



Genetic Variability and Performance of Bread Wheat (*Triticum aestivum* L.) Genotypes under High Temperature Environments of Ethiopia

Bayisa Asefa*, Berhanu Sim, Demeke Zewdu, Alemu Dabi, Negash Geleta, Tafesse Solomon, Gadisa Alemu, Rut Duga, Habtemariam Zegeye, Abebe Delesa, Dawit Asneke and Abebe Getamesay

Ethiopian Institute of Agricultural Research, Kulumsa Agricultural Research Center, P.O. Box -489, Asella, Ethiopia

Corresponding Author

Bayisa Asefa
e-mail: bayisa5@yahoo.com

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Abstract

This study was conducted during May to December, 2022 at Kulumsa and Melkassa, in Ethiopia, evaluated 49 CIMMYT-introduced genotypes including the check variety across two locations using an alpha lattice design. The Combined analysis of variance revealed highly significant genetic variability for most of the traits, including grain yield (GYLD), thousand kernel weight (TKW) and hectoliter weight (HLW). Genotypes EBW222059, EBW222088 and EBW222079 were the top yielders, consistently outperforming the check. High genotypic (GCV) and Phenotypic (PCV) coefficients of variation for GYLD (22.24% and 24.42%) and TKW (13.38% and 15.32%) at Kulumsa indicated a strong genetic base for improvement. Very high broad-sense heritability for grain yield (83%) and days to heading (92%), coupled with high genetic advance as a percent of mean (GAM) for grain yield (41.72%), suggested the predominance of additive gene action, making phenotypic selection highly effective. However, maturity traits and plant height showed significant environmental influence, rendering direct selection for these traits ineffective. Correlation analysis confirmed that grain yield was strongly and positively associated with TKW and HLW at both genotypic and phenotypic levels. These results demonstrated that selecting for heavier, denser grains was a reliable strategy for yield enhancement. The study concluded that the identified elite genotypes should advance to multi-environment stability trials, while TKW and HLW should be prioritized as key selection markers to accelerate the development of high-yielding, adaptable wheat varieties. Thus, genetic variability in these genotypes could be exploited to enhance bread wheat yields under high-temperature conditions of Ethiopia.

Keywords: Correlation, genetic advance, heritability, genetic gain, variability

1. Introduction

In Ethiopia, bread wheat (*Triticum aestivum* L.) represents one of the most critical cereal crops regarding both production volume and national consumption. It serves as strategic commodity that generates essential farm income and bolsters food security, acting as a primary staple that provides an estimated 12% of the daily per capita caloric intake for the country's population (Anonymous, 2020). The crop is predominantly cultivated by small-scale farmers under rain-fed conditions within an altitudinal range of 1500 to 3000 m.a.s.l. (Bekele et al., 2000). However, despite the presence of diverse agro-ecologies suitable for production and the inherent elasticity of wheat to grow from extreme lowlands to highlands, production still lags behind domestic demand by 25 to 30% (Gadisa et al., 2020). This deficit is driven by increased demand resulting from population growth, urbanization, and the expansion of agro-industries (Hodson

et al., 2020). Bread wheat is more widely adapted than other cultivated species, a characteristic that has established it as one of the most cultivated food crops globally (Rajaram, 2005). Grain yield remains the most significant trait of interest; consequently, breeders frequently seek to identify genotypes that demonstrate high and stable yields across varying environments (Alemu et al., 2023). In Ethiopia, approximately 4.6 million farmers are engaged in wheat production on small-scale plots. Despite the country's potential, productivity remains below the global average of 3.3 t ha⁻¹. This shortfall is primarily due to productivity constraints such as biotic and abiotic stresses, with wheat rust identified as a major factor limiting national output (Haydar et al., 2020). It is essential that bread wheat yields increase in parallel with the growing population (Karaman, 2019). To effectively improve grain yield, the selection of genotypes should not rely on yield alone; rather, other yield components must be integrated into the



