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Analyzing Yield Performance of Farmers' and Improved Varieties of a Selected Genotype of Bread Wheat (*Triticum Aestivum L.*) in Goro, Bale, Oromia Region

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Abstract

The study focused on Analyzing yield performance of farmers' and improved varieties of a selected genotype of bread wheat (Triticum aestivum L.). The research was conducted in the Bale Zone, Agarfa Woreda, Oromia Region, Ethiopia. Testing was conducted on sixteen bread wheat varieties, comprising eight farmers' varieties and eight improved variants. During the 2021/22 season, these genotypes were cultivated at the Goro Community Seed Bank using a Randomized Complete Block Design. The analysis of variance revealed significant differences among the genotypes for most traits at the individual level. The majority of traits exhibited a significant ($p \leq 0.05$) variety and genotype-by-environment (G×E) interaction. The mean grain yield of the varieties, ranging from 6.67 to 4 tons per hectare, showed considerable variation. Phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for most traits. PCV varied from 2.6% (kernel number per spike) to 36.2% (grain yield), while GCV ranged from 2.23% (kernel number per spike) to 29.9% (grain yield). The heritability estimates for plant height (95.7%) and spike length (91.1%) were both above 80%, indicating a high degree of genetic influence. When considering the percentage of mean, the expected genetic improvement ranged from 0.95% for spike length to 49.14% for grain yield. Positive and negative genotypic and phenotypic relationships were also identified among the yield components. Among the varieties, Tikur Goshmber had the highest grain yield at 33.34kunt/hect, while Tate had the lowest at 11.6 kunt/hect. The improved varieties Kekeba and Digalu had the highest and lowest yields at 39.01 kunt/hect and 10.01 kunt/hect, respectively. It has been observed that the genotypes being studied demonstrate have significant variability, heritability, and correlations among the traits examined that consequently for the advancement of bread wheat yield in the respective area.

Keywords: Bread wheat (*Triticum aestivum L.*), Correlation, Heritability, landrace, released varieties.

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Introduction

Ethiopia is considered as secondary genetic diversity for tetraploid (2n = 4x = 28) wheat, having cultivated these varieties since ancient times Vavilov N.I. (1997). Wheat (*Triticum aestivum*) is considered a vital food crop globally and its significance is increasing due to political issues between Russia and Ukraine. Wheat is considered a valuable cash crop due to its high yield per unit area, its ability to thrive in a temperate climate with a moderate growing season, and the production of high-quality, versatile flour Habte L, (2020).

In 2020, the global production of wheat was 760 million tons, with China, India, and Russia accounting for 41% of total production (Central Statistical Agency, CSA, 2014). Ethiopia, Egypt, and South Africa are the top wheat-producing countries in Africa, and they also import a substantial quantity of wheat. Egypt is the leading wheat-producing and importing country in Africa. The wheat yield was 6.50 tons in 2019 which was the highest among the top wheat-producing countries. About 97% of the rise in wheat yield has been achieved through the adoption of new improved varieties, new production techniques, agricultural mechanization and modern irrigation techniques, and the remaining percentage increase in yield has been attributed to planting area expansion Abdelmageed et al., (2019).

The largest amount of area cultivated is allocated for wheat production which is not a guarantee to reduce the wheat yield gap in Ethiopia. The average wheat area cultivated increased from 1963/64wheat production area was 988 hectares to 2019/20 1.789 million hectares with production ton/hectares 0.71 t0 2.64 respectively which clearly showed that Ethiopian wheat yield was the lowest among the top wheat-producing countries in Africa due to a lack of technical knowledge and information, and poor seeds/inputs delivery systems which resulted in a big wheat yield gap (Food and Agriculture Organization Corporate Statistical Database, FAOSTAT, 2022) Ethiopia Wheat production for 2022/23 is projected at 5.7 million tons, up by

3.26 percent over the 2021/22 production estimate and harvested area is forecast at nearly 2 million hectares and the wheat yield is estimated at a record 2.85 tons/hectare (United States Department of Agriculture, USDA Report, 2022).

Ethiopian agriculture is largely traditional, with a focus on farming landrace crops. Bread wheat landraces exhibit significant variability in characteristics, making them valuable sources of genetic variation for breeding programs aimed at achieving high and consistent production in low-input environments (Evangelos Korpetis *et al*., 2023). Landraces play a crucial role in expanding the genetic diversity of cultivated bread wheat and mitigating biodiversity erosion, enabling crops to better withstand the challenges of low-input agriculture .The yield performance of bread wheat landraces compared to released varieties is a significant aspect of the research on these landraces. The studies show that landraces generally have lower yields compared to commercial cultivars, but they also exhibit adaptability to low-input and organic environments. However, in the organic environment, landraces demonstrated a significant difference in yield performance. While commercial cultivars showed a significant reduction in yield (around 68%) compared to the conventional environment, landraces showed a much smaller reduction (around 33-85%). Landraces are a valuable source of genetic variation, which provides increased adaptability and enables crops to better withstand the challenges of low-input and organic agriculture. Landraces play a crucial role in expanding the genetic diversity of cultivated bread wheat and mitigating biodiversity erosion (Evangelos Korpetis et al., 2023). To ensure appropriate and sustainable production of wheat, it is important to understand the environmental and climatic conditions of its cultivation, including the planting date, cultivar ripening time, plant density, soil and meteorological data (Zewdie Habte Shikur 2022).

