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RESEARCH ARTICLE

Genetic variability, heritability and correlation analysis in bread wheat (*Triticum aestivum* L.) genotypes in North Western Ethiopia

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Abstract

Wheat productivity in Ethiopia remains low (3.1 ton ha^{-1}), highlighting the need for genetic improvement programs. This study assessed genetic variability, heritability and correlation analysis in 160 bread wheat genotypes tested across 2 sites and seasons using an alpha lattice design. The study revealed substantial variation in yield and related traits, indicating a strong potential for selection. Grain yield showed high genetic and phenotypic coefficients of variation, while those for 1000 kernel weight (TKW) and spike length were moderate and for most other traits, they were low. Genetic advance was notable only for yield and TKW, with high genetic advance as a percentage of mean (GAM) observed for yield, TKW and spike length. Spikelet number and kernel number per spike displayed moderate GAM, whereas remaining traits were low. High heritability (>60 %) for most studied traits indicate that the observed variations were predominantly under genetic control and less influenced by the environment. Moreover, a significant positive correlation was observed between agronomic traits. These findings provide valuable guidance for breeders in developing high yielding wheat varieties adapted to diverse environments.

Keywords: genetic variability; genotype; heritability; selection

Introduction

Global wheat production relies almost exclusively on 2 main species: hexaploid bread wheat (*Triticum aestivum* L., 2n = 6X = 42, AABBDD) and tetraploid durum wheat (*Triticum turgidum* sub sp. *durum*, 2n = 4X = 28, AABB) (1). Bread wheat (*T. aestivum*) holds worldwide importance because of its broad adaptability, rich dietary profile, wide cultivation range and strong potential for both production and yield (2).

Bread wheat (*T. aestivum*) is a key staple food for a significant portion of the global population, including Ethiopia. In Ethiopia, wheat is grown at altitudes ranging from 1500–3000 m above sea level, within 6–16 °N latitude and 35–42 °E longitude. The most suitable agro-ecological zones, however, fall between 1900 and 2700 m above sea level (3). However, wheat productivity per hectare in Ethiopia is low (3.1 ton/ha) compared to most other countries, such as Germany (7.43 ton/ha), France (7.20 ton/ha), Egypt (7.18 ton/ha) and China (5.78 ton/ha) (4).

Variations in wheat yield arise from differences in genetic makeup, climatic conditions, soil characteristics and the influence of both biotic and abiotic stresses, as well as management practices (5). The narrow genetic base of improved varieties has reduced their resilience to environmental and disease pressures (6). Declining genetic diversity further heightens crop vulnerability to pathogens and unfavorable climate shifts (7). To address these challenges, it is essential to identify and promote wheat genotypes that combine high yield with quality traits across diverse ecological settings (8, 9). Accordingly, this study aimed to evaluate genetic variability and develop bread wheat varieties with superior performance under the tested environments.

Materials and Methods

A set of 160 bread wheat (*T. aestivum*) genotypes (Supplementary Table 1), consisting of advanced lines and commercial varieties, was used. Advanced lines (156) were obtained from the International Maize and Wheat Improvement Center (CIMMYT Mexico) while, 4 were commercial cultivars grown in Ethiopia.

The study was carried out during the 2023 and 2024 main cropping seasons at 2 sites: the Dabat station of Gondar Agricultural Research Center (12°59′03″ N, 37°45′54″ E; 2607 m above sea level) and Adet Agricultural Research Center (11°16′32″ N, 37°29′30″ E; 2216 m above sea level). An alpha lattice design with 2 replications and 4 sub-blocks per replication was employed. Each genotype was hand-sown in 2 rows, 1 m in length, with 20 cm spacing between rows and 40 cm between entries. Distances of 1 and 1.5 m were maintained between blocks and replications, respectively. A seeding rate of 150 kg ha^{-1} was used. Fertilisation at Dabat consisted of 100 kg ha^{-1} NPS (Nitrogen-Phosphorus-Sulfur) applied at sowing and 300 kg ha^{-1} urea (one-third at sowing and two-thirds 40 days later). At Adet, 181 kg ha^{-1} NPS was applied at sowing, while 300 kg ha^{-1} urea was split (one-third at sowing and two-thirds 40 days later). Weeding was performed manually 3 times during the season.

Data were recorded on key agronomic traits including days to heading (from emergence to 50 % spike exertion), grain filling duration (days to maturity minus heading) and days to physiological maturity (from sowing to 90 % caryopsis nail impression). Plant height was measured on 10 matured plants from ground to spike tip (excluding awns), while 1000 kernel weight was determined using an electric balance. Grain yield was harvested, weighed and converted to t/ha. Yield components such as kernels per spike, spikelets per spike and spike length (cm) were assessed from 5 representative plants or spikes per genotype. To ensure consistency and reliability, agronomic traits were recorded following established protocols (10, 11).

The analysis of variance (ANOVA) was performed using SAS software version 9.2 (12) for the alpha lattice design, which has been shown to improve efficiency in large-scale genotype evaluations (13). Genotype and block were considered as fixed and random factors, respectively. The least significant difference (LSD) was used to compare 2 means at the 5 % level of significance.

