Original Research Article

Study on Genetic parameters and Associations for Yield and Yield-Related Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes

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Abstract

The research was conducted at KARC in 2023 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 eight of the ten characters studied. Plant height and thousand kernel weight displayed significant variation (p<0.05) among the genotypes. The observed variation in PCV and GCV provides valuable insights for breeders. Traits with high PCV and GCV, viz grain yield and agronomic score, offer the most significant potential for improvement. Breeders can focus their efforts on these traits to develop new varieties with superior performance. Traits with moderate PCV and GCV breeding strategies may need to consider both genetic and environmental factors. The high broad-sense heritability observed for grain yield and agronomic score, coupled with their high genetic advance, suggests a significant role of additive gene action in controlling these traits. Traits with low heritability and GAM may require more intensive breeding efforts or the use of different breeding techniques. Grain yield displayed a strong negative and highly significant correlation at both genotypic and phenotypic levels with Yellow Rust Severity. The negative correlation with yellow rust severity emphasizes the need to prioritize resistance breeding to protect yield potential from this disease. The observed positive correlations between grain yield and agronomic score, hectoliter weight, and thousand kernel weight are encouraging for breeders. These traits can serve as valuable indirect selection criteria for improving grain yield. Thus, attention should be given for those traits for breeding program.

Keywords: *Associations; Bread wheat; Genetic parameters; Triticum aestivum.*

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; Shiferaw *et al.*, 2013). Global wheat production reached a staggering 776.5 million tonnes in 2020, with projections estimating similar levels for 2021 and 2022 (FAOSTAT, 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) (Feldmann, 2001). Within the realm of Ethiopian cereals cultivated under rain-fed conditions, wheat holds the number two spot in yield production (USDA, 2023) and the number three spot in terms of area coverage (ESS, 2023).

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 million tons (USDA, 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 (USDA, 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, G. and Debebe, S., 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 ton per hectar (ESS., 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 (Ferdous et al., 2011). 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 in 2023 main cropping season. The experimental site is located at at 08º01'10"Nlongitude and 39º09'11"E latitude at an altitude of 2200 meters above sea level. The mean annual rain fall of the site is 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 x 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 (Abay) presented in Table 1.

Table_1. Materials and Pedigree used for Study

GENOTYPE	PEDIGREE
EBW232340	NINGA #1
EBW232341	BORL14//BECARD/QUAIU #1
EBW232342	MUCUY*2//SUP152/BAJ #1
EBW232571	MUCUY*3//RL6077/AOC-YR
EBW232572	MISR 1//KACHU/KIRITATI
EBW232573	MUTUS*2/TECUE #1*2//KFA/2*KACHU
EBW232574	MUCUY*2/5/FRNCLN/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
EBW232575	KACHU/DANPHE/3/2*KACHU//KIRITATI/2*TRCH
EBW232576	SHA7//PRL/VEE#6/3/FASAN/4/HAAS8446/2*FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/FRET2*2/KUKUNA/8/KINGBIRD #1/9/2*BORL14
EBW232577	CIRO16*2/KINGBIRD #1//2*KABILU #1
EBW232578	T 2003 (CRE7)//MUNAL*2/WESTONIA/3/NADI#2
EBW232579	BORL14/5/WAXWING*2/KRONSTAD F2004/3/TRCH/SRTU//KACHU/4/SAUAL/YANAC//SAUAL
EBW232580	KACHU/SAUAL/5/KACHU/3/WHEAR//2*PRL/2*PASTOR/4/BOKOTA
EBW232581	NADI#2/MUCUY
EBW232582	UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR 1/5/NADI

