

Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticumaestivum.L*) Genotypes at Gurage Zone, Ethiopia

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Abstract: In Ethiopia, a number of improved bread wheat (*Triticumaestivum L.*) varieties have been released by different research centers for the existence of genetic variability, heritability and genetic advance. However nothing has been done at Gurage Zone and therefore a total of twenty five bread wheat (*Triticumaestivum L.*) genotypes were evaluated for genetic variability, heritability and genetic advance at Gurage zone at two different environments. The genotypes were grown in randomized complete block design. Data were collected on 13 agronomic characters. Analysis of variance at each location showed highly significant ($P \leq 0.01$) difference for all characters, except harvest index at Fereziye, and harvest index and days to heading at Kotergedra. The combined analysis of variance over the two locations showed highly significant ($P \leq 0.01$) variations among the genotypes in all studied traits. The medium values of PCV and GCV were recorded from above ground biomass and tillers per plant across two locations. High estimates of heritability across a location were obtained in the case of spikelets per spike (98.06%), 1000 kernel weight (93.01%) and plant height (85.08%). Across location high values of genetic advance was obtained from above ground biomass (22.83%) and tillers per plant (21.61%).

Keywords: Wheat, Genetic Advance, GCV, PCV, Heritability

1. Introduction

Wheat, a self-pollinating annual plant in the true grass family *Gramineae (Poaceae)*, is extensively grown as staple food sources in the world [20]. It is exclusively produced under rain fed conditions in *meher* and *belg* (long and short rainy seasons), respectively.

China is the leading wheat producing country in the world with a production of 121.023, million tons or 18% of the world total. India, United States of America, France and Russian Federation follow respectively. Wheat is a strategic crop in Africa, as an essential element of food security, yet African countries spend more on importing wheat every year. North Africa is the largest wheat producing part of Africa and the production is estimated at about 20.2 million tons. Egypt

is the leading wheat producing country in Africa, Morocco, Algeria and Tunisia are the respective countries [10].

Wheat is grown at an altitude ranging from 1500 to 3000 m.a.s.l, between 6-16° N latitude and 35-42° E longitude in our country. The most suitable agro-ecological zones, however, fall between 1900 and 2700 m.a.s.l [1]. Wheat in Ethiopia is an important cereal crop and it ranks fourth in total area coverage next to teff, maize and sorghum; also fourth in total production next to maize, teff and sorghum. 4.23 million tons of wheat is produced on an area of 1.7 million ha and about 4.6 million farmers are 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. Furthermore, 47259 farmers were involved with

unestimated area coverage in Gurage Zone in 2015 main production season [7].

In Ethiopia, bread wheat improvement has started in 1949 and up to now many varieties have been released by the national and regional research institutes. However, those varieties are not widely distributed to all parts of the country. This is because of several constraints including the remoteness and inaccessibility of the growing areas that limited testing of adaptability and yields of the varieties in such areas. It is necessary to evaluate varieties for the intended growing regions since varieties are recommended as high yielding after evaluating at a few representative wheat growing areas. At Gurage Zone of South Nation, Nationality Region is one of the areas where improved varieties are not widely distributed so far, most probably due to the above indicated problems. Particularly, the potential of the area to wheat crop is not exploited due to lack of improved varieties. There is no detailed information indicating the adaptability and production status of the improved bread wheat varieties in the area. Therefore, it is important to evaluate those varieties at Gurage Zone to study the genetic variability, heritability and genetic advance since it provides information that can be utilized to improve wheat yield through breeding and to identify high yielding and more adaptable varieties to improve productivity and production of wheat.

Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised [2], [9]. Heritability in broad sense can be defined as the proportion of the total genetic variability to the total phenotypic variance [2]. Heritability estimates can be used to predict genetic advance under selection so that breeders can anticipate improvement from different types and intensities of selection. Heritability values (estimates) vary not only within the environment but also with the nature of the test population [11]. In view of this the present study was undertaken with the following specific objectives to:

- (1) Quantify the variability among genotypes for yield and yield related traits.
- (2) Estimate heritability and genetic advance among genotypes for yield and yield contributing characters.

2. Materials and Methods

2.1. Experimental Materials

Experimental materials comprised of twenty five bread

wheat genotypes released from different agricultural research centers (Table 1).

Table 1. List of Genotypes.

