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Evaluation of Selected Common Wheat (*Triticum aestivum* L.) Genotypes for Diverse Traits at Kokate and Hossana, Southern Ethiopia

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Abstract

During the 2018/19 cropping season, a field trial involving 49 bread wheat (Triticum aestivum L.) genotypes was conducted at the Kokate and Hossana research sub-stations in Southern Ethiopia. The aim was to assess various characteristics within these genotypes. A simple lattice design was employed, and data on 11 quantitative traits were gathered and analyzed using SAS statistical software. The analysis of variance (ANOVA) revealed that there were notable differences in most of the traits studied, based on location, genotype, and the interaction between genotype and location. Particularly, biological yield and harvest index exhibited high phenotypic and genotypic coefficient of variation (PCV and GCV), suggesting their suitability for effective selection and prediction of genotypic potential based on their phenotypic expressions. Traits, such as days to 50% heading, biological yield, and harvest index showed high heritability and genetic advance as a percentage of the mean, suggesting the involvement of additive gene action. Therefore, selecting for these traits would be beneficial.

Keywords: Wheat, genetic advance, heritability, grain yield, genetic gain, PCV, GCV

INTRODUCTION

Common wheat (*Triticum aestivum* L.) holds a pivotal position globally, prized for its economic advantages, including its widespread utilization for ensuring food security and generating income. In Ethiopia, wheat grain serves as a key ingredient in various culinary traditions, being utilized in the making of traditional bread ("injera"), regular bread ("dabo"), and local beer ("tella") [1].

Wheat significantly contributes to meeting the dietary needs of individuals worldwide, constituting 20% of their nutritional intake. It supplies approximately 55% of carbohydrates, 20% of daily protein, and 21% of calories for nearly 40% of the global population [2, 3]. Enhancing yield and traits that contribute to it stands as a primary focus in wheat enhancement initiatives. The success of crop improvement largely hinges on the extent and type of genetic diversity available, as well as the heritability and successful transfer of desired characteristics into new cultivars. Assessing the level of variability and heritability within a specific population for a target trait is crucial for the effectiveness of wheat breeding endeavors. This process aids in the identification of genotypes carrying favorable traits that can be reliably passed down through successive generations [4]. Consequently, the advancement of economically significant traits through sufficient variability creation, including methods, such as hybridization,

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is key to genetic enhancement.

In this study, bread wheat genotypes sourced from ICARDA were systematically assessed across multiple study sites, aiming (1) to scrutinize the lines for diverse variability parameters like genetic variability encompassing heritability, PCV, and GCV, and (2) to appraise the wheat lines for grain yield and its associated components within and across the designated sites.

MATERIALS AND METHODS

Description of the Study Area

The study took place in Kokate and Hossana, situated within the Wolaita and Hadya Zones, respectively, in the Southern Nations, Nationalities, and Peoples Regions (SNNPR) of Ethiopia. These locations were selected to reflect the main regions of Common wheat cultivation in Ethiopia. Kokate and Hossana are sub-stations located at distances of 378 km and 232 km from Addis Ababa, respectively. Both sub-stations are among the research sites managed by the Areka Agricultural Research Center (ArARC). The experiment was conducted during the 2018/2019 cropping season under rain-fed conditions.

Experimental Materials

This research incorporated 49 bread wheat genotypes, comprising 48 sourced from ICARDA and one recently released variety, all acquired from Kulumsa Agricultural Research Center (KARC). These genotypes, initially bred by ICARDA, were specifically designed for optimal performance in potential regions and were selected for their anticipated high yield, as well as resistance to diseases and insect pests. The list of genotypes utilized in this investigation is detailed in Table 1.

Table 1. List of genotypes used in the study.