Different study results indicate that there is significant genetic diversity among bread wheat landraces in Ethiopia, which provides potential for selection and improvement of important agronomic traits. Several studies have evaluated the performance of released bread wheat varieties and landraces in different agro-ecological zones of Ethiopia. The landraces showed moderate to high heritability and genetic advance for traits like spike length, seeds per spike, thousand seed weight, biomass yield and harvest index Evangelos Korpetis et al., (2023)

Despite significant efforts to enhance the productivity and production of this crop, insufficient research has been conducted on landraces to characterize and comprehend the nature and degree of GCV, PCV, heritability, genetic gain, the relationship between yield and yield-related traits, and the performance of bread wheat varieties developed for the southeast highlands of Ethiopia.: Assessing the morpho-agronomic characteristics and yield performance of farmer-selected bread wheat (*Triticum aestivum L.*) varieties in comparison to enhanced cultivars for on-farm conservation of yield and yield-related variables.

Specific objectives

- To compare farmer's varieties of bread wheat (*Triticum aestivum* L.) with improved cultivars in terms of morpho-agronomic characteristics
- To evaluate the bread wheat farmer's varieties' product performance against enhanced varieties.
- To evaluate the degree of correlation between the agronomic traits of farmer-grown bread wheat varieties and enhanced variants

Methods

Description of the study site

The study was carried out at the Goro Community Seed Bank, which is 487 kilometers southeast of Addis Ababa, in the Oromia regional state's Bale Zone Goro Woredas. The mean annual temperature is 18 0C during the day and 24 0C at night. The Goro Community Seed Bank is situated at a height of 2034 meters above sea level at longitudes 770 56'25'N and latitudes 650 37' 75' E. With an average annual rainfall of 700–1560 mm, the central region represents the highlands of Bale. Brown, slightly acidic soil is the predominant kind.

Experimental material

As explained in table 1 below, there were 16 types of bread wheat used. Eight of these were farmer's varieties, and the remaining eight were released varieties. SARC and the EBI Gene Bank provided the several wheat types, which were planted during the 2021/2022 study's main summer planting season.

Table 1. Description of released and farmers varieties of bread wheat in ethiopia was used in the study

No.	Accessions names	Farmers varieties /Released	Source
1	Tate	Farmers varieties	EBI
2	Garando	>>	EBI
3	Tikur goshmber	>>	EBI
4	Nech goshmber	>>	EBI
5	Konte	>>	EBI
6	Bawunde	>>	EBI
7	Bokate	>>	EBI

8	Setakur	>>	EBI
9	Danda’a	Improved varieties	OSE
10	Eerso	>>	OSE
11	Huluka	>>	OSE
12	Sherume	>>	OSE
13	Hidase	>>	OSE
14	Digalu	>>	OSE
15	Kekeba	>>	OSE
16	Ogolcho	>>	OSE

Experimental design and trial management

The experiment was conducted twice using a Randomized Complete Block Design (RCBD). Each plot consisted of six rows, 20 cm apart and 2.5 meters in length, covering an area of 3 m^2 (2.5 m x 1.2 m). A 1.5 m space separated the replications. To collect data on 12 quantitative traits, the four central rows were harvested, dried, threshed, and cleaned. A week before planting, 20 Qt/ha of organic compost was applied, and 150 kg/ha of seedlings were sown. Hand drilling ensured even distribution of seeds and organic fertilizer. Local recommendations for weeding and other agronomic practices were adhered to, with no pesticides or herbicides used..

Data to be collected

Data on quantities and qualitative was collected either on the plot bases or from four central rows randomly selected plants of wheat genotypes on the following characters.

1. Plant height (PH)- the height was measured in cm from the ground level to the top of the plant.

2. Number of tillering (NT) - The number of tillering at which the 50% tillering appears per plots.

3. Spike length (SL):- the average length of the longest spike expressed in cm at physiological maturity from four central rows randomly selected.

4. Kernel number per spike (KNS):- the number of kernels was counted for each spike of the four central rows randomly selected

5. Day to emergence (DE):- day to emergence was record when 50% of the plant in each plot emerged out. .

6. Day to head emergence (DHE):- The days from the date of sowing to the date at which the first head appears per plots.

7. Day to physiological maturity (DM):- was recorded as the day from emergence to maturity when 50% of the plant population per plot have turned yellowish or showed sign of senescence.

8. Grain yield per plot (GYP) (kg):- The ratio of grain yield in kilogram per plot.

9.1000 kernel weight (TKW): the weight of 1000 kernel was selected randomly from five plants per Plots.

