Genetic variability and Heritability and yield related traits among Bread wheat (*Triticum aestivum* L.) Accessions in West Shewa, Central Ethiopia

Gelgu Feyisa¹, B. Chandra Sekhar Singh^{2*} and Gudeta Nepir³

 ^{1,3}Department of Plant Sciences, College of Agriculture and Veterinary Sciences, Gudar Mamo Mezemir Campus, Ambo University, Ambo, Ethiopia (East Africa)
 ²Department of Agriculture, Faculty of Agriculture, Mangalayatan University, Jabalpur - 483001 (India)
 *Corresponding author Email: <u>singhsekhar960@gmail.com</u>

Abstract

Bread wheat (Triticum aestivum L.) is a staple food crop in Ethiopia. This study aimed to assess the genetic variability, heritability, genetic advance, and identify promising bread wheat genotypes for further breeding programs. A total of 100 bread wheat genotypes were evaluated using an alpha-lattice design in Ethiopia. Analysis of variance revealed significant differences (p < 0.01) among the genotypes for all traits studied. The highest genotypic and phenotypic coefficients of variation were observed for biomass yield, productive tillers, harvest index, grain yield, and awn length, whereas low genotypic and phenotypic coefficients of variation were detected for days to heading, days to maturity, and grain-filling period. Broad-sense heritability ranged from 55.55% for flag leaf width to 96.8% for awn length, while genetic advance as a percent of mean (GAM) ranged from 7.38% for the number of days to maturity to 90.13% for awn length. Investigated, genotypes such as 31790 (58.93 qt/ha), EBW192299 (57.97 qt/ha), 33682 (56.51 qt/ ha), 34737 (55.38 qt/ha), and Acc.34159 (52.51 qt/ha) were identified as high yielders compared to other tested genotypes. This investigation highlights the importance of genetic diversity in bread wheat and emphasize the potential targeted selection in breeding programs to enhance food security and sustainable agricultural practices in Ethiopia.

Key words : Bread wheat, Genetic Variability, Heritability, Genetic Advance, Yield traits.

Wheat stands as a basic staple food crop in global agriculture¹². particularly bread wheat (*Triticum aestivum* L.), revered

as the "king of cereals" for its pivotal role in the world's food supply. Belonging to the family Poaceae, tribe Triticeae, and genus Triticum, bread wheat is an allohexaploid species characterized by 42 chromosomes and perfect flowers, facilitating high levels of self-pollination with minimal cross-pollination. Bread wheat holds a prominent position in global food grain trade, accounting for approximately 95% of worldwide wheat production¹³. In contrast, the remaining 5% is represented by tetraploid durum wheat, primarily used in pasta and semolina products²¹. Despite its importance, wheat production faces challenges in meeting increasing demand, particularly in countries like Ethiopia, where wheat is cultivated under rainfed and irrigation conditions. Although Ethiopia boasts diverse agro-ecological zones suitable for wheat cultivation, demand often outstrips supply due to factors such as population growth, urbanization, and expanding agro-industries. Consequently, there exists a significant gap between wheat production and demand in the country. Wheat serves as a major cereal crop in Ethiopia, occupying substantial land area and contributing significantly to food security and economic growth.

However, productivity levels remain relatively low compared to global averages, highlighting the need for enhanced breeding efforts and improved agronomic practices. The report on wheat production reveals that the world annual production was 765.4 million metric tons with average yield of 3.48 t/ha, and it accounts for nearly 30% of global cereal production¹¹. Wheat is occupying 1.79 million hectares of land with total production of 5.8 million tons and productivity was 3.046 t/ha in Ethiopia⁸. Addressing this disparity requires a comprehensive understanding of genetic variability and heritability among bread wheat genotypes, crucial for developing superior varieties with desirable traits such as high yield, stress tolerance, and nutritional quality. This study aims to assess the Phenotypic variability and performance of bread wheat accessions to identify promising breeding materials with desirable traits for further improvement^{1,3}.