Entry	Variety Name	Source Center	Year of Release
1	ETBW 5879	Kulumsa	2014
2	ETBW 6095	Kulumsa	2014
3	WORRAKATTA/PASTOR	Sinana	2014
4	UTQUE96/3/PYN/BAU//MILLAN	Sinana	2014
5	Hidasse	Kulumsa	2012
6	Ogolcho	Kulumsa	2012
7	Hoggana	Kulumsa	2011
8	Hulluka	Kulumsa	2012
9	Mekelle-3	Mekelle	2012
10	Mekelle-4	Mekelle	2013
11	Shorima	Kulumsa	2011
12	Mekelle-1	Mekelle	2012
13	Mekelle-2	Mekelle	2011
14	Ga'ambo	Werer	2011
15	Kakaba	Kulumsa	2010
16	Danda'a	Kulumsa	2010
17	Gassay	Adet	2007
18	Alidoro	Holleta	2007
19	Digelu	Kulumsa	2005
20	Tay	Adet	2005
21	Sofumar	Sinana	1999
22	Mada-Wolabu	Sinana	1999
23	Pavon-76	Kulumsa	1982
24	Jefferson	Kulumsa	2012
25	King Bird	Kulumsa	2014

2.2. Experimental Design and Field Management

The genotypes were planted in early July 2015 at Wolkite University stations (Kotergedra and Fereziye) (Table 2 & Fig. 1). The genotypes were grown in randomized complete block design (RCBD) with three replications. Each plot consisted of six rows spaced 20cm X 2.5m long. The plot area was 3m² (2.5m X 1.2m). A 1.5 meter distance was maintained between replication and 50cm between plots used for both sites.

Fertilizers (both N and P₂O₅) was applied at the rate of 150 kg/ha urea and 100 kg/ha DAP at the time of planting and tillering. Seeding was done at the rate of 125Kg/ha. Seed and fertilizer was drilled uniformly by hand. Weeding and other agronomic practice was carried out as per recommendations of the respective sites.

Table 2. Location and descriptions of weather conditions for the two testing sites.

Sites	Seasonal Temperature (°C)		Soil type	Soil PH	Seasonal Rainfall (mm)	Location		
	Max	Min				Latitude	Longtiude	Altitude
Fereziye	24.37	10.2	EutricNitisols	5.4	1336.8	8.2 ⁰ N	37.9 ⁰ E	1980 masl
Kotergedra	23	8	EutricNitisols	5.7	1450	8.05 ⁰ N	37.5 ⁰ E	2600 masl

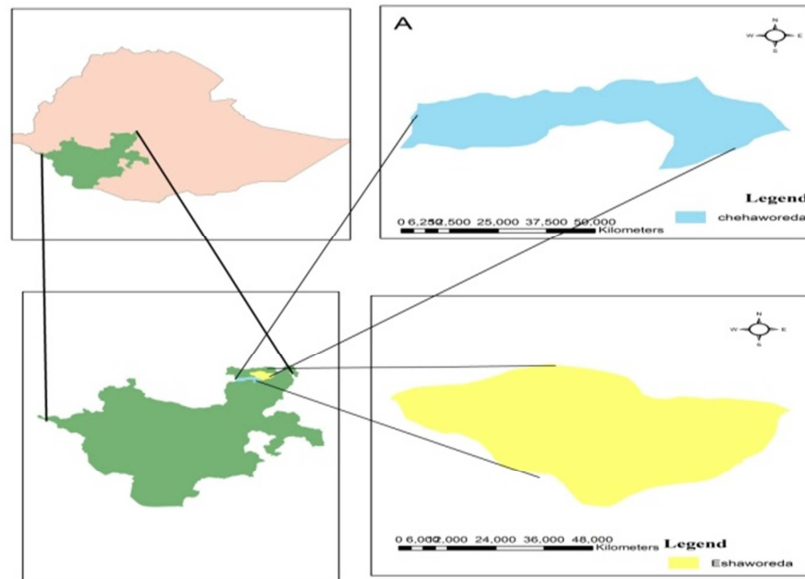


Figure 1. Geographical Map of Gurage Zone for the study area.

2.3. Data Collection

The data on the following attributes was collected on the basis of the central four rows in each plot.

