



Estimation of Genetic Parameters and Character Associations, and Disease Resistance of Bread Wheat (*Triticum aestivum* L.) Genotypes

Demeke Zewdu¹ , Gadisa Alemu¹, Rut Duga¹, Alemu Dabi¹, Negash Geleta¹, Berhanu Sime¹, Tafesse Solomon¹, Abebe Delesa¹, Habteamriam Zegeye¹, Abebe Getamesay¹, Bayisa Asefa¹, Dawit Asnake¹, Getnet Muche¹, Alemu Ayele¹, Daniel Kassa¹, Bekele Abeyo² and Ayele Badebo²

¹Dept. of Wheat Breeding, Ethiopian Institute of Agricultural Research, Kulumsa Agricultural Research Center, Asella, Ethiopia

²Dept. of Wheat Breeding, CIMMYT Ethiopia Office, Addis Ababa, Ethiopia



Corresponding  demekezewdu21@gmail.com

 0009-0000-7816-5006

ABSTRACT

The experiment was conducted during July–November in 2023 main cropping season at Kulumsa Agricultural Research Center to assess the extent of genetic variability and the association among traits in bread wheat genotypes. Analysis of variance revealed significant genetic variation ($p < 0.01$) among genotypes for seven of the nine studied characters. Grain yield exhibited the widest range, varying from 891 (EBW232651) to 1682.5 (EBW232625) kg ha⁻¹, with an average of 1325.96 kg ha⁻¹. Encouragingly, 78% of studied genotypes exhibited superior grain yield compared to check Balcha (1242.5 kg ha⁻¹). A moderate range of PCV and GCV were obtained for agronomic score, grain yield and thousand kernel weight, offer the most significant potential for improvement through selection. The high broad-sense heritability observed for days to heading days to maturity, hectoliter weight and thousand kernel weight, and traits with high GAM viz. grain yield and agronomic score, suggested a significant role of additive gene action in controlling these traits. Grain yield exhibited strong positive and highly significant correlations ($p < 0.01$) at both genotypic (rg) and phenotypic (rp) levels with Agronomic Score, Thousand kernel weight and hectoliter weight. Grain yield displayed a strong negative and highly significant correlation ($p < 0.01$) at both genotypic and phenotypic levels with yellow rust severity. The negative correlation with yellow rust severity emphasized the need to prioritize resistance breeding to protect yield potential from this disease. This finding suggested that selecting for improved agronomic score, hectoliter weight, and thousand kernel weight could be effective indirect selection strategies for enhancing grain yield in this breeding population.

KEYWORDS: Bread wheat, character associations, disease resistance, genetic parameters

Citation (VANCOUVER): Zewdu et al., Estimation of Genetic Parameters and Character Associations, and Disease Resistance of Bread Wheat (*Triticum aestivum* L.) Genotypes. *International Journal of Bio-resource and Stress Management*, 2026; 17(7), 01-14. [HTTPS://DOI.ORG/10.23910/1.2026.7073a](https://doi.org/10.23910/1.2026.7073a).

Copyright: © 2026 Zewdu et al. This is an open access article distributed under the terms of the Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International License, that permits unrestricted use, distribution and reproduction in any medium after the author(s) and source are credited.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, author have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The author has declared that no conflict of interest exists.

1. INTRODUCTION

Wheat (*Triticum aestivum* L.), is a self-pollinating annual plant, it is in the true grass family, *Gramineae*, is extensively grown as staple food source in the world (Mollasadeghi and Shahryari, 2011). It ranks second only next to rice in global food importance, providing roughly 20% of global caloric and protein intake and sustaining an estimated 40% of the world's population (Braun et al., 2010). Global wheat production reached a staggering 776.5 mt in 2020, with projections estimating similar levels for 2021 and 2022 (Anonymous, 2023). Beyond its role in food security, wheat is increasingly recognized as a valuable cash crop on the international market (Tadesse et al., 2017). Ethiopia stands out as one of Africa's leading wheat producers (Yasin et al., 2017). World wheat production is based almost entirely on two modern species: common or hexaploid bread wheat (*Triticum aestivum* L, $2n=6x=42$, AABBDD) and durum or tetraploid wheat (*T. turgidum* subsp. durum, $2n=4x=28$, AABB) (Yen et al., 2020). Within the realm of Ethiopian cereals cultivated under rain-fed conditions, wheat holds the number two spot in yield production (Anonymous, 2023a) and the number three spot in terms of area coverage (Anonymous, 2023b). Recent projections for the 2021/22 Ethiopian wheat harvest indicate an increase of 1.6% compared to the previous year, reaching an estimated 5.18 mt (Anonymous, 2021). This growth is attributed to factors like the Ethiopian government's focus on irrigation development, improved input availability for farmers, and the rise of mechanized farming in specific regions (Anonymous, 2021). Several other contributing factors include rapid population growth with increasing urbanization, and a shift in dietary preferences towards convenient, fast foods like bread, biscuits, pasta, and porridge. The socio-economic and food security significance of wheat in Ethiopia cannot be overstated. Wheat is a staple food crop that constitutes a significant portion of the daily caloric intake for both rural and urban households, especially in the form of injera, bread, and other wheat-based products (Tadesse et al., 2018). In fact, wheat accounts for approximately 15% of the national caloric intake, placing it second only to maize. (Abebe and Debebe, 2019) Moreover, the wheat industry provides livelihoods and employment opportunities for millions of smallholder farmers, processors, and other value chain actors, contributing to the overall economic development of the country. Despite the importance of wheat in Ethiopia, the country's production and productivity levels lag behind other major wheat-producing countries, such as China and India. But national average wheat yield in Ethiopia is around 3.1 t ha^{-1} (Anonymous, 2023), it is low compare to other nations average wheat yield. The primary culprit lies in the dominance of rain-fed subsistence farming by small-scale farmers, with limited adoption of irrigation practices

(Anteneh et al., 2020). A comprehensive understanding of germplasm variability, heritability, genetic advance, and trait association is crucial for successful crop improvement programs. This knowledge empowers scientists to develop superior recombinants with desired traits (Rauf et al., 2012; Tilahun et al., 2020). The presence of substantial genetic diversity is essential to address current and future challenges in wheat breeding, such as yield enhancement, wider adaptability, improved quality characteristics, drought tolerance, and resistance to insects and diseases. Therefore the present study was conducted to assess the extent of genetic variability and the association among traits in bread wheat genotypes.

2. MATERIALS AND METHODS

2.1. Experimental site and year

The research was conducted at Kulumsa agricultural research center during July–November in 2023 main cropping season. The experimental site was located at $08^{\circ}01'10''$ N longitude and $39^{\circ}09'11''$ E latitude at an altitude of 2200 m above sea level. The mean annual rain fall of the site was 820 mm with an average annual temperature of 16.5°C .

2.2. Experimental materials and design

The experiment was laid out in an 8×5 simple lattice design with two replications. Materials used for study were forty nine (49) bread wheat genotypes introduced from International Maize and Wheat Improvement Center (CIMMYT) and one (1) released variety (Balcha) presented in Table 1 below.

2.3. Data collected

Data were collected characters such as days to heading, days to maturity, grain filling period plant height, grain yield, hectoliter weight, thousand kernels weight, agronomic score, yellow rust and stem rust severity and reaction.

