.48	24.10
GY	2.94-4.93	3.95	0.15	0.71	0.86	23.43	21.28	82.49	1.57	39.82



## Shey Bench site

Traits	Range	Mean	$\sigma^2_e$	$\sigma^2_g$	$\sigma^2_p$	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GA	GAM(%)
DH	54-80.75	67.35	6.34	61.46	67.80	12.23	11.64	90.65	15.38	22.83
DM	107.5-135.25	129.5	5.86	78.32	84.18	7.09	6.84	93.04	17.58	13.58
GFP	57.35-72.9	59.36	6.28	23.49	29.77	9.19	8.16	78.90	8.87	14.94
PH	83-118.6	96.18	19.32	49.77	69.09	8.64	7.33	72.03	12.33	12.82
NT	1.8-3.75	3.25	0.66	0.76	1.42	36.69	26.85	53.57	1.32	40.48
NGS	37.3-44.25	39.56	21.25	16.32	37.57	15.49	10.21	43.44	5.48	13.86
NSS	12.5-16.25	13.25	0.98	0.24	1.22	8.32	3.66	19.34	0.44	3.31
SL	7.1-10.81	7.25	0.19	1.39	1.58	17.34	16.26	87.97	2.28	31.42
TKW	27.52-42.33	28.45	8.24	10.70	18.94	15.30	11.49	56.48	5.06	17.80
BMY	6.06-10.83	7.62	1.18	0.70	1.88	17.97	10.94	37.07	1.05	13.72
HI	27.18-60.74	38.95	6.91	21.18	28.09	13.61	11.81	75.40	8.23	21.13
GY	2.19-4.23	3.06	0.12	0.22	0.34	19.06	15.33	64.71	0.78	25.40

Where,  $\sigma^2_e$ = Error variance,  $\sigma^2_g$ = Genotypic variance,  $\sigma^2_p$ = Phenotypic variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, H<sup>2</sup>= Broad-sense heritability, GA= Genetic advance, GAM (%)= Genetic advance as percent of mean, DH= Days to heading, DM= Days to maturity, GFP= Grain filling period, PH= Plant height, NT= Number of tillers per plant, NGS= Number of grains per spike, NSS= Number of spikelets per spike, SL= Spike length, TKW= Thousand-kernel weight, BMY= Biomass yield, HI= Harvest index, GY= Grain yield (t ha<sup>-1</sup>).

Similar results depicting closer values of the PCV to the GCV estimates for most characters thereby showing little environmental effect on the expression of the characters (Dawit *et al.* 2012).

### Estimates of heritability (broad-sense heritability)

Heritability estimate for the 12 characters studied at three locations are shown in Table 4 (top, middle, bottom) which ranged from 32.17% for the number of productive tillers to 98.70 % for harvest index at Chena, from 16.83% for biomass to 93.63% for days to heading at Masha and from 19.34% for the number of spikelets per spike to 93.04% for days to maturity at Shey Bench, respectively.

In general, high heritability estimates were obtained for most of the characters studied at experimental locations. High estimates of heritability have been also reported by other researchers for most of these characters (Obsa *et al.*, 2017; Berhanu *et al.* 2017a,b). On the contrary, low estimates of heritability have been reported for days to heading, days to maturity and grain filling period (Kifle *et al.*, 2016a,b). However, medium estimates of heritability were obtained for biomass yield (48.72%) at Chena and for the number of productive tillers (55.63%) and the number of kernels per spike (56.32%) at Masha and for the number of productive tillers (53.57), number of kernels (43.44%) and thousand-kernel weight (56.48%) at Shey Bench. Low estimates of heritability were obtained for the number of productive tillers

(32.10%) at Chena and biomass yields (16.83% and 37.07%) at Masha and Shey Bench accompanied by the number of spikelets per spike (19.34%).

### *Estimates of genetic advance*

The present study revealed high heritability is coupled with moderate genetic advance for days to heading, days to maturity, spikelet length and grain filling period at all the locations. This indicates that it is most likely that the heritability of these characters is due to additive gene effects, and selection might be effective for these characters (Salman *et al.*, 2014; Rahman *et al.*, 2016). Salman *et al.* (2014) also reported high and moderate heritability and genetic advance for days to heading, days to maturity, and thousand-seed weight. Besides, high heritability estimates together with genetic advance were observed for grain yield at Chena, for thousand-kernel weight, harvest index and grain yield at Masha and for harvest index and grain yield at Shey Bench. A number of workers have also reported similar findings for high heritability associated with high genetic advance for grain yield and harvest index which support the present findings. (Mohammed *et al.*, 2011; Dergicho *et al.*, 2015; Berhanu *et al.* (2017a,b).

A low value for both heritability and genetic advance was computed for biomass yield at Masha and the number of spikelets per spike at Shey Bench. This suggests that the low heritability of traits due to the influence of environment limits the scope of improvement by selection. The low heritability of traits may be due to the presence of non-additive type of gene action (Ali *et al.*, 2007) and the presence of higher environmental factors along with non-additive gene action might be the possible causes for the lower values of heritability and genetic advance.

### **Conclusion**

The study results indicated the presence of wide genetic variation among wheat genotypes at all the three locations which can be exploited to develop high-yielding varieties. Therefore, there is higher chance of selecting genotypes for different quantitative traits and exploiting high yielding varieties within the study areas and similar agro-ecologies of the south western Ethiopia. The range and mean values in this study suggest the existence of sufficient variability among the tested genotypes for the majority of the characters studied which imply that there was reasonably sufficient

variability which provides ample scope for selecting superior and desired genotypes by plant breeders for further improvement of bread wheat in the study areas.

High heritability (>80%) coupled with moderate genetic advance as percent of mean (10 to 20%) was observed for days to heading, days to maturity, spikelet length and grain filling period at all locations. This indicates that it is most likely that heritability of these characters is due to additive gene effects, and selection might be effective for these characters. Therefore, direct selection for these characters, and incorporation therein of selected individual genotypes in breeding program would bring improvement in the genotypes. Thus, selection for high performance of these traits could also result in increased grain yield and those traits could be taken as selection criteria in bread wheat improvement program.

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### **Authors' Contributions**

Senior author developed concept, experimental design, conducted the experiment and collected data. Second author helped in statistical analyses and manuscript preparation.

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