1. Days to heading (DTH): The number of days from date of sowing to the stage where 75% of the spikes have fully emerged.
2. Days to maturity (DTM): The number of days from sowing to the stage when 90% of the plants in a plot have reached physiological maturity.
3. Grain filling period (GFP): The number of days from heading to maturity, i.e. the number of days to maturity minus the number of days to heading.
4. Grain yield (GY): Grain yield in grams obtained from the central four rows of each plot and converted to kilograms per hectare at 12.5% moisture content.
5. 1000-kernel weight (TKW): Weight of 1000 seeds in gram.
6. Above ground biomass (AGB): The plants within the four central rows were harvested and weighed in grams.
7. Harvest index (HI): On a plot basis, the ratio of dried grain weight to the dried above ground biomass weight multiplied by 100.

Ten plants were randomly selected from the four central rows for recording the following observations:

1. Tillers/plant (TPP): The average number of tillers
2. Plant height (PHT): The average height in cm from ground level to the tip of the spike.
3. Kernels per spike (KPS): The average number of kernels per spike.
4. Spikelet per spike (SkPS): The average number of spikelet's per spike.
5. Spike length (SL): The average spike length in cm from its base to the tip.
6. Spikes per plant (SPP): The average number fertile spikes per plant including tillers.

2.4. Data Analysis

The data were recorded were subjected to analysis by using General Linear Model procedure and the statistical package SAS version 9.1 was used for the following statistical procedures.

2.5. Analysis of Variance

The analysis of variance was conducted using randomized complete block design (RCBD). Before computing the combined analysis, error variance homogeneity test was performed using the procedure suggested by [12]. In the combined analysis of variance, locations were considered random and genotypes were considered fixed. The least significant difference (LSD) was used to compare two means at the 5% and 1% level of significance.

Analysis of variance of randomized complete block design for each test location was computed using the following mathematical model:

$$Y_{ij} = \mu + r_j + g_i + \epsilon_{ij}$$

Where: Y_{ij} = the observed value of the trait Y for the i^{th} genotype in j^{th} replication

μ = the general mean of trait Y

r_j = the effect of j^{th} replication

g_i = the effect of i^{th} genotypes and

ϵ_{ij} = the experimental error associated with the trait y for the i^{th} genotype in j^{th} replication.

Analysis of variance of randomized complete block design for combined location was computed using the following mathematical model:

$$Y_{ijk} = \mu + g_i + E_j + GE_{ij} + Bk(j) + \epsilon_{ijk}$$

Where: Y_{ijk} = observed value of genotype i in block k of location j

μ = grand mean
 G_i = effect of genotype i
 E_j = environment or location effect
 GE_{ij} = the interaction effect of genotype i with location/environment j
 $Bk(j)$ = effect of block k in location/environment j
 ϵ_{ijk} = random error or residual effect of genotype i in block k of location j
 Least significant Difference (LSD) among genotypes and coefficient of variation in percent (CV%) for all characters was computed [12].

$$LSD = \alpha (2\sigma^2 e/r)^{1/2}$$

CV% = $[(\sigma^2 e)^{1/2} / \bar{x}] \times 100$ where, α = t- value at 5% and 1% probability level.

2.6. Estimation of Genetic Parameters

The genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability was estimated as follows:

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

Where: MS_g = mean square due to genotypes,

MS_e = error mean square

r = the number of replication

Environmental variance ($\sigma^2 e$) = error mean square = MSe

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2_g + \sigma^2_e$$

Variance components for the data combined over locations were computed in a similar fashion as for individual locations by using the following formula [14], [15].

$$\sigma^2 e = MSe$$

$$\sigma^2 gl = \frac{MSgl - MSe}{r}$$

$$\sigma^2 g = \frac{MSg - MSgl}{rl}$$

$$\sigma^2 p = \sigma^2 g + \frac{\sigma^2 gl}{l} + \frac{\sigma^2 e}{rl}$$

Where: σ^2_{gl} = variance of genotype by location interaction

MSe = error mean square

$MSgl$ = genotype by location interaction mean square

MSg = genotype mean square

r = replication

l = location

Phenotypic coefficient of variation (PCV)

$$= \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

Genotypic Coefficient of variation (GCV)

$$= \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where: \bar{x} = grand mean of character

Heritability (H^2): heritability in broad sense for all characters was computed using the formula given by [9]. Broad sense heritability (h^2) expressed as a percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and was estimated on genotype mean base as described by [2] as:

$$\text{Heritability } (H^2) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where: H^2 = heritability in broad sense

σ_p^2 = Phenotypic variance

σ_g^2 = Genotypic variance

Genetic advance in absolute unit (GA) and present of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by [14] as:

$$GA = K\sigma P H^2$$

Where: K =the standardized selection differential at 5% selection intensity ($k=2.06$)

σ_p =phenotypic standard deviation on mean basis

H^2 =heritability in broad sense

Genetic advance as percent of mean was calculated to compare the extent of predicted advance of different traits under selection, using the following formula.