selection process. The relationships among different traits in wheat can be elucidated using genotypic and phenotypic correlation analysis, which serves as an effective tool for enhancing crop improvement for specific traits of interest (Johnson et al., 1956). Furthermore, studies of correlation coefficients and heritability provide detailed information necessary to identify important characters for improving genotypes through selection. The development of high-yielding, stable, and rust-resistant genotypes is a fundamental strategy in variety development and multi-location evaluation (Alemu et al., 2023). The national wheat research program in Ethiopia focuses on developing and releasing bread wheat varieties characterized by rust resistance, high grain yield, and satisfactory quality (Alemayehu et al., 2024). Consequently, breeding for grain yield, disease resistance, and wide adaptability has become a priority for the national wheat improvement program (Alemu, et al., 2019; Alemu, 2024). The Ethiopian Wheat Research Program introduces thousands of bread wheat germplasms annually from international research institutes, evaluating them in quarantine blocks and through serial yield trials across various locations and years. Knowledge regarding the genetic variability present in existing crop species for specific characters is paramount to the success of any plant breeding program (Gadisa et al., 2021). Thus, estimating genetic parameters such as heritability and genetic advance provides essential knowledge for predicting the transfer of traits from parental plants to offspring. Moreover, heritability and genetic advance are critical selection parameters that assist breeders in determining which characters should be targeted for selection (Johnson et al., 1956). The phenotypic and genotypic coefficients of variation are also vital genetic parameters; the magnitude of the difference between PCV and GCV values indicates the level of environmental influence on genotypic performance. Hence, this study was carried out to evaluate the performance of genotypes and analyze quantitative genetic parameters for yield and other related traits of wheat genotypes under investigation.

2. Materials and Methods

The experiment was conducted during May to December, 2022 cropping season across two locations: Kulumsa and Melkassa. The agroecological descriptions of the study sites have been depicted in Table 1. A total of forty-nine bread wheat genotypes, introduced by the National Wheat Research breeding program from CIMMYT, were evaluated in this study alongside a check variety (Hidasse). The trials were laid out using an alpha lattice design with two replications. Each experimental plot occupied an area of 3m², arranged in 10 rows and 5 columns. All agronomic management practices were implemented according to the specific recommendations for each location to ensure optimal crop performance.

2.1. Analysis of variance and estimation of genetic parameters

The analysis of variance (ANOVA) for an alpha lattice design was performed for each trait using R-Software version 4.0.1.

The genotypic and phenotypic components of variance were computed according to Formulae given by Johnson et al. (1955) for the observed characteristics.

Genotypic variance (σ^2g)=(MSG-MSe)/r, Environmental variance (σ^2e) =MSe/r

Phenotypic variance (σ^2p)= σ^2g + σ^2e , Where: MSG=mean square due to genotypes, MSe=Environmental variance (error mean square), error variance= σ^2e , r=number of replication.

The genotypic and phenotypic coefficients of variation were computed according to Burton et al (1953) and expressed as a percentage using R-software version 4.0.1.

PCV= ($\sqrt{\sigma^2p}$ /grand mean)×100 and GCV= ($\sqrt{\sigma^2g}$ /grand mean) ×100, Where, σ^2p =Phenotypic variance, σ^2g =Genotypic variance, PCV=Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation. PCV and GCV values were categorized as: 0–10%: low, 10–20%: moderate, and >20: high as indicated by Subramanian and Menon (1973).

2.2. Broad sense heritability (h^2bs)

Broad sense heritability was estimated as the ratio of genotypic variance to phenotypic variance and expressed in percentage (Hanson et al., 1956).

$H^2=\sigma^2g/\sigma^2p \times 100$, Where: σ^2g =Genotypic variance, σ^2p =Genotypic variance.

2.3. Genetic advance

The extent of genetic advance to be expected for each character was computed using the formula given by Johnson et al. (1956) and Allard (1960).

$G.A=i \times h^2 \times \delta p$ where, G.A=Genetic advance, i=Selection differential (at 5% selection intensity, $k=2.06$), h^2 =Heritability in a broad sense, δp =Phenotypic standard deviation.

2.4. Genetic advance as percent of mean (GAM)

GAM was categorized as low, moderate, and high as given by Johnson et al. (1956) 0–10%: low, 10–20%: moderate, and 20 and above: high.

$GAM=(GA/\text{grand mean}) \times 100$, where GA was the genetic advance

2.5. Genotypic and phenotypic correlations

The formula used to compute genotypic and phenotypic correlation was given (Singh, et al., 1997); phenotypic correlation coefficient= $COV_{p_{xy}}/\sqrt{(\sigma^2p_x)(\sigma^2p_y)}$, Genotypic correlation coefficient(rg_{xy})= $COV_{g_{xy}}/\sqrt{(\sigma^2g_x)(\sigma^2g_y)}$, Environmental correlation coefficient (re_{xy})= $COV_{e_{xy}}/\sqrt{(\sigma^2e_x)(\sigma^2e_y)}$, Where: rp_{xy} =Phenotypic correlation coefficient between traits x and y, rg_{xy} =Genotypic correlation coefficient between traits x and y, $pcov_{xy}$ =Phenotypic covariance between traits x and y, $gcov_{xy}$ =Genotypic covariance between traits x and y, $ecov_{xy}$ =Environmental covariance between character x and y.