10. **Above ground Biomass Weight per plant (AGB in kg/m2):-** Whole above ground plant parts on the plant were harvested, sun dried and weighted from four selected rows from each plot. This value again converted to kg hectare.

11. Harvest index (HI):- this will be calculated by the following formula:

$$\text{Harvest Index (HI)} = \frac{\text{seed yield per plot(kg)}}{\text{Biomass per plot (kg)}} \times 100\%$$

Data analysis method

The descriptive statistics of each trait was conducted and followed by an analysis of variance (ANOVA). These statical analysis was performed using appropriate procedures of the SAS software version 9.1 (SAS 9.1 Institute Inc. Cary .NC, USA).

Analysis of variance

Data was collected and are subjected to analysis of variance using the linear model equation yij= Ti +Bi+ ij , where yij = the overall mean , Ti = the effect of the ith treatment Bj = the effect of the jth block, and ij= the random effect associated with the experimental unit assigned to the ith treatment and occurring in the jth plot to determine the differences existing among the 16 wheat genotypes. The variance was analyzed using the standard procedure applicable to Randomized Complete Block Design (RCBD) as suggested by Gomez, (1984) using appropriate procedures of the SAS software version 9.1 (SAS 9.1 Institute Inc. Cary .NC,USA).The least significance difference (LSD) was also worked out for mean separation at 1% and 5% probability levels explained in table 2. below.

Table.2 Analysis of variance

S.V	D.F	Mss	EMS
Replication	r-1	Mr	$\delta^{2e}+\delta 2r$
Genotypes	g-1	Mg	$\delta^{2}+r\delta^{2}g$
Error	(r-1)(g-1)	Me	$\delta^{2}e$

Where S.V=source of variation D.F=degree of freedom , mss=mean sum square, EMS=expected mean square Mr =mean sum square of replication , Mg =mean sum square of genotype , Me = mean sum square of error, $\delta^{2}e$ =error variance, $\delta^{2}g$ =genotypic variance, r= number of replication

Phenotypic and genotypic variability

The variability present in the population was estimated by simple measures namely range, mean, standard error, phenotypic and genotypic variance coefficient of variations. The phenotypic and genotype according to the methods suggested by Burton and Derane (1952) as follows:

$\delta^{22p\ =}\ \delta^{2}\ {}^{2}g^{+}\delta^{2e}$ where ∂ p = phenotypic variance

$\partial^{2}g = \frac{Mg - me}{r}$ g= Genotypic variance

me= environmental (error) variance (error mean square)

Ms= Mean sum square of genotype

M<= Mean sum square of error

R= number of replication

Phenotypic coefficient of variation (PCV) $= \frac{\sqrt{\delta 2 \delta 2p}}{x}$ X 100

Genotypic Coefficient of Variation (GCV) = $\frac{\sqrt{\delta 2g}}{x}$ 100

Where x =population mean.

Estimates of heritability in broad sense

Heritability was computed for each character based on formula developed by Allard RW (1960) as.

$h^{2} = \frac{\sqrt{\delta 2g}}{\delta 2\ \mathrm{p}}$ X 100 δ^{2}

Where 2 p= Phenotypic Variance

,δ^{2} g= Genotypic Variance

δ^{2} p =∂2 g +δ^{2} e ,δ^{2} e =Environmental (error) variance.

Estimation of expected genetic advance

The genetic advance (GA) for selection intensity (K) at 5% was calculated by formula suggested by Allard RW,(1960)as:

GA= (K) (δp) (h^2)

Where, GA= Expected genetic advance, δp= the phenotypic standard deviation, h^{2} = the heritability, k=selection differential (K= 2.06 at 5% ^{X} selection intensity).

The genetic advance as percent of mean is calculated as $\frac{GA}{X}X^{100}$ Where , X= population Mean

Correlation analysis

To estimate the correlation, it is necessary to calculate the covariance. The covariance was computed from the analysis of covariance table 3. Below.

Table 3. Analysis of covariance

S.V	D.F	MSP	EMSp
Replication	(r-1)	Mspr	δ exy+g δ rxy
Genotype	(g-1	Mspg	δ exy+r δ gxy
Error	(r-1)(g-1	Mspe	δ exy

where, S.V =source of variation

D.F =degree of freedom

Mspg= mean sum products due to genotypes for character x and y

Mspe = mean sum product of environment (error) for character x and y

Emsp = expected mean sum product

r= number of replications

COV exy = Mspg-Mspe

COV pxy = COV gxy +COV (exy)

Where, COV (gxy)=genotype covariance between characters x and y

COV pxy= phenotypic covariance between characters x and y,

COV exy = environmental covariance between x and y

The correlation was estimated using the formal suggested by [26].

where rp= phenotypic correlation coefficient

rp = $\sqrt{(\delta 2px*\delta 2py)}$

pcov xy = phenotypic covariance b/n character x and y

px = phenotypic variance for character x.

rg = $\frac{P\operatorname{cov}xy}{\sqrt{(\delta 2gx*\delta 2by}}$ py = phenotypic variance for character y .

where , rg = Genotypic correlation coefficient

Gcov x.y = Genotypic covariance between character x and y

gx = Genotypic variance for character x

gy = Genotypic variance for character y.