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

Where: GAM = genetic advance as percent mean

GA = genetic advance under selection

\bar{X} = Mean of the population in which selection employed

3. Results and Discussion

3.1. Analysis of Variance

The analysis of variance for different characters at Fereziye and Kotergedra are presented in Appendices Table A1 and A2, respectively. Genotypes differed highly significantly ($p \leq 0.01$) at Fereziye in all measured characters, except harvest index. Highly significant ($p \leq 0.01$) variation was observed for days to maturity, 1000 kernel weight, above ground biomass, plant height, kernels per spike, spikelets per spike, spike length and spikes per plant and significant ($p \leq 0.05$) variation was observed for grain filling period, grain yield and tillers per plant but non-significant variation was observed for days to heading and harvest index at

Kotergedra. [17], observed non-significant differences among bread wheat genotypes for days to maturity, spike length, fertile tillers, spikelets per spike, grains per spike and grain yield per plot in contrary to the present study. [22], reported that significant differences among genotypes for all the characters to support this result.

Before pooling of the data across environments, the ANOVA assumption was tested for its homogeneity using Bartlett test. The ratio of the highest error means square and the smallest error mean square the value was compared with the F table and, if it is significant no need of pooling across the environments [12]. Hence, the test of homogeneity of variance showed uniformity except kernel per spike, grain yield and harvest index and the data were pooled across

environments and analyzed. The results of the combined analysis of variance across the two locations are presented in Table 3. The combined analysis of variance over the two locations showed highly significant ($P \leq 0.01$) variations among the genotypes in all studied traits. However, location effects were highly significant ($P \leq 0.01$) for days to heading, days to maturity, grain filling period, above ground biomass, tillers per plant, plant height and spikes per plant.

Locations x genotype interaction was highly significant ($P \leq 0.01$), for days to heading, days to maturity, grain filling period, above ground biomass, tillers per plant, spike length and spikes per plant and plant height ($p \leq 0.05$). However significant interaction was not evident for 1000 kernel weight and spikelets per spike.

Table 3. Analysis of variance for 10 characters across the two locations.

Source	Loc (df=1)	Rep (df=2)	Genotype (df=24)	Loc*Genotype(df=24)	Error (df=98)	CV%
Days to heading	7017.80**	14.13	70.87**	68.38**	7.79	3.86
Days to maturity	40574.00**	51.81	231.04**	125.15**	17.22	3.14
Grain filling period	13843.00**	25.85	95.68**	48.82**	20.43	7.55
1000-kernel weight	8.17	7.17	67.06**	4.69	7.68	6.33
Above ground biomass	497078424.00**	3438273.50	15499552.40**	4597724.30**	1575433.00	12.43
Tillers/plant	15.68**	4.84*	9.92**	3.87**	1.03	13.69
Plant height	3864.87**	29.74	166.67**	24.86*	12.52	5.77
Spikelets per spike	0.00	0.06	12.35**	0.24	0.94	5.88
Spike length	1.06	0.37	3.95**	0.98**	0.36	7.08
Spikes per plant	23.36**	3.45*	3.20**	2.03**	0.78	12.36

*, ** Indicate significant and highly significant at the 0.05 and 0.01 probability levels, respectively

3.2. Phenotypic and Genotypic Variations

Estimated variance components, phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) of the characters studied at Fereziye, Kotergedra and combined locations are presented in Tables 4, 5 and 6 respectively.

According to [8], PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% as medium. High PCV values were observed at Fereziye for spikes per plant (29.80%), grain yield (26.61%), tillers per plant (26.33%), above ground biomass (26.03%) and kernels per spike (20.99%). Highest PCV was also reported by [18] for number of tillers (40.4%) followed by grain yield per plant (16.97%), spike length (12.99%), plant height (10.37%) and days to flowering (7.69%). The PCV values for grain filling period (13.57%), spike length (11.77%), days to heading (10.27%) and plant height (10.12%) were medium at Fereziye. Days to maturity (9.54%) and 1000 kernel weight (9.52%) had low PCV values. Spikes per plant (26.15%), grain yield (25.29%), tillers per plant (23.49%) and above ground biomass (23.13%) had higher GCV values at Fereziye. The high PCV and GCV observed indicate their high variability that in turn offers good scope for selection. [18], has reported GCV of 37% observed for tiller number per plant.