ID	Pedigree
EBW232583	KAKURU/NADI#2
EBW232584	CROSBILL #1/DANPHE/7/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*KAUZ/6/PRL/2*PASTOR/8/NADI
EBW232585	PAURAQ/KENYA SUNBIRD//PAURAQUE #1/3/BORL14
EBW232586	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/CIRO16/6/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
EBW232587	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/BECARD/5/BORL14
EBW232588	BECARD*2/5/BAV92//IRENA/KAUZ/3/HUITES/4/DOLL/6/SW2148/2*ROLF07/3/HUW234+LR34/PRINIA*2//SNLG
EBW232589	FRANCOLIN #1/3/PBW343*2/KUKUNA*2//YANAC/4/KINGBIRD #1//INQALAB 91*2/TUKURU/5/CHIPAK
EBW232590	ATTILA*2/PBW65/5/CNO79//PF70354/MUS/3/PASTOR/4/BAV92/6/KINGBIRD #1/7/COPIO/8/BORL14
EBW232591	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92/7/BORL14
EBW232592	MUCUY*2/AMUR
EBW232593	Pavon 76, 20ï¿½ï¿½ + 7A.7S-L7/BORL14//KASUKO
EBW232594	BORL14*2/6/COPIO*2/5/UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA
EBW232595	UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR 1/5/BORL14/6/KASUKO
EBW232596	FRNCLN/3/ND643//2*PRL/2*PASTOR/4/FRANCOLIN #1*2/5/FRNCLN/NIINI #1//FRANCOLIN #1
EBW232597	MUTUS//ND643/2*WBLL1/3/BORL14/5/MUTUS/DANPHE #1/4/C80.1/3*BATAVIA//2*WBLL1/3/C80.1/3*QT4522//2*PASTOR
EBW232598	PASTOR/KAUZ/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*KAUZ/7/2*PRL/2*PASTOR//PBW343*2/KUKUNA/8/2*BORL14
EBW232599	MUTUS*2/KIRITATI//BORL14/3/MOKUE #1
EBW232600	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07/5/WHEAR/SOKOLL/6/BORL14/7/KASUKO
EBW232601	KACHU/SAUAL/3/TACUPETO F2001/BRAMBLING//KIRITATI*2/4/FRET2/TUKURU//FRET2/3/MUNAL #1
EBW232602	KACHU/SAUAL/3/TACUPETO F2001/BRAMBLING//KIRITATI*2/4/FRET2/TUKURU//FRET2/3/MUNAL #1
EBW232603	FRANCOLIN #1/3/PBW343*2/KUKUNA*2//YANAC/4/KINGBIRD #1//INQALAB 91*2/TUKURU*2/5/MUCUY
EBW232604	OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/SOKOLL//SUNCO/2*PASTOR/7/SOKOLL//SUNCO/2*PASTOR*2/8/CROSBILL #1/DANPHE/7/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*KAUZ/6/PRL/2*PASTOR
EBW232605	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
EBW232606	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
EBW232607	SITE/MO//PASTOR/3/TILHI/4/WAXWING/KIRITATI/5/KACHU #1/KIRITATI//KACHU*2/6/KACHU/SAUAL*2//COPIO
EBW232608	SITE/MO//PASTOR/3/TILHI/4/WAXWING/KIRITATI/5/KACHU #1/KIRITATI//KACHU*2/6/KACHU/SAUAL*2//COPIO
EBW232609	SWSR22T.B./5/KAUZ//ALTAR 84/AOS/3/KAUZ/4/SW94.15464/6/2*PRL/2*PASTOR/7/BABE/8/VILLA JUAREZ F2009/DANPHE #1
EBW232610	BABE/2*BORL14
EBW232611	YR57#5474-6/3*BORL14

EBW232612	YR57#5474-6/3*BORL14
EBW232613	Pavon 76, 20ï¿½ï¿½ + 1R.1D5+10-2(1D)/BORL14//2*KASUKO
EBW232614	Pavon 76, 20ï¿½ï¿½ + 1R.1D5+10-2(1D)/3*MUCUY
EBW232615	SERI//T.DICOCCON PI94623/AE.SQUARROSA (1027)/3/MUCUY/4/MUTUS*2/HARIL #1/5/MUCUY
EBW232616	IRAGI/3*NADI#2
ETBW9396	ABAY

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 (R core team, 2021). The ANOVA was conducted using the following mathematical model:

$P_{ijk} = \mu + g_i + r_j + b_{k(j)} + e_{ijk}$, Where: $P_{ijk} ==$ phenotypic value of ith genotype under j^{th} replication and k^{th} incomplete block within replication j; $\mu ==$ grand mean; $g_i ==$ the effect of ith genotype; $r_j ==$ the effect of replication j; $b_{k(j)} ==$ 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 estimated according to the statistical procedure of SAS software (SAS, 2014) 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 ($\sigma^2 g$) $== \frac{MSg - MSe}{r}$,

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

Where: -, $\sigma^2 e ==$Environmental variance, r == number of replications, 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) $== \frac{\sqrt{\sigma 2p}}{\overline{X}} * 100$,

Genotypic Coefficient of Variation (GCV) $== \frac{\sqrt{\sigma 2g}}{\overline{X}} * 100$, Where: - $\overline{X} ==$ grand mean.

2.4.3. Estimates of Heritability in Broad Sense

Heritability is a useful technique that estimates the performance of parents in hybrids. The highest heritability in any character shows 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 $H^2 == \frac{\sigma 2g}{\sigma 2p} * 100$

Where: - $\sigma^2 p==$ phenotypic Variance, $\sigma^2 g==$ genotypic variance and $H^2 ==$ broad sense heritability.

2.4.4. Estimation of Expected Genetic Advance

There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is called genetic advance (GA). High genetic advance coupled with high heritability estimates offers 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) (σp) (H^2) Where:- GA == Expected genetic advance at 5% selection intensity, σp = 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 $== \frac{GA}{\overline{X}} * 100$ Where: - GAM == Genetic advance as percent of mean, GA == Genetic advance at 5% selection intensity, $\overline{X} ==$ Population Mean

2.4.5. Phenotypic and Genotypic Correlation Analysis

Correlation coefficient analysis was done using R software (R core team, 2021), it helps to determine the nature and degree of relationship between any two measurable characters (Fellahi *et al.*, 2013). The various characteristics of crop plants are generally interrelated or correlated (Abderrahmane *et al.*, 2013). Phenotypic and genotypic correlation coefficients was estimated (Miller *et al.*, 1958) as:

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

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

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

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

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

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

MSPg = Mean square product for genotypes

MSPe = Means square products of error

r = Number of replications

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 is number of genotypes. Accordingly, the phenotypic correlation coefficient value was tested for its significance by employing the following

formula: $t = \dfrac{r_p}{SE(r_p)}$, $SE_{(r_p)} = \sqrt{\dfrac{1-r_p^2}{n-2}}$ 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:

$t_{cal} = \dfrac{r_g}{SE(r_g)}$, $SE_{rg} = \sqrt{\dfrac{1-r_g^2}{2H_x^2 * H_y^2}}$

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. Results and Discussion
2.1 Analysis of Variance (ANOVA)

Analysis of variance (ANOVA) revealed significant genetic variation (p<0.01) among the 50 wheat genotypes for eight of the ten characters studied. These characters included days to 50% heading, days to 90% maturity, grain filling period, grain yield, hectoliter weight, agronomic score, yellow rust severity, and stem rust severity. Plant height and thousand kernel weight also displayed significant variation (p<0.05) among the genotypes.

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

This finding aligns with previous research by Alemu et al. (2017), Wani et al. (2018), Semahegn et al. (2021), and Getachew et al. (2021), 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	34.81	2.81	**23.68**[**]	1.10	1.56	0.96
DTM	92.16	5.87	**17.65**[**]	3.85	1.7	0.86
GFP	0.97	13.69	**11.66**[**]	3.73	4.10	0.80
PHT	676.00	38.50	**50.43**[*]	26.00	6.17	0.76
AgrSc	0.32	0.09	**0.67**[**]	0.18	21.00	0.83
TKW	1.96	42.26	**38.61**[*]	20.93	14.23	0.73
HLW	7.75	4.63	**10.00**[**]	3.27	2.61	0.80
YrS	1332.25	45.85	**11.20**[**]	38.08	19.11	0.97
SrS	7.84	8.32	**283.55**[**]	3.60	21.43	0.84
GYLD	92659.36	82061.22	**249445.71**[**]	37670.70	15.86	0.89

*Note. * and ** indicates significant at (5%) and highly significant at (1%) probability levels respectively. DTH: days to heading; DTM: days to Maturity; GFP: grain filling period; 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 R^2: Coefficient of determination*

3.2. Estimation of genotypic and phenotypic coefficient of variations

This section explores 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).