The Coefficient of correlation at phenotypic level are tested for their significance by comparing the values of correlation with tabulated r; value at g-2 degree of freedom however, the tested for their significance using the formula described by Robertson G.E,(1959) indicated below

$$Z=\frac{rgxy}{SEgxy}$$

Where g= number of accessions

SEgxy= standard error of the genotypic correlation rgxy= Genotypic correlation rgxy=Genotypic correlation coefficient of x and y calculated t value is compared with the tabulated “Z” value at g-2 degree of freedom at 5% level of significance.

$$SEgxy=\sqrt{\frac{(1-r2gx)2}{2hx.hy}}$$

Where. g= number of genotypes

Hx= heritability of character x

Hy= heritability of character y

Results and Discussions

According to the study result indicated in table 4 highlights the significant diversity in the attributes being studied, presenting the minimum, maximum, and average values for 11 different characteristics. Setakur may take up to nine days to emerge, in contrast to the Kekeba species, which can emerge in as few as seven days. The tillering number ranges from a low of 8 in Sherume to a high of 28 in Tikur Goshmber, which matures between 66 and 80 days for Huluka and 142 days for Setakur. Heights of Tate plants vary from 73 cm to 150 cm, while spike lengths for Setakur range from 11.2 cm to 6.2 cm. Kernels per spike can vary from 43.2 in Tate to 80 in Tikur Goshmber. Digalu has a grain yield of 0.2 tons, Tikur Goshmber yields 1.2 tons, and the weight of 1000 seeds ranges from 24 grams forBawunde. Harvest indices ranged from 20% for Digalu to 50% for Kekeba, while above-ground biomass varied from 1 ton for Digalu to 3.0 tons for Tikur Goshmber. Comparable trends were noted in research .The result of the present study agrees with the finding of Kochito G/Mariam, (2019) who reported high variation among the genotype].

Table 4. Minimum and Maximum scoring genotypes and Mean values for the 11 character of the 16 bread wheat genotypes evaluated

Characters	Minimum		Maximum		Mean	Variance	SD(±)
	Value	Genotypes	Value	Genotypes			
Days to emergence	7	Kekeba	9	Setakur	7.9	1.04	0.91
Days heading	66	Kekeba	80	Bawunde	72.5	59.3	4.02
Number of tillering	8	Sherume	28	Tikur goshmber	16.12	14.9	1.08
Days of Maturity	112	Huluka	142	Setakur	127.4	33.6	9.75
Plant Height(cm)	73	Tate	150	Setakur	100.7	193.2	22.60
Spike length(cm)	6.2	Digalu	11.6	Setakur	8.39	10.04	1.46
Kernel per spike(g)	43.2	Tate	80	Tikurgoshmber	59.2	82.8	7.98
GrainYieldper plot(g)	0.2	Digalu	1.2	Tikurgoshmber	0.71	0.22	0.25
ThousandSeedWeight(g)	24	Tate	42	Bawunde	36.6	10.9	4.81
AbovegroundBiomass(g)	1.0	Digalu	3.0	Tikurgoshmber	1.92	0.19	0.56
Harvest index(g)	20	Digalu	50	Kekeba	36.6	256	7.40

According to research result Reported by Alemu Debi (2016) indicated that the harvest index (HI), which is the ratio of harvestable to total biomass, ranged from 0.45 to 0.50 for spring wheat and from 0.50 to 0.55 for winter wheat. The HI for winter wheat neared the theoretical maximum of 0.64. The average HI observed in this study was 0.45, spanning from 0.2 to 0.91; however, it fell short of the expected 0.64 at the study locations. Grain yields varied from 666.6 kg/ha to 4000 kg/ha, with an average yield of 2366.6 kg/ha.The genotype Digalu yielded the least, whereas Tikur Goshmber yielded the most provided a comprehensive range from 2115 kg/ha for Menze to 5955 kg/ha for Alidoro in bread wheat.

Analysis of Variance of studied traits

The majority of the traits studied in table 5 showed considerable variation across the 11 characters whose ANOVA results were analyzed. The genotypes exhibited significant differences (P<0.01) in various parameters, including plant height and days to maturity. Notable genotypic variations were observed in: days to heading, days to tillering, grain yield, 1000 kernel weight, spike length, harvest index, and above-ground biomass. Significant genetic variability in grain yield and its components was reported for Ethiopian bread wheat genotypes by Alemu Dabi (2016), among others. Other researchers also noted significant genetic variability for durum wheat grain yield and its components. According to Gezahegn F.et al.,(2015), significant genotype differences (P<0.01) exist in plant height, spike length, grain yield per plot, days to heading, days to maturity, days to tillering, and harvest index. However, (ElAbidim Fellahi 2017) reported no significant differences in plant height or spike length among bread wheat genotypes. The significant statistical significance of genotypic variances indicates heterogeneity in the genotypes studied. Thus, selection might be advantageous for varying quantitative traits or for inclusion in a breeding program to create diversity. The same genotype variability was noted by Delesa *et al*., (2023).