2.4. Data analysis

2.4.1. Analysis of variance (ANOVA)

The analysis of variance (ANOVA) was performed using the R software version 4.1.2 for simple Lattice Design. The ANOVA was conducted using the following mathematical model:

$P_{ijk} = \mu + g_i + r_j + bk(j) + e_{ijk}$, Where: P_{ijk} =phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within replication j ; μ =grand mean; g_i =the effect of i^{th} genotype; r_j =the effect of replication j ; $bk(j)$ =the effect of incomplete block k within replication j and e_{ijk} =the residual or effect of random error

2.4.2. Estimation of phenotypic and genotypic variance

Genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability were

Table 1: Materials and pedigree used for study		
Entry	Genotype	Pedigree
1	Balcha	BALCHA
2	EBW232617	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI
3	EBW232618	NAINA #1
4	EBW232619	BAVIS #1//ND643/2*WBLL1/3/BORL14
5	EBW232620	SUP152/BAJ #1/5/PBW65/2*PASTOR/3/KIRITATI//PBW65/2*SERI.1B/4/DANPHE #1
6	EBW232621	BAJ #1*2/WHEAR*2/3/PRL/2*PASTOR*2//FH6-1-7
7	EBW232622	MUTUS*2/TECUE #1*2//KFA/2*KACHU
8	EBW232623	MUTUS//ND643/2*WBLL1/3/2*KACHU//KIRITATI/2*TRCH
9	EBW232624	CHYAK1*2/3/HUW234+LR34/PRINIA//PFAU/WEAVER*2/4/TAITA
10	EBW232625	KABILU #1*2/TAITA
11	EBW232626	BORL14/5/MUTUS/DANPHE #1/4/C80.1/3*BATAVIA//2*WBLL1/3/C80.1/3*QT4522//2*PASTOR
12	EBW232627	BORL14/5/KACHU/3/WHEAR//2*PRL/2*PASTOR/4/BOKOTA
13	EBW232628	CHIPAK/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
14	EBW232629	KACHU/BECARD//WBLL1*2/BRAMBLING/3/KACHU//KIRITATI/2*TRCH
15	EBW232630	KACHU//KIRITATI/2*TRCH/3/CHIPAK
16	EBW232631	BAVIS/NAVJ07/3/FRANCOLIN #1*2//ND643/2*WBLL1
17	EBW232632	WBLL1*2/SHAMA//KACHU/3/CIRO16/5/TRCH/3/ROLF07/YANAC//TACUPETO F2001/BRAMBLING/4/PRL/2*PASTOR
18	EBW232633	BABAX/LR42//BABAX/3/ER2000/5/ATTILA/4/WEAVER/TSC//WEAVER/3/WEAVER/6/KA/NAC//TRCH/7/BECARD/CHYAK
19	EBW232634	TRCH/3/ROLF07/YANAC//TACUPETO F2001/BRAMBLING/4/PRL/2*PASTOR/5/BORL14
20	EBW232635	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92/9/BORL14
21	EBW232636	BECARD/AKURI*2/4/MUU #1//PBW343*2/KUKUNA/3/MUU/5/KUTZ//KFA/2*KACHU
22	EBW232637	KASUKO/4/BECARD/AKURI*2/3/PBW343*2/KUKUNA*2//FRTL/PIFED
23	EBW232638	KASUKO/4/BECARD/AKURI*2/3/PBW343*2/KUKUNA*2//FRTL/PIFED
24	EBW232639	KUTZ//KFA/2*KACHU/5/BECARD/AKURI*2/4/MUU #1//PBW343*2/KUKUNA/3/MUU
25	EBW232640	WBLL1*2/SHAMA//BAJ #1/3/BORL14/4/KASUKO
26	EBW232641	MUCUY*2/AMUR
27	EBW232642	MUNAL #1/CHIPAK//KASUKO
28	EBW232643	CHEWINK #1/MUTUS//MUCUY/3/MOKUE #1
29	EBW232644	FRNCLN/3/ND643//2*PRL/2*PASTOR/4/FRANCOLIN #1*2/5/BORL14
30	EBW232645	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1*2/4/KENYA SUNBIRD/5/2*KACHU/3/WHEAR//2*PRL/2*PASTOR
31	EBW232646	ATTILA*2/PBW65/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI/6/PFUNYE #1/7/BORL14/8/MELON//FILIN/MILAN/3/FILIN/4/TRCH/SRTU//KACHU
32	EBW232647	MELON//FILIN/MILAN/3/FILIN/4/TRCH/SRTU//KACHU*2/5/ATTILA*2/PBW65*2//MURGA
33	EBW232648	MUTUS*2/KIRITATI//BORL14/3/MOKUE #1

Entry	Genotype	Pedigree
34	EBW232649	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/CIRO16/6/BORL14/7/KASUKO
35	EBW232650	CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07/6/2*WBLL1*2/BRAMBLING//CHYAK
36	EBW232651	FRET2/KUKUNA//FRET2/3/WHEAR/4/FRET2*2/KUKUNA/7/TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/8/2*BORL14
37	EBW232652	TRCH/3/ROLF07/YANAC//TACUPETO F2001/BRAMBLING/4/PRL/2*PASTOR/5/BORL14/6/KASUKO
38	EBW232653	TRCH/7/TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/8/CIRO16/9/BORL14/10/MOKUE #1
39	EBW232654	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/SHAMA//PARUS/PASTOR/5/BORL14/7/SOKOLL/3/PASTOR//HXL7573/2*BAU*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI
40	EBW232655	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI*2/7/FRANCOLIN #1/3/PBW343*2/KUKUNA*2//YANAC/4/KINGBIRD #1//INQALAB 91*2/TUKURU
41	EBW232656	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI*2/7/BORL14
42	EBW232657	WBLL1*2/KKTS//PASTOR/KUKUNA/3/KINGBIRD #1//INQALAB 91*2/TUKURU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL/6/KUTZ//KFA/2*KACHU/7/KUTZ//KFA/2*KACHU
43	EBW232658	KASUKO/4/CIRO16*2/3/MUU #1/SAUAL//MUU/5/KASUKO
44	EBW232659	JINMAI 33//MUTUS*2/MUU/3/MOKUE #1
45	EBW232660	YR51#5515-1/3*BORL14
46	EBW232661	YR57#5474-6/3*BORL14
47	EBW232662	SR50/4/3*KACHU*2/3/ND643//2*PRL/2*PASTOR
48	EBW232663	TAM200/PASTOR//TOBA97/3/FRNCLN/4/WHEAR//2*PRL/2*PASTOR/5/BORL14
49	EBW232664	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/4/PAURAQ/5/BORL14
50	EBW232665	SWSR22T.B./5/KAUZ//ALTAR 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*PASTOR/7/WA8124/8/BAJ #1/CIRO16

estimated according to the statistical procedure of SAS software using mixed model (i.e. treatment as random and replication and block as fixed to generated genotypic variance and residual (error variance)) and calculated other components with excel by using the formula as follows (Burton and Devane, 1953):

Genotypic variance (σ^2_g)=(MSG-MSe)/r,

Phenotypic variance (σ^2_p)= σ^2_g + σ^2_e

Where:-, σ^2_e =Environmental variance, r=number of replication, MSe=Error, MSG=Mean square of genotype. Phenotypic and genotypic coefficients of variations were expressed as a percentage of the corresponding phenotypic and genotypic standard deviations as described by Johnson et al. (1955)

Phenotypic coefficient of variation (PCV)=($\sqrt{\sigma^2_p/\bar{X}}$) $\times$ 100, Genotypic Coefficient of Variation (GCV)=($\sqrt{\sigma^2_g/\bar{X}}$) $\times$ 100, Where:- $\bar{X}$ = grand mean.