Kernels per spike (11.39%) and spike length (10.10%) had medium GCV values. Days to heading (9.67%), grain filling period (9.64%), plant height (8.86%), spikelets per spike

(8.61%), days to maturity (8.51%) and 1000 kernel weight (7.11%) had low GCV values at Fereziye. Low GCV and PCV values indicate lesser scope of selection as they are under the influence of environment. Therefore, the high values of PCV and GCV for grain yield, spikes per plant, above ground biomass and tillers per plant indicated the existence of high variability and therefore, can respond positively to selection at Fereziye. Similar result was found by [21], who reported high values of GCV and PCV recorded for tiller number and grain yield. Higher magnitudes of GCV and PCV were recorded for grain yield, biological yield, productive tillers per plant and plant height [5].

Higher PCV and GCV values were not estimated at Kotergedra. Medium PCV values on tillers per plant (19.34%), spikes per plant (19.19%), above ground biomass (17.14%), grain yield (14.75%), kernels per spike (12.46%), spike length (12.43%) and plant height (10.59%) were estimated at Kotergedra that in turn offers good scope for selection. [19], reported medium PCV and GCV obtained from plant height and kernels number per spike.

Spikelets per spike (9.66%), 1000 kernel weight (9.42%), grain filling period (7.73%) and days to maturity (3.02%) showed low PCV values at Kotergedra. Similarly [19], reported low PCV values obtained from days to heading, days to maturity, spikelets per spike, spike length and 1000 kernel weight. In the present study medium GCV values were estimated on spikes per plant (12.97%), above ground biomass (11.74%), tillers per plant (11.66%) and kernels per spike (10.89%) that in turn offers good scope for selection. Low GCV values on grain yield (9.64%), spike length

(9.54%), plant height (8.11%), spikelets per spike (7.52%), 1000 kernel weight (6.87%), grain filling period (4.79%) and days to maturity (2.11%) at Kotergedra indicating that less scope of selection as they were under the influence of environment. Similar studies by [5] reported that number of spikelets per spike, days to heading, test weight, harvest index, grain filling period and days to maturity exhibited least genotypic and phenotypic coefficients of variation.

Estimates of phenotypic coefficients of variation ranged from 9.52% (1000 kernel weight) to 29.80% (spikes per plant). The genotypic coefficients of variation also ranged from 7.11% (1000 kernel weight) to 26.15% (spikes per plant) at Fereziye. PCV value ranged from 3.02% (days to maturity) to 19.34% (tillers per plant) and the GCV values ranged from 2.11% (days to maturity) to 12.97% (spikes per plant) at Kotergedra.

For combined analysis PCV ranged from 4.69% to 17.37% and GCV ranged from 0.89% to 13.56%. With this range medium value of PCV was obtained by tillers per plant (17.37%) followed by above ground biomass (15.91%) and spikes per plant (10.21%). Low PCV values obtained from spike length (9.52%), spikelets per spike (8.69%), plant height (8.59%), 1000 kernel weight (7.64%), grain filling period (6.67%), days to heading (4.75%) and days to maturity (4.69%). Medium GCV values were obtained for tillers per plant (13.56%) and above ground biomass (13.34%). Low GCV was obtained for spikelets per spike (8.61%), spike length (8.26%), plant height (7.93%), 1000 kernel weight (7.37%), spikes per plant (6.18%), grain filling period (4.67%), days to maturity (3.18%) and days to heading (0.89%). [16], has reported low GCV obtained for days to maturity (7.91%) and this supports this result. The medium values of PCV and GCV in the case of above ground biomass and tillers per plant reveal the existence of high amount of variability in the case of these characters, so that they can respond positively to selection across a location.

3.3. Heritability

According to [23], if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to phenotype. But, for a character with low heritability, say less than 40%, and selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Estimated heritability in the case of the characters studied are presented in Tables 4, 5 and 6.

Heritability estimates are expected to be lower in poor environments where heritability is concealed due to a greater genotype x environment interaction component. Lower heritability was obtained for kernels per spike (29.45%) at Fereziye. Tillers per plant (36.34%) and grain filling period (38.37%) had lower heritability at Kotergedra and therefore there is less scope of selection in the case of such characters.