For the individual environment, phenotypic response of the i^{th} genotype in j^{th} replication and l^{th} sub-block was computed using the following model:

$$y_{ijl} = \mu + g_i + \gamma_j + bl\,(_j) + \epsilon_{ij} \qquad \text{(Eqn. 1)}$$

Where, y_{ijl} = observed phenotype, μ = grand mean, g_i = fixed effect of the i^{th} genotype, γ_j = effect of the j^{th} replication, $bl\,(_j)$ = random effect of the l^{th} block nested within the j^{th} replication and ϵ_{ij} = random error term.

The ANOVA for over all seasons and locations were executed by considering genotype as a fixed effect and the block, location and year as random effect according to the following model:

$$Y_{ijklm} = \mu + g_m + \gamma_{ijk} + y_{ij} + e_j + b_{ijk}l + (gy)_{im} + (ge)_{jm} + (ye) + (yeg)_{ijm} + \varepsilon ijklm \qquad \text{(Eqn. 2)}$$

Where, Y_{ijklm}= observed response of genotype m, replication k of block l of location j and year i; μ = grand mean; g_m = fixed effect of genotype m; γ_{ijk} = effect of replication k in location j and year i; y_{ij} = random effect of year i at location j and is ~ normally and independently distributed (NID) (0, $\delta^2 y$); e_j = random effect of location j and is ~ NID(0, $\delta^2 e$); b_{ijkl} = random effect of block l nested with replication k in location j and year i and is ~ NID(0, $\delta^2 b$); $(gy)_{im}$ = random effect of the interaction between genotype m and year i and is ~ NID(0, $\delta^2 gy$); $(ge)_{jm}$ = random effect of the interaction between genotype m and location j and is ~ NID(0, $\delta^2 ge$); $(ye)_{ij}$ = random effect of the interaction between year i and location j and is ~ NID(0, $\delta^2 ye$); $(yeg)_{ijm}$ = random effect of the three-way interaction of genotype m in location j and year i and is ~ NID (0, δ^2_{gey}) and $\varepsilon ijklm$ = random residual effect and ~ NID(0, δ^2).

Combined analyses were performed to know average genotypic effects, environment effects and genotype × environment effects; as well as to get the estimates of environmental and genotype × environment interaction variances. Significant means were separated using LSD procedure at 5 % significance level.

Variance components including genotypic, phenotypic and genotype × environment interaction variances along with coefficients of genotypic and phenotypic variability, were derived from the ANOVA results using the following formulas (14).

$$\sigma^2 gl = (MSgl - Mse)/r \qquad \text{(Eqn. 3)}$$

$$\sigma^2 p = \sigma^2 g + \sigma^2 gy + \sigma^2 gl + \sigma^2 gyl + \sigma^2 e \qquad \text{(Eqn. 4)}$$

Where, $\sigma^2 p$ is the total phenotypic variance, $\sigma^2 g$ is genotypic variance, $\sigma^2 gy$ is the genotype by year interaction variance, $\delta^2 gl$ is the genotype-by-location interaction variance, $\sigma^2 gyl$ is the genotype-by-year-by location interaction variance and $\delta^2 e$ is environmental variance.

The traits estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated using the formula as follows (15):

$$PCV = (\sqrt{(\sigma^2 p)} / \bar{x}) \ast 100 \text{ and } GCV = (\sqrt{(\sigma^2 g)} / \bar{x}) \ast 100 \qquad \text{(Eqn. 5)}$$

Where, $\sigma^2 p$ and $\sigma^2 g$ are the total phenotypic and genotypic variations, respectively and $\bar{x}$ = grand mean of the characters under study.

Computed GCV and PCV values were categorised as low (<10 %), moderate (10–20 %) and high (>20 % and above) as suggested by previous researchers (15).

Broad-sense heritability across environments was estimated by the formula:

$$H^2 = \sigma^2 g / (\sigma^2 g + \sigma^2 g\, y/y + \sigma^2 ge/l + \sigma^2 gye/yl + \sigma^2 \varepsilon/ylr) \qquad \text{(Eqn. 6)}$$

Where, $\sigma^2 g$ is the genotypic variance, $\sigma^2 gy$ is the genotype-by-year interaction variance, $\sigma^2 ge$ is the genotype-by-location interaction variance, $\sigma^2 gye$ is the genotype-by-year-by-location interaction variance and $\sigma^2 e$ is the location variance and l, r and y represent the numbers of locations, replicates and years, respectively.

Genetic advance (GA) in absolute unit and percent of the mean (GAM), were estimated in accordance with the methods illustrated previously (16) as:

$$GA = K \ast \sigma p \ast H^2 \qquad \text{(Eqn. 7)}$$

Where, GA = Expected genetic advance from selection, H^2 = Heritability in broad sense, σp = phenotypic standard deviation and k = the standardise selection differential at 5 % selection intensity (K=2.063) (14). The calculated GA was categorised as low (<10 %), moderate (10–20 %) and high (>20 %) based on (16).

Genetic advance as percent of mean (GAM was also calculated following the formula described earlier (17) as:

$$GAM = (GA / \bar{x}) \ast 100 \qquad \text{(Eqn. 8)}$$

Where, GAM = genetic advance as a percentage of the mean, GA = genetic advance under selection, $\bar{x}$ = grand mean of the trait.

Computed GAM values were categorised as low (<10 %), moderate (10–20 %) and high (>20 %) (18).