Table 5. Analysis of variance (Mean squares) for the 11 characters of 16 bread wheat genotypes grown evaluated

Characters	Error (df= 30)	Genotypes (df= 15)	Replication (df= 1)	CV(%)	LSD
Days to emergence	0.52	0.86	5.6**	9.1	0.54
Days heading	7.6	28.6**	1.87	3.8	2.05
Number of tillering	2.9	6.61**	2.04	3.9	1.9
Days of Maturity	26.4	190.6*	2.3**	4.0	3.8
Plant Height(cm)	25.4	1173.8*	141.6**	5.0	3.8
Spike length(cm)	0.59	4.08**	0.024	9.2	0.57
Kernel per spike(g)	58.7	70.8**	56.8**	12.9	5.7
Grain Yield per plot(g)	0.021	0.11**	0.15**	20.4	0.11
Thousand Seed Weight(g)	14.7	5.9**	0.91	10.5	2.8
Above ground Biomass(g)	0.13	0.57**	0.29**	18.8	0.27
Harvest index(g)	29.6	82.7**	123.6**	14.8	4.1

Goro in 2021/22. df = degree of freedom, CV = Coefficient of Variance, G = Genotype and **,* = Indicate significance at the 0.05 and 0.01 probability levels, respectively.

Mean and Range of grain yield and yield components

Table 4 displays the range and mean values for 11 characteristics, as well as the average performance of 16 genotypes across these traits. Table 5 shows that the minimum coefficients of variation range from 3.8% for days to maturity to 20.4% for grain yield. The coefficients of variation span from 3.7% for days to maturity to 35.8% for grain yield. The experimentation's precision was assessed using coefficients of variation (CV%), where lower CV% means for most traits indicated data reliability Girma Gerema *et al*,. (2020) also reported the existence of an enormous amount of genetic variability for phonological, yield and associated characters

Phenotypic and Genotypic Coefficients of Variation

The level of genotypic and phenotypic variability is crucial when selecting improved varieties and initiating a breeding program. As shown in table 6, the lowest phenotypic variance ranged from 0.066 (grain yield) to 599.6 (plant height), while the lowest genotypic variance ranged from 0.045 (grain yield) to 574.2 (plant height).

PCV ranged from 2.6% (kernel number per spike) to 36.2% (grain yield), and GCV ranged from 2.23% to 29.9% (grain yield). High GCV values were noted for plant height, spike length, and grain yield, whereas the harvest index (14.1%) showed moderate values. Traits like thousand-kernel weight (10.47%) and days to emergence had moderate PCV values, but above-ground biomass (30.8%), spike length (30.9%), harvest index (20.5%), plant height (24.3%), and grain yield (36.2%) exhibited high PCV values. These traits' phenotypic expression would be a reliable indicator of genotypic potential, suggesting that selection based on these traits would be effective. Comparable results of moderate PCV and GCV for wheat grain yield and thousand-kernel weight have been reported. Low PCV and GCV for the grain filling phase (1.82%, 1.59%) and days to maturity (3.63%, 3.50%), respectively, were also observed Girma Gerem et al.,(20200. The study noted that, despite minor variations, the phenotypic coefficient of variation estimates were generally higher than the genotypic ones, indicating the influence of environmental factors on these traits.These findings are in agreement with a previous study in wheat Aavula N. et al.,(2023)

Table. 6. Phenomenological (σ2p), genotypic (σ2g), and environmental (σ2e) components of variance estimation, phenotypic and genotypic coefficients of variability (PCV and GCV), broad sense heritability (H), expected genotypic advance (GA), and genetic advance expressed as a percentage of the mean (GA%) for the 11 studied characters

Characters	MsTr	δ^2e	δ^2g	δ^2p	GCV	PCV	h^2	GA	GA%
Days to emergence	7.9	0.52	0.17	0.67	5.2	10.4	25.4	0.47	6.02

Days heading	72.6	7.6	10.5	18.1	4.4	5.8	58.0	4.8	6.61
Number of tillering	16.12	2.9	6.61	9.51	6.2	7.3	72.0	6.05	8.9
Days of Maturity	127.4	26.4	82.1	108.5	7.1	8.2	75.6	15.18	11.9
Plant Height(cm)	100.7	25.4	574.2	599.6	23.8	24.3	95.7	44.6	44.2
Spike length(cm)	8.37	0.59	6.05	6.64	29.4	30.8	91.1	0.08	0.95
Kernel per spike(g)	59.2	58.7	1.75	2.34	2.23	2.6	74.8	12.02	20.3
GrainYieldper plot(g)	0.71	0.021	0.045	0.066	29.9	36.2	68.2	0.35	49.5
ThousandSeed Weight(g)	36.6	14.7	10.6	25.3	8.9	13.7	41.9	4.14	11.3
Aboveground Biomass(g)	1.92	0.13	0.22	0.35	24.4	30.8	62.9	0.72	37.8
Harvest index(g)	36.6	29.6	26.6	56.2	14.1	20.5	47.3	7.21	19.7