Grain filling period (50.50%), 1000 kernel weight (55.83%), spikelets per spike (68.76%), spikes per plant

(76.97%), spike length (73.65%), plant height (76.67%), tillers per plant (79.61%) and days to maturity (79.67%) had medium heritability at Fereziye. Days to maturity (48.84%), grain yield (42.74%), 1000 kernel weight (53.16%), above ground biomass (46.86%), plant height (58.57%), spikelets per spike (60.56%), spike length (58.87%), spikes per plant (45.68%) and kernels per spike (76.40%) at Kotergedra had medium heritability estimate indicating low influence of external environment. At Fereziye higher heritability values were found for grain yield (90.33%) and days to heading (88.64%) and therefore these characters show potential to respond positively to selection due to additive gene effect and low environmental influence. Similar results were obtained by [3], for higher heritability of days to heading (89.08%) and grain yield plot⁻¹ (84.64%), indicating the possibility of success in selection. Grain filling period (62.72%), days to maturity (76.17%), plant height (74.04%), number of tillers plant⁻¹ (69.23%), number of grains spike⁻¹ (68.34%) and 1000 grain weight (60.23%) showed moderately higher heritability.

Higher estimates of heritability across a location was obtained for spikelets per spike (98.06%), 1000 kernel weight (93.01%) and plant height (85.08%) indicating their potential to respond positively to selection across the locations. [19], reported high estimate of heritability obtained from plant height (98.3%). [4], [6] and [3] also reported high level of heritability for days to heading, days to maturity, grain filling period, plant height and grain yield/ plot and moderate heritability estimates for number of spikelets per spike and tillers per plant. Medium heritability was obtained for spike length (75.19%), above ground biomass (70.34%), tillers per plant (60.99%), grain filling period (48.98%) and days to maturity (45.83%). Low estimates of heritability have been obtained for spikes per plant (36.56%) and days to heading (3.51%) from the present study.

3.4. Estimates of Expected Genetic Advance

The estimated genetic advance and expected genetic advance as percent of the mean for the characters considered at Fereziye, Kotergedra and combined location are also presented in Tables 4, 5 and 6, respectively. Expected genetic advance as percent of the mean was generally medium for most characters at both locations. [8], classified genetic advance as percent of mean as low (<10%), moderate (10-20%) and high (>20%). Among the characters, the highest genetic advance as percent of mean was recorded for grain yield (49.04%), spikes per plant (46.79%), tillers per plant (42.76%), above ground biomass (41.95%) and medium genetic advance was recorded for days to heading (18.57%), spike length (17.68%), plant height (15.83%) and days to maturity (15.50%) at Fereziye. [18], reported that high genetic advance was observed for grain yield per plant (32.84%), plant height (20.35%), spike length (16.30%) and flowering day (14.36%). In the case of kernels per spike (19.42%), spikes per plant (17.88%) and above ground biomass (16.39%) it was moderately high when compared to other traits at Kotergedra. Emphasis should be given to these characters which showed high genetic advance for

formulating reliable selection indices for the development of high yielding bread wheat genotypes.

Estimates of genetic advance as percentage of mean ranged from 10.84% for 1000 kernel weight to 49.04% for grain yield at Fereziye, and from 3.01% for days to maturity to 19.42% for kernels per spike at Kotergedra. Generally, grain filling period and days to maturity at Kotergedra depicted genetic advance values lower than 10%. [3], reported high genetic advance as percent of mean for days to heading, grain filling period, number of tillers, 1000 seed weight, plant height, peduncle length and spike length in contradiction to the present study.

Across locations high values of genetic advance were obtained for above ground biomass (22.83%) and tillers per plant (21.61%). Medium genetic advance was obtained from

spikelets per spike (17.49%), plant height (14.92%), spike length (14.61%) and 1000 kernel weight (14.49%) but minimum genetic advance was obtained for spikes per plant (7.62%), grain filling period (6.66%), days to maturity (4.39%) and days to heading (0.34%). Therefore tillers per plant and above ground biomass were positively selected across different environments because of their high genetic advance. [13], has reported high genetic advance for biological yield (46.6%). [19], reported high expected genetic advance estimates for plant height, kernel number per spike, productive tillers and thousand kernel weight. According to [14], high heritability estimates along with high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone.