Despite its agricultural significance, wheat productivity in Ethiopia lags behind global averages, attributed to various constraints such as limited access to improved varieties, suboptimal use of production inputs, adverse climatic conditions, and pest and disease pressures. Furthermore, there is a dearth of comprehensive information on genetic variability and heritability of yield-related traits among bread wheat genotypes, hindering effective breeding strategies and varietal development efforts. Accurate estimation of phenotypic and genotypic variability, heritability, and genetic advance is imperative for guiding breeding programs and selecting superior genotypes with desirable traits. While extensive genetic diversity exists within wheat populations, harnessing this potential requires a systematic evaluation of breeding materials to identify promising candidates for further improvement. This research aims to address this knowledge gap by conducting a thorough assessment of bread wheat genotypes, laying the groundwork for targeted breeding efforts aimed at enhancing wheat productivity and resilience in Ethiopia.

Description of the study area :

The experiment was conducted at Liban Jawi District, West Shewa Zone, Oromia Regional State of Ethiopia. Liban Jawi is located at 173 km away from Addis Ababa and 47 km from Ambo town. The altitude of

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S.	Acce-	Source	S N	Acce-	Source	S N	Accession	Source
no.	ssion	Source	5.1	ssion	Source	5.IN	Accession	Source
1	31169	Amara	35	33907	Amara	69	34737	Tigray
2	31224	Oromia	36	33909	Amara	70	34804	Amara
3	31257	Oromia	37	33911	Amara	71	34821	Oromia
4	31258	Oromia	38	33915	Tigray	72	34856	Amara
5	31296	Amara	39	33917	Amara	73	36255	Oromia
6	31394	Oromia	40	33919	Amara	74	36503	Amara
7	31395	Oromia	41	33921	Amara	75	EBW192364	KARC
8	31430	Amara	42	33924	Amara	76	EBW192398	KARC
9	31542	Oromia	43	33972	Oromia	77	EBW192299	KARC
10	31543	Oromia	44	34029	Amara	78	EBW192344	KARC
11	31600	Oromia	45	34037	Amara	79	EBW192345	KARC
12	31551	Oromia	46	34039	Amara	80	EBW192362	KARC
13	31554	Oromia	47	34043	Oromia	81	EBW192610	KARC
14	31593	Amara	48	34045	Amara	82	BW184033	KARC
15	31627	Oromia	49	34053	Oromia	83	EBW192875	KARC
16	31630	Oromia	50	34073	Amara	84	EBW192865	KARC
17	31632	Oromia	51	34086	Amara	85	EBW192348	KARC
18	31643	Oromia	52	34097	Oromia	86	EBW192489	KARC
19	31644	Oromia	53	34098	Oromia	87	EBW192872	KARC
20	31786	Amara	54	34137	Oromia	88	BWKU13383	KARC
21	31790	Amara	55	34145	Oromia	89	EBW192398	KARC
22	31813	Amara	56	34152	Amara	90	EBW194030	KARC
23	31818	Amara	57	34157	Amara	91	EBW192870	KARC
24	33206	Amara	58	34159	Amara	92	Alidoro	HARC
25	33387	Oromia	59	34161	Oromia	93	Danda,a	HARC
26	33389	Oromia	60	34169	Oromia	94	Digelu	KARC
27	33516	Amara	61	34190	Oromia	95	Enkoy	KARC
28	33556	Oromia	62	34239	SNNP	96	Hidase	KARC
29	33597	Amara	63	34280	Tigray	97	Kingbird	KARC
30	33682	Amara	64	34667	Oromia	98	Kubsa	KARC
31	33794	Amara	65	34706	Oromia	99	Ogolcho	KARC
32	33828	Amara	66	34720	Tigray	100	Wane	KARC
33	33893	Amara	67	34728	Tigray			
34	33901	Tigray	68	34735	Tigray			

Table-1. List of 100 bread wheat accessions grown in 2021

Foot Note: S.N =Serial Number, KARC=Kulumsa Agricultural Research, HARC = Holeta Agricultural Research Center the district ranges from 1800 to 3098 m.a.s.l (meters above sea level) and receives an annual rain fall of 1000 mm to 1800 mm with average temperature of 10.4-29°C. It has three different agro-climatic conditions namely high land, moderate altitude and low land constituting 27%, 65% and 8%, respectively. The dominant soil type of the test site is loamy soil with PH of 6-7.

Planting materials :

A total of hundred bread wheat accessions were grown at Liban Jawi in 2021-2022 cropping season. These bread wheat accessions were collected from different sources such as: Ethiopian Biodiversity Institute (EBI), Kulumsa Agricultural Research Center (KARC) and Holeta Agricultural Research Center (HARC). Nine released varieties (Alidoro, Dandaa, Digelu, Enkoy, Hidase, King bird, Kubsa, Ogolcho and Wane) were used as check varieties (Table-1).