Range of Variation: PCV and GCV ranged from 2.58% to 28.86% and 2.22% to 26.59%, respectively. These values are categorized as low (<10%), moderate (10-20%), and high (>20%) (Sivasubramanian and Menon, 1973).

High PCV and GCV: Notably, high values (>20%) for both PCV and GCV were observed for grain yield (maximum value) and agronomic score. This indicates substantial phenotypic and genotypic variation for these traits, suggesting a high potential for improvement through breeding. These findings align with previous research by Kumar et al. (2019), Dutamo et al. (2015), and Tilahun et al. (2020), who also reported high PCV and GCV for grain yield.

Moderate PCV and GCV: A moderate range of PCV (13.67%) was observed for thousand kernel weight, with a lower genotypic coefficient of variation (9.25%). This suggests 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.

Low PCV and GCV: Days to heading, days to maturity, grain filling period, plant height, and hectoliter weight displayed low values for both PCV and GCV (all less than 10%). This indicates relatively low phenotypic and genotypic variation for these traits in this set of genotypes. These results are 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 provides valuable insights for breeders. Traits with high PCV and GCV, like grain yield and agronomic score, offer the most significant potential for improvement through selection. Breeders can

focus their efforts on these traits to develop new wheat varieties with superior performance. For traits with moderate PCV and GCV, like thousand kernel weight, breeding strategies may 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, may 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 highlights the presence of significant genetic variation for key traits in these wheat genotypes. Breeders can leverage this information to guide their selection strategies and develop new wheat varieties with improved yield, agronomic performance, and other desired characteristics.

3.3. Estimation of heritability and Genetic advance

Broad-sense heritability (H^2) estimates ranged from 45.79% for thousand kernel weight to 95.35% for days to heading. These values are categorized as low (0-40%), medium (40-59%), moderately high (60-79%), and very high (>80%) (Singh, 2001).

High Heritability Traits: Several traits exhibited moderately high to very high heritability (>60%). These included days to heading (95.35%), grain yield (84.90%), days to maturity (78.19%), agronomic score (73.13%), grain filling period (68.01%), and hectoliter weight (67.30%). This indicates a strong genetic influence on these traits and a high likelihood of improvement through selection. These findings align with previous research by Rajput et al. (2019), Upadhyay et al. (2019), and Sami et al. (2021), who also reported high heritability estimates for days to heading and days to maturity.

Medium Heritability Traits: Thousand kernel weight (45.79%) and plant height (48.44%) displayed medium broad-sense heritability. While still influenced by genetics, these traits may also be somewhat affected by environmental factors.

Genetic Advance: Genetic advance as a percentage of the mean (GAM) ranged from 4.19% for days to maturity to 46.79% for grain yield. GAM is categorized as low (0-10%), moderate (10-20%), and high (>20%) (Johnson et al., 1955).

High Genetic Advance Traits: Traits with high GAM (>20%) were grain yield (46.79%), followed by agronomic score (46.46%) and thousand kernel weight (22.17%). This suggests substantial genetic progress can be achieved through breeding for these traits. Similar findings were reported by Kabir et al. (2017), Upadhyay et al. (2019), and Kumar et al. (2020), who observed high GAM for grain yield and thousand kernel weight.

Moderate and Low Genetic Advance Traits: The remaining traits (days to heading, days to maturity, grain filling period, and plant height) displayed low GAM (<10%). While improvement may still be possible, it might be slower for these traits within this set of genotypes. Kabir et al. (2017) also reported low GAM for plant height. However, contrasting results were found by Fikre et al. (2015) and Chimdesa et al. (2017), who observed moderate GAM for plant height.

These variations highlight 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, suggests a significant role of additive gene action in controlling these traits. This is consistent with Upadhyay et al. (2019). Breeders can effectively select for these traits to develop improved wheat varieties.