2.4.3. Estimates of heritability in broad sense

Heritability was a useful technique that estimates the performance of parents in hybrids. The highest heritability in any character showed its highest transmitting ability to the next generation (Ajmal et al., 2009). Broad sense heritability was categorized as low (0–40%), medium (40–59%), moderately high (60–79%) and very high (>80%) as suggested by Singh (2001). Heritability (H^2) was computed by excel for each character based on a formula developed by Allard, 1960 as $H^2=(\sigma^2_g/\sigma^2_p)\times 100$

Where, σ^2_p =phenotypic Variance, σ^2_g =genotypic variance and H^2 =broad sense heritability

2.4.4. Estimation of expected genetic advance

There was a direct relationship between heritability and response to selection, which was referred to as genetic progress. The expected response to selection was called genetic advance (GA). High genetic advance coupled with high heritability estimates offered the most effective condition for selection (Tesfaye et al., 2014). Genetic advance as percent mean (GAM) was categorized as low (0–10%), moderate (10–20%) and high (>20%) as suggested by Johnson et al. (1955). The genetic advance (GA) for selection intensity (K) at 5% was calculated with excel by the formula suggested by Allard (1960) as: $GA = (K)(\sigma_p)(H^2)$ Where, GA=Expected genetic advance at 5% selection intensity, σ_p =Phenotypic standard deviation, H^2 =Heritability, K=selection differential (K=2.063 at 5% selection intensity). Genetic advance as percent of the mean (GAM) was calculated by excel used the formula as (Johnson et al., 1955). $GAM = (GA/\bar{X}) \times 100$. Where, GAM=Genetic advance as percent of mean, GA=Genetic advance at 5% selection intensity, $\bar{X}$ =Population mean

2.4.5. Phenotypic and genotypic correlation analysis

Correlation coefficient analysis was done using R software, it helped to determine the nature and degree of relationship between any two measurable characters (Fellahi et al., 2013). Phenotypic and genotypic correlation coefficients was estimated (Miller et al., 1958) as:

Phenotypic correlation coefficient = $COV_{pxy} / \sqrt{(\sigma_{px}^2)(\sigma_{py}^2)}$

Genotypic correlation coefficient (r_{gxy}) = $COV_{gxy} / \sqrt{(\sigma_{gx}^2)(\sigma_{gy}^2)}$

Phenotypic covariance ($pcov_{xy}$) = $gcov_{xy} + ecov_{xy}$

Genotypic covariance ($gcov_{xy}$) = $(MSPg - MSPe) / r$

Environmental correlation coefficient (r_{exy}) = $Cov_{exy} / \sqrt{(\sigma_{ex}^2)(\sigma_{ey}^2)}$

Where, r_{xy} = Phenotypic correlation coefficient between traits x and y

r_{gxy} = 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

MSPg = Mean square product for genotypes

MSPe = Means square products of error

r = Number of replication

The level of significance of phenotypic and genotypic correlation coefficients was tested using the formula suggested by Robertson (1959) using a t-table at ($g-2$) degree of freedom at 5% level of significance: where, g was number of genotypes. Accordingly, the phenotypic correlation coefficient value was tested for its significance by employing

the following formula: $t = rp / (SE(r_p))$, $SE(r_p) = \sqrt{((1-r_p^2)/(n-2))}$
Where, r_p = Phenotypic correlation

$SE(r_p)$ = Standard error of phenotypic correlation

n = Number of genotypes to be tested

The genotypic correlations coefficients were tested for their significance by the formula indicated below:

$t_{cal} = r_g / (SE(r_g))$, $SE(r_g) = \sqrt{(1-r_g^2)/(2H_x^2 \times H_y^2)}$

Where, $SE(r_g)$ = Standard error of genotypic correlation coefficient

r_g = Genotypic correlation coefficient; n is the number of genotypes test

H^2 = Heritability

2.4.6. Disease scoring

To evaluate these genotypes for yellow and Leaf rust diseases scoring were made for both yellow and stem rust. Host responses to both rusts were recorded based on the modified Cobb scale (Peterson et al., 1948). This scale combined several infection types; resistant (R), moderately resistant (MR), moderately susceptible (MS), moderately Resistant to Moderately Susceptible (MRMS) and susceptible (S). Severity was recorded on 0–100% scale where 0% was considered as immunity while 100% was completely susceptible.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance (ANOVA)

Analysis of variance (ANOVA) revealed significant genetic variation ($p < 0.01$) among the 50 wheat genotypes for seven of the nine characters studied (Table 2). These characters included days to 50% heading, days to 90% maturity, grain yield, hectoliter weight, agronomic score and yellow rust severity, and stem rust severity. Stem rust severity also displayed significant variation at ($p < 0.05$) among the genotypes. Plant height showed not statistically significant variation among the genotypes.

The observed significant differences among genotypes for most of the assessed traits indicated substantial genetic diversity within the 50 wheat genotypes tested. This diversity presented a valuable resource for breeders aiming to develop new wheat varieties with specific desired characteristics. Breeders could leverage this variation to select genotypes excelling in traits of interest, such as high yield, early maturity, or disease resistance.

This finding aligned with previous research by Alemu et al. (2017b), Wani et al. (2018) and Zewdu et al. (2024a) who also reported significant genetic variability among wheat genotypes for days to heading, maturity, plant height, grain filling period, thousand kernel weight, and grain yield.

Table 2: Mean squares, coefficient of variation and R-square for 10 traits of 50 bread wheat genotypes evaluated at Kulumsa Agricultural Research center in 2023

Traits	Replication (DF=1)	Block (Replication) (DF=8)	Genotype MS (DF=49)	Error MS (DF=41)	CV (%)	R ²
DTH	10.24	1.47	15.96**	1.32	1.8	0.94
DTM	14.44	5.80	12.80**	1.44	1.10	0.92
PHT	53.29	18.62	38.80 ^{ns}	23.71	5.92	0.76
AgrSc	1.00	0.03	0.22**	0.08	13.10	0.83
TKW	1.00	7.90	33.90**	7.75	7.27	0.84
HLW	3.62	0.80	5.98**	1.03	1.43	0.88
YrS	33.64	31.83	595.28**	50.75	36.31	0.93
SrS	51.84	54.64	162.94*	88.56	41.27	0.78
GYLD	70596.49	28590.43	70549.23**	24528.36	11.81	0.88

* and **: Indicates significant at ($p=0.05$) and highly significant at ($p=0.01$) probability levels respectively; DTH: Days to heading; DTM: Days to Maturity; PHT: Plant height; AgrSc: Agronomic score; TKW: Thousand kernel weight; HLW: Hectoliter weight; YrS: Yellow rust severity; SrS: Stem rust severity; GYLD: Grain yield; MS: Mean square; CV: Coefficient of variations; DF: Degree of freedom and R²: Coefficient of determination

3.2. Mean performance of studied bread wheat genotypes

This section detailed the variation observed among 50 wheat genotypes for several key traits (Table 3).

3.2.1. Days to 50% heading

This ranged from 57.5 to 66.5 days, with an average of 62.14 days. 34 genotypes (74%) head earlier and 12 genotypes (42%) heading later than the check Balcha. Nearly even distribution observed with 19 genotypes head significantly earlier than the mean and 31 genotypes heading later than the mean.

3.2.2. Days to 90% maturity

This ranged from 110 to 115 days, with an average of 114.2

days. Here, a higher proportion (88%) of genotypes matured earlier than the check (Balcha) and 5 genotypes matured later than the check (Balcha). 26 genotypes (52% of the studied genotypes) matured earlier and 24 (48% of the studied genotypes) matured later than the mean.

3.2.3. Plant height

Plant height ranged from 74 to 94 cm, with an average of 82.7 cm. All genotypes showed short in plant height than the check (Balcha). The half (50%) of the genotypes had lower than average plant height, while the remaining half (50%) genotypes had higher values.