Experimental Design and Trial Management:

The field experiment was conducted in a 4x25 alpha lattice design with two replications during the main rainy season in 2021. The total area, including borders, measured 18.8 m x 17 m (319.6 m2), with an effective trial area of 12.8 m x 11 m (140.8 m2). Each replication consisted of four blocks, with each block containing twenty-five plots. To minimize bordering effects, two plots were placed at the border of each block. Each plot measured 27 rows of 2 m length, with a row spacing of 0.20 m. This arrangement included twenty-five entries and two border rows per block. The width of each block was 5.4 m (0.2 m x 27), resulting in a total area of 10.8 m2 per replication. The spacing between blocks was maintained at 1 m, while the spacing between plots within a block was 0.2 m and terraces were constructed over the blocks to prevent soil erosion. Planting was performed using the hand drilling method, with seeds sown at a depth of 5 cm and a seed rate of 150 kg/ ha during the first week of July. Fertilization included the application of NPS and urea at a rate of 100 kg/ha. Urea was split into two applications: one-third at planting and two-thirds at the mid-tillering stage. Weed control was carried out manually within the experimental field.

Data collection :

Data were collected at both the plant and plot levels using random sampling techniques and descriptors for wheat¹⁴.

Plant-based Data collection :

- 1. Plant Height (cm): Measured as the distance in centimeters between the ground level and the tip of the spike (excluding awns) of ten randomly selected plants at maturity.
- 2. Number of Productive Tillers per Plant (PT): Counted as the actual number of fertile tillers on ten randomly selected plants.
- 3. Spike Length (cm): Measured from the base of the spike to the tip of the highest spikelet (excluding awns) on ten randomly selected plants at maturity.
- 4. Spikelets per Spike (SPS): Total number of spikelets on the main spike of all ten sampled plants at maturity.

- 5. Number of Kernels per Spike (KPS): Average number of seeds recorded from the ten sampled plants.
- 6. Flag Leaf Length (cm) and Width (cm): Average length and width of the uppermost leaf on ten randomly selected plants at physiological maturity.
- 7. Peduncle Length (cm): Length of the peduncle from the last node to the tip during maturity on ten randomly tagged plants.
- 8. Awn Length (cm): Length from the end of the spike to the tip of the awn measured and averaged for ten randomly tagged plants.

Plot-based Data collection :

- 1. Days to 50% Heading (DH): Number of days from sowing to when at least 50% of heads in the plot were fully exerted or flowered.
- 2. Grain Filling Period (GFP): Calculated as the difference between the number of days to maturity and the number of days to heading.
- 3. Days to 90% Maturity: Number of days from sowing to when 90% of heads in the plot were physiologically matured.
- 4. Grain Yield per Plot (g): Adjusted for moisture content and converted to quintals per hectare after threshing.
- 5. Thousand Seed Weight (g): Weight of 1000 seeds from randomly sampled seeds per plot measured using a sensitive balance.
- 6. Biological Yield or Biomass (g): Determined by weighing the total air-dried aboveground biomass of the plot and converted

to quintals per hectare.

7. Harvest Index (%): Calculated by dividing grain yield per plot by total above-ground dry biomass yield per plot and multiplying by one hundred.

Data Analysis

Analysis of Variance (ANOVA) :

All data collected were subjected to analysis of variance (ANOVA) using the general linear model (GLM) procedure of SAS statistical version 9.4 software²⁰.

Statistical model :

The analysis of variance was conducted using the following statistical model: Analysis of variance was done by means of the following model:

$Yijl = \mu + \tau i + \gamma j + \rho l (j) + \varepsilon ijl$

Where; μ is the overall (grand) mean, τ i is the effect due to the ith treatment, (i=1, 2, 3..., t), γ j is the effect due to the jth replication, and (j=1, 2..., r), ρ l (j) is block inside replicate effect, ϵ ijl is that the error term wherever the error terms, are independent observations from an approximately normal distribution with mean = 0 and constant variance $\sigma^2 \epsilon$.

Least significant Difference (LSD):

To determine significant differences in parameter means among genotypes, the least significant difference (LSD) test was employed at a probability level of 5%. This post-hoc test allows for the identification of significant differences between pairs of means.