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

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

Table 3: 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	$\sigma2g$	$\sigma2p$	$\sigma2e$	GCV	PCV	ECV	H^2B	GA	GAM
DTH	11.29	11.84	0.55	5.00	5.12	1.10	95.35	5.58	8.30
DTM	6.90	8.83	1.93	2.29	2.58	1.21	78.19	4.82	4.19
GFP	3.97	5.83	1.87	4.17	5.06	2.86	68.01	3.92	8.20
PHT	12.22	25.22	13.00	4.23	6.07	4.36	48.44	8.14	9.85
AgrSc	0.25	0.34	0.09	24.50	28.65	14.85	73.13	0.94	46.46
TKW	8.84	19.31	10.47	9.25	13.67	10.07	45.79	7.12	22.17
HLW	3.37	5.00	1.64	2.65	3.23	1.85	67.30	3.63	5.23
GYLD	105887.50	124722.90	18835.35	26.59	28.86	11.21	84.90	572.66	46.79

Note. $\sigma2g$: genotypic variance; $\sigma2p$: phenotypic variance; $\sigma2e$: environmental variance; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; ECV: environmental coefficient of variation; H^2B: broad sense heritability; GA: genetic advance; GAM: genetic advance as percent of mean; DTH: days to heading; DTM: days to Maturity; GFP: grain filling period; PHT: plant height; AgrSc: agronomic score; GY: grain yield; HLW: hectoliter weight; TKW: thousand kernel weight

3.4. 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=0.75, rp=0.73**): This indicates that genotypes with higher agronomic scores (potentially better overall agronomic performance) also tended to have higher grain yield. Hectoliter Weight (rg=0.73, rp=0.69**): A positive correlation exists between grain yield and hectoliter weight, suggesting denser grains may contribute to higher yield. Thousand Kernel Weight (rg=0.58, rp=0.51**): This positive correlation indicates that genotypes with larger kernels generally produced higher grain yield. These findings suggest 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 (Oury et al. 2017; Ashebr *et al.*, 2020; Guo et al. 2020; Getachew *et al.*, 2021). Molla et al. (2018); Feyissa et al. (2019) reported a significant positive correlation between grain yield and agronomic score at at both genotypic and phenotypic correlation coefficient. Grain yield showed positively and significantly correlated with thousand kernel weight at both genotypic and phenotypic correlation coefficient (Ibrahim et al. 2018; Ashebr *et al.*, 2020; Getachew *et al.*, 2021; Li et al. 2021).

Grain yield displayed a strong negative and highly significant correlation (p<0.01) at both genotypic and phenotypic levels with Yellow Rust Severity (rg=-0.70, rp=-0.65**). This indicates that genotypes susceptible to yellow rust disease (higher severity scores) had lower grain yield. This highlights the importance of incorporating yellow rust resistance into breeding programs to protect yield potential.

Plant height exhibited a positive and significant correlation (p<0.01) at the phenotypic level (rp=0.28**) with grain yield, but the genotypic correlation (rg=0.25ns) was not significant. This suggests a possible environmental influence on this association. Days to heading, days to maturity, grain filling period, and stem rust severity were not significantly correlated with grain yield at either genotypic or phenotypic levels.

The observed positive correlations between grain yield and agronomic score, hectoliter weight, and thousand kernel weight are encouraging for breeders. These traits can serve as valuable indirect selection criteria for improving grain yield. The negative correlation with yellow rust severity emphasizes the need to prioritize resistance breeding to protect yield potential from this disease. This result aligned with Chen et al. (2018); Bedane et al. (2019) 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 suggests 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. The result agreement with previous finding that reported by Obsa *et al*., (2017) days to heading were not significantly correlated with grain yield at both genotypic and phenotypic level. Molla et al. (2017) who reported no significant correlation between grain yield and days to heading and days to maturity at both genotypic and phenotypic correlation coefficient.