Table 1: Agro-ecological description of the study Sites

Location	Geographic position		Altitude (m)	Temperature (°C)		Rainfall (mm)
	Latitude	Longitude		Min.	Max.	
Kulumsa	08°01'10"N	39°09'11"E	2200	10.5	22.8	820
Melkasa	08°24'N	39°12'E	1550	13.6	28.6	763

3. Results and Discussion

3.1. Analysis of variance (ANOVA)

The results of the combined analysis of variance (ANOVA) across the two locations (Kulumsa and Melkassa) were presented in Table 2. The analysis revealed highly significant differences among the genotypes for all traits under study. This indicated the presence of a substantial amount of genetic variability within the 49 bread wheat genotypes, which was a fundamental prerequisite for any successful breeding program.

The existence of such variability suggested that there was ample room for improving these characters through selection or by utilizing these genotypes as diverse parental lines in future crossing programs. These findings were consistent with previous reports by Singh et al. (2019) and Kumar et al. (2021), who also observed significant genetic diversity for quantitative traits in bread wheat. Furthermore, Dabi et al. (2019) emphasized that such variability was the primary tool for breeders to identify and isolate elite genotypes with superior performance.

Table 2: Combined analysis of variance for agronomic traits of bread wheat genotypes

Sources of variation	DTH	DTM	PHT	TKW	HLW	GYLD
Genotype variance (Df=49)	11.88**	10.00**	1.31**	5.66**	2.03**	1210.00**
Loc Variance (Df=1)	1725.25**	4525.32**	523.47**	458.25**	11.25*	13212.65**
Gen x Loc Variance(G*Loc) (Df=49)	1.43**	3.01**	13.19**	4.39**	5.40**	1.04**
Residual Variance (Df=82)	2.84	1.91	22.24	18.90	2.60	0.32
Grand Mean	60.76	107.91	83.70	29.46	63.87	3.91
CV (%)	2.77	1.28	5.63	14.76	2.53	14.50
Genotype significance	0.00	1.00	0.72	0.05	0.11	1.00
GenxEnv significance	0.00	0.00	0.00	0.14	0.00	0.00

DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield; CV (%): Coefficient of Variation; Df: Degree of freedom

The effect of location was also highly significant for nearly all measured traits, with the exception of Hectoliter Weight, which showed a significant difference at a lower threshold. This highlighted that the two environments-Kulumsa and Melkassa-exerted distinct pressures on the expression of these traits, likely due to differences in soil type, temperature, and moisture levels during the 2022 cropping season. Importantly, the Genotype by Location (G L) interaction showed highly significant differences among genotypes (Gadisa et al., 2020). This interaction implied that the genotypes did not maintain a consistent ranking or performance level across the two locations. For instance, a genotype that performed exceptionally well at Kulumsa might not have expressed the same potential at Melkassa. Such a strong interaction complicated the selection process, as it indicated that specific genotypes might be better suited to particular environments rather than being broadly adapted.

In contrast, the variation due to replications within locations was non-significant for most traits, except for grain yield and Hectoliter weight, which exhibited highly significant differences. This suggested that the experimental field layout

and alpha lattice design were generally effective in controlling local soil heterogeneity, though yield-related traits remained sensitive to micro-environmental shifts. Given these results, it was essential to consider the magnitude of environmental interaction when evaluating varietal performance. Identifying genotypes that performed well in relation to specific location effects was vital for developing varieties tailored to the diverse agro-ecologies of Ethiopia, a conclusion also supported by Dabi et al. (2019) in similar bread wheat studies.

The combined analysis of variance across locations, as well as the site-specific analysis at Kulumsa, revealed highly significant differences among the bread wheat genotypes for all studied traits. This indicated a robust presence of genetic variability, suggesting that the germplasm possessed sufficient diversity for effective selection and breeding. In contrast, the results from Melkassa showed a more varied response among the genotypes.