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SV	DF	Mean square	F values	Expected mean square
Replication(r)	r-1	Msr	Msr/Mse	$\sigma_{r}^{2} + \sigma_{b}^{2} + \sigma_{g}^{2} + \sigma_{e}^{2}$
Block(rep)	r(b-1)	Msb	Msb/Mse	$r\sigma_b^2 + \sigma_g^2 + \sigma_e^2$
Genotypes(g)	g-1	Msg	Msg/Mse	$rb\sigma^2_g + \sigma^2_e$
Error	rg-rb-g+1	Mse		σ_{e}^{2}
Total	rg-1	Mst		

Table-2. Skeleton of analysis of variance table for alpha lattice design

Foot Note: SV= source of variation, DF= degree of freedom, r= number of replications, b= block, g= genotypes, Msr= mean square of replication, Msg= mean square of genotypes, Msb= mean square of block with in replication, Mse= mean square of error, Mst= mean square of total.

Estimation of Variance components :

The presence of genotypic and phenotypic variations within a crop species is crucial for initiating a breeding program. These variations were estimated to assess the extent of variability among the genotypes. The phenotypic and genotypic variability of each trait was estimated using phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic coefficients of variation were calculated following the formula proposed by Burton and Devane⁷ as follows:

Environmental variance($\sigma^2 e$)=MSe ; Genotypic variance($\sigma^2 g$) = MSg-MSe/r;

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$.

Where, $\sigma^2 g$ = genotypic variance Msg= mean square of genotype Mse= mean square of error r= number of replications $\sigma^2 e$ = Environmental variance, $\sigma^2 p$ = phenotypic variance and r= replication.

Phenotypic coefficient of variation (PCV)= $\sqrt{\sigma^2 p/x^* 100}$

Genotypic coefficient of variation (GCV)= $\sqrt{\sigma^2 g/x^*} 100$

Where, PCV represent Phenotypic coefficient of variation, GCV represent Genotypic coefficient of variation and x^- represent population average of the trait. According to Sivasubramaniah and Menon²² and GCV values were classified as high (>20%), medium (10-20%) and low (0-10%).

Estimation of Broad sense Heritability and Expected Genetic Advance :

Broad-sense heritability values were estimated using the formula adopted by Falconer and Mackay¹⁰:

$Hb2 = \sigma g 2\sigma p 2 \times 100 Hb2 = \sigma p 2\sigma g 2 \times 100$

Where:

Hb2Hb2 = heritability in broad sense

 $\sigma g 2\sigma g 2 =$ genotypic variance

 $\sigma p 2\sigma p 2 =$ phenotypic variance

According to Johnson *et al.*,¹⁵ the percentage of heritability was classified as follows: low (0-30%), moderate (30-60%), and high (>60%). Estimation of genetic advance (GA) and genetic advance as a percentage of means

(GAM) were calculated.

Genetic advance (GA) can be calculated using the formula :

 $GA = K \times \sigma p \times Hb2GA = K \times \sigma p \times Hb2$

Where:

GAGA = Genetic advance

 $\sigma p \sigma p$ = Phenotypic standard deviation on a mean basis

Hb2Hb2 = Heritability in the broad sense

KK = Standardized selection differential at 5%

selection intensity (2.063)

Genetic advance as percentage of mean (GAM)

Genetic advance as a percentage of the mean (GAM) can be estimated using the formula:

GAM=GAx⁻×100GAM=x⁻GA×100

Where:

- *GAMGAM* = Genetic advance as a percentage of the mean
- GAGA = Genetic advance
- $x^{-}x^{-}$ = Mean of the population

According to Johnson *et al.*,¹⁵ Genetic advances as a percentage of the mean (GAM) was classified as follows: low (0-10%), moderate (10-20%), and high (>20%)

Analysis of Variance (ANOVA) :

Analysis of variance (ANOVA) revealed highly significant differences (P < 0.01) among the 100 bread wheat genotypes for all the studied traits, including days to 50%

heading, days to maturity, grain filling period, plant height, spike length, spikelet per spike, kernel per spike, biomass yield, harvest index, thousand seed weight, productive tillers, flag leaf length, flag leaf width, awn length, peduncle length, and grain yield (Table-3). The results of the analysis of variance demonstrated the presence of substantial variability among bread wheat accessions for yield and its components. This variability provides breeders with an opportunity to select the best bread wheat genotypes through selection, as variability within the population is a fundamental prerequisite for a successful plant breeding program.

