

## Research Article

# Evaluation of Bread Wheat (*Triticum aestivum* L.) Germplasm at Kafa Zone, South West Ethiopia

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Bread wheat germplasm has wide genetic diversity, which means it can withstand a lot of biotic and abiotic stresses. Despite the presence of bread wheat germplasm diversity in Ethiopia, wheat production in the Kafa Zone is significantly lower than the national average. The ultimate goal of this research was to determine the genetic diversity of grain yield and yield components of bread wheat. One hundred bread wheat accessions with 3 local checks were evaluated in augmented randomized complete block design at Kafa Zone, Gewata Woreda Shupa site, during the 2018–19 growing season. The mean performance of the accessions revealed that accession number 29812 yielded more grain than the others. Spike length, number of seeds per spike, biomass yield, and harvest index all had moderate genotypic coefficients of variation. Spike length, number of seeds per spike, thousand seed weight, biomass yield, and harvest index all had moderate-to-high heritability and also all the above-listed traits had moderate-to-high genetic advance as a percentage of the mean. This means that practical improvement of these essential traits can be achieved by effective and satisfactory selection. Grain yield has positive correlations with grain filling period, number of productive tillers, spike length, number of seeds per spike, thousand seed weight, and biomass yield. The principal component analysis grouped all of the traits into four main components. Seven clusters and one ungrouped accession were formed from the accessions. Cluster IV and cluster VI had the greatest intercluster distance ( $D_2 = 104.77$ ) among the clustered groups, suggesting the probability of selecting a parental genotype for hybridization. However, the current result is merely indicative and cannot be used to draw firm conclusions. As a result, the experiment should be replicated in different locations and seasons for greater consistency.

## 1. Introduction

Wheat has long been one of Ethiopia's most common cereals, dominating food habits and dietary practices alongside teff “injera” and considered to be a major source of energy and protein for the people [1].

Ethiopia produces the most wheat in sub-Saharan Africa, followed by South Africa [2]. In the 2016/17 cropping season, the crop ranked fourth in terms of area covered (1,696,082.59 ha) and quantity generated 4537853.339 metric tons, behind maize, teff, and sorghum [3].

Wheat grows in Ethiopia under a variety of environmental conditions, ranging from 1500 to 3200 meters above sea level [4], allowing for the existence of various wheat varieties. For genetic improvement programs and efficient

genetic diversity utilization of plant materials, knowing the extent of heterogeneity among bread wheat (*Triticum aestivum* L.) accessions is extremely valuable [5]. High genetic diversity available in gene banks increases the chance of adaptability and plays a great role in crop breeding [6].

Regarding genetic diversity of bread wheat in Ethiopia, many studies have been conducted across various regions of the country [7–10]. Despite Ethiopia's bread wheat diversity, wheat is grown on 7137.64 hectares per year in the Kafa Zone, with a production of 1.902 tons per hectare, which is lower than the national production (2.675 tons per hectare) [3]. This lower production of bread wheat in the Kafa Zone is due to a lack of adaptable, high-yielding varieties. As a result, determining the variation present in collections conserved at the Ethiopian Biodiversity Institute is a crucial step toward

crop improvement. With the above facts in mind, the following objectives were set for the current investigation to determine the genetic diversity of bread wheat yield and yield contributing traits.

## 2. Materials and Methods

The experiment was conducted in the Kafa Zone, Gewata Woreda, Bonga Agricultural Research Center, Shupa sub-station in the 2018/19 cropping season. The planting material used in the study comprised a hundred accessions of bread wheat collected from different regions of Ethiopia and obtained from the Ethiopian Biodiversity Institute. Three varieties were used as a check. The accessions were selected randomly from major wheat-producing regions. The experiment was laid out in an Augmented Randomized Complete Block Design (ARCB) with ten blocks. Each block comprised ten accessions and three checks, a total of thirteen accessions in one block. All the checks were repeated in all the blocks randomly, while the accessions were unreplicated. Each accession was grown in 2 rows of 1.5 m long plots with 20 cm distance between rows. Data were recorded on plant height, the number of productive tillers per plant, spike length, number of seed per spike, days to heading, days to maturity, grain filling period, thousand-grain weights, grain yield, biomass yield, and harvest index. Harvest index was calculated as grain yield divided by biological yield multiplied by hundred. All of the usual recommended agronomic practices and plant protection measures were implemented, as recommended by EIAR [11]. Statistical analysis for ANOVA, Pearson's correlation, clustering, and principal component analysis were analyzed by using SAS software version 9.3. The significance of correlation and cluster distance was determined by using the *r*-table from Gomez and Gomez [12]. Genetic variance, phenotypic variance, genetic coefficient of variance, and phenotypic coefficient of variance were calculated based on the formula proposed by Burton and De Vane [13]. Heritability and genetic advance as percent of mean were determined based on the formula proposed by Falconer et al. [14].

## 3. Results and Discussion

**3.1. Analysis of Variance.** The mean square of all the traits studied showed the presence of significant differences ( $P < 0.05$ ) among the tested accessions (Table 1). This suggests that the studied breeding materials have an adequate genetic variation for all of the traits. This indicates that crop improvements through selection are possible.

### 3.2. Mean and Range

**3.2.1. Days to Heading, Grain Filling Period, and Maturity.** Days to heading ranged from 57 to 84 with a mean of 67.95 whereas the early check had 60 days. Days to maturity ranged from 95 to 136 with a mean of 112.39. The check variety was the earliest to maturity with 95 days, which is 41 days earlier than that of late-maturing accession while

accession number 214115 was late to maturity with 136 days. The result of the present study agrees with the finding of [15] who reported the presence of high variation among the genotypes for days to heading and days to maturity. Accession number 222785 was the earliest to fill the grain with 26 days, which is 37 days earlier than the late grain filling period while accession number 214115 was late to fill the grain with 63 days. The differences in days to heading, days to maturity, and grain filling period that are seen among the accessions are attributable to the combined effect of genetic and environmental variables.

**3.2.2. Number of Productive Tillers.** The mean value of all the accessions for the number of productive tillers was 4.1 with a range from 1.5 to 7.2. The lowest number of productive tillers was observed in accession number 7341, whereas accession number 29812 recorded the highest number of productive tillers while the check had 3.6 and 5.4 minimum and maximum tiller numbers, respectively. A number of reports [16–18] stated the presence of a high range of variation for the number of productive tillers. The genetic and environmental factor is the main reason for the variation observed among accessions for the number of productive tillers.

**3.2.3. Plant Height and Number of Seeds per Spike.** The mean plant height was 113.89 cm with a range of 77.6 cm to 154.2 cm. The check had the lowest plant height of 77.6 cm and the highest plant height of 154.2 cm was observed for accession number 214116. The mean value of all the accessions for the number of seeds per spike was 40.78 with a range from 16.2 to 66.8. In line with the present study, Yaqoob [19] reported a high range of variation for plant height. The cumulative influence of genetic and environmental variables is responsible for the differences in plant height and quantity of seeds per spike seen among the accessions.

**3.3. Thousand Seed Weight and Grain Yield.** The overall mean value for thousand seed weight was 23 g. The range value of thousand seed weight was 7 g to 39.5 g. The lowest seed weight was exhibited by accession number 213309 while the highest thousand seed weight was recorded by accession number 6885. The minimum grain yield recorded was 1.047 tons ha<sup>-1</sup> for accession number 7341, whereas a maximum of 5.70 tons was for accession number 29812 with a mean value of 3.35 tons ha<sup>-1</sup>. The checks had 2.791 and 4.678 tons ha<sup>-1</sup> lowest and the highest grain yields, respectively. Some accessions, 6883, 6884, 29811, 29813, 242429, and 243702, exhibited higher grain yield than the check variety (Shorima). Many studies [15, 20–22] reported a high range of variation among genotypes for grain yield. In general, a higher range of variation among accession for days to heading, days to maturity, grain filling period, number of productive tillers, plant height, spike length, number of seeds per spike, thousand seed weight, and grain yield was due to genetic and environmental variation.

TABLE 1: Mean squares from the analysis of variance for eleven quantitative traits of bread wheat landraces.

SV	DF	Mean squares										
		DH	DM	GFP	NPT	PH (cm)	SPL	NSPS	TSW	GY	BY	HI
Block	9	1.35 ns	39.56 ns	39.37 ns	1.17 ns	60.38 ns	0.93 ns	3.12 ns	0.08 ns	0.29 ns	0.44 ns	0.0036 ns
Entries	102	47.67**	122.55**	74.87*	4.25**	280.07**	21.97**	230.44**	32.1**	2.82**	3.88**	0.0694**
Nacc	99	30.87**	97.47**	40.23 ns	1.34**	126.27**	3.32 ns	96.04**	0.56**	0.91**	1.09**	0.0069**
Checks	2	150.03**	27.03 ns	51.03 ns	0.16 ns	95.21 ns	0.95 ns	248.44**	1.04 ns	1.29**	1.74**	0.0013 ns
Ch vs. acc	1	77.85**	961.05**	491.85**	5.76**	9144.20**	16.28**	1260.28**	4.80**	4.08**	4.89**	0.015**
Error	18	1.18	2.7	9.70	0.33	10.89	1.04	3.38	1.3	0.20	0.22	0.0018
CV (%)		1.60	4.93	11.45	15.79	6.85	10.18	7.10	15.70	13.39	12.85	6.20
Total	129											

\* = significant at probability level of 0.05 and \*\* = significant at probability level of 0.01, SV = source of variation, Nacc = new accessions, Ch vs. acc = check vs. accessions, ns = nonsignificant, df = degree of freedom, CV% = coefficient of variation in percentage, DH = days to heading, DM = days to maturity, GFP = grain filling period, NPT = number of productive tillers, PH = plant height (cm), SPL = spike length (cm), NSPS = number of seeds per spike, TSW = thousand grain weight (g), GY (t ha<sup>-1</sup>) = grain yield in tons per hectare, BY (t ha<sup>-1</sup>) = biomass yield in tons per hectare, and HI = harvest index.

#### 3.4. Genotypic and Phenotypic Coefficients of Variation.

According to Burton and Devane [13], GCV and PCV are classified as high (>20%), medium (10–20%), and low (<10%). In the present study, GCV ranged from 3.173 for days to heading to 15.279 for grain yield. PCV ranged from 3.553 for days to heading to 21.818 for the number of productive tillers. High PCV values were observed for the number of productive tillers (21.81%) and grain yield (20.28) (Table 2). The present result revealed that the magnitude of the difference was relatively low for days to heading, days to maturity, plant height, spike length, thousand seed weight, number of seeds per spike, and thousand seed weight. This suggested that the marked influence of environmental factors for the phenotype expression of genotypes was low and the higher chance of improvement of these traits through selection. In support of the present result, Arya et al. [16] and Adhiana et al. [23] reported low magnitude of differences between PCV and GCV that was observed for days to heading, days to maturity, plant height, spike length, thousand seed weight, and harvest index.

In the present study, the magnitude of differences between PCV and GCV was high for the grain filling period, the number of tillers, grain yield, and biomass yield. This implies the greater influence of environmental factors for the phenotypic expression of these traits that enhances breeder to use heterosis/hybridization/breeding strategy. In relation to the present result [24–26], a high magnitude of differences between PCV and GCV was observed for the number of productive tillers, grain, and biomass yield.

#### 3.5. Estimation of Heritability in the Broad Sense and Genetic Advance.

The estimated heritability was studied for all traits (Table 2). The heritability values ranged from 40.186 for the grain filling period to 87.042% for the number of seeds per spike. Robinson et al. [27] classified heritability values as low (0–30%), moderate (30–60%), and high (60 and above). Thus, high heritability was observed for days to heading (79.75%), days to maturity (81.61%), plant height (71.19%), spike length (66.80%), number of seeds per spike (87.04%), thousand seed weight (70.31%), biomass yield (62.45%), and harvest index (76.21%), which indicates that environment had a low influence on the expression of the traits suggesting

direct selection for improvement. In support of the present study, Alemu et al. [28] reported high heritability for days to heading and spike length. Many studies [8, 29, 30] and [31] reported heritability from low to high.

Heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance. In the present study, high heritability coupled with high genetic advance as percent of the mean was observed for spike length, the number of seeds per spike, biomass yield, and harvest index (Table 2). This suggests that these traits are not much influenced by environmental factors and substantial improvement for these traits could be achieved through direct selection and also these traits are considered to be governed by additive genes. In support of the present finding, Arya et al. [16] found high heritability coupled with high genetic advance as percent of the mean for spike length, the number of seeds per spike, biomass yield, and harvest index.

Moderate heritability coupled with high genetic advance as percent of the mean was observed for the number of productive tillers and grain yield indicating improving these traits through selection would be effective. In agreement with these, Kumar et al. [18] reported moderate heritability coupled with high genetic advance as a percent of the mean for the number of productive tillers. Alemayehu et al. [24] reported moderate heritability coupled with high GAM for grain yield. The present study was supported by the work of [17, 28, 30, 32, 33].

#### 3.6. Correlation of Grain Yield with Other Traits at the Genotypic Level.

Grain yield exhibited a positive significant correlation with the grain filling period, number of productive tillers, spike length, number of seeds per spike, thousand seed weight, and biomass yield at both genotypic levels (Table 3). Therefore, any improvement of these traits would result in a substantial increment in grain yield. This also implies that selection of accessions based on the grain filling period, number of productive tillers, number of seeds per spike, and biomass yield would be beneficial for increasing wheat grain yield. Grain filling period, number of tillers, spike length, thousand seed weight, and biomass yield had a positive correlation with grain yield, according to Alemu et al. [34]; Din et al. [31]; and Salehi et al. [35].

TABLE 2: Mean, range, phenotypic and genotypic variances, and coefficient of variations; heritability in broad sense and genetic advance for eleven quantitative traits of bread wheat germplasm.

Traits	Min	Max	Range	Mean	SE	s <sup>2</sup> <sub>g</sub>	s <sup>2</sup> <sub>p</sub>	GCV	PCV	H <sup>2</sup>	GA	GAM
DH	57	84	27.00	67.95	1.08	4.649	5.829	3.17	3.55	79.75	3.97	5.846
DM	95	136	41.00	112.3	5.69	11.98	14.68	3.08	3.40	81.61	6.45	5.740
GFP	26	63	37.00	44.10	5.44	6.517	16.21	5.78	9.13	40.18	3.33	7.570
NPT	1.5	7.2	5.70	4.13	0.65	0.382	0.812	14.9	21.8	47.04	0.87	21.17
PH	77.6	154.2	76.60	113.8	7.80	26.91	37.80	4.55	5.3	71.19	9.03	7.929
SPL	6.2	15.4	9.20	10.02	1.01	2.093	3.133	14.4	17.6	66.80	2.43	24.34
NSPS	16.2	66.8	50.60	40.78	2.89	22.70	26.08	11.6	12.5	87.04	9.17	22.48
TSW	7	39.5	32.5	23	0.36	3.08	4.38	7.63	9.09	70.31	3.03	13.20
GY	1.047	5.701	4.65	3.35	0.44	0.262	0.462	15.2	20.2	56.71	0.79	23.73
BY	2.012	6.788	4.78	4.42	0.56	0.366	0.586	13.6	17.3	62.45	0.98	22.31
HI	0.448	0.969	0.52	0.75	0.04	0.006	0.008	10.9	12.3	78.97	0.15	20.09

DH: days to heading, DM: days to maturity, GFP: grain filling period, NPT: number of productive tillers, PH: plant height (cm), SPL: spike length (cm), NSPS: number of seeds per spike, TSW: thousand seed weight (g), GY: grain yield (t ha<sup>-1</sup>), BY: biomass yield (t ha<sup>-1</sup>), HI: harvest index, SE: standard error, s<sup>2</sup><sub>g</sub>: genotypic variance, s<sup>2</sup><sub>p</sub>: phenotypic variance, PCV (%): phenotypic coefficient of variations, GCV