Table 4. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficients of variability and genetic advance as percent of mean for the 12 characters of bread wheat genotypes tested at Fereziye.

Characters	Range	Mean±SE mean	σ^2_g	σ^2_p	H ² (%)	GCV%	PCV%	GA	GA%
Days to heading	53.00-75.33	65.53±0.77	40.14	45.28	88.64	9.67	10.27	12.17	18.57
Days to maturity	101.00-135.33	115.80±1.26	97.16	121.96	79.67	8.51	9.54	17.95	15.50
Grain filling period	40.00-61.33	50.27±0.78	23.50	46.55	50.50	9.64	13.57	7.03	13.98
Grain yield	1983.30-4941.70	2941.00±86.23	515429.06	570615.87	90.33	25.29	26.61	1391.96	49.04
1000-kernel weight	35.00-50.00	43.53±0.47	9.58	17.17	55.83	7.11	9.52	4.72	10.84
Above ground biomass	4858.30-12508.30	8281.20±246.18	3676343.17	4653064.67	79.01	23.13	26.03	3476.78	41.95
Tillers/plant	5.03-12.83	7.73±0.23	3.24	4.07	79.61	23.49	26.33	3.28	42.76
Plant height	54.70-82.57	66.40±0.77	34.63	45.17	76.67	8.86	10.12	10.51	15.83
Kernels per spike	35.83-66.00	47.92±1.16	29.80	101.17	29.45	11.39	20.99	6.04	12.61
Spikelets per spike	13.53-21.30	16.50±0.19	2.02	2.94	68.76	8.61	10.38	2.40	14.56
Spike length	6.73-11.30	8.61±0.12	0.76	1.03	73.65	10.10	11.77	1.52	17.68
Spikes per plant	4.03-11.83	6.69±0.12	3.03	3.94	76.97	26.15	29.80	3.12	46.79

σ^2_g =Genotypic Variance, σ^2_p =Phenotypic Variance, H²=Heritability, GCV%=Genotypic Coefficient of Variation, PCV%=Phenotypic Coefficient of variation, GA=Genetic Advance

Table 5. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficients of variability and genetic advance as percent of mean for the 11 characters of bread wheat genotypes tested at Kotergedra.

Characters	Range	Mean±SE mean	σ^2_g	σ^2_p	H ² (%)	GCV%	PCV%	GA	GA as%
Days to maturity	142.67-156.00	148.69±0.52	9.86	20.19	48.84	2.11	3.02	4.48	3.01
Grain filling period	64.33-78.00	69.48±0.62	11.06	28.82	38.37	4.79	7.73	4.20	6.05
Grain yield	3166.70-5366.70	3742.33±64.38	130230.67	304710.67	42.74	9.64	14.75	481.28	12.86
1000-kernel weight	33.33-53.33	44±0.47	9.13	17.17	53.16	6.87	9.42	4.49	10.21
Above ground biomass	9842.00-16992.00	11922±235.29	1957369.67	4176786.67	46.86	11.74	17.14	1953.81	16.39
Tillers/plant	5.40-10.43	7.08±0.16	0.68	1.88	36.34	11.66	19.34	1.02	14.34
Plant height	46.00-66.83	56.25±0.68	20.79	35.50	58.57	8.11	10.59	7.12	12.66
Kernels per spike	44.17-70.60	53.11±0.78	33.46	43.79	76.40	10.89	12.46	10.31	19.42
Spikelets per spike	14.20-21.40	16.51±0.18	1.54	2.54	60.56	7.52	9.66	1.97	11.93
Spike length	6.87-10.07	8.44±0.12	0.65	1.10	58.87	9.54	12.43	1.26	14.93
Spikes per plant	5.30-10.27	6.75±0.15	0.77	1.68	45.68	12.97	19.19	1.21	17.88

σ^2_g =Genotypic Variance, σ^2_p =Phenotypic Variance, H²=Heritability, GCV%=Genotypic Coefficient of Variation, PCV%=Phenotypic Coefficient of variation, GA=Genetic Advance

Table 6. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficients of variability and genetic advance as percent of mean for the 10 characters of bread wheat genotypes for combined locations.