Relationships between agronomic traits were computed using Pearson's correlation. The correlation analysis was carried out using pooled data from the 6 environments, referred to as best linear unbiased estimator (BLUE) values. Correlation coefficients between every pair of traits were computed using the PROC CORR procedure in SAS based on the standard formula:

$$r = \mathrm{Cov}(x, y) / \sqrt{(\sigma x \star \sigma y)} \qquad \text{(Eqn. 9)}$$

Where, r = correlation coefficient, Cov (x, y) = covariance of traits x and y, σx = standard deviation of trait x (square root of variance of x), σy = standard deviation of trait y (square root of variance of y).

Results

Table 1 summarises the mean performance of genotypes, descriptive statistics and the significance levels of phenotypic traits across all test locations. The results show that the longest durations for heading (78.45 days), flowering (85.72 days) and physiological maturity (139.45 days) were recorded at E3 (GARC-2024), whereas the shortest durations (66.45, 74.51 and 132.32 days, respectively) were observed at E4 (AARC-2024). The longest grain filling duration (65.92 days) was observed at E4 (AARC-2024), whereas the shortest duration (61.0 days) was recorded at E3 (GARC-2024). The tallest plants (102.14 cm) and longest spikes (8.89 cm) were measured at E1 (GARC-2023), while the shortest plant height (99.15 cm) and spike length (8.41 cm) were noted at E4 (AARC-2024). The highest mean performance for the number of spikelets (15.62) and 1000 kernel weight (43.82 g) recorded at E2 (AARC-2023), whereas the lowest values (14.82 spikelets and 40.16 g 1000 kernel weight) were recorded at E4 (AARC-2024). Similarly, the number of kernels per spike was greatest at E2 (43.82) and lowest at E4 (41.84). Grain yield was highest at E3 (4143.03 kg) and lowest at E4 (3952.24 kg) (Table 1).

The ANOVA based on pooled data, the main effect due to genotype, year and location were highly significant ($p < 0.0001$) for all traits (Table 2). Similarly, the interaction effects of genotype × year, genotype × location and location × year were highly significant ($p < 0.0001$) on most agronomic traits. However, for

Table 1. Descriptive statistics of phenotypic values in wheat genotypes evaluated at 4 environments

Trait	Environment	Mean	Range	SD	CV	P > F
DH	E1(GARC-2023)	75.62	70.5–81.5	2.60	3.44	***
	E2(AARC-2023)	69.93	64.0–78.0	3.11	4.45	***
	E3(GARC-2024)	78.45	70.5–86.5	4.19	5.34	***
	E4(AARC-2024)	66.45	61.5–75.5	2.91	4.38	***
DF	E1(GARC-2023)	81.51	75.5–89.5	3.48	4.27	***
	E2(AARC-2023)	75.89	69.5–84	3.15	4.15	***
	E3(GARC-2024)	85.72	77.5–93.5	4.59	5.35	***
	E4(AARC-2024)	74.51	68–82	3.57	4.79	***
GFD	E1(GARC-2023)	61.16	53–70.0	3.75	6.13	**
	E2(AARC-2023)	63.33	54.50–74	3.89	6.14	***
	E3(GARC-2024)	61.00	51.5–69.5	3.38	5.54	**
	E4(AARC-2024)	65.92	58.0–76.0	3.48	5.28	***
DM	E1(GARC-2023)	136.77	124.5–146.5	5.58	4.08	***
	E2(AARC-2023)	133.46	122–144.5	5.3	3.97	***
	E3(GARC-2024)	139.45	128–144	5.63	4.04	***
	E4(AARC-2024)	132.32	122–143.5	4.97	3.76	***
PH	E1(GARC-2023)	102.14	96–109.3	3.66	3.58	***
	E2(AARC-2023)	99.74	93.2–107.2	3.83	3.84	***
	E3(GARC-2024)	102.04	95.1–109.25	4.14	4.06	***
	E4(AARC-2024)	99.15	93.15–105.7	3.3	3.33	***
SL	E1(GARC-2023)	8.89	7.2–11.5	0.97	10.91	***
	E2(AARC-2023)	8.81	7.3–10.65	0.94	10.67	***
	E3(GARC-2024)	8.73	7–11.1	1.03	11.80	***
	E4(AARC-2024)	8.41	5.05–10.5	0.8	9.51	***
NSS	E1(GARC-2023)	15.10	12.9–17.7	1.16	7.68	***
	E2(AARC-2023)	15.62	13.5–18.3	1.22	7.81	***
	E3(GARC-2024)	14.84	12.9–16.9	1.18	7.95	***
	E4(AARC-2024)	14.80	12.8–17.1	1.17	7.91	***
NKS	E1(GARC-2023)	42.26	36.5–48.9	3.47	8.21	***
	E2(AARC-2023)	43.82	37–50.75	3.57	8.15	***
	E3(GARC-2024)	42.64	35.7–49.9	3.89	9.12	***
	E4(AARC-2024)	41.84	36.1–48.5	3.49	8.34	***
NKPS	E1(GARC-2023)	2.83	2.22–3.18	0.18	6.36	***
	E2(AARC-2023)	2.81	2.6–2.9	0.14	4.98	ns
	E3(GARC-2024)	2.88	2.48–3.19	0.18	6.25	***
	E4(AARC-2024)	2.83	2.62–3.19	0.11	3.89	**
GY	E1(GARC-2023)	3768.62	2857.19–5291.0	716.8	19.02	***
	E2(AARC-2023)	3847.23	2757.6–5408.50	702.5	18.26	***
	E3(GARC-2024)	4143.05	3004.8–4996.61	636.7	15.37	***
	E4(AARC-2024)	3952.24	2847.0–5191.65	650.6	16.46	***
TKW	E1(GARC-2023)	42.36	32.46–57.14	6.6	15.58	***
	E2(AARC-2023)	43.82	32.95–55.72	6.1	13.92	***
	E3(GARC-2024)	43.05	32.11–51.95	5.6	13.01	***
	E4(AARC-2024)	40.16	30.09–48.50	5.76	14.34	***