3.2.4. Thousand kernel weight

This ranged widely, from 33–45 g, with the mean of 38

Table 3: Minimum and Maximum values with their corresponding genotype, Ranges, means and standard errors of the means for 7 quantitative traits among 50 bread wheat genotypes tested at Agricultural Research center in 2023

Traits	Minimum		Maximum		Range	Mean	Standard error
	Values	Genotype	Values	Genotype			
DTH	57.5	EBW232663	66.5	EBW232636	57.50-66.50	62.14	0.87
DTM	110	EBW232663	115	EBW232636	110.00-115.00	114.2	0.91
PHT	74.00	EBW232639	94.	Balcha (check)	74.00-94.00	82.7	3.71
AgrSc	1.50	Some	2.5	Some	1.50-2.50	2.09	0.21
TKW	33	Some	45	EBW232627, EBW232654	33.00-45.00	38.30	2.12
HLW	68.03	EBW232651	72.79	EBW232640	68.03-72.79	70.76	0.77
GYLD	891	EBW232651	1682.50	EBW232625	891.00-1682.50	1325.96	119.28

DTH: Days to heading; DTM: Days to Maturity; PHT: Plant height; AgrSc: Agronomic score; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield

g 42 genotypes (84% of the studied genotypes) had lower kernel weight than the check (Balcha), while the remaining 7 genotypes (14%) had higher kernel weight values than the check (Balcha). Notably, 21 genotypes had lower kernel weight than the mean (38 g), while 29 genotypes had greater than the mean.

3.2.5. Hectoliter weight

Ranged from 68.03 to 72 hl kg⁻¹, with an average of 70.76 hl kg⁻¹. Here, 42% of the genotypes had lower than average hectoliter weight, while 58% had higher hectoliter weight values. Compared to the check variety Balcha (69.28 hl kg⁻¹), 4 genotypes had lower hectoliter weight, but a positive sign was that 45 genotypes displayed superior values.

3.2.6. Agronomic score

This ranged from 1.5–2.5, with an average of 2.09. Interestingly, 54% of the genotypes had a lower score than the average, while 46% had a higher agronomic score. However, compared to the check variety Balcha (2.25), a high proportion (27 genotypes) had a lower score.

3.2.7. Grain yield

This exhibited the widest range, varying from 891 (EBW232651) to 1682.5 (EBW232625) kg ha⁻¹, with an average of 1325.96 kg ha⁻¹. 27 genotypes (54% of the studied genotypes) yielded less than the average, while the remaining 23 genotypes (46%) produced more. Encouragingly, 39 genotypes (78% of studied genotypes) exhibited superior grain yield compared to check Balcha. Only seven genotypes yielded lower than the check variety Balcha (1242.5 kg ha⁻¹).

Generally, the study revealed substantial genetic diversity among the wheat genotypes for all measured traits. There's potential for breeding efforts to target earlier heading combined with faster maturity, improved kernel weight,

and even higher grain yield. Many genotypes displayed superior performance compared to the check variety Balcha, highlighting the potential for breeding advancements. These findings were consistent with previous research by Fikre et al. (2015), Naik et al. (2015) and Alemu et al. (2017b) who also reported significant variations in grain yield and related traits among bread wheat genotypes.

3.3. Estimation of genotypic and phenotypic coefficient of variations

This section explored the extent of phenotypic and genotypic variation among the 50 wheat genotypes using the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV).

3.3.1. Range of variation

PCV and GCV ranged from 2.34% to 18.53% and 2.09% to 12.66%, respectively. These values were categorized as low (<10%), moderate (10–20%), and high (>20%) (Sivasubramanian and Menon, 1973).

3.3.2. Moderate PCV and GCV

A moderate range of PCV and GCV were obtained for agronomic score (18.53% and 12.66%) and grain yield (16.44% and 11.44%) respectively and moderate PCV (11.91%) was observed for thousand kernel weight, with a lower genotypic coefficient of variation (9.44%) (Table 4). This suggested some environmental influence on this trait, but also the presence of some heritable genetic variation for improvement. Similar findings for moderate PCV for thousand kernel weight were reported by Fikre et al. (2015). However, Dutamo et al. (2015a) observed high PCV and GCV for thousand kernel weight, highlighting potential environmental variation depending on the specific genotypes and growing conditions used in each study.

3.3.3. Low PCV and GCV

Days to heading, days to maturity, plant height, and

Table 4: Estimation of variance components, heritability and genetic advance as percent of means for 8 quantitative traits of 50 bread wheat genotypes tested at Kulumsa agricultural research center in 2023

Trait	σ^2_g	σ^2_p	σ^2_e	GCV	PCV	ECV	H ² B	GA	GAM
DTH	7.32	8.64	0.66	4.35	4.73	1.31	84.72	4.77	7.67
DTM	5.68	7.12	0.72	2.09	2.34	0.74	79.78	4.33	3.79
PHT	7.55	31.26	11.86	3.32	6.76	4.16	24.14	9.07	10.96
AgrSc	0.07	0.15	0.04	12.66	18.53	9.57	46.67	0.63	30.05
TKW	13.08	20.83	3.88	9.44	11.91	5.14	62.79	7.40	19.32
HLW	2.48	3.51	0.52	2.22	2.65	1.01	70.61	3.04	4.29
GYLD	23010.44	47538.80	12264.18	11.44	16.44	8.35	48.40	353.55	26.66

σ^2_g : Genotypic variance; σ^2_p : Phenotypic variance; σ^2_e : Environmental variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; ECV: Environmental coefficient of variation; H²B: Broad sense heritability; GA: Genetic advance; GAM: Genetic advance as percent of mean; DTH: Days to heading; DTM: Days to Maturity; PHT: Plant height; AgrSc: Agronomic score; GYLD: Grain yield; HLW: Hectoliter weight; TKW: Thousand kernel weight

hectoliter weight displayed low values for both PCV and GCV (all less than 10%). This indicated relatively low phenotypic and genotypic variation for these traits in this set of genotypes. These results were consistent with previous reports by Tilahun et al. (2020), Kabir et al. (2017), and Chimdesa et al. (2017), who also found low PCV and GCV for plant height, days to heading, days to maturity, and hectoliter weight.

The observed variation in PCV and GCV provided valuable insights for breeders. Traits with moderate PCV and GCV, like grain yield, agronomic and thousand kernel weight score offered the most significant potential for improvement through selection. Breeders could focus their efforts on these traits to develop new wheat varieties with superior performance. For these traits breeding strategies might need to consider both genetic and environmental factors. Breeders might employ selection methods that minimize environmental influences or incorporate environmental stability testing alongside selection for genetic improvement. Traits exhibiting low PCV and GCV, like days to heading and plant height, might have limited potential for further improvement within this set of genotypes. However, these traits might be important for breeding programs with specific breeding objectives, such as developing varieties adapted to particular planting windows or requiring specific plant stature.

Overall, the analysis of PCV and GCV highlighted the presence of significant genetic variation for key traits in these wheat genotypes. Breeders could leverage this information to guide their selection strategies and develop new wheat varieties with improved yield, agronomic performance, and other desired characteristics.

3.4. Estimation of heritability and genetic advance

Broad-sense heritability (H^2) estimates ranged from 24.14% for plant height to 84.72% for days to heading. These values were categorized as low (<40%), medium (40–59%), moderately high (60–79%), and very high (>80%) (Singh, 2001).