While days to heading, days to maturity, and hectoliter weight maintained highly significant differences, other traits were less differentiated at this specific site. Notably, plant



height and thousand kernel weight showed non-significant differences, whereas grain yield exhibited only significant differences among the tested genotypes (Table 3). This discrepancy suggested that the environmental conditions at Melkassa might have exerted a more uniform influence on certain developmental traits, or perhaps masked the genetic potential of the genotypes for height and seed weight compared to the Kulumsa site. Such variation between

locations underscored the importance of multi-environment trials in identifying genotypes with stable performance across diverse Ethiopian agro-ecologies (Girma et al., 2021).

3.2. Mean performance of genotypes

The mean performance of the fifty bread wheat genotypes evaluated across the Kulumsa and Melkassa locations was summarized in Table 4. The results revealed substantial variation among the genotypes for all studied traits, with

Table 3: Analysis of variance of the 6 traits of 50 bread wheat genotypes

Sources of variation	DTH		DTM		PHT		TKW		HLW		GYLD	
	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK
Replication (df=1)	0.49	4.00	0.20	1.00	88.36	324.00	4.84	1.96	74.82	0.15***	77340.0	481914.0**
Genotype variance (df= 49)	17.39***	2.45***	16.5***	5.79**	45.09***	69.51 ^{ns}	45.02***	16.43 ^{ns}	31.47***	14.8***	344489.0***	127089.0*
Residuals (df=49)	0.69	0.76	2.01	1.84	13.58	54.10	6.06	7.18	13.07	3.75	32156.0	54846.0
Max. Mean	73.00	56.00	-	103.00	120.00	90.00	44.00	36.00	72.44	68.60	2816.00	1687.00
Min. mean	58.00	51.00	-	93.00	90.00	55.00	22.00	20.00	31.76	54.18	616.00	174.00
Grand mean	65.55	52.52		95.82	102.00	71.30	32.00	26.54	65.83	62.15	1776.73	846.58

DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield; KU: Kulumsa; MK: Melkassa

grain yield (GYLD) exhibiting the widest range of performance, extending from 488.30 kg ha⁻¹ for the check variety (Hidasse) to 1834.15 kg ha⁻¹ for genotype EBW222059. Out of the fifty genotypes tested, EBW222059 (1834.15 kg ha⁻¹), EBW222088 (1783.02 kg ha⁻¹) and EBW222079 (1707.81 kg ha⁻¹) appeared as the top-yielding lines across locations. These genotypes significantly exceeded the grand mean of 1311.66 kg ha⁻¹ and the check variety, suggesting they were outstanding candidates for potential variety release after further stability testing. These findings aligned with Gezahegn et al. (2015), who reported similarly wide ranges of variation for yield traits in bread wheat. Particularly, EBW222059 was not only the highest yielder but also demonstrated superior performance for most associated traits, indicating its high genetic potential compared to the check.

Significant variability was also recorded in phenological traits, which were essential for determining the adaptation of genotypes to specific growing seasons. Days to heading (DTH) ranged from 54.50 days (EBW222096) to 63.00

Table 4: Mean performance of different characters among fifty bread wheat genotypes

Genotype	DTH	DTM	PHT	TKW	HLW	GYLD
EBW222050	59.25	62.93	28.50	88.00	106.50	1290.46
EBW222051	56.50	64.97	29.50	82.25	108.25	1306.39
EBW222052	57.75	62.60	25.50	86.25	106.25	922.47
EBW222053	58.00	63.22	27.00	84.00	107.00	1200.55
EBW222054	58.75	56.61	26.50	86.25	107.00	1299.46
EBW222055	56.25	66.89	28.50	78.00	107.00	1250.89
EBW222056	58.25	65.25	28.00	81.25	108.58	1142.72
EBW222057	62.25	64.18	35.50	88.00	108.00	1297.86
EBW222058	59.25	59.45	28.00	85.25	104.25	992.86
EBW222059	59.75	67.77	30.00	84.50	107.42	1834.15
EBW222060	58.25	64.74	24.00	88.25	105.25	929.23
EBW222061	60.00	62.90	28.50	88.00	108.00	1183.32

Table 4: Continue...