Several authors have also reported significant variation among bread wheat genotypes for different traits. Kali Mullah et al., ¹⁶ found a highly significant difference (P < 0.01) among forty-one bread wheat genotypes concerning days to heading, days to maturity, grain filling period, plant height. thousand seed weight, biomass yield, and grain vield. Similarly, Adhiena et al.,² observed a significant difference among 64 bread wheat genotypes for days to heading, days to maturity, grain filling period, number of tillers per plant, spike length, number of kernels per spike, thousand kernel weight, biomass yield, harvest index, and grain yield. Similarly, significant differences in days to heading, days to maturity, grain filling period, biomass yield, harvest index, thousand kernel weight, plant height, fertile tillers per plant, spike length, number of spikelets per spike, number of kernels per spike, and grain yield were reported by Birhanu et al.,^{5,6}.

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Traits	Replication	Block(rep)	Genotype	Error	\mathbb{R}^2						
	(df= 1)	(df= 6)	(df=99)	(df=9)							
DH	11.52	23.05	104.54**	4.29	96.40						
DM	95.22	61.12	55.94**	6.74	90.7						
GFP	44.18	9.25	32.45**	7.53	83.6						
FLL	36.52	14.83	22.77**	2.89	90						
FLW	0.02	0.09	0.09**	0.04	84.6						
AL	1.98	0.88	27.69**	0.45	98.6						
PEL	116.4	12.24	156.15**	20.48	89.39						
РН	2337	154.92	449.62**	51.56	91.06						
SL	12.61	1.24	3.12**	0.46	89						
SPS	8.08	3.54	5.65**	1.28	83.9						
KPS	1007.6	80.06	34.53**	22.29	88.35						
BY	1965.6	83.40	2719.9**	55.46	98.17						
HI	8.69	2.66	64.87**	3.32	95.51						
TSW	38.91	8.16	57.22**	10.02	86.64						
РТ	12.10	0.18	3.28**	0.2	94.90						
GY	212.79	4.61	225.58**	8.29	96.72						

Table-3. Analysis of variance for 16 traits of bread wheat genotypes evaluated at Liban Jawi during 2021 growing season.

Foot Note :** = highly significant at 0.01, df= degree of freedom, DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height, SL= spike length, SPS = number of spikelet per spike, KPS= number of kernels per spike, BY= biomass yield quintal per hectare, HI= harvest index, TSW= thousand seed weight, PT= productive tillers, FL= Flag Leaf length, FLW= flag leaf width, AL= awn length, PEL= peduncle length and GY= grain yield quintal per hectare.

Mean and Ranges of Bread wheat Genotypes for Studied Traits :

The descriptive statistics revealed a wide range of variations among the studied genotypes (Table-4). Particularly, there was considerable diversity observed in both days to heading and days to maturity. The range for the date of heading among genotypes spanned from 58 to 101 days, while the range for days to maturity was from 114.5 to 145 days. On average, the number of days to heading and maturity were 77.69 and 122.63 days, respectively. Some genotypes exhibited early heading, such as 34706 (58 days), EBW-192299 (60 days), and EBW192344 (61 days), while others, like 33389 (101.5 days) and 31542 (91 days), headed later. Similarly, the range for days to maturity varied widely among genotypes, with some, like EBW192362, Ogolcho, and EBW192299, maturing as early as 114.5 days, and others, such as 33389, taking as long as 145 days. Understanding days to heading and maturity is crucial, particularly in selecting genotypes for terminal stress conditions²³. This study's results are consistent with findings by Tesfay²³ *et al.* (2014), who also observed high variation among genotypes for days to heading and maturity. Yohannes *et al.*,²⁴ similarly reported a wide range of variation among bread wheat genotypes for these traits.

Additionally, the studied genotypes displayed extensive variability in spike length (5.55-14.55 cm), spikelets per spike (15.45-24.2), kernels per spike (34.15-76.2), biomass yield (36.25-243.75 qt/ha), harvest index (9.36-37.59), thousand seed weight (22.69-56.28g), productive tillers (2.1-8.4), flag leaf length (19.7-36.1), flag leaf width (1.05-1.95), awn length (0-15.58), and peduncle length (27.13-

63.2), with mean values of 9.67, 18.44, 54.14, 151.78, 21.88, 40.88, 4.99, 28.8, 1.47, 8.31, and 48.76, respectively. Furthermore, the grain yield of bread wheat genotypes exhibited wide variability (ranging from 58.93 qt/ha to 6.86 qt/ha), with a mean of 32.8 qt/ha. Some genotypes, such as 31790, EBW192299, and 33682, displayed the highest grain yields, while others, like 34667 and Ogolcho, had lower yields. These findings align with those of Alemu *et al.*,⁴ who also reported significant variation among genotypes for grain yield.