Several traits exhibited moderately high to very high heritability (>60%). These included days to heading (84.72%), days to maturity (79.78%), hectoliter weight (70.61%) and thousand kernel weight (62.79%). This indicated a strong genetic influence on these traits and a high likelihood of improvement through selection. These findings aligned with previous research by Rajput et al. (2019), Upadhyay et al. (2019), and Sami et al. (2021), who also reported high heritability for these traits. Grain yield (48.40%) and agronomic score (46.67%) displayed medium broad-sense heritability. While still influenced by genetics, these traits might also be somewhat affected by environmental factors. Whereas, plant height showed

low heritability (24.14%) which highly affected by environmental factors. Genetic advance as a percentage of the mean (GAM) ranged from 4.19% for days to maturity to 46.79% for grain yield. GAM was categorized as low (0–10%), moderate (10–20%), and high (>20%) (Johnson et al., 1955).

Traits with high GAM (>20%) were grain yield (30.05%) and agronomic score (26.66%), and traits with moderate GAM thousand kernel weight (19.32%) and plant height (10.96%). This suggested substantial genetic progress could be achieved through breeding for these traits. Similar findings were reported by Kabir et al. (2017), who observed high GAM for grain yield and Fikre et al. (2015) and Chimdesa et al. (2017), who observed moderate GAM for plant height. The remaining traits (days to heading, days to maturity, grain filling period, and plant height) displayed low GAM (<10%). While improvement might still be possible, it might be slower for these traits within this set of genotypes. However, contrasting results was found by Kabir et al. (2017) who reported low GAM for plant height.

These variations highlighted the potential influence of the specific genotypes and environments used in different studies. The high broad-sense heritability observed for grain yield and agronomic score, coupled with their high genetic advance, suggested a significant role of additive gene action in controlling these traits.

For traits with moderate heritability and GAM (like thousand kernel weight), breeding strategies might need to account for both genetic and environmental factors. Selection methods that minimized environmental influence or incorporate environmental stability testing alongside selection for genetic improvement could be employed. Traits with low heritability and GAM might require more intensive breeding efforts or the use of different breeding techniques to achieve significant improvement within this set of genotypes. However, these traits might still be important for breeding programs with specific objectives.

Overall, the analysis of heritability and genetic advance provided valuable insights into the potential for improvement of various traits in these wheat genotypes. Breeders could leverage this information to prioritize breeding efforts and develop new wheat varieties with enhanced yield, agronomic performance, and other desired characteristics.

3.5. Genotypic and phenotypic correlations of grain yield with other traits

Grain yield exhibited strong positive and highly significant correlations ($p < 0.01$) at both genotypic (rg) and phenotypic (rp) levels with Agronomic Score (rg=0.72^{**}, rp=0.65^{***}) (Table 5). This indicated that genotypes with higher agronomic scores (potentially better overall agronomic

performance) also tended to have higher grain yield. Thousand Kernel Weight ($rg=0.53^{**}$, $rp=0.49^{**}$). This positive correlation indicated that genotypes with larger kernels generally produced higher grain yield. Hectoliter Weight ($rg=0.46^{**}$, $rp=0.46^{**}$). A positive correlation existed between grain yield and hectoliter weight, suggesting denser grains might contribute to higher yield. These findings suggested that selecting for improved agronomic score, hectoliter weight, and thousand kernel weight could be effective indirect selection strategies for enhancing grain yield in this breeding population.

Similar result reported that grain yield showed positively and significantly correlated with hectoliter weight at both genotypic and phenotypic correlation coefficient (Ashebr et al., 2020). Grain yield showed positively and significantly correlated with thousand kernel weight at both genotypic and phenotypic correlation coefficient (Ashebr et al., 2020).

Grain yield displayed a strong negative and highly significant correlation ($p<0.01$) at both genotypic and phenotypic levels with Yellow Rust Severity ($rg=-0.64^{**}$, $rp=-0.51^{**}$). This indicated that genotypes susceptible to yellow rust disease (higher severity scores) had lower grain yield. This highlighted the importance of incorporating yellow rust resistance into breeding programs to protect yield potential.

Days to heading, days to maturity, plant height and stem rust severity were not significantly correlated with grain yield at either genotypic or phenotypic correlation. The observed positive correlations between grain yield and agronomic score, hectoliter weight, and thousand kernel weight were encouraging for breeders. These traits could serve as valuable indirect selection criteria for improving grain yield. The negative correlation with yellow rust severity emphasized the need to prioritize resistance breeding to protect yield

potential from this disease. This result aligned with Zewdu and Yimam (2024b) who demonstrated a significant negative correlation between grain yield and yellow rust severity. The lack of significant correlations with days to heading, days to maturity, grain filling period, and stem rust severity suggested minimal influence of these traits on grain yield within this set of genotypes. However, these traits might still be important for breeding programs with specific objectives, such as developing varieties adapted to particular planting windows or resistant to a wider range of diseases.

Overall, the analysis of correlation coefficients provided valuable insights into the relationships between grain yield and other traits. Breeders could leverage this information to develop selection strategies that enhanced grain yield while also considering other important agronomic characteristics and quality traits.

3.6. Genotypic and phenotypic correlations among yield related traits

Days to 50% heading exhibited positive and highly significant ($p<0.01$) correlations with days to 90% maturity at both genotypic ($rg=0.51^{**}$) and phenotypic ($rp=0.57^{**}$) levels (Table 5). This positive correlation indicated that earlier heading lines also tended to mature earlier. Days to 50% heading also displayed negative significant ($p<0.05$) correlations with Plant height ($rp=-0.22^{*}$) and yellow rust severity ($rp=-0.22^{*}$) at phenotypic correlation. This implied that earlier heading lines were generally had short plant height and better resistance to yellow rust.

Days to 90% maturity displayed positive significant ($p<0.05$) at phenotypic correlation ($rp=0.23$) with agronomic score. Hectoliter weight displayed positive and highly significant correlations with thousand kernel weight at both genotypic

Table 5: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for 10 traits of 50 bread wheat genotypes tested at Kulumsa Agricultural Research Center in 2023

Variable	DTH	DTM	PHT	YrS	SrS	AgrSc	TKW	HLW	GYLD
DTH	1	0.61 ^{**}	-0.28 ^{ns}	-0.27 ^{ns}	0.01 ^{ns}	0.21 ^{ns}	-0.16 ^{ns}	0.02 ^{ns}	-0.10 ^{ns}
DTM	0.57 ^{**}	1	-0.32 ^{ns}	-0.07 ^{ns}	-0.09 ^{ns}	0.21 ^{ns}	0.08 ^{ns}	0.14 ^{ns}	0.11 ^{ns}
PHT	-0.22 [*]	-0.19 ^{ns}	1	0.05 ^{ns}	0.23 ^{ns}	0.14 ^{ns}	0.16 ^{ns}	0.24 ^{ns}	0.07 ^{ns}
YrS	-0.22 [*]	-0.05 ^{ns}	0.04 ^{ns}	1	-0.17 ^{ns}	-0.52 ^{**}	-0.48 ^{**}	-0.36 [*]	-0.64 ^{**}
SrS	-0.01 ^{ns}	-0.08 ^{ns}	0.26 [*]	-0.14 ^{ns}	1	-0.01 ^{ns}	-0.04 ^{ns}	-0.22 ^{ns}	-0.03 ^{ns}
AgrSc	0.20 [*]	0.23 [*]	0.13 ^{ns}	-0.41 ^{**}	0.01 ^{ns}	1	0.37 ^{**}	0.24 ^{ns}	0.72 ^{**}
TKW	-0.13 ^{ns}	0.04 ^{ns}	0.07 ^{ns}	-0.45 ^{**}	-0.05 ^{ns}	0.27 ^{**}	1	0.39 ^{**}	0.53 ^{**}
HLW	0.05 ^{ns}	0.12 ^{ns}	0.09 ^{ns}	-0.31 ^{ns}	-0.19 ^{**}	0.24 [*]	0.38 ^{**}	1	0.46 ^{**}
GYLD	0.12 ^{ns}	0.11 ^{ns}	0.05 ^{ns}	-0.51 ^{**}	0.01 ^{ns}	0.65 ^{**}	0.49 ^{**}	0.46 ^{**}	1