Genotype	DTH	DTM	PHT	TKW	HLW	GYLD
EBW222062	59.00	65.77	27.50	80.75	107.25	1219.28
EBW222063	58.00	64.72	32.50	89.25	109.25	1568.82
EBW222064	58.50	64.10	31.00	92.00	106.75	1168.53
EBW222065	58.25	64.37	30.50	88.75	107.50	1207.98
EBW222066	57.25	65.00	33.50	95.00	108.50	1252.38
EBW222067	59.75	62.89	31.50	91.25	108.00	1638.65
EBW222068	61.75	59.37	25.00	87.50	107.50	1351.38
EBW222069	62.75	64.27	33.00	87.00	111.75	1617.07
EBW222070	58.25	66.48	31.00	93.50	106.00	1638.42
EBW222071	58.75	64.98	32.00	91.25	109.00	1421.68
EBW222072	59.50	64.89	29.00	91.25	108.25	1486.86
EBW222073	58.25	65.16	32.00	82.50	107.50	1469.77
EBW222074	61.50	64.11	33.00	80.50	108.00	1537.68
EBW222075	61.00	61.67	26.50	80.25	107.50	1352.86
EBW222076	63.00	60.95	26.50	88.75	108.50	1152.77
EBW222077	59.75	62.95	27.50	91.25	107.25	1404.07
EBW222078	60.25	65.43	28.50	90.00	108.75	1522.92
EBW222079	60.50	62.95	36.00	91.75	109.00	1707.81
EBW222080	57.00	67.96	37.00	84.50	107.50	1474.89
EBW222081	60.00	65.57	32.50	83.25	108.50	1366.72
EBW222082	59.25	64.48	32.00	88.25	108.00	1316.62
EBW222083	59.75	63.90	32.50	84.00	109.25	1524.27
EBW222084	58.00	65.01	26.00	83.75	104.75	1034.64
EBW222085	61.50	64.32	29.00	92.50	107.75	1142.97
EBW222086	60.75	62.12	29.00	90.75	108.42	709.62
EBW222087	57.00	64.77	30.50	79.50	104.00	1363.56
EBW222088	59.00	67.55	35.50	93.25	108.25	1783.02
EBW222089	56.00	68.67	33.50	88.75	107.25	1660.57
EBW222090	60.25	64.87	31.50	97.50	109.00	1413.36
EBW222091	57.75	66.89	29.00	85.25	105.50	1337.69
EBW222092	61.00	65.85	31.50	90.00	110.75	1388.19
EBW222093	59.25	64.27	28.00	89.50	107.75	1300.82
EBW222094	59.50	64.00	26.00	81.00	106.50	1170.92
EBW222095	55.50	68.74	31.00	85.50	108.25	1304.61
EBW222096	54.50	62.15	29.50	85.75	103.50	1135.77
EBW222097	57.50	63.51	30.00	87.25	104.25	1288.02
EBW222098	59.50	58.32	23.50	84.50	105.25	1008.92
Hidasse	58.50	55.07	24.50	86.25	104.00	488.30
Mean	59.04	63.99	29.76	87.07	107.36	1311.66

DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; TKW: Thousand kernel weight, HLW: Hectoliter weight, GYLD: Grain yield

days (EBW222076), with an overall mean of 59.04 days. Regarding days to maturity (DTM), the check variety Hidasse was the earliest to mature at 55.07 days, while genotypes such as EBW222095 (68.74 days) and EBW222089 (68.67 days) were among the latest maturing lines, against a grand mean of 63.99 days. The presence of both early and late-maturing genotypes within this population provided breeders with options to select for different agro-ecological zones, such as early-maturing types for moisture-stressed areas or late-maturing types for high-rainfall highlands.

Morphological and seed quality traits also showed distinct differences across the germplasm. Plant height (PHT) varied from a minimum of 23.50 cm (EBW222098) to a maximum of 37.00 cm (EBW222080), with a grand mean of 29.76 cm. Thousand kernel weight (TKW), a critical yield component, peaked in genotype EBW222090 (97.50 g) and was lowest in EBW222055 (78.00 g), resulting in a grand mean of 87.07 g. Furthermore, hectoliter weight (HLW), an indicator of grain density and milling quality, ranged from 103.50 kg hl⁻¹ (EBW222096) to 111.75 kg hl⁻¹ (EBW222069), with a grand mean of 107.36 kg hl⁻¹.

Generally, the extensive variability observed across these six traits among the fifty bread wheat genotypes underscored a reasonably sufficient genetic base within the introduced CIMMYT germplasm. Especially, genotype EBW222059 stood out as an elite line, delivering the highest grain yield while maintaining superior performance for several associated traits. This diversity provided an excellent opportunity for the national wheat improvement program to select superior and desired genotypes for direct production or as parental lines for future hybridization efforts aimed at improving wheat productivity in Ethiopia (Alemu et al., 2024). The high degree of variability observed across these six traits among the fifty genotypes indicated a reasonably sufficient genetic base. This diversity provided an excellent opportunity for selecting superior genotypes to advance the national wheat improvement program.