Overall, the substantial variability observed across 16 traits in the 100 bread wheat genotypes indicates ample opportunity for selecting superior and desired genotypes. The wide range of variation observed for all traits studied underscores the potential for wheat improvement through selection. These results, along with the identification of highyielding genotypes, provide valuable insights for future wheat improvement programs.

 Table-4. Mean performance genotypes for selected traits among bread wheat genotypes evaluated at Liban Jawi 2021/22.

No	Genotypes	GY	No	Genotypes	KPS	No	Genotypes	РН
1	34667	6.86	1	33389	34.15	1	EBW192344	75.57
2	Ogolcho	13.43	2	33556	39.6	2	BW184033	76.05
3	33901	13.45	3	33924	39.85	3	31543	76.16
4	Digelu	14.09	4	31813	40.05	4	EBW192364	77.23
5	34706	15.08	5	31600	40.45	5	EBW192398	77.27
6	31542	16.43	6	33919	41.45	6	EBW192345	77.55
7	33389	16.64	7	33516	41.8	7	EBW194030	77.62
8	EBW192872	16.75	8	34145	42.45	8	EBW192362	78.18
9	33556	19.21	9	Ogolcho	42.45	9	EBW192875	78.6
10	33972	19.45	10	31554	42.65	10	EBW192348	79.85

Bottom ten genotypes

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	Top ten genotypes										
1	33828	48.99	1	EBW192344	65.3	1	31542	120.75			
2	EBW192345	49.51	2	31786	66.25	2	31600	121.85			
3	King bird	51.22	3	EBW192870	67.55	3	34169	122.1			
4	Enkoy	51.97	4	EBW192364	68.75	4	34157	123.57			
5	Alidoro	52.46	5	31543	70.65	5	31813	125			
6	34159	52.51	6	EBW192348	70.75	6	31643	126.2			
7	34737	55.38	7	EBW192398	70.8	7	33915	130.8			
8	33682	56.51	8	EBW192610	71	8	34098	133.55			
9	EBW192299	57.97	9	33893	73.2	9	34856	135.48			
10	31790	58.93	10	34157	76.2	10	36255	135.5			
	Mean	32.8			54.14			104.76			
	Min	6.86			34.15			75.57			
	Max	58.93			76.2			135.5			
	CV%	8.78			6.13			6.85			
	LSD (0.05)	5.72			9.37			14.26			

Foot Note:_ GY= grain yield (qt/ha), KPS= kernels per spike, PH= plant height (cm), CV= coefficient of variation, LSD= least significance difference.

Table-5. The range and mean performance of bread wheat genotypes for 16 traits.

	Entry	Range								
Traits		Minimum	Entry	Maximum	Mean	CV(%)	LSD (0.05)			
DH	34706	58	33389	101.5	77.69	2.67	4.11			
DM	EBW192362	114.5	33389	145	122.63	2.12	5.16			
GFP	31169	37	EBW192364	57.5	44.96	6	5.45			
PH	EBW192344	75.57	31542	135.5	104.76	6.85	14.26			
SL	34667	5.55	34157	14.55	9.67	7.01	1.34			
SPS	31395	15.45	31818	24.2	18.44	6.13	2.24			
KPS	33389	34.15	34157	76.2	54.14	8.72	9.37			
BY	34667	36.25	34159	243.75	151.78	4.91	14.79			
HI	31542	9.36	EBW192348	37.59	21.88	8.33	3.62			
TSW	Ogolcho	22.69	34169	56.28	40.88	7.74	6.28			
РТ	34667	2.1	34137	8.4	4.99	8.9	0.89			
FLL	EBW192362	19.7	33597	36.1	28.8	5.91	3.38			
FLW	EBW192362	1.05	34053	1.95	1.47	12.94	0.38			
AL	34667	0	33911	15.58	8.31	8.07	1.33			
PEL	EBW192362	27.13	34169	63.2	48.76	9.28	8.99			
GY	34667	6.86	31790	58.93	32.8	8.78	5.72			

Foot Note: C.V= coefficient of variation, LSD= Least significant difference, DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height (cm), SL= spike length (cm),

SPS= spikelet per spike, KPS= kernel per spike, BY= biomass yield(qt/ha),HI=harvest index, TSW= thousandseed weight, PT= productive tillers, FLL= flag leaf length(cm), FLW= flag leaf width(cm), AL= awn length (cm), PEL= peduncle length (cm) and GY= grain yield (qt/ha).