Characters	Range	Mean±SE mean	σ^2_{gl}	σ^2_g	σ^2_p	H ² (%)	GCV	PCV	GA	GA as% mean
Days to heading	64.67-78.17	72.37±0.71	20.20	0.42	11.81	3.51	0.89	4.75	0.25	0.34
Days to maturity	122.17-145.67	132.25±1.51	35.98	17.65	38.51	45.83	3.18	4.69	5.80	4.39
Grain filling period	53.67-69.5	59.87±0.93	9.46	7.81	15.95	48.98	4.67	6.67	3.99	6.66
1000-kernel weight	34.17-51.67	43.77±0.33	-1.00	10.40	11.18	93.01	7.37	7.64	6.34	14.49
Above ground biomass	7487.5-13920.8	10101.60±225.91	1007430.43	1816971.35	2583258.73	70.34	13.34	15.91	2306.19	22.83
Tillers/plant	5.62-11.63	7.40±0.14	0.95	1.01	1.65	60.99	13.56	17.37	1.60	21.61
Plant height	50.93-74.7	61.33±0.66	4.11	23.64	27.78	85.08	7.93	8.59	9.15	14.92

Characters	Range	Mean±SE mean	σ^2_{gl}	σ^2_g	σ^2_p	H ² (%)	GCV	PCV	GA	GA as% mean
Spikelets per spike	13.87-21.35	16.50±0.13	-0.23	2.02	2.06	98.06	8.61	8.69	2.87	17.39
Spike length	6.85-10.45	8.52±0.08	0.21	0.50	0.66	75.19	8.26	9.52	1.24	14.61
Spikes per plant	5.98-9.18	7.15±0.10	0.42	0.20	0.53	36.56	6.18	10.21	0.54	7.62

σ^2_{gl} = Genotype x location variance, σ^2_g =Genotypic Variance, σ^2_p =Phenotypic Variance, H²=Heritability, GCV%=Genotypic Coefficient of Variation, PCV%=Phenotypic Coefficient of variation, GA=Genetic Advance

4. Conclusions

This study generally indicated that there was significance genetic variability among the genotypes studied. Thus, there is an opportunity in selection of superior varieties among advanced bread wheat genotypes through direct selection at the study locations as short term strategy rather than a lengthy crossing program.

Abbreviation

CSA Central Statistical Agency
 FAOSTAT Food and Agriculture Organization Statistics
 GCV Genotypic Coefficient of Variation

PCV Phenotypic Coefficient of Variation
 RCBD Randomized Complete Block Design
 SAS Statistical Analysis System
 SNNP South Nation, Nationality and People

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Appendices

Table A1. Analysis of variance for 13 characters at Fereziye site.

Source	Rep (df=2)	Gen (df=24)	Error (df=48)	CV%
Days to heading	27.21**	125.56**	5.14	3.46
Days to maturity	29.64	316.28**	24.79	4.30
Grain filling period	32.69	93.56**	23.04	9.55
Grain yield (GY):	91975	1601474**	55186.81	7.98
1000-kernel weight	1.33	36.33**	7.58	6.33
Above ground biomass	668367	12005751**	976721.5	11.93
Harvest index	0.01	0.01	0.002	14.59
Tillers/plant	0.43	10.55**	0.83	11.79
Plant height	21.85	114.44**	10.54	4.89
Kernels per spike	67.57	160.77**	71.37	17.63
Spikelet per spike	0.07	6.97**	0.92	5.80
Spike length	0.35	2.54**	0.27	6.04
Spikes per plant	0.13	10.004**	0.91	14.23

*, ** Indicate significant and highly significant at the 0.05 and 0.01 probability levels, respectively

Table A2. Analysis of variance for 13 characters at Kotergedra site.

Source	Rep (df=2)	Gen (df=24)	Error (df=48)	CV%
Days to heading	2.29	13.69	10.11	4.01
Days to maturity	23.05	39.91**	10.33	2.16
Grain filling period	14.68	50.95*	17.76	6.06
Grain yield (GY):	532908	565172*	174480	11.16
1000-kernel weight	7	35.42**	8.04	6.44
Above ground biomass	3258775	8091526**	2219417	12.49
Harvest index	0.001	0.001	0.001	7.49
Tillers/plant	6.13*	3.23*	1.19	15.43
Plant height	15.65	77.08**	14.71	6.81
Kernels per spike	92.96**	110.70**	10.33	6.05
Spikelet per spike	0.06	5.62**	1.00	6.06
Spike length	0.52	2.39**	0.45	7.97
Spikes per plant	5.90**	3.21**	0.91	14.14

*, ** Indicate significant and highly significant at the 0.05 and 0.01 probability levels, respectively

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