* and **: Indicates significant at ($p=0.05$) and highly significant at ($p=0.01$) probability levels respectively; ns: Non-significant; DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; AgrSc: Agronomic score; TKW: Thousand kernel weight; HLW: Hectoliter weight; YrS: Yellow rust severity; SrS: Stem rust severity; GYLD: Grain yield

and phenotypic correlation ($r_g=0.39^{**}$ and $r_p=0.38^{**}$), hectoliter weight also had positive significant correlations with and agronomic score ($r_p=0.24^*$) at phenotypic levels. However, hectoliter weight showed negative and highly significant correlations with stem rust severity at phenotypic correlation ($r_p=-0.19^{**}$), This indicated that larger seeds were associated with denser grains and better overall plant performance. This was in line with the observations of (Xu et al., 2015) who documented positive correlations between thousand kernel weight, hectoliter weight, and agronomic score in barley. Similar positive correlations between these traits were expected in wheat.

Yellow rust severity exhibited negative and highly significant correlations with thousand kernel weight ($r_g=-0.48^{**}$ and $r_p=-0.45^{**}$) and agronomic score ($r_g=-0.52^{**}$ and $r_p=-0.41^{**}$)

at both genotypic and phenotypic levels respectively. Yellow rust severity exhibited negative significant correlations with hectoliter weight at genotypic level ($r_g=-0.39^{**}$). This suggested that higher yellow rust infection led to reduced seed size.

Our study revealed a network of positive and significant correlations between several wheat traits, suggesting that improving one trait can have a cascading effect on others, ultimately leading to increased grain yield. Analyses of genotypic and phenotypic correlation showed that, genotypic correlations were generally higher than phenotypic correlations, indicating a strong underlying genetic basis for these relationships. Traits significantly associated with grain yield also exhibited correlations with each other, highlighting their inherent interconnectedness.

Table 6: Studied genotypes yellow and stem rust severity and reactions

Entry	Genotype	YrS	YrR	SrS	SrR	Entry	Genotype	YrS	YrR	SrS	SrR
1	Balcha	30	MR	30	S	26	EBW232641	20	MS	10	MS
2	EBW232617	40	MR	20	MS	27	EBW232642	40	S	20	MRMS
3	EBW232618	30	MS	30	MS	28	EBW232643	10	MRMS	15	MS
4	EBW232619	25	MRMS	1	MRMS	29	EBW232644	40	S	5	MS
5	EBW232620	5	MR	5	MRMS	30	EBW232645	10	MR	1	MR
6	EBW232621	25	MR	15	MS	31	EBW232646	50	MR	10	MS
7	EBW232622	60	S	5	MS	32	EBW232647	40	S	1	MRMS
8	EBW232623	50	S	5	MS	33	EBW232648	20	MR	15	0
9	EBW232624	80	MRMS	10	MS	34	EBW232649	15	MS	10	MS
10	EBW232625	15	MRMS	1	MS	35	EBW232650	10	MR	20	S
11	EBW232626	20	MS	5	MRMS	36	EBW232651	90	S	30	S
12	EBW232627	40	MRMS	20	MS	37	EBW232652	40	S	5	MRMS
13	EBW232628	40	MS	15	MS	38	EBW232653	20	S	1	0
14	EBW232629	30	MRMS	15	MS	39	EBW232654	30	MRMS	1	MR
15	EBW232630	20	MRMS	5	MS	40	EBW232655	5	MR	30	MS
16	EBW232631	60	MR	85	MRMS	41	EBW232656	30	MR	5	MRMS
17	EBW232632	15	MRMS	5	MRMS	42	EBW232657	50	S	5	MS
18	EBW232633	60	S	0	0	43	EBW232658	50	S	30	0
19	EBW232634	20	MRMS	5	MRMS	44	EBW232659	5	MR	5	0
20	EBW232635	40	MR	10	MRMS	45	EBW232660	5	MR	5	MS
21	EBW232636	10	MRMS	20	MRMS	46	EBW232661	5	MR	15	MS
22	EBW232637	20	MRMS	1	MR	47	EBW232662	40	S	10	0
23	EBW232638	15	MRMS	1	MR	48	EBW232663	40	MS	5	MR
24	EBW232639	15	MR	10	MR	49	EBW232664	40	MRMS	1	MS
25	EBW232640	30	MS	10	MS	50	EBW232665	10	MRMS	15	MS

MR: Moderately Resistance; MS: Moderately Susceptible; MRMS: Moderately resistant to moderately susceptible; S: Susceptible; R: Resistance

This suggested that breeding programs focused on improving multiple, interrelated traits, such as thousand kernel weight, and hectoliter weight, yellow rust severity hold promise for significant grain yield advancements.

The findings from this study had important implications for breeding programs aimed at improving grain yield. Breeders could leverage the identified correlations to develop selection strategies that focus on traits that were directly or indirectly associated with higher yields. By selecting for genotypes with superior agronomic scores, larger kernels, denser grains, and resistance to diseases like yellow rust, breeders could increase the likelihood of developing high-yielding varieties.

3.7. Rust severity and reaction

The final rust severity for yellow rust severity showed from 5–90% (Table 6). Based on final rust severity, for yellow rust 24 genotypes (48% of the studied genotypes) showed high adult plant resistance (0–29% of severity), 17 genotypes (34% of studied genotypes) observed as medium resistance (30–40% of severity) and 9 genotypes (18% of studied genotypes) observed above 41% yellow rust severity (Table 6). The result line up with Pathan and Park (2006) who categorized the level of adult plant resistance such as high, medium and low APR based on their severity percentage. Tested genotypes showed diverse reactions for yellow rust ranging from moderately resistance (MR) to susceptible (S) responses. 16 genotypes (32% of the studied genotypes) were observed moderately resistance (MR), and 15 genotypes (30% of the studied genotypes) were showed moderately resistant to moderately susceptible (MRMS) reaction type. 7 genotypes (14% of the studied genotypes) were showed moderately susceptible (MS) reaction, and 12 genotypes (24% of the studied genotypes) were observed susceptible (S) reactions for yellow rust response (Table 6). Similar work also done by different researchers such as Bayisa et al. (2023); Shewaye et al. (2021); Zewdu and Yimam (2024b) and Zewdu et al. (2024c) who reported a range of severity and reactions of yellow rust disease observed on Bread wheat genotypes.

The final rust severity for stem rust severity showed from immune (0) to 85%. Based on final rust severity percentage, for stem rust 44 genotypes (88% of the studied genotypes) showed 0–29% of severity, and 6 genotypes (12% of studied genotypes) were observed >30% of stem rust severity (Table 6). Tested genotypes showed diverse reactions for stem rust ranging from immune (0) to susceptible (S) responses. 6 genotypes (26% of the studied genotypes) were observed immune (0), 6 genotypes (12% of the studied genotypes) were observed moderately resistant (MR), 12 genotypes (24% of the studied genotypes) were observed moderately resistant to moderately susceptible (MRMS) reaction type, 23 genotypes (46% of the studied genotypes) were displayed

moderately susceptible (MS) reaction, and 3 genotypes (6% of the studied genotypes) were showed susceptible (S) reaction for stem rust disease response (Table 6). Similar work also done by different researchers such as Shewaye et al. (2021) and Zewdu and Yimam (2024b) who reported a range of severity and reactions of stem rust disease observed on Bread wheat genotypes

4. CONCLUSION

Analysis of variance revealed significant genetic variation ($p < 0.01$) among genotypes. High heritability observed for days to heading, days to maturity, hectoliter weight and thousand kernel weight, and high GAM viz. grain yield and agronomic score. Grain yield exhibited strong correlations at both genotypic and phenotypic levels with agronomic score, thousand kernel weight and hectoliter weight and negative correlation with yellow rust severity. This finding suggested that selecting for improved agronomic score, hectoliter weight, and thousand kernel weight could be effective for enhancing grain yield.