G*	Genotype (Pedigree)	Seed Source
G1	WBLL4//OAX93.24.35/WBLL1/4/SHUHA-1/3/MON'S'/ALD'S'//ALDAN'S'/IAS58	ICARDA
G2	KAUZ/STAR/3/MUNIA/ALTAR 84//MILAN/4/LEITH-1	ICARDA
G3	FARIS-22/4/BOW/PRL//BUC/3/WH576/5/NING MAI 9558//CHIL/CHUM18	ICARDA
G4	FILIN/3/CROC-1/AE.SQUARROSA (205)//KAUZ/4/FILIN/5/VEE/MJI//2*TUI/3/PASTOR/6/ASEEL-4	ICARDA
G5	WBLL1*2/BRAMBLING//ZAFIR-3	ICARDA
G6	WEAVER/TSC//WEAVER/3/WEAVER/4/WAXWING/5/DURRA-8	ICARDA
G7	CHAMRAN/4/OPATA/BOW//BAU/3/OPATA/BOW/5/SAMIRA-9	ICARDA
G8	KOUKAB-1//PFAU/MILAN/3/SOSSI-3	ICARDA
G9	VEE/NAC//MILAN/PASTOR/5/HUITES/4/CS/TH.SC//3*PVN/3/MIRLO/BUC	ICARDA
G10	SERI.1B//KAUZ/HEVO/3/AMAD/4/ESWYT99#18/ARRIHANE/5/SKAUZ/BAV92	ICARDA
G11	OPATA/RAYON//KAUZ/3/ETBW 4922/4/MILAN/PASTOR	ICARDA
G12	SHIHAB-19/KHIDER-1/5/YANAC/3/PRL/SARA//TSI/VEE#5/4/CROC-1/AE.SQUARROSA (224)//OPATA	ICARDA
G13	HUITES/4/CSTH.SC//3*PVN/3/MIRLO/BUC/5/ETBW 4922/6/QADANFER-4	ICARDA
G14	KINGBIRD/IZAZ-11	ICARDA
G15	KIRITATI/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/SHUHA-4/CHAM-8	ICARDA
G16	KRICHAUFF/2*PASTOR//SHUHA-8/DUCULA	ICARDA
G17	P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN-a	ICARDA
G18	P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN-b	ICARDA
G19	ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA 86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'-a	ICARDA
G20	ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA 86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'-b	ICARDA

G21	PFAU/MILAN//ABIER-2/3/SHUHA-3//TURACO/CHIL	ICARDA
G22	TEVEE-1/STAR'S'//ETBW 4920/3/TEPOCA+LR34/2*BORL95	ICARDA
G23	KAUZ/FCT//ETBW 4920/3/MILAN/PASTOR	ICARDA
G24	CHAM-10/3/PASTOR//MUNIA/ALTAR 84/4/PFAU/MILAN	ICARDA
G25	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-a	ICARDA
G26	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-b	ICARDA
G27	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-c	ICARDA
G28	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-d	ICARDA
G29	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-e	ICARDA
G30	THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B-a	ICARDA
G31	THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B-b	ICARDA
G32	CHAM-8/ETBW 4919//PFAU/MILAN	ICARDA
G33	ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/GHALI-1	ICARDA
G34	KAUZ/FCT//ETBW 4920/3/MILAN/PASTOR	ICARDA
G35	FARIS-17//PFAU/MILAN/3/SOSSI-3	ICARDA
G36	ZERBA-6/FLAG-6/3/TAM200/PASTOR//TOBA97	ICARDA
G37	BABAX/LR42//BABAX*2/3/VIVITSI/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ	ICARDA
G38	TEMPORALERA M 87*2/TUKURU//FAYEQ-2	ICARDA
G39	NESMA*2/14-2//2*SAFI-3/4/PASTOR//HXL7573/2*BAU/3/WBLL1	ICARDA
G40	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/NESMA*2/14-2//2*SAFI-3	ICARDA
G41	FAYEQ-2/3/NESMA*2/14-2//2*SAFI-3	ICARDA
G42	QT6581/4/PASTOR//SITE/MO/3/CHEN/AEGILOPSSQUARROSA (TAUS)//BCN/5/PAVON 76/JADIDA-2	ICARDA
G43	WAXWING*2/VIVITSI//SHUHA-8/DUCULA	ICARDA
G44	WBLL1//TEVEE/KAUZ/3/MILAN/SHA7//POTAM*3KS811261-5	ICARDA
G45	KINGBIRD/3/NESMA*2/14-2//2*SAFI-3a	ICARDA
G46	KINGBIRD/3/NESMA*2/14-2//2*SAFI-3b	ICARDA
G47	KAUZ/STAR//ETBW 4920/3/QAMAR-2	ICARDA
G48	ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA 86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'	ICARDA
G49	WANE(ETBW6130)	KARC

Note: G = genotypes used in the study, KARC = Kulumsa Agricultural Research Center, ICARDA = International Center for Agricultural Research in Dry Area.