E1 = Gondar Agricultural Research Center, Dabat site in 2023; E2 = Adet Agricultural Research Center in 2023; E3 = Gondar Agricultural Research Center, Dabat site in 2024 = E4 = Adet Agricultural Research Center in 2024; DF = Days to 50 % Flowering; DM = Days to 90 % Maturity; GDF = Grain filling duration; PH = Plant height (cm); SL= Spike length (cm); NSS = Number of spikelet per spike; NKPS = Number of kernel per spikelet; NKS = Number of kernel per spike; GY = Grain yield. TKW = Thousand kernel weight; Sig = significance level.

Table 2. Combined analysis of variance for 11 traits across 4 environments

Mean squares								
Trait	**G(df = 159)**	**L(df = 1)**	**Y(df = 1)**	**G*L(df = 318)**	**G*Y(df = 159)**	**L*Y(df = 1)**	**G*L*Y(df = 318)**	**Residual**
DH	52.0^{***}	25054.3^{***}	41.69^{***}	4.57^{***}	17.98^{***}	3260.82^{***}	5.87^{***}	1.44
DF	68.40^{***}	24047.1^{***}	439.45^{***}	6.72^{***}	24.40^{***}	2332.80^{***}	5.54^{***}	1.74
GFD	36.9^{***}	4136.4^{***}	417.4^{***}	12.09^{***}	29.5^{***}	506.2^{***}	10.3^{***}	4.18
DM	128.8^{***}	8830.5^{***}	195.3^{***}	11.1^{***}	68.9^{***}	1197.3^{***}	7.2^{***}	3.9
PH	100.1^{***}	2243.9^{***}	37.4^{***}	1.9^{*}	1.9^{*}	20.0^{***}	2.2^{***}	1.56
SL	6.3^{***}	9.05^{***}	30.7^{***}	0.30^{***}	0.33^{***}	2.42^{***}	0.36^{***}	0.17
NSS	8.0^{***}	22.7^{***}	101.14^{***}	0.25^{ns}	0.62^{*}	29.95^{***}	0.40^{ns}	0.47
NKS	92.9^{***}	46.4^{***}	206.3^{***}	3.13^{***}	1.94^{***}	450.6^{***}	2.47^{***}	0.99
NKPS	0.05***	0.54***	0.35***	0.03***	0.02*	0.06^{ns}	0.02^{ns}	0.02
GY	3013497.6^{***}	1038739.4^{***}	18985282^{***}	268154.5^{***}	206534.2^{***}	5957883.9^{***}	184823.05^{***}	9454.9
TKW	219.6^{***}	157.4^{**}	711.9^{***}	24.3^{***}	19.5^{ns}	1538.4^{***}	29.9^{***}	16.2

G = Genotype; L = Location; Y = Year; G*Y = Genotype-by-year interaction; G*L = Genotype-by-location interaction; Y*L = Year-by-location interaction; G*Y*L = Genotype-by-year-by location interaction; DH = days to 50 % heading; DF = days to 50 % flowering; DM = days to 90 % maturity; GDF = Grain filling duration; TKW = 1000 kernel weight; PH = Plant height (cm); SL = Spike length (cm); NSS = number of spikelet per spike; NKPS = Number of kernel per spikelet; and NKS = Number of kernel per spike; *** = very highly significant at $p< 0.001$, * = significant at $p < 0.05$, ns = non-significant at $p = 0.05$ significance level and df = degree of freedom.

number of spikelets per spike, number of kernels per spikelet and TKW, the effects of genotype × location, location × year and genotype × year interactions were non-significant, respectively. Likewise, their three-way interactions (genotype × year × location) were highly significant ($p < 0.0001$) on all the agronomic traits except number of spikelets per spike and number of kernels per spikelet, where the three-way interactions were non-significant (Table 2).

Genotypic and phenotypic variability are critical in breeding programs for improving yield and disease resistance. Their extent is measured through coefficients of variation, genetic variance (σ^2g), heritability and genetic advance, as shown in Table 3. All agronomic traits showed very high significance ($p < 0.0001$) and the largest genetic variance across environments (Table 3). Moreover, for all agronomic traits, the genotype × year (σ^2gy), genotype × location (σ^2gl) and year × location (σ^2yl) interactions were highly significant but lower in magnitude as compared to genotypic variance (Table 3).

In a broad sense, heritability of the agronomic traits across the entire environment ranged from 58 % (grain filling duration) to 98 % (number of kernels per spike and plant height) (Table 3). High broad-sense heritability ($H^2 > 60$ %) values were observed for all agronomic traits except grain filling duration (Table 3). This high heritability indicates that the variations observed were mainly under genetic control and were less influenced by the environment.