5. ACKNOWLEDGEMENT

The authors would like to express gratitude for Ethiopian Institute of Agricultural Research and Kulumsa Agricultural Research Center, and we are also grateful to CIMMYT for its support in providing experimental materials to conduct this study. We would like to thank Mr Nigussie Degefa, Mr. Mamuye Tesema, Mrs. Banchi Simie and mrs. Etenesh Melese for their supports.

6. REFERENCES

- Abebe, G., Debebe, S., 2019. The role of wheat in Ethiopian food security. *Ethiopian Journal of Agricultural Sciences* 28(1), 45–57. Available from: <https://gjrpublication.com/wp-content/uploads/2024/11/GJRALs20314.pdf>.
- Ajmal, S.U., Zakir, N., Mujahid, M.Y., 2009. Estimation of genetic parameters and character association in wheat. *Journal of Agricultural Biological Sciences* 1(1), 15–18. Available from: https://www.uaar.edu.pk/jabs/files/jabs_1_1_2.pdf.
- Allard, R.W., 1960. *Principles of plant breeding*. John Wiley & Sons, 485p. Available from: <https://acsess.onlinelibrary.wiley.com/doi/10.2134/agronj1962.00021962005400040037x>.
- Alemu, A., Debele, A., Mekonen, A., 2017a. Genetic variability and heritability of wheat traits in Ethiopia. *African Journal of Agricultural Research* 12(4), 282–290. DOI: <https://doi.org/10.5897/AJAR2016.1159>.
- Alemu, D., Tadesse, W., Tesfaye, K., 2017b. Genetic variability and association among yield and yield-related traits in bread wheat (*Triticum aestivum* L.)

- genotypes. African Journal of Agricultural Research 12(21), 1808–1816. DOI: <https://doi.org/10.5897/AJAR2017.12321>.
- Anteneh, A., Asrat, D., 2020. Wheat production and marketing in Ethiopia: Review study. Cogent Food and Agriculture 6(1), 1778893. Available from: <https://www.tandfonline.com/doi/full/10.1080/23311932.2020.1778893>.
- Anonymous, 2023a. World Food and Agriculture Statistical Yearbook 2023. Rome. Available from: <https://doi.org/10.4060/cc8166en>. Accessed on: March 30, 2026
- Anonymous, 2023b. World agricultural supply and demand estimates (WASDE-643). World Agricultural Outlook Board. Available from: <https://www.usda.gov/oce/commodity/wasde>. Accessed on: March 30, 2026.
- Anonymus, 2021. Ethiopia: grain and feed annual (Report No. ET2021-0008). Available from: https://apps.fas.usda.gov/newgainapi/api/Report/DownloadReportByFileName?fileName=Grain%20and%20Feed%20Annual_Addis%20Ababa_Ethiopia_03-15-2021. Accessed on: April 2, 2026.
- Anonymous, 2023. Report on agricultural sample survey: area and production of major crops (Private Peasant Holdings, Meher Season). Statistical Bulletin 594. Addis Ababa, Ethiopia. Available from: <https://www.ess.gov.et>. Accessed on: April 4, 2026.
- Ashebr, T., Tadesse, Z., Abate, M., 2020. Correlation and path coefficient analysis of yield and yield-related traits in durum wheat (*Triticum durum* Desf.) genotypes. Journal of Plant Breeding and Crop Science 12(3), 86–91. DOI: <https://doi.org/10.5897/JPBCS2020.0899>.
- Bayisa, T., Terefe, H., Letta, T., 2023. Screening of bread wheat genotypes for slow rusting resistance to yellow rust (*Puccinia striiformis* f.sp. tritici) and association among parameters in Southeastern Ethiopia. Journal of Plant Pathology & Microbiology 14, 674. Available from: <https://www.walshmedicalmedia.com/open-access/screening-of-bread-wheat-genotypes-for-slow-rusting-resistance-to-yellow-rust-empuccinia-striiformis-fsp-triticiem-and-association-120724.htm>.
- Braun, H.J., Atlin, G., Payne, T., 2010. Multi-location testing as a tool to identify plant response to climate change. In: Reynolds, M.P., (ed.), Climate change and crop production. CABI Climate Change Series, U.K. pp. 115–138. Available from: <https://www.sciepub.com/reference/127602>.
- Burton, G.W., Devane, E.H., 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal 45(10), 478–481. Available from: <https://access.onlinelibrary.wiley.com/doi/10.2134/agronj1953.00021962004500100005x>.
- Chimdesa, O., Mohammed, W., Eticha, F., 2017. Analysis of genetic variability among bread wheat (*Triticum aestivum* L.) genotypes for growth, yield and yield components in Bore district, Oromia regional state. Agriculture, Forestry and Fisheries 6(6), 188–199. Available from: https://www.researchgate.net/publication/326510779_analysis_of_genetic_variability_among_bread_wheat_triticum_aestivum_l_genotypes_for_growth_yield_and_yield_components_in_bore_district-oromia_regional_state.
- Dutamo, D., Alamerew, S., Eticha, F., Assefa, E., 2015. Genetic variability in bread wheat (*Triticum aestivum* L.) germplasm for yield and yield component traits. Journal of Biology, Agriculture and Healthcare 5, 140–147. Available from: https://www.researchgate.net/publication/358117651_genetic_variability_in_bread_wheat_triticum_aestivum_l_germplasm_for_yield_and_yield_component_traits.
- Fikre, G., Alamerew, S., Tadesse, Z., 2015. Genetic variability studies in bread wheat (*Triticum aestivum* L.) genotypes at Kulumsa agricultural research center, South East Ethiopia. Journal of Biology, Agriculture and Healthcare 5, 89–98. Available from: https://www.researchgate.net/publication/308764540_genetic_variability_studies_in_bread_wheat_triticum_aestivum_l_genotypes_at_kulumsa_agricultural_research_center_south-east-ethiopia.
- Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955. Estimates of genetic and environmental variability in soybeans. Agronomy Journal 47(7), 314–318. Available from: <https://access.onlinelibrary.wiley.com/doi/10.2134/agronj1955.00021962004700070009x>.
- Kabir, R., Israr, A., Rehman, A.U., Qamar, M., Intikhab, A., 2017. Evaluation of bread wheat genotypes for variability and association among yield and yield related traits. International Journal of Biosciences 11(1), 7–14. ISSN: 2220-6655 (Print), 2222-5234. Available from: https://www.researchgate.net/publication/320444105_Evaluation_of_bread_wheat_genotypes_for_variability_and_association_among_yield_and_yield_related_traits.
- Mollasadeghi, N., Shahryari, M., 2011. Wheat production and its global importance. International Journal of Plant Production 5(2), 77–84. Available from: https://www.researchgate.net/publication/288765421_Important_morphological_markers_for_improvement_of_yield_in_bread_wheat.
- Naik, V.R., Biradar, S.S., Yadawad, A., Desai, S., Veerasha, B., 2015. Study of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes. Research Journal of Agricultural Science 6(1), 123–125. Available from: https://www.researchgate.net/publication/288765421_Important_morphological_markers_for_improvement_of_yield_in_bread_wheat.