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

3.5. 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=0.73) and phenotypic (rp=0.67**) levels.** This indicates that earlier heading lines also tended to mature earlier. This aligns with observations reported by Liu et al., (2023) who found a similar positive correlation with Days to 50% heading and with days to 90% maturity at both genotypic and phenotypic (rp=0.67**) correlations coefficient in wheat genotypes. Days to 50% heading also displayed negative and highly significant (p<0.01) correlations with grain filling period at both genotypic (rg=-0.53) and phenotypic (rp=-0.44**) levels.** This suggests that earlier heading lines had shorter grain filling durations. Furthermore, days to 50% heading exhibited a negative and significant (p<0.05) genotypic correlation (rg=-0.33) and a negative and highly significant (p<0.01) phenotypic correlation (rp=-0.29*) with plant height.** This implies that earlier heading lines were generally had short plant height. This corroborates the findings of Chen et al., (2022) who documented a negative correlation between heading time and plant height in wheat genotypes.

Days to 90% maturity displayed a negative and highly significant (p<0.01) genotypic correlation (rg=-0.3) with stem rust severity.** This indicates that earlier maturing lines tended to have lower stem rust infection. This is consistent with the work of Singh et al., (2020) who observed a negative association between heading date and stem rust susceptibility in wheat. Days to 90% maturity exhibited a positive and highly significant (p<0.01) phenotypic correlation (rp=0.35) with grain filling period.** This suggests that longer maturity lines had longer grain filling durations, potentially leading to higher yields. While not directly studied in wheat, Sun et al., (2019) reported a positive correlation between maturity and grain filling period in rice, suggesting a possible parallel mechanism in wheat. Further research is needed to confirm this in wheat cultivars.

Grain filling period exhibited positive and significant correlations with hectoliter weight (grain density) at both genotypic (rg=0.32) and phenotypic (rp=0.27) levels, and with yellow rust severity at both genotypic (rg=0.33*) and phenotypic (rp=0.32**) levels.** This indicates that longer grain filling periods were associated with denser grains and potentially higher susceptibility to yellow rust. The link between grain filling duration and hectoliter weight is well-documented in wheat, as reported by Li et al., (2018).

Plant height displayed significant correlations with thousand kernel weight (seed size) at both genotypic (rg=0.35) and phenotypic (rp=0.23) levels.** This suggests that taller plants tended to produce larger seeds. This finding aligns with the observations of [Zhang et al., 2017] in soybean, but research specific to wheat is needed to confirm this relationship. Plant height also exhibited significant correlations with agronomic score (overall plant performance) and hectoliter weight at the phenotypic level (rp=0.24 and rp=0.26, respectively).** This suggests that taller plants generally performed better agronomically and produced denser grains. These findings partially align with the work of [Yang et al., 2016] who reported a positive association between plant height and agronomic score in wheat.

Thousand kernel weight displayed positive and highly significant correlations with hectoliter weight (rg=0.58 and rp=0.55**) and agronomic score (rg=0.55** and rp=049**) at both genotypic and phenotypic levels.** This indicates that larger seeds were associated with denser grains and better overall plant performance. This is 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 are expected in wheat.

Yellow rust severity exhibited negative and highly significant correlations with thousand kernel weight at both genotypic (rg=-0.45) and phenotypic (rp=-0.36**) levels.** This suggests that higher yellow rust infection led to reduced seed size. This finding aligns with the work of [Hassan et al., 2014] who reported a negative association between yellow rust severity and thousand kernel weight in wheat. However, the association with yellow rust severity requires further investigation in wheat genotypes.

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. This suggests that breeding programs focused on improving multiple, interrelated traits, such as days to maturity, plant height, thousand kernel weight, and hectoliter weight, hold promise for significant grain yield advancements.

Table:4. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for10 traits of 50 bread wheat genotypes tested at Kulumsa Agricultural Research Center in 2023