PCV = Phenotypic coefficient variance, GCV = Genotypic coefficient variance, GA = Genetic Advance, and GA% = Genetic Advance as percent of Mean, σ2p = Phenotypic variance, σ2g = Genotypic variance, σ2e = Environmental variance, and σ2gl = Genotype and Location interaction variance

Estimates of heritability

Broad-sense heritability (H2), estimated for 11 traits, ranged from 25.4% for days to emergence to 95.7% for plant height table 6. Heritability estimates were categorized by Zewdie Habte Shikur (2022)) as low (<40%), medium (40-59%), moderately high (60-79%), and very high (≥80%). Analysis in table 6 revealed very high heritability estimates (>80%) for plant height (95.7%), spike length (91.1%), and days to maturity (75.6%), among others. These results indicate that the observed variation is predominantly due to genetics rather than environmental factors, suggesting strong potential for selective breeding. Low heritability for days to emergence (25.4%) and harvest index (43.3%) implies environmental influence. Moderate heritability was observed for 1000 seed weight (41.9%) and days to heading (58%). These findings align with Girma Gerem et al.,(2020), which reported strong heritability for days to heading, and are supported by Aavula N et al .,(2023), who found high heritability for plant height and other traits.Genetic advance as a percentage of the mean, categorized as low (0-10%), moderate (10-20%), and high (20% and above) by [19]. Table 6 shows that selecting the top 5% of the base population could result in a genetic advance ranging from 0.17% to 19.14% over the mean. The expected genetic advance varied from 0.95% for spike length to 49.14% for grain yield. High genetic advance was noted for grain yield (49.3%), plant height (44.2%), and other traits, contrasting with moderate advances for days to maturity, 1000 kernel weight, and harvest index. Grain yield showed a significant advance of 14.85%, along with days to 50% heading.

Association of Characters

For each feature pair, the genotypic and phenotypic correlation coefficients were analyzed, as shown in table 7 for the sites under study. The genotypic correlation coefficients, indicative of inherent genetic connections among various traits and less influenced by the environment, generally exhibited greater values than the phenotypic correlation coefficients. This study made it clear that an inherent association exists between different traits, as evidenced by the larger genotypic correlation coefficients compared to phenotypic ones for most of the traits examined.

Table. 7. Genotypic and phenotypic correlation coefficients among 11 characters of 16 bread wheat genotype studied

	EM	NT	MAT	DHE	KNS	SL	PH	TKW	AM	HI	PY
EM	1	-0.779*	0.198	0.038	-0.346	0.432	-.0226	0.341**	0.146	-0.636	-0.505
NT	0.774*	1	0.64*	-0.416	0.502	0.732*	0.663*	-0.283	-0.236	-0.455	-0.475
MAT	0.246	0.64*	1	0.532**	0.721*	0.197	0.316**	0.591	-0.241	-0.359	0.366**
DHE	0.743*	0.96*	0.675*	1	0.531*	0.421**	0.743*	0.123	-0.218	-0.421	0.439
KNS	0.542**	0.74*	-0.246	-0.749*	1	0.364**	0.643*	0.246	0,318	0.378	0.459*

SL	0.497**	0.50*	0.19*	0.531	0.457**	1	0.453**	0.359	-0.272	-0.093	0 221**
PH	0.453	0.63*	0.316	0.70*	0.453*	0.118	1	0.521	0.476	-0.201	-0.172
TKW	-0.232	0.59*	-0.123*	0.20*	0.359*	0.271**	0.439**	1	0.643*	0.139	0.607*
AGB	0.014	-0.236	-0.241	-0.218	-0.271	0.895*	0.770*	0.181	1	0.174	0.649*
HI	-0.063	-0.454	-0.359	-0.421	-0.095	0.729	0.560	0.369	0.125	1	0.850*
PY	0.220	0.63*	-0.366	-0.439**	0.723*	0.434*	0.162	0.929*	0.227	0.936*	1