- .net/publication /284119713_study_of_genetic_variability_parameters_in_bread_wheat_triticum_aestivum_l_genotypes.
- Pathan, A.K., Park, R.F., 2006. Evaluation of wheat cultivars, landraces and breeding lines for resistance to stripe rust (*Puccinia striiformis* f. sp. tritici) in a field environment. *Euphytica* 149(1-2), 271-282. DOI: <https://doi.org/10.1007/s10681-005-9081-4>.
- Peterson, R.F., Campbell, A.B., Hannah, A.E., 1948. A diagrammatic scale for estimating rust intensity on leaves and stems of cereals. *Canadian Journal of Research* 26(5), 496-500. Available from: <https://cdnsiencepub.com/doi/10.1139/cjr48c-033>.
- Rajput, R.S., 2019. Path analysis and genetic parameters for grain yield in bread wheat (*Triticum aestivum* L.). *Annual Research & Review in Biology* 31(3), 1-8. Available from: <https://journalarrb.com/index.php/ARRB/article/view/1327>.
- Rauf, S., Tariq, S.A., Hassan, S.W., 2012. Estimation of pedigree based diversity in Pakistani wheat (*Triticum aestivum* L.) germplasm. *Communications in Biometry and Crop Science* 7(1), 14-22. Available from: https://www.researchgate.net/publication/235910150_estimation_of_pedigree_based_diversity_in_pakistani_wheat_triticum_aestivum_l_germplasm.
- Robertson, A., 1959. The sampling variance of the genetic correlation coefficient. *Biometrics* 15(2), 469-485. Available from: <https://www.jstor.org/stable/2527750>.
- Sami, U.A., Azeem, A., Sher, A., Ijaz, M., Sattar, A., Saleem, M.A., Bibi, M., Abbas, N., Hussain, M., 2021. Assessment of genetic variability and direct-indirect contribution of post-anthesis traits to the grain yield in bread wheat (*Triticum aestivum* L.) at different sowing dates. *International Journal of Agriculture and Biology* 26(1), 193-200. Available from: <https://www.cabidigitallibrary.org/doi/pdf/10.5555/20210355187>.
- Shewaye, Y., Zegaye, H., Tadesse, Z., 2021. Impact of stem and yellow rusts on grain yield of bread wheat (*Triticum aestivum* L.) genotypes under rainfed conditions of Ethiopia. *International Journal of Bioorganic Chemistry* 6(1), 7-13. Available from: https://www.researchgate.net/publication/353216075_impact_of_stem_and_yellow_rusts_on_grain_yield_of_bread_wheat_triticum_aestivum_l_genotypes_under_rainfedconditions_of_ethiopia.
- Singh, R.K., 2001. *Plant breeding principles and methods*. Kalyani Publishers. <https://archive.org/details/in.ernet.dli.2015.271669>.
- Sivasubramanian, S., Menon, N., 1973. Heterosis and inbreeding depression in rice. *Advances in Agronomy* 47, 85-140. Available from: <https://www.sciencedirect.com/reference/127212>.
- Tadesse, W., Halila, H., Jamal, M., 2017. Role of sustainable wheat production to ensure food security in the cwana region. *Journal of Experimental Biology and Agricultural Sciences* 5, 15-32. Available from: https://www.researchgate.net/publication/319616190_role_of_sustainable_wheat_production_to_ensure_food_security_in_the_cwana_region.
- Tadesse, W., Bishaw, Z., Assefa, S., 2018. Wheat production and breeding in Sub-Saharan Africa: Challenges and opportunities in the face of climate change. *International Journal of Climate Change Strategies and Management* 11(5), 696-715. DOI: <https://doi.org/10.1108/IJCCSM-02-2018-0015>. <https://www.emerald.com/ijccsm/article/11/5/696/129408/Wheat-production-and-breeding-in-Sub-Saharan>.
- Tilahun, B., Habtamu, T., Tesfaye, L., 2020. Genetic variability, heritability and genetic advance among bread wheat genotypes at Southeastern Ethiopia. *Agriculture, Forestry and Fisheries* 9(2), 128-134. DOI: 10.11648/j.aff.20200904.15.
- Tesfaye, T., Tsige, G., Tadesse, D., 2014. Genetic variability, heritability and genetic diversity of bread wheat (*Triticum aestivum* L.) genotype in western Amhara region, Ethiopia. *Wudpecker Journal of Agricultural Research* 3(1), 026034. Available from: [https://www.semantic.scholar.org/paper/Genetic-variability-%2C-heritability-and-genetic-of-\(-Tesfaye-Genet/a0bea71df63a22c1a161343b744ac6d44208d427](https://www.semantic.scholar.org/paper/Genetic-variability-%2C-heritability-and-genetic-of-(-Tesfaye-Genet/a0bea71df63a22c1a161343b744ac6d44208d427).
- Upadhyay, K., Adhikari, N., Sharma, S., 2019. Genetic variability and cluster analysis of wheat (*Triticum aestivum* L.) genotypes in foot hill of Nepal. *Archives of Agriculture and Environmental Science* 4, 350-355. Available from: <https://journals.Aesacademy.org/index.php/aaes/article/view/aaes-04-03-013>.
- Wani, S.H., Sheikh, F., Najeeb, S., Iqbal, A.M., Kordrostami, M., Parry, G., Jeberson, M.S., 2018. Genetic variability study in bread wheat (*Triticum aestivum* L.) under temperate conditions. *Current Agriculture Research Journal* 6(3), 268-277. Available from: <https://www.agriculturejournal.org/volume6number3/genetic-variability-study-in-bread-wheat-triticum-aestivum-l-under-temperate-conditions/>.
- Yasin, G., 2015. Effect of integrated nutrient management on wheat: A Review. *Journal of Biology, Agriculture and Healthcare* 5(13), 68-76. Available from: <http://www.iiste.Org/Journals /index.php/JBAH/article/view/23955/24526>.
- Yen, C., Yang, J., Yuan, Z., Ning, S., Liu, D., 2020. Geographic and historical origin of wheat. In: *Biosystematics of triticeae*. Springer, Singapore. DOI: 10.1007/978-981-13-9931-2_10.

- Zewdu, D., Yimam, K., 2024b. Evaluation of bread wheat (*Triticum aestivum* L.) genotypes for yellow and stem rust adult plant resistance and disease impact on grain yield. *Agricultural and Biological Research* 40(2), 974–979. Available from: https://www.researchgate.net/publication/380039253_evaluation_of_bread_wheat_triticum_aestivum_l_genotypes_for_yellow_and_stem_rust_adult_plant_resistance_and_disease_impact_on_grain_yield [accessed May 27 2026].
- Zewdu, D., Solomon, T., Alemu, G., Dabi, A., Geleta, N., Sime, B., Duga, R., 2024c. Phenotypic screening of bread wheat (*Triticum spp.* L.) germplasm collection for yellow and leaf rust disease resistance. *International Journal of Economic Plant* 11(3), 310–315. DOI: <http://doi.org/10.23910/2/2024.5452a>.
- Zewdu, D., Mekonnen, F., Geleta, N., 2024a. Correlation and path analysis for yield and yield component traits on bread wheat (*Triticum aestivum* L.) genotypes. *International Journal of Bio-resource and Stress Management* 15(1), 01–13. DOI: [HTTPS:// DOI. ORG/ 10.23910/1.2024.5040](https://doi.org/10.23910/1.2024.5040).