Variable	DTH	DTM	GFP	PHT	AgrSc	TKW	HLW	YrS	SrS	GYLD
DTH	1	0.73^{**}	-0.53^{**}	-0.33^{*}	0.046^{ns}	-0.03^{ns}	-0.05^{ns}	-0.19^{ns}	-0.25^{ns}	**0.03^{ns}**
DTM	0.67^{**}	1	0.20^{ns}	-0.26^{ns}	0.10^{ns}	0.06^{ns}	0.20^{ns}	0.05^{ns}	-0.43^{**}	**0.11^{ns}**
GFP	-0.44^{**}	0.35^{**}	1	0.15^{ns}	0.06^{ns}	0.12^{ns}	0.32^{*}	0.33^{*}	-0.18^{ns}	**0.10^{ns}**
PHT	-0.29^{**}	-0.25^{*}	0.06^{ns}	1	0.25^{ns}	0.35^{*}	0.23^{ns}	-0.04^{ns}	0.11^{ns}	**0.25^{ns}**
AgrSc	0.02^{ns}	0.07^{ns}	0.059^{ns}	0.24^{*}	1	0.55^{**}	0.70^{**}	-0.59^{**}	-0.25^{ns}	**0.75^{**}**
TKW	-0.06^{ns}	0.03^{ns}	0.12^{ns}	0.23^{ns}	0.49^{**}	1	0.58^{**}	-0.45^{**}	-0.03^{ns}	**0.58^{**}**
HLW	-0.11^{ns}	0.10^{ns}	0.27^{**}	0.26^{**}	0.64^{**}	0.55^{**}	1	-0.47^{**}	-0.17^{ns}	**0.73^{ns}**
YrS	-0.14^{ns}	0.11^{ns}	0.32^{**}	-0.09^{ns}	-0.51^{**}	-0.36^{**}	-0.43^{**}	1	-0.18^{ns}	**-0.70^{**}**
SrS	-0.20^{ns}	-0.35	-0.18^{ns}	0.20^{ns}	-0.28	-0.08^{ns}	-0.16^{ns}	-0.16^{ns}	1	**0.08^{ns}**
GYLD	**0.01^{ns}**	**0.06^{ns}**	**0.07^{ns}**	**0.28^{**}**	**0.73^{**}**	**0.51^{**}**	**0.69^{**}**	**-0.65^{**}**	**0.05^{ns}**	1

*Note. * and ** indicates significant at (5%) and highly significant at (1%) probability levels respectively. DTH: days to heading; DTM: days to Maturity; GFP: grain filling period; PHT; plant height; AgrSc: agronomic score; TKW: thousand kernel weight; HLW; hectoliter weight; YrS: yellow rust severity; SrS: stem rust severity; GYLD; grain yield*

Conclusion

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. The research was conducted at Kulumsa agricultural research center in 2023 main cropping season. Analysis of variance (ANOVA) revealed significant genetic variation (p<0.01) among the 50 wheat genotypes for eight of the ten characters studied. Plant height and thousand kernel weight also displayed significant variation (p<0.05) among the genotypes.The observed variation in PCV and GCV provides valuable insights for breeders. Traits with high PCV and GCV, like grain yield and agronomic score, offer the most significant potential for improvement through selection. Breeders can focus their efforts on these traits to develop new wheat varieties with superior performance. For traits with moderate PCV and GCV, like thousand kernel weight, breeding strategies may need to consider both genetic and environmental factors.

The high broad-sense heritability observed for grain yield and agronomic score, coupled with their high genetic advance, suggests a significant role of additive gene action in controlling these traits. For traits with moderate heritability and GAM (like thousand kernel weight), breeding strategies may need to account for both genetic and environmental factors. Selection methods that minimize environmental influence or incorporate environmental stability testing alongside selection for genetic improvement could be employed. Traits with low heritability and GAM may require more intensive breeding efforts or the use of different breeding techniques to achieve significant improvement within this set of genotypes. However, these traits may still be important for breeding programs with specific objectives.

Grain yield displayed a strong negative and highly significant correlation (p<0.01) at both genotypic and phenotypic levels with Yellow Rust Severity (rg=-0.70, rp=-0.65**). The observed positive correlations between grain yield and agronomic score, hectoliter weight, and thousand kernel weight are encouraging for breeders. These traits can serve as valuable indirect selection criteria for improving grain yield. The negative correlation with yellow rust severity emphasizes the need to prioritize resistance breeding to protect yield potential from this disease.

Thus, attention should be given for those traits for breeding program.

5. Acknowledgement

6. Conflict of Interest

The authors have declared that no conflict of interest exists

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