**,* = Indicate significance at the P< 0.05 and 0.01, probability levels, respectively

The findings in table 7 revealed that a strong association between select characteristics and grain yield at both genotypic and phenotypic levels. Grain yield showed a highly significant positive correlation at the phenotypic level with kernels per spike (r = 0.459*), 1000-kernel weight (r = 0.607*), and harvest index (r = 0.850*). Days to maturity (r = 0.366**) and spike length (r = 0.221**) also demonstrated a notable positive correlation with grain yield. At the genotypic level, grain yield was significantly correlated with spike duration (r = 0.221**), kernels per spike (r = 0.456*), and 1000-kernel weight (r = 0.866*). Additionally, grain yield had a substantial positive correlation with harvest index (r = 0.988*), above-ground biomass (r = 0.253*), and days to maturity (r = 0.476**). Biomass yield (r = 0.8) exhibited a strong positive association with grain yield, as the result supporting by, Evangelos Korpetis et al.,(2023) also reported a highly significant positive phenotypic correlation between grain yield and both above-ground biomass and harvest index. The current study identified a robust positive association between plant height, hectoliter weight, and grain yield, suggesting that selecting for these traits could effectively enhance wheat grain yield. No significant correlation was found between grain yield and the remaining characteristics. Days to heading showed a strong positive correlation with days to maturity, plant height, kernels per spike, and spike length at both genotypic and phenotypic levels, implying that increasing days to heading could enhance these traits. However, its correlation with days to tillering, days to emergence, 1000-kernel weight, and harvest index was negative. Days to heading, days to maturity, and spikelets per spike were found to be highly significantly correlated, as reported by Aavula N. *et al.,* (2023).

Days to maturity showed a significant positive association with plant height, days to heading, 1000-kernel weight, and grain yield at the phenotypic level. It also demonstrated a strong genetic link with days to heading and spike length. This indicates that a longer phenological period may lead to a substantial accumulation of biomass, contributing significantly to the weight of 1000 kernels and grain yield. A strong, positive correlation was observed with spike length, 1000-kernel weight, harvest index, plant height, days to maturity, and grain yield at both genotypic and phenotypic levels, suggesting that an extended interval between heading days and days to maturity significantly increases 1000-kernel weight and the number of kernels per spike.

At both levels, the harvest index had a strong positive association with plant height, kernels per spike, and days to maturity, and a significant negative correlation with spike length. The study "Estimation of Genetic and Phenotypic Correlation Coefficients Among Grain Yield and Its Components in Bread Wheat" reported that biomass per plant had positive and highly significant correlations with grain yield per plant and a negative association with harvest index. Negative correlations between the harvest index and above-ground biomass were found, indicating that the harvest index ratio decreases as above-ground biomass increases. Hectoliter weight had a significant positive association with 1000-kernel weight and harvest.

Significant negative correlations were observed between plant height and both 1000 kernel weight and harvest index at the phenotypic level. In contrast, significant positive correlations were noted with days to tillering, days to heading, kernels per spike, spike length, and days to maturity at both genotypic and phenotypic levels. This conclusively demonstrates that higher plant height results in greater above-ground biomass. Similarly Girma .Gerem *et al*.,(2020) reported a substantial positive correlation (r=0.34) between plant height and biomass yield. However, this study contradicts the same author's earlier findings, which indicated a positive correlation between plant height and 1000 kernel weight. Consistent with common observations, the number of kernels per spike was highly positively correlated with the number of tillers per plant and spikelets per spike, and negatively correlated with the 1000 kernel weight, the genotypic level, thousand seed weight showed a strong positive correlation with plant height, spike length, day to heading, day to tillering, and kernel per spike. According to Alemu Dabi,(2016), there is a positive and substantial link between the length of the peduncle and the number of kernels per spike and plant height. This suggests that genotypes with longer peduncle lengths may also have longer plant heights and more kernels per spike. Additionally, it demonstrated a strong positive link between the days to maturity and emergence at the phenotypic level. At both the genotypic and phenotypic levels, the number of spikes per plant was positively correlated and statistically significant, suggesting that a higher number of tillers per plant may lead to a higher number of spikes per plant. demonstrating that determining the ultimate spike number for each plant is a crucial aspect of tillering.Significant negative association with 1000 kernel weight, which is frequently observed in wheat, and correlation with tiller per plant and spikelet per spike.Frankin, S.*et al*.,(2021) reported a similar finding, showing a persistent negative correlation between grains per spike and 1000 kernel weight.

Table 8. Average Grain yield in kunt/hectar of bread wheat farmer's varieties in contrast to improved varieties of by using compost.

No	Treatments	Average yield kunt/hect	Rank	No	Treatments	Averageyield kunt/hect	Rank
	Wheat Farmers varieties				Wheat Improved varieties		
1	Bawunde	26.67	6	1	Sherume	21.67	3
2	Tikur seregegna	27.17	5	2	Ejerso	18.34	6
3	Tate	11.67	8	3	Ogolcho	18.44	5
4	Setakur	21.67	7	4	Danda'a	18.64	4
5	Bokate	28.54	3	5	Digalu	10.01	8
6	Nech goshmber	28.34	4	6	Huluka	23.4	2
7	Ayubo	31.67	2	7	Hidase	10.41	7
8	Tikur goshmber	33.34	1	8	Kekeba	30.01	1