3.2. Estimation of genetic parameters

3.2.1. Genotypic and phenotypic coefficients of variation (GCV and PCV)

The estimates for the mean, range, genotypic and phenotypic variances, and the corresponding coefficients of variation (GCV and PCV) for the six quantitative traits were presented in Table 5. According to the results, the Phenotypic Coefficient of Variation (PCV) was consistently higher than the Genotypic Coefficient of Variation (GCV) for all characters across both locations. This disparity indicated that environmental factors influenced the expression of these traits to varying degrees (Salman et al., 2014). At Kulumsa, the PCV and GCV values for grain yield were 24.42% and 22.24%, respectively, while at Melkassa, these were 35.63% and 22.45%. The wider gap between PCV and GCV at Melkassa, particularly for grain yield and plant height, suggests a stronger environmental influence



Table 5: Estimation of genetic parameters for different traits in bread wheat genotypes

Statistics	DTH		DTM		PHT		TKW		HLW		GLD	
	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK
Genotype variance	8.35	0.85	7.22	1.98	15.75	7.70	19.48	4.62.4	9.20	5.52	1561.23	3612.57
Phenotypic variance	9.04	1.65	9.23	3.81	29.34	61.81	25.54	11.80	22.27	9.28	1883.31	9096.48
Envt (Residual) variance	0.69	0.76	2.01	1.41	13.58	54.10	6.06	7.18	13.07	3.75	3215.08	5484.90
GCV	4.41	1.75		1.47	3.86	3.89	13.38	8.10	4.61	3.78	22.24	22.45
PCV	4.59	2.41		2.04	5.27	11.03	15.32	12.95	7.17	4.90	24.42	35.63
ECV	1.27	1.60		1.41	3.59	10.32	7.47	10.10	5.49	3.12	10.09	27.66
GA	5.72	1.38	4.89	2.09	5.99	2.02	7.94	2.77	4.02	3.74	74.32	24.71
GAM (%)	8.73	2.62		2.18	5.83	2.83	24.07	10.44	6.10	6.01	41.72	29.14
Heritability	0.92	0.53	0.78	0.52	0.54	0.12	0.76	0.39	0.41	0.60	0.83	0.40
Max mean	73.0	56.00		3.00	120.00	90.00	44.00	36.00	72.44	68.60	2816.00	1687.00
Min mean	58.0	51.00		93.00	90.00	55.00	22.00	20.00	31.76	54.18	616.00	174.00
Grand mean	65.55	52.52		95.82	102.84	71.30	32.98	26.54	65.83	62.15	1776.73	846.58

KU: Kulumsa; MK: Melkasa; DTH: Date to heading; DTM: Date to maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYD: Grain yield; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; ECV: Environmental coefficient of variation; GA: Genetic advance; GAM(%): Genetic advance as percent of mean

at that site compared to Kulumsa.

High GCV and PCV values (>20%) were recorded for grain yield at both locations, indicating a substantial level of genetic diversity and offering a superior opportunity for crop improvement through direct selection. These findings aligned with Geneti et al. (2022), who also reported high PCV for grain yield in bread wheat. At Kulumsa, thousand kernel weight (TKW) also showed high variability (PCV=15.32, GCV=13.38), whereas at Melkassa, its variability was slightly lower (PCV=12.95, GCV=8.10). Moderate values were observed for plant height at Kulumsa (PCV=5.27, GCV=3.86). In contrast, the lowest estimates of PCV and GCV were recorded for days to heading (PCV=2.41, GCV=1.75) and days to maturity (PCV=2.04, GCV=1.47) at Melkassa, revealing that phenological traits at this site were highly influenced by environmental factors and might be difficult to manipulate through direct selection. These results were supported by Ashfaq et al. (2014), and Hassani et al. (2022).

3.2.2. Broad-sense heritability and genetic advance

Heritability values were instrumental in predicting the expected progress achievable through the selection process. Traits characterized by high broad-sense heritability estimates tend to respond more effectively to selection, as the environmental influence on phenotypic expression was relatively low in such cases (Haydar et al., 2020). This indicated a higher relative magnitude of genotypic variance compared to the total variation among the studied genotypes. Consequently, selection based on phenotypic expression for

traits with high to very high broad-sense heritability was likely to be successful, as there was a close correlation between phenotypic and genotypic appearance (Singh, 2001). The estimates of heritability, genetic advance (GA), and genetic advance as a percent of the mean (GAM) for all characters studied were represented in Table 5.