Estimation of Phenotypic and Genotypic Variance, and environmental influence on Traits :

The evaluation of phenotypic variance $(\delta 2p)$, genotypic variance $(\delta 2g)$, and environmental variance ($\delta 2e$), alongside the computation of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and environmental coefficient of variation (ECV), offers crucial insights into the variability and the impact of genetic and environmental factors on trait expression. Table-6 presents the outcomes, revealing notable disparities between phenotypic and genotypic variances across the studied traits. Among the traits, biomass yield exhibited the highest phenotypic variance (1387.68), while flag leaf width displayed the lowest (0.09). Genotypic variances ranged from 1332.22 for biomass yield to 0.05 for flag leaf width. Generally, phenotypic variances exceeded genotypic variances for all traits, indicating a significant influence of environmental factors on trait expression.

Following Burton and Devane's⁷ classification, PCV and GCV values exceeding 20% are considered high, those between 10% and 20% are moderate, and values below 10% are low. Phenotypic coefficient of variation (PCV) ranged from 4.56% for days to maturity to 45.14% for awn length, while genotypic coefficient of variation (GCV) ranged from 4.04% for days to maturity to 44.41% for awn length. Traits such as awn length, grain yield, harvest index, productive

tillers, and biomass yield exhibited high PCV and GCV values (>20%), indicating substantial variability and potential for selection based on phenotypic performance. Conversely, traits such as days to heading, days to maturity, and grain filling period displayed low PCV and GCV values (<10%), suggesting limited scope for selection due to narrow variability. Moderate PCV and GCV values (10%-20%) were observed for traits such as number of kernels per spike, flag leaf length, spike length, thousand seed weight, plant height, and peduncle length, indicating the potential effectiveness of selection based on these traits.

The values of PCV were generally higher than those of GCV for all traits, suggesting a significant environmental influence on trait expression. However, the close proximity of PCV and GCV values suggests minimal environmental impact on phenotypic expression. Moderate ECV was observed only for flag leaf width, while all other traits exhibited minimal ECV, indicating low environmental variance. These findings underscore the importance of considering both genetic and environmental factors in wheat breeding programs and highlight traits with substantial variability and potential for selection to drive genetic improvement effectively.

Estimation of Heritability and Expected Genetic Advance in Bread Wheat Genotypes:

Heritability, delineating the inheritance of traits from parents to offspring, is a pivotal parameter in breeding programs. In our study,

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	u ans evaluated at west Shewa											
No	Trait	$\delta^2 g$	δ ² e	δ²p	GCV %	PCV %	ECV%	H ² b %	GA	GAM		
1	DH	50.12	4.29	54.41	9.11	9.49	2.66	92.11	14	18.02		
2	DM	24.6	6.74	31.34	4.04	4.56	2.11	78.49	9.05	7.38		
3	GFP	12.46	7.53	19.99	7.85	9.94	6.09	62.33	5.75	12.79		
4	РН	199.03	51.56	250.59	13.47	15.11	6.85	79.42	25.94	24.76		
5	SL	1.33	0.46	1.79	11.93	13.83	7.04	74.30	2.05	21.19		
6	SPS	2.18	1.28	3.46	8	10.08	6.13	63.00	2.41	13.07		
7	KPS	6.12	22.29	28.41	14.19	17	8.72	69.58	13.2	24.38		
8	BY	1332.22	55.46	1387.68	24.05	24.54	4.91	96.00	73.77	48.60		
9	HI	30.77	3.32	34.09	25.35	26.68	8.32	90.26	10.87	49.68		
10	TSW	23.6	10.02	33.62	11.88	14.18	7.73	70.19	8.38	20.49		
11	РТ	1.54	0.2	1.74	24.87	26.43	9.02	88.50	2.4	48.09		
12	FLL	9.94	2.89	12.83	10.9	12.44	5.90	77.47	5.7	19.79		
13	FLW	0.05	0.04	0.09	15.21	20.40	13.6	55.55	0.34	23.13		
14	AL	13.62	0.45	14.07	44.41	45.14	8.06	96.80	7.49	90.13		
15	PEL	67.83	20.48	88.31	16.89	19.27	9.27	76.80	14.88	30.52		
16	GY	108.64	8.29	116.93	32.57	32.97	8.78	92.91	20.72	63.17		