According to the result indicated in table 8 that among the farmer varieties, Tikur Goshmber had the highest grain yield at 33.34 quintals per hectare, while Tate had the lowest at 11.67 quintals per hectare. Among the improved varieties, Digalu had the lowest yield of 10.01 quintals per hectare, and Kekeba had the highest at 39.01 quintals per hectare. The yield performance of bread wheat landraces compared to released varieties is a significant aspect of the research on these landraces. The studies show that landraces generally have lower yields compared to commercial cultivars, but they also exhibit adaptability to low-input and organic environments. However, in the organic environment, landraces demonstrated a significant difference in yield performance. While commercial cultivars showed a significant reduction in yield (around 68%) compared to the conventional environment, landraces showed a much smaller reduction (around 33-85%). Landraces are a valuable source of genetic variation, which provides increased adaptability and enables crops to better withstand the challenges of low-input and organic agriculture. Evangelos Korpetis *et al*.,(2023)

Summary and Conclusion

In Goro, sixteen bread wheat genotypes were cultivated (eight released and eight farmer varieties) to evaluate genetic diversity, the relationship between yield components and grain yield, and the performance of farmer-grown varieties compared to improved varieties using compost. Highly significant ($p \leq 0.01$) variations were observed in genotypes for 11 of the parameters studied, indicating potential for enhancing bread wheat yield and its components. Table 8 reveals that the Tikur Goshmber variety had the highest grain yield (33.34 quintals/hectare) among the farmer's varieties, while the Tate variety had the lowest (11.67 quintals/hectare). Among the improved varieties, the Digalu variety yielded the least (10.01 quintals/hectare), and the Kekeba variety the most (39.01 quintals/hectare). Consequently, for further yield improvement of bread wheat in the area, it is advisable to select and crossbreed farmer and released varieties with high GCV, heritability, genetic advance, positive correlation coefficient, and high grain yield. The study demonstrated significant genetic variability in the genotypes tested, which is beneficial for both direct and indirect selection.

- To effectively enhance grain yield, features with moderate to high heritability and genetic gain should be prioritized.
- Genotypic and phenotypic correlations among plant traits are valuable when formulating, evaluating, and implementing selection criteria for desired traits in a breeding program.
- Significant phenotypic and genotypic correlations were observed between grain yield and traits such as thousand kernel weight, above-ground biomass, harvest index, and plant height.
- The above-ground biomass and harvest index showed a highly significant direct impact on grain yield at both genotypic and phenotypic levels, indicating these traits should be emphasized to improve bread wheat grain yield..

Consequently, traits with high Genotypic Coefficient of Variation (GCV), heritability, genetic progress, positive correlation coefficients, and high grain yield were prioritized in the selection and hybridization of farmer-used and commercially released varieties. The heritability, variability, and correlations observed in the evaluated characteristics of the genotypes confirmed the potential to enhance wheat productivity in the targeted region for both farmers and released varieties. Thus, traits exhibiting high GCV, heritability, genetic advancement, and positive correlation should be the focus of selection and hybridization in these genotypes.

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Appendix

Mean values of 11 characters of 16 bread wheat genotypes studied

No.	EM	NT	MAT	DHE	KNS	SL	PH	GY	TKW	AGB	HI
Sherume	7	12	129	71	62.4	8.2	86.2	0.5	33	1.3	38.4
Ejerso	9	8	139	70	62.4	6.2	79.0	0.6	31	1.4	42.8
Ogolcho	7	10	139	77	60.8	7.6	87.0	0.4	32	1.2	33.3
Danda’a	7	15	137	77	68.8	7.4	85.4	0.3	37	1.1	27.2
Digalu	9	13	134	76	62.4	7.2	78.0	0.2	36	1.0	20.0
Huluka	9	18	116	77	65.6	7.6	76.8	0.6	38	1.5	40.0
Hidase	9	14	118	70	60.8	8.4	85.6	0.7	42	2.6	26.9
Kekeba	9	9	113	66	64.0	8.2	80.0	1.0	40	2.0	50.0
Bawunde	9	18	134	79	58.0	11	141	0.8	42	2.4	33.3
Tikur Seregegna	9	22	128	70	55.2	8.8	118	1.0	39	2.4	41.6
Tate	9	16	113	67	65.6	8.6	73.6	0.3	26	1.1	27.2
Setakur	9	24	141	76	66.0	11	146	0.6	38	1.6	37.5
Bokate	9	20	134	74	51.2	8.0	104	0.7	41	2.0	35.0
Nechgoshmber	9	16	130	68	48.0	7.8	115	0.9	40	2.5	36.0
Ayebo	7	15	116	69	50.4	8.2	116	1.1	39	2.6	42.3
Tikur goshmber	7	28	129	68	61.6	11	117	0.8	28	3.0	26.6
Mean	**7.9**	**16.12**	**127.4**	**72.5**	**59.2**	**8.39**	**100.7**	**0.71**	**36.6**	**1.92**	**36.6**
CV	**9.1**	**3.9**	**4.0**	**3.8**	**12.9**	**9.2**	**5.0**	**20.4**	**10.5**		**14.8**

										18.8	
LSD (5%)	**0.54**	**1.9**	**3.8**	**2.05**	**5.7**	**0.57**	**3.8**	**0.11**	**2.8**	**0.27**	**4.1**