Following the classification by Singh (2001)—where heritability values greater than 80% were very high, 60–79% was moderately high, 40–59% was medium, and values less than 40% were low. Thus, this study observed distinct patterns for heritability across the two locations. At Kulumsa, very high broad-sense heritability estimates were revealed for days to heading (92%) and grain yield (83%), while hectoliter weight (60%) showed moderately high values. Moreover, moderate heritability was observed for plant height, days to maturity and thousand kernel weight (TKW). These findings of very high heritability for days to heading were consistent with previous research by Negasa et al. (2016) and Bayisa et al. (2020). On the other hand, at Melkassa, moderately high broad-sense heritability was observed for days to heading (78%) and thousand kernel weight (76%), whereas plant height exhibited low heritability (12%). Low heritability estimates for yield-related traits have also been noted by Adhiena et al. (2016), suggesting that site-specific environmental pressures could significantly alter heritability outcomes.

However, heritability alone could not provide a full indication of the genetic progress resulting from the selection of

individual genotypes. Knowledge of heritability must be coupled with genetic advance for a more comprehensive understanding of the traits under study. As stated by Hamdi et al. (2003), genetic advance (GA) was essential for predicting the expected genetic gain from a single cycle of selection, representing the improvement in genotypic value of the new population compared to the base population at a given selection intensity (Singh, 2001). According to Johnson et al. (1955), genetic advance as a percent of the mean (GAM) was categorized as low (<10%), moderate (10–20%), and high (>20%).

At Kulumsa, the GAM in this study ranged from 2.18% for days to maturity to 41.72% for grain yield. Markedly, the combination of moderate to high heritability with high genetic gain was observed for TKW (24.07%) and grain yield (41.72%), indicating the significant involvement of additive gene action. This suggested that selection for the improvement of these characters would be highly rewarding. Similar results were reported for days to heading and spike length by Obsa et al. (2017). However, lower values of heritability and GAM for other traits might be attributed to higher environmental factors or non-additive gene action. Generally, the high and moderate heritability estimates found for most traits indicated that the variation was primarily under genetic control and less affected by the environment. As noted by Raia et al. (2016), the expression of economically important characters through additive gene action made selection for crop improvement most effective when high broad-sense heritability was paired with high GAM.

Furthermore, at Melkassa, the highest expected genetic advance as a percent of the mean was observed for grain yield (29.14%) and TKW (10.44%). The presence of high heritability alongside moderately high GAM for these traits suggested they were favorable for improvement through selection, which aligned with findings by Salman et al. (2014) and Mohammedamin et al. (2022). In contrast, days to maturity showed high heritability, it was paired with low genetic advance. Furthermore, plant height exhibited low heritability (12%) and low genetic advance, indicating that selection for this character would be ineffective at this location due to the predominant influence of non-additive genes and environmental factors. This was consistent with Desalegn and Chauhan (2016), who also reported low heritability for traits such as harvest index and tillers plant⁻¹.

3.2.3. Genotypic and phenotypic correlation for grain yield and other traits

The results of the correlation analysis revealed that, for the majority of the traits studied, phenotypic correlation coefficients were generally higher than their corresponding genotypic correlations. The genotypic correlation coefficients between grain yield and other agronomic characters (Tables 6 and 7) demonstrated varying trends, highlighting the complex nature of yield determination at the genetic level.

In this study, grain yield exhibited highly significant and positive genotypic correlations with thousand kernel weight (TKW) and hectoliter weight (HLW). These strong associations indicated that TKW and HLW were major contributors to grain yield, a finding that aligned with Surma et al. (2012), who reported similar positive and significant correlations between yield, kernel weight and starch content. Furthermore, a significant positive correlation was observed between TKW and HLW. At the phenotypic level, grain yield also showed highly significant positive correlations with HLW, followed by TKW and plant height (PHT). While Ashebr et al. (2020) confirmed the strong link between yield and HLW. These results collectively suggested that genotypes characterized by higher TKW and HLW were likely to be more productive.

Regarding phenological traits, grain yield showed positive and significant phenotypic correlations with plant height. However, at the genotypic level, grain yield exhibited non-significant negative correlations with both days to heading (DTH) and days to maturity (DTM). The significant associations found in this study at the genotypic level suggested a pleiotropic effect or genetic linkage, where genes favoring an increase in one trait simultaneously influence another (Tables 6 and 7).

Table 6: Estimate of Correlation coefficient at phenotypic (above diagonal) and genotypic (below diagonal) level among six traits at Kulumsa

Traits	DTH	DTM	PHT	TKW	HLW	GYLD
DTH	1	0.556 ^{ns}	0.102 ^{ns}	-0.175 ^{ns}	-0.063 ^{ns}	-0.163 ^{ns}
DTM	0.631 ^{**}	1	0.173 ^{ns}	0.070 ^{ns}	0.103 ^{ns}	0.089 ^{ns}
PHT	0.122 ^{**}	0.251 ^{**}	1	0.378 ^{ns}	0.177 ^{ns}	0.509 [*]
TKW	-0.162 ^{**}	0.105 ^{**}	0.557 ^{ns}	1	0.788 ^{ns}	0.864 ^{**}
HLW	-0.005 ^{ns}	0.139 ^{**}	0.082 [*]	0.585 ^{**}	1	0.851 ^{**}
GYLD	0.131 ^{ns}	0.112 ^{ns}	0.620 ^{**}	0.963 ^{**}	0.561 [*]	1

Signif. 0 ****: 0.001; **: 0.01; *: 0.05

Table 7: Estimate of Correlation coefficient at phenotypic (above diagonal) and genotypic (below diagonal) level among six traits at Melkassa

Traits	DTH	DTM	PHT	TKW	HLW	GYLD
DTH	1	-0.419 ^{ns}	0.234 ^{ns}	-0.219 ^{ns}	-0.303 ^{ns}	-0.046 ^{ns}
DTM	-0.511 ^{**}	1	-0.449 ^{ns}	-0.236 ^{ns}	-0.232 ^{ns}	-0.482 ^{ns}
PHT	0.325 ^{**}	-0.527 ^{**}	1	0.257 ^{ns}	0.330	0.573 [*]
TKW	-0.736 ^{**}	-0.629 ^{**}	1.000	1	0.425 ^{ns}	0.498 ^{**}
HLW	-0.421 ^{ns}	-0.099 ^{**}	0.518	0.919	1	0.679 ^{**}
GYLD	-0.174 ^{ns}	-0.330 ^{ns}	0.719 ^{**}	1.000 ^{**}	0.716 [*]	1

Signif. 0 ****: 0.001; **: 0.01; *: 0.05; DTH: Date to heading; DTM: Date to maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield



At the Kulumsa site, DTH showed positive but non-significant genotypic associations with DTM and PHT, while it was negatively and non-significantly correlated with TKW and HLW. Phenotypically, however, DTH was highly significantly and positively correlated with both DTM and PHT. These results were consistent with Geneti et al. (2022), who reported highly significant phenotypic associations between heading and maturity. Similarly, DTM showed positive but non-significant genotypic correlations with DTH and HLW, while exhibiting non-significant negative correlations with PHT, TKW, and grain yield—findings that were supported by Ashebr et al. (2020). At the phenotypic level, DTM was highly significantly and positively correlated with PHT, but showed a significant negative correlation with TKW.

Furthermore, plant height revealed positive but non-significant genotypic correlations with TKW and HLW, as also noted by Ashebr et al. (2020). At the phenotypic level, plant height showed a highly significant association with grain yield and a significant positive correlation with hectoliter weight (HLW). Remarkably, thousand-kernel weight (TKW) was highly and positively associated with both HLW and grain yield. These significant positive correlations among most agronomic traits align with the findings of Asefa et al. (2026). Overall, the prevalent positive and significant correlations—both genotypic and phenotypic—among the majority of the studied traits suggested that simultaneous selection for these characters could effectively enhance grain yield in bread wheat.

4. Conclusion

Substantial genetic variability existed among the 49 bread wheat genotypes evaluated, particularly for primary yield-determining traits such as grain yield and thousand kernel weight (TKW). This diversity represented a critical genetic reservoir for wheat improvement program, providing a robust foundation for selecting superior lines tailored to diverse agro-ecologies of Ethiopia. The identification of elite genotypes; EBW222059, EBW222088, and EBW222079, which outperformed the standard check variety, Hidasse, provided immediate candidates for enhancing regional wheat productivity.

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