Table-6. Variance and genetic parameters of bread wheat traits evaluated at West Shewa

Foot Note :DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height, SL= spike length, SPS= spikelet per spike, KPS= kernels per spike, GY= grain yield, BY= biomass yield, HI= harvest index, TSW= thousand seed weight, PT= productive tillers, FLL= flag leaf length, FL= flag leaf width, AL= awn length, PEL= peduncle length, δ^2 g= genotypicvariance, δ^2 e = environmental variance, δ^2 p= phenotypic variance, GCV= genotypic coefficient of variation, PCV= phenotypic coefficient of variation, H²b= broad sense heritability, GA= genetic advance and GAM= genetic advance as percent of mean

we evaluated broad-sense heritability and genetic advance for 16 quantitative traits in bread wheat genotypes, providing insights into their genetic potential and suitability for selection strategies (Table-6).

The broad-sense heritability, classified as low (0-30%), moderate (30-60%), and high (>60%), ranged from 55.55% for flag leaf width to 96.8% for awn length. Traits with high heritability, including grain filling period, spikelet per spike, kernels per spike, thousand seed weight, spike length, peduncle length, flag leaf length, days to maturity, plant height, productive tillers, harvest index, days to heading, grain yield, biomass yield, and awn length, indicate substantial genetic control over their variation, rendering them amenable to selection. The high heritability, validated by moderate to high genetic advance, suggests additive gene effects and underscores the efficacy of selection for these traits. Previous studies by Destaw *et* al.^{9,17,18,19} support our findings, emphasizing the genetic basis of these traits in bread wheat.

Moderate heritability values, such as for flag leaf width (55.55%), imply a need for delayed selection to more advanced generations. Additionally, the utility of heritability is enhanced when used in conjunction with genetic advance estimates, as high heritability does not always guarantee high genetic gain. The genetic advance, expressed as a percentage of the mean, ranged from low to high across traits, with significant potential for improvement observed for traits like thousand seed weight, spike length, and grain yield. Moderate heritability coupled with high genetic advance, as observed for flag leaf width, indicates the efficacy of selection for trait improvement. Conversely, traits governed by non-additive gene actions, like days to maturity, may exhibit high heritability but low genetic advance, highlighting the complexity of genetic regulation. These results provide valuable insights into the heritability and expected genetic advance of key traits in bread wheat genotypes, facilitating informed decision-making in breeding programs. Consideration of both heritability and genetic advance is essential for maximizing genetic gain and developing superior wheat cultivars with enhanced agronomic traits.

The analysis of variance revealed highly significant differences among the genotypes for all traits studied, highlighting the potential trait for improvement through both direct and indirect selection. Such variability within the population is critical for advancing crop characteristics. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits, with values ranging from 4.04% for days to maturity to 44.41% for awn length, and the GCV ranged from 4.56% for days to maturity to 45.14% for awn length. Broad-sense heritability values ranged from 55.55% for leaf width to 96.8% for awn length, while genetic advance as a percentage of the mean ranged from 7.38% for days to maturity to 90.13% for awn length. Traits such as productive tillers, biomass yield, harvest index, grain yield, and awn length exhibited both high GCV and high heritability, along with substantial genetic advance, suggesting these traits are primarily controlled by additive gene action and are, therefore, amenable to improvement through recurrent selection. In contrast, days to maturity, despite its high heritability, showed a lower genetic advance, indicating it is predominantly governed by non-additive gene action and may not be easily fixed through selection. These findings suggest that traits like productive tillers, biomass yield, harvest index, grain yield, and awn length, with their high heritability and genetic advance, are strong contestants for improvement through selection. Based on the present analysis, genotypes 31790, EBW192299, 33682, 34737, and 34159 were identified as high-yielding, outperforming other genotypes in the study. Understanding that extent of genetic variability is essential for successful plant breeding programs, as it forms the foundation for selection processes.

Data Availability

Data is available in the manuscript.

Conflict of Interest

The authors do not have any possible conflicts of interest.

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