For all traits, PCV slightly exceeded GCV, reflecting environmental influence on trait expression (Table 3). Genotypic coefficient of variation ranged from 3.45 % for kernels per spikelet to 22.06 % for grain yield, with most traits (63.6 %) showing low values (<10 %), 27.3 % moderate (10–20 %) and 9.1 % high (>20 %). Phenotypic coefficient of variation values varied between 5.13 % (plant height) and 25.24 % (grain yield). Grain yield and 1000 kernel weight had high PCV, spike length and kernels per spike were moderate, while the remaining traits were low (<10 %) (Table 3).

Genetic advance as a percentage mean was categorised as low (0–10 %), moderate (10–20 %) and high (20 % and above) (17). Accordingly, GA ranged from 0.11 % (number of kernels per spikelet) to 1129.48 % (grain yield). Except for grain yield (1129.48 %) and thousand-kernel weight (10.07 %), other traits showed low genetic advance (Table 3).

Grain yield (28.76 %), 1000 kernels weight (25.09 %) and spike length (20.38 %) showed high genetic gains from at 5 % selection as percent of mean. Whereas numbers of spikelet per spike and number of kernels per spike showed moderate genetic gains from selection as percent of mean and the rest of the traits showed low (<10 %) GAM values (Table 3).

The genotypes GY varied from 2897.4 to 5164.1 kg ha^{-1} (mean = 3927.6), TKW varied from 29.72 to 51.71 g (mean = 40.12 g), NKS ranged from 37.15 to 49.25 (mean = 42.65) and kernels per spikelet varied from 2.63 to 3.01. Among tested bread wheat genotypes, G37 and G143 were found to be the highest (5164.12 kg ha^{-1}) and the lowest (2897.43 kg ha^{-1}) performing genotypes, respectively (Supplementary Table 2).

Table 3. Variance components, heritability, phenotypic and genotypic coefficient of variations and genetic advance for 11 traits in 160 wheat genotypes based on pooled data

Trait	**σ^2g**	**σ^2gy**	**σ^2gl**	**σ^2gyl**	**σ^2e**	**PV**	**H^2**	**GCV**	**PCV**	**GA**	**GAM**
DH	12.65^{***}	3.03^{***}	1.56^{***}	2.22^{***}	1.44	20.90	0.80	4.85	6.23	4.38	5.96
DF	16.67^{***}	4.72^{***}	2.49^{***}	1.90^{***}	1.74	27.51	0.79	5.14	6.60	4.78	6.02
GFD	8.19^{***}	4.82^{***}	3.96^{***}	3.07^{***}	4.18	24.21	0.58	4.55	7.82	2.59	4.11
DM	31.22^{***}	15.44^{***}	3.59^{***}	1.64^{***}	3.94	55.83	0.75	4.12	5.51	6.18	4.56
PH	24.65^{***}	-0.07^{***}	0.20^{***}	0.35^{***}	1.56	26.69	0.98	4.93	5.13	7.18	7.13
SL	1.53^{***}	-0.009^{***}	0.06^{***}	0.09^{***}	0.17	1.86	0.95	14.24	15.66	1.77	20.38
NSS	1.88^{***}	0.054^{***}	-0.11^{***}	-0.03^{***}	0.47	2.26	0.98	9.08	9.95	2.02	13.36
NKS	22.99^{***}	-0.13	1.07^{***}	0.74^{***}	0.99	25.65	0.97	11.24	11.87	6.79	15.92
NKPS	0.01^{***}	0.0003^{***}	0.005^{***}	0.0015^{***}	0.02	0.03	0.63	3.45	6.28	0.11	3.75
GY	751010.70^{***}	5427.8^{***}	129349.9^{***}	87684.1^{***}	9454.9	982927.33	0.89	22.06	25.24	1129.48	28.76
TKW	50.85^{***}	-2.6^{***}	4.04^{***}	6.9^{***}	16.27	75.40	0.91	17.77	21.64	10.07	25.09

DH = Days to 50 % heading; DF = Days to 50 % flowering; DM = Days to 90 % maturity; GDF = Grain filling duration; TKW = 1000 kernel weight; PH = Plant height (cm); SL= Spike length (cm); NSS = Number of spikelet per spike; NKPS = Number of kernel per spikelet; NKS = Number of kernel per spike; *** = very highly significant at $p< 0.001$, * = significant at $p < 0.05$ and ns = non-significant at $p = 0.05$ significance level.

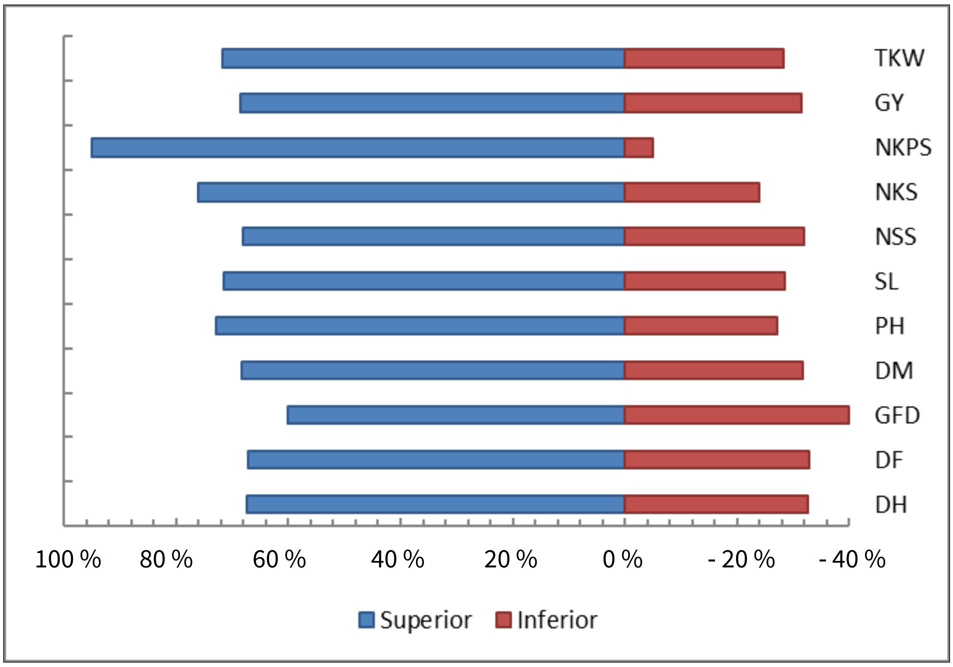

Fig. 1. Proportion of the wheat genotypes superior and inferior to the check, King-bird.

DH = Days to 50 % heading; DF = Days to 50 % flowering; DM = Days to 90 % maturity; GFD = Grain filling duration; TKW = Thousand-kernel weight; PH = Plant height (cm); SL = Spike length (cm); NSS = Number of spikelet per spike; NKPS= Number of kernel per spikelet; NKS = Number of kernel per spike.

Fig. 1 shows the proportion of genotypes performing above or below the standard check, King-bird. When compared with King-bird and the mean of 4 released cultivars (Alidero, Medawolabu, Danda'a and King-bird), many tested genotypes demonstrated superior grain yield and other agronomic traits.

The top 5 % of genotypes (G37, G81, G34, G30, G129, G108, G80 and G149) demonstrated superior grain yield performance, with yields ranging from 35.71 to 49.03 % over the standard check and 39.71 to 53.42 % over commercial cultivars. The top 5 % of thousand kernels weight genotypes outperformed King- Bird and released varieties by 27.89 % to 43.36 % and 25.58 % to 38.37 %, respectively. Similarly, the comparative advantage of the best genotypes over the standard check and commercial varieties varied from 20.12 to 26.96 % and 20.86 to 27.65 % for kernels per spike and 10.00 to 11.48 % and 7.6 to 9.05 % for kernels per spikelet, respectively (Table 4).

Pearson's correlation among agronomic traits was computed based on across-environments data. A significant positive correlation was observed between agronomic traits. Most traits showed strong positive correlation and some traits are moderately associated. A very highly significant ($p < 0.0001$) and nearly perfect positive correlation (r = 0.98) was observed between

Table 4. Comparison of mean performances of top 5 % selected genotypes for grain yield and related traits performance with King-bird and with mean off 4 released varieties

Genotype	GY means of selected genotype	Comparative advantage (%)		Genotype	NKPS means of selected genotype	Comparative advantage (%)	
		King bird	MRV			King bird	MRV
G37	5164.12	49.03	53.42	G37	3.01	11.48	9.05
G81	5160.88	48.94	53.32	G81	3.01	11.48	9.05
G34	5115.51	47.50	51.97	G34	3.00	11.11	8.69
G30	5104.57	47.31	51.65	G30	2.99	10.74	8.33
G129	4768.89	37.63	41.67	G129	2.99	10.74	8.33
G108	4714.87	36.07	40.07	G108	2.98	10.37	7.97
G80	4713.81	36.04	40.01	G80	2.97	10.00	7.6
G149	4702.66	35.71	39.71	G149	2.97	10.00	7.6
King-bird	3465.00	-	-2.85	King-bird	2.70	-	2.17
MRV	3366.00	2.85	-	MRV	2.76	-2.22	
Genotype	**NKS means of selected genotype**	**Comparative advantage (%)**		**Genotype**	**TKW means selected genotype**	**Comparative advantage (%)**	
		King bird	**MRV**			**King bird**	**MRV**
G30	49.20	26.96	27.65	G34	51.71	43.36	38.37
G34	48.85	26.06	26.75	G81	51.47	43.12	37.73
G37	48.75	25.80	26.49	G37	50.48	39.95	35.08
G81	48.60	25.41	26.31	G30	49.45	37.09	32.32
G146	47.33	22.14	22.80	G149	48.25	33.76	29.11
G119	46.75	20.64	21.30	G100	47.18	30.80	26.25
G47	46.63	20.33	20.99	G76	46.96	30.19	25.66
G149	46.58	20.12	20.86	G129	46.93	27.89	25.58
King bird	38.75	-	0.54	King bird	36.07	-	-3.47
MRV	38.54	-0.54	-	MRV	37.37	3.53	-

GY = Grain yield; NKPS = Number of kernels per spikelet; NKS = Number of kernels per spike; MRV = Mean of 4 selected released varieties.

Table 5. Association between agronomic traits in 180 bread wheat genotypes

	DH	DF	GFD	DM	PH	SL	NSS	NKS	NKPS	GY	TKW
DH	1	0.98^{**}	0.45^{***}	0.88^{**}	0.68^{**}	0.66^{**}	0.61^{**}	0.65^{**}	0.47^{**}	0.68^{**}	0.68^{**}
DF		1	0.51^{***}	0.90^{**}	0.73^{**}	0.71^{**}	0.67^{**}	0.70^{**}	0.49^{**}	0.73^{**}	0.73^{**}
GFD			1	0.82^{**}	0.43^{**}	0.39^{**}	0.41^{**}	0.42^{**}	0.27^{*}	0.47^{**}	0.47^{**}
DM				1	0.66^{**}	0.63^{**}	0.61^{**}	0.64^{**}	0.44^{**}	0.69^{**}	0.68^{**}
PH					1	0.93^{**}	0.90^{***}	0.94^{**}	0.64^{**}	0.92^{**}	0.89^{**}
SL						1	0.92^{***}	0.96^{**}	0.64^{***}	0.94^{**}	0.93^{**}
NSS							1	0.94^{**}	0.43^{**}	0.92^{**}	0.91^{**}
NKS								1	0.70^{***}	0.95^{**}	0.93^{**}
NKPS									1	0.62^{**}	0.58^{**}
GY										1	0.98^{**}
TKW											1

DH = Days to 50 % heading; DF = Days to 50 % flowering; DM = days to 90 % maturity; GDF = Grain filling duration; TKW = 1000 kernel weight; PH = Plant height (cm); SL = Spike length (cm); NSS = Number of spikelet per spike; NKPS = Number of kernel per spikelet; NKS = Number of kernel per spike; *** = very highly significant at $p < 0.001$, * = significant at $p < 0.05$ and ns = non-significant at $p = 0.05$ significance level.

days to heading and days to flowering (Table 5). Grain yield showed significant positive association with TKW (r = 0.98), NKS (r = 0.95), NSS (r = 0.92), NKPS (r = 0.95), PH (r = 0.92) and SL (r = 0.94). A significant positive correlation was observed between PH and SL (0.95), PH and NSS (r = 0.90), PH and NKS (0.94) and DM and DF (r = 0.90) (Table 5).

Discussion

The primary objectives of this study were to assess genotypic diversity, explore trait associations for direct and indirect selection and identify high-yielding, stable bread wheat genotypes under diverse environments. Consistent with these objectives, the combined analysis demonstrated that grain yield, yield components and other agronomic traits were strongly influenced by genotypes, environments, years and their interactions. Similar findings of substantial genetic variability in bread wheat have been reported by previous researchers (19–22). The highly significant ($p <$ 0.0001) genotypic differences observed across sites confirm the presence of inherent genetic diversity among the tested materials, underscoring the potential for effective genetic improvement through selection.

The pooled analysis revealed that year effects accounted for the largest share of phenotypic variance, followed by location effects. All traits exhibited significant genotypic variance, confirming strong genetic control. Genotype × year interactions were generally greater than genotype × location effects, except for plant height and spike length. Traits such as days to maturity and grain yield showed high genotype × year variance (σ^2gy), reflecting sensitivity to seasonal fluctuations. The pronounced year effect highlights the need for stable genotypes capable of consistent performance across environments. Grain yield also displayed a high genotype × location variance (σ^2gl underscoring the importance of location specific adaptation. In contrast, traits including plant height, flowering time, spikelet number, kernel number per spike and per spikelet, spike length and thousand-kernel weight showed low but significant genotype × location effects, indicating minor environmental influence.

For all traits, the genotype × location × year variance (σ^2gyl) was much lower than the genotypic variance, indicating strong genetic control and limited environmental influence (23). The analysis highlights grain yield (GY), days to maturity (DM) and number of kernels per spike (NKS) as traits with high genetic and interaction variances, making them key targets for breeding programs. Traits with low interaction variances, such as spike length and number of kernels per spikelet, may be more stable across environments.

The existence of sufficient genetic variability among tested bread wheat genotypes was evidenced by wide ranges of grain yield and yield components mean performances at individual and across environments. In the present study, the mean grain yield ranges from 2757.63 to 5408.50 kg ha^{-1} at individual environments, which is higher than an earlier reports (24), that described grain yield mean performances of 1284.4–4683.3 kg ha^{-1}. This result is similar to the result of previous researchers (21), who described grain yield mean performances of 2115–5955 kg ha^{-1} and lower than another report described a maximum grain yield of 7840 kg ha^{-1} (22). Moreover, considerable variation was observed for pooled grain yield (2897.4–5164.1 kg), yield components like TKW (32.40–52.7 g), number of kernels per spike (37.20–49.20). The current finding supported by the finding of earlier reports which stated that the existence of genetic variability among genotypes gives the possibility of genetic improvement of various traits through exploiting the variability existing within the materials (23). Similar substantial genetic variability for grain yield and yield component trait performances has been reported for wheat in Ethiopia (19, 25) and elsewhere in the world (26, 27).

Among tested bread wheat genotypes, G37 and G143 were found to be the highest (5164.1 kg ha^{-1}) and the lowest (2897.41 kg ha^{-1}) performing genotypes. The top 5 % of genotypes (G37, G81, G34, G30, G129, G108, G80 and G149) outperformed the standard check by 35.71–49.03 % and exceeded the yield of commercial cultivars by 39.71–53.42 %. These results highlight the value of genetic variability analysis across environments and years in identifying superior and stable genotypes, reinforcing its importance for successful wheat breeding.

Broad sense heritability (H^2) estimates ranged from 58–98 % across environments, with most traits showing high heritability (≥60 %). High heritability indicates that observed variation is largely genetic, suggesting good prospects for selection (28). However, the study also revealed that many traits with high heritability were coupled with low genetic advance, such as spike length and kernels per spike, which recorded heritability values of 95 and 63 % but genetic advances of only 1.7 and 0.11 %, respectively. This combination suggests that these traits are predominantly governed by non-additive gene action (29). This distinction is crucial for breeding. Traits with high heritability but low genetic advance are less responsive to direct selection because additive genetic variance is limited. For such traits, breeders should consider alternative strategies such as recurrent selection, hybrid development, or exploiting heterosis rather than simple pedigree selection. Conversely, traits with high heritability and high genetic advance, such as grain yield, 1000 kernel weight and spike length are more amenable to direct selection, as additive gene action plays a stronger role (29). These traits therefore represent promising targets for immediate genetic improvement.

In the present study, PCV values were consistently higher than GCV values across traits, reflecting environmental influence on trait expression. However, the relatively small differences between PCV and GCV observed suggest that phenotypic selection remains reliable. Grain yield showed the highest variability (GCV = 22.06 %, PCV = 25.64 %), supporting its potential as a key trait for genetic improvement. These results are consistent with earlier reports that also highlighted high variability in grain yield and related traits in bread wheat (21, 22, 28, 30). Similarly, the moderate variability observed for 1000 kernel weight, spike length and kernels per spike agrees with findings of previous authors (26, 31), while the low variability recorded for traits such as heading, flowering, maturity, plant height and kernels per spikelet aligns with earlier studies that emphasised limited scope for improvement through selection (31, 32).

The expected genetic advance expressed as a percentage of the mean ranged from 3.75 % for the number of kernels per spikelet to 28.76 % for grain yield, indicating that selecting the top 5 % of the base population could result in an advance of 3.75 to 28.76 % over the respective population mean. Genetic advance expressed as a percentage of the mean from the combined analysis was high for grain yield (28.76 %), 1000 kernel weight (20.38 %) and spike length (20.38 %). Studies have reported high genetic advance (as a percentage of the mean) for grain yield and 1000 kernel weight, which are consistent with the present findings (22, 27, 33). Other authors have also reported high genetic advance for spike length, which aligns with this study (20, 21). This suggested selection could be effective in genotypes for these traits and the possibility of improving bread wheat grain yield through direct selection for grain yield related traits. Genetic advance expressed as percentage of mean from the combined analysis was moderate for numbers of spikelet per spike (13.36 %) and number of kernels per spike (15.92 %). This result agrees with previous studies (22). Low genetic advance as percent of the means were recorded for the traits like days of heading, days of flowering, days of maturity, grain filling duration, spike length and number of kernels per spikelet. The low results of genetic advance as percent of grain filling duration, days to maturity and number of kernels per spikelet agrees with earlier reports (22) and other trait like days of heading, days of flowering and days of maturity in line with previous studies (21).

Correlation analysis further clarified trait associations. Grain yield was strongly and positively correlated with 1000 kernel weight (r = 0.98; p < 0.0001), kernels per spike, spike length and plant height. These associations suggest that indirect selection for yield can be achieved by targeting these correlated traits (34). A strategic breeding approach would therefore combine direct selection for grain yield with indirect selection for 1000 kernel weight and kernels per spike, thereby maximising genetic gain (35).

Finally, the identification of superior genotypes such as G37 and G81 is a key outcome. These genotypes not only demonstrate exceptional yield performance but also stability across environments. They could be considered for direct release as new varieties to enhance productivity in Ethiopian wheat systems. Alternatively, they may serve as valuable parents in crossing programs, given their desirable trait combinations, thereby contributing to long-term genetic improvement.

Conclusion

This study revealed significant genetic variability among bread wheat genotypes, with high heritability estimates across most traits. However, the nuanced interpretation of genetic parameters showed that traits with high heritability, but low genetic advances are likely governed by non-additive gene action, limiting the effectiveness of direct selection. For such traits, breeding strategies should emphasise hybrid development or recurrent selection to exploit non-additive variance. In contrast, traits with both high heritability and high genetic advance, such as grain yield and 1000 kernel weight, are ideal candidates for direct selection.

The strong positive correlations between grain yield and associated traits (1000 kernel weight, kernel per spike, spike length and plant height) provide a clear basis for strategic indirect selection. The identification of superior genotypes (G37, G81, G34, G30, G129, G108, G80 and G149), which outperformed both standard checks and commercial cultivars, underscores their potential for direct release or use as parents in breeding programs.

The next practical steps include validating the performance of these superior genotypes across broader agro-ecological zones, integrating them into crossing pipelines and applying marker-assisted selection to accelerate genetic gain. Together, these strategies will strengthen wheat improvement programs and contribute to enhanced productivity and food security in Ethiopia and beyond.

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Authors' contributions

WF was involved in conceptualisation, methodology, statistical analysis and preparation of the original draft. AS was involved in project administration, supervision and editing. TM contributed materials and was involved in data visualisation. TA was involved in investigation and validation. KT was involved in review. All authors read and approved the final version of the manuscript.

Compliance with ethical standards

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