Experimental Design and Trial Management

The field experiment was arranged in 7 x 7 simple lattice designs at each location. Each plot measured 2.5 meters in length and 1.2 meters in width, totaling 3 square meters with 6 rows. Replications were spaced 2 meters apart, plots were spaced 0.5 meters apart, and rows were spaced 0.2 meters apart. The experiment was conducted in the 2018/2019 cropping season. In accordance with national recommendations, a seed rate of 150 kg/ha (equivalent to 45 grams per plot) was utilized. Fertilizers, including Urea at 150 kg/ha and NPS at 100 kg/ha, or 45 and 30 grams per plot, respectively, were applied. All NPS (100 kg/ha) was applied at sowing, while Urea was applied in two splits: one-third at sowing and the remaining two-thirds after 35-40 days post-sowing, following the guidelines provided [5]. Hand weeding was employed for weed management, and all other agronomic practices were uniformly implemented.

Data Collection

The data were recorded in accordance with the updated descriptor lists for wheat provided by the International Board for Plant Genetic Resources [6]. Information was gathered both at the plot level and on individual plants. Data collection at the plot level was conducted on the four central rows, while data collection at the plant level involved selecting five plants randomly from these four central rows of each plot. The mean data obtained from these five sample plants were utilized for subsequent data analysis.

Data Analysis

The efficacy of the simple lattice design compared to the randomized complete block design (RCBD) was evaluated and found to be superior. Consequently, ANOVA was performed based on the simple lattice design. Before conducting statistical analysis for each location, the data were assessed for normality, and all datasets met the normality assumption. The quantitative data from each site were analyzed using analysis of variance (ANOVA), which was performed with the Proc Lattice and Proc GLM procedures in SAS version 9.3 [7], in accordance with the simple lattice design. Prior to computing the combined analysis, a homogeneity test for the error variance of the two locations was conducted using Hartley's test (1950), as recommended by [8], and confirmed by the F-test (ratio of the largest mean square error to the smallest mean square error in the set), indicating homogeneity. Therefore, a joint analysis was conducted. Comparisons of the mean values across the treatment groups were performed using the least significant difference (LSD) test at the 5% significance level.

ESTIMATION OF GENETIC PARAMETERS

Phenotypic and Genotypic Variances and Coefficients of Variation

Estimates of variance components were computed using the formula suggested by [9–32] as follows:

Phenotypic Variance $(\sigma^2 p) = \sigma 2g + \frac{\sigma 2gl}{L} + \sigma 2e / LR = MSG/RL$

where,
$\sigma^2 p$ = Phenotypic variance,
$\sigma^2 g$ = Genotypic variance,
$\sigma^2 gl$ = genotype by location variance,
$\sigma^2 e$ = Environmental variance,
R = number of replications,
L = number of locations, and
MSG = mean square of genotype.

Genotypic Variance $(\sigma^2 g) = (MSG - MSGXL/RL)$

where,
$\sigma^2 g$ = genotypic variance,
MSG = mean square of genotype,
MSGxL = mean square of genotype by location,
R = number of replications, and
L = number of locations.

Genotype x Location Interaction Variance $(\sigma^2 gl) = (MSGXL - MSE)/R$

where,
$\sigma^2 gl$ = genotype by environmental interaction variance,
MSGxL = mean square of genotype by location interaction,
MSE = mean square of error, and
R = number of replications.

Environmental Variance (mean square error) $(\sigma^2 e)$ = MSE

Phenotypic and genotypic coefficient of variation was estimated by using the methods suggested by [32] as follows:

1. Phenotypic Coefficients of Variation (PCV) $= \frac{\sqrt{\sigma^2 p}}{\bar{x}} 100$
2. Genotypic Coefficients of Variation (GCV) $= \frac{\sqrt{\sigma^2 g}}{\bar{x}}$ x 100

where,
σ^2p = Phenotypic variance,
σ^2g = Genotypic variance, and
$\bar{x}$ = Grand mean of the traits under consideration.

Broad sense heritability values were estimated using the formula adopted from Falconer and Mackay (1996).

$$\text{Heritability } (h^2b) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where,
h^2b = heritability in broad sense,
σ^2p = Phenotypic variance, and
σ^2g = Genotypic variance.

The genetic advance (GA) and percent of the mean (GAM) were calculated by assuming selection of superior 5% of the genotypes estimated in accordance with the methods illustrated [10]:

$$\text{Expected genetic advance (GA)} = k * \sigma p * h^2 b$$

where,
GA = expected genetic advance,
K = constant (selection differential where K = 2.06 at 5% selection intensity),
σp = phenotypic standard deviation on mean basis, and
h^2b = heritability in broad sense.

Genetic advance as percent of mean (GAM) was calculated by using the subsequent formula [10] and classified as low (<10%), moderate (10–20%) and high (>20%):

$$\text{Genetic advance as percent mean (GAM)} = \frac{GA}{\bar{x}} \times 100$$

where,
GAM = genetic advance as percent of mean,
GA = genetic advance under selection,
$\bar{x}$ = mean of the population in which selection is effective.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

The mean squares for the characters derived from the analysis of variance (ANOVA) at each location (Kokate and Hossana), as well as the combined data from both locations, are shown in Tables 2, 3, and 4, respectively.

At both individual locations and across all locations, the analysis revealed highly significant differences ($P < 0.01$). Among the evaluated characteristics were the duration to reach 50% heading, the grain filling period, the time taken to reach 90% physiological maturity, plant height, spike length, kernel count per spike, and 1000-seed weight. These findings signify the presence of sufficient variability that can be utilized through selective breeding.

The combined analysis revealed significant ($P < 0.01$) location effects for all traits examined, except for days to 90% physiological maturity. This suggests that the phenotypic expression of this trait remains consistent across both locations, while other traits displayed varied responses to the testing sites. Genotypic effects were highly significant ($P < 0.01$) for all traits evaluated across locations, except for the number of productive tillers per square meter area. This suggests a significant level of diversity within the genetic materials examined.

Table 2. Analysis of variance summary for 12 quantitative yield and yield related characters evaluated at Kokate, 2018/19 cropping season.

Characters			**Mean Square**					**CV (%)**
	Replication (Df = 1)	Blocks With In Rep. (ad) (df = 12)	Trmt. (df = 48)		Error			
					Intra block (df = 36)	RCBD (df = 8)	Rel. E. to RCBD (%)	
			Unadju.	Adju.				
HD	0.16	3.15	26.91	24.1**	2.20	2.43	103.07	2.38
GFP	4.94	52.17	50.53	50.52**	29.50	35.17	107.53	10.28
MD	3.31	57.69	71.51	71.50**	29.93	36.87	109.96	4.75
PH	50.57	23.31	51.50	48.57**	14.71	16.86	104.94	4.98
SL	0.34	0.28	0.68	0.58**	0.22	0.24	101.33	5.46
KPS	224.11	49.64	53.39	53.38**	38.67	41.41	101.49	14.80
SPS	102.04	1.48	3.24	3.13^{ns}	2.94	2.57	87.54	10.27
PT	445.72	801.69	946.50	1029.09^{ns}	918.24	889.10	96.83	21.50
BY	0.85	0.03	0.11	0.09^{ns}	0.08	0.07	85.43	18.47
GY	0.54	0.14	0.21	0.19^{ns}	0.19	0.19	92.21	14.38
TSW	2.32	11.38	38.52	29.3**	7.88	8.76	103.17	7.19
HI	164.35	16.64	63.56	59.4^{ns}	37.26	32.11	86.17	15.10

Table 3. Analysis of variance summary for 12 quantitative yield and yield related characters evaluated at Hossana, 2018/19 cropping season.

Characters			**Mean Square**					**CV (%)**
	Replication (Df = 1)	Blocks With In Rep. (ad) (df = 12)	Trmt. (df = 48)		Error			
					Intra Block (df = 36)	RCBD (df = 48)	Rel.E. to RCBD (%)	
			Unadju.	Adju.				
HD	0.26	3.08	63.50	54.49**	1.93	2.21	105.11	2.14
GFP	2.61	8.28	86.36	79.73**	13.11	11.90	90.78	7.04
MD	4.50	5.67	133.23	121.2**	14.58	12.35	84.71	3.27
PH	12.93	21.89	44.63	37.30**	8.45	11.81	121.15	3.31
SL	0.69	0.17	0.98	0.80**	0.25	0.23	91.90	6.01
KPS	202.87	18.78	80.11	66.28*	33.65	29.93	88.95	10.69
SPS	29.32	1.19	1.85	1.83*	0.94	1.01	101.30	5.64
PT	392.00	718.39	1140.61	1064.79^{ns}	1372.31	1208.83	88.09	19.71
BY	0.29	0.14	0.43	0.40*	0.20	0.18	92.24	16.31
GY	1.50	0.28	1.07	0.94**	0.16	0.19	106.39	11.20
TSW	24.59	25.43	55.93	52.11**	18.49	20.23	102.40	13.89
HI (%)	81.28	13.17	44.33	37.31**	15.63	15.02	96.07	14.40

Table 4. Mean squares of combined analysis of variance for 12 quantitative traits of 49 bread wheat genotypes evaluated in 2018/2019 cropping season at Kokate and Hossana, SNNPR.

Traits	**MSL (df =1)**	**MSG (df = 48)**	**MSGxL (df = 48)**	**MSE (df = 84)**	**CV (%)**
HD	374.70**	170.63**	8.00**	2.44	2.39
GFP	105.80**	150.80**	40.98*	22.67	9.48
MD	82.29^{ns}	143.85**	47.00**	23.84	4.31
PH	5620.72**	64.08**	23.12*	11.65	4.54
SL	5.76**	1.11**	0.32^{ns}	0.23	5.61
KPS	7583.92**	72.09**	56.85*	35.37	12.39
SPS	13.80**	3.57**	1.33^{ns}	1.87	7.22
PT	108852.86**	1033.10^{ns}	1020.29^{ns}	1079.48	19.99
BY	66.91**	1.259**	0.23**	0.14	15.69
GY	10.25**	1.774**	0.47**	0.20	13.14
TSW	3173.55**	75.85**	26.14**	14.69	10.58
HI	8091.77**	220.17**	33.25*	25.98	13.57

The analysis of mean squares for genotype x location interaction revealed significant effects ($p < 0.05$) on grain filling period, plant height, kernels per spike, and harvest index, while highly significant effects ($p < 0.01$) were observed for days to 50% heading, days to 90% physiological maturity, biological yield, grain yield, and 1000-seed weight. Conversely, spike length, spikelet per spike, and productive tillers displayed non-significant differences among the tested bread wheat genotypes.

The significant interaction effects suggest that the genotypes performed differently across various test locations, whereas the lack of significant interaction effects indicates similar trait performances in both locations. This finding is consistent with findings reported by several researchers [11–14].

The estimated PCV and GCV values from combined analysis over the two test locations were presented in Table 5.

Table 5. Estimates of ranges, mean, standard deviation (SD) and Variance components for 11 quantitative characters combined over the two locations, Kokate and Hossana, SNNPR, 2018/19.

						PCV	GCV	h^2b	GA	GAM
Traits	**Range**	**Mean ± SD**	**σ^2e**	**σ^2p**	**σ^2g**	**%**	**%**	**%**		**%**
HD	54.25–73.50	63.69 ± 1.56	2.44	42.66	40.66	10.26	10.01	95.31	12.82	20.14
GFP	39.50–67.50	52.12 ± 4.76	22.67	37.70	27.45	11.78	10.05	72.82	9.21	17.67
MD	103.25–130.75	115.81 ± 4.88	23.84	35.96	24.21	5.18	4.25	67.33	8.31	7.18
PH	74.500–91.15	82.27 ± 3.41	11.65	16.02	10.24	4.87	3.89	63.92	5.27	6.41
SL	7.25–9.85	8.44 ± 0.48	0.23	0.28	0.20	6.24	5.26	71.10	0.77	9.14
KPS	37.50–57.40	48.00 ± 5.95	35.37	18.02	3.81	8.85	4.07	21.15	1.85	3.85
SPS	14.90–18.90	16.96 ± 1.37	1.87	0.89	0.561	5.57	4.42	62.81	1.22	7.21
BY	1.58–2.90	2.14 ± 0.37	0.14	0.32	0.26	26.26	23.69	81.40	0.53	24.71
GY	2.34–4.41	3.38 ± 0.45	0.20	0.44	0.25	19.74	14.87	56.78	0.52	15.37
TSW	25.84–42.39	34.98 ± 3.83	14.69	18.96	12.43	12.45	10.08	65.54	5.88	16.81
HI	22.32–42.30	33.87 ± 5.01	25.98	55.04	46.73	21.90	20.19	84.90	12.98	38.31

Note:

1. HD (Days to 50% heading): The number of days it takes for the crop to reach 50% heading stage.
2. GFP (Days to Grain Filling Period): The duration it takes from anthesis to the end of grain filling.
3. MD (Days to 90% Physiological Maturity): The time taken to reach 90% physiological maturity of the crop.
4. PH (Plant Height in cm): The measurement of plant height, typically recorded in centimeters.
5. SL (Spike Length in cm): The length of the spike, measured in centimeters.
6. KPS (Number of Kernels Per Spike): The total number of kernels found on each spike.
7. SPS (Number of Spikelet Per Spike): The total number of spikelets on a single spike.
8. BY (Biological Yield in kg/ha): The total biological yield, usually measured in kilograms per hectare.
9. GY (Grain Yield in tons/ha): The yield of grains, often expressed in tons per hectare.
10. TSW (Thousand Seed Weight in grams): The weight of one thousand seeds, usually in grams.
11. HI (Harvest Index in %): The ratio of grain yield to total biological yield, expressed as a percentage.
12. MSL (Mean Square of Location): A statistical value representing the variation due to different locations.
13. MSG (Mean Square of Genotype): The variation caused by the genotype of the plants.
14. MSGxL (Mean Square of Genotype by Location Interaction): The interaction between genotype and location, reflected in the mean square value.
15. MSE (Mean Square of Error): A statistical term that accounts for random errors or variations in the data.
16. CV (Coefficient of Variation): A statistical measure of the relative variability in the data, often expressed as a percentage.
17. df (Degree of Freedom): Refers to the number of independent values or quantities that can vary in an analysis without breaking any constraints.
*18. * Significant at ($p \leq 0.05$), and ** = highly significant at ($p \leq 0.01$)*
19. Ns indicated non-significant among treatments.

The PCV value ranged from 4.87% for plant height to 26.26% for biological yield and the GCV value ranged from 3.89% for plant height to 23.69% for biological yield, which indicated a wide range of estimates for all the characters. Researchers [15–17] classified PCV and GCV values greater than 20% as high, values between 10% and 20% as moderate, whereas values less than 10% are considered low. The classification revealed high phenotypic and genotypic coefficients of variation (PCV and GCV) for biological yield (26.26% and 23.69%) and harvest index (21.91% and 20.19%). Moderate PCV and GCV values were noted for days to 50% heading (10.26%, 10.01%), grain filling period (11.78%,

10.05%), grain yield (19.74%, 14.87%), and thousand-seed weight (12.43%, 10.08%). These results indicate that selecting based on these traits could be beneficial.

While the PCV values exceeded the GCV values for all traits examined in this study (see Table 5), the difference in magnitude was minimal across all traits. This suggests that the variability among genotypes for each trait may primarily stem from genetic rather than environmental factors. Consequently, selecting based on phenotypic characteristics for these traits is likely to lead to the improvement of other correlated traits. Similar findings in previous research, where PCV values closely aligned with GCV estimates for most traits, indicating minimal environmental influence on trait expression, have also been reported [18–21].

In this study, the broad sense heritability values spanned from 21.15% for the number of kernels per spike to 95.31% for days to 50% heading (refer to Table 5). Johnson et al. [10] categorized heritability as low, moderate, and high for values ranging from 0% to 30%, 30% to 60%, and above 60%, respectively.

In this study, all the examined traits displayed moderate to high heritability values, except for the number of kernels per spike, which exhibited a heritability value of 21.15%. Notably, high heritability values were observed for days to 50% heading (95.31%), harvest index (84.90%), biological yield (81.40%), grain filling period (72.82%), spike length (71.10%), days to 90% physiological maturity (67.33%), thousand-seed weight (65.54%), plant height (63.92%), and number of spikelets per spike (62.81%). These high heritability values suggest that the observed variation was predominantly governed by genetic factors and was less influenced by environmental factors, indicating the potential for progress through selection. These findings align with results reported by the researchers Abebe et al. and Dutamo et al. [22, 23].

A moderate heritability value of 56.78% was documented for grain yield. These results align with those observed by the researchers Meles et al. [24, 25] in bread wheat, who reported moderate grain yield values of 43.57% and 52.83%, respectively. Conversely, a low heritability value of 21.15% was observed for the number of kernels per spike, indicating that this trait was largely influenced by environmental factors, making genetic improvement through selection challenging. Similarly, Girma et al. [11] reported a low heritability value of 29.62% for the number of kernels per spike in bread wheat.

Johnson et al. [10] emphasized that heritability alone does not provide sufficient information for effective selection of the best individual, but when considered alongside genetic advance, it offers a more dependable index for selection. Genetic advance (GA) and genetic advance as a percent of mean (GAM) are categorized as low if they fall below 10%, moderate between 10% and 20%, and high if they exceed 20%. As a result, traits, such as grain filling period, days to maturity, plant height, spike length, number of kernels per spike, spikelet per spike, biological yield, grain yield, and thousand-seed weight exhibited low genetic advance, whereas days to 50% heading and harvest index showed a moderate level of genetic improvement.

Genetic advance as a percentage of the mean (GAM) varied from 3.85% for the number of kernels per spike to 38.31% for harvest index. The lowest GAM values were observed for traits, such as number of kernels per spike, days to maturity, plant height, spike length, and number of spikelets per spike. Moderate GAM values were noted for traits including grain filling period, grain yield, and thousand-seed weight. In contrast, high GAM was observed for days to 50% heading, biological yield, and harvest index.

In this study, traits, such as days to 50% heading, biological yield, and harvest index showed both high heritability and a significant genetic advance as a percentage of the mean. This suggests that these traits are mainly controlled by additive gene effects, implying that selection for these characteristics could be effective in the early generations. Similar results were reported in a recent wheat study [33],

where the authors also found high heritability and a substantial genetic advance as a percentage of the mean for these same traits [26].

The grain filling period and thousand-seed weight exhibited substantial heritability, accompanied by a moderate genetic advance as a percentage of the mean (GAM). Comparable results were reported by several other researchers [24, 25, 27]. Moderate heritability with moderate GAM was observed for grain yield, consistent with findings by the resarchers Ganno et al. [28] and Khan et al. [3] in bread wheat genotypes. However, these results contradict the findings of Girma et al. [11], who reported low heritability along with low genetic advance as a percent of the mean. The discrepancies in findings may be attributed to various factors, including differences in the genetic materials used and variations in environmental conditions during the experiments.

Traits like days to maturity, plant height, spike length, and number of spikelets per spike exhibited high heritability but low genetic advance as a percentage of the mean (GAM), indicating that environmental factors have minimal impact on their expression. However, the presence of significant non-additive genetic effects suggests that selection for these traits may be less efficient. To improve these traits, employing heterosis breeding or hybridization, followed by recurrent selection, is recommended. These results align with previous studies conducted on bread wheat genotypes [29–31].

On the other hand, the number of kernels per spike showed low heritability and a low genetic advance as a percentage of the mean, suggesting that these traits are largely controlled by non-additive genetic factors and are strongly affected by environmental conditions. For these traits, breeders may not benefit significantly from selection or hybridization due to the high involvement of environmental factors. Therefore, it may be more effective to induce variation through genetic engineering or mutation rather than relying solely on selection.

CONCLUSION AND RECOMMENDATION

Examining the extent and pattern of genetic variability provides valuable insights for plant breeders to develop future breeding strategies. The average values for most traits showed wide variations, suggesting significant differences among the genotypes tested. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for the traits ranged from high to low. High to moderate PCV and GCV values were observed for biological yield, harvest index, days to 50% heading, grain filling periods, grain yield, and thousand-seed weight, suggesting that selection based on these traits may be effective. Additionally, their phenotypic expression could serve as a good indicator of genetic potential.

Moderate to high heritability estimates, coupled with significant genetic gain as a percentage of the mean, were observed for traits, such as days to 50% heading, grain filling duration, biological yield, grain yield, thousand seed weight, and harvest index. These results indicate that these traits are largely controlled by genetic factors, with additive gene effects playing a major role. Consequently, early generation selection could be an effective strategy for enhancing these traits.

The current study identified notable genetic diversity among the evaluated genotypes, highlighting a valuable potential for further enhancement through selection and other breeding strategies. Therefore, it is recommended that biological yield, harvest index, number of kernels per spike, thousand seed weight, and grain yield be considered as important selection criteria for further improvement of bread wheat yield.

Declarations

Author Contribution Statement

Mathewos Chumamo Bunaro conceived, designed and performed the experiments, analyzed and interpreted the data, wrote the paper.

*Sentayehu Alamerew and Mathewos Ashamo g*ave supportive ideas, edited the written paper.

Data Availability Statement

Data included in article/supplementary material/referenced in article.

Declaration of Interest's Statement

The authors declare no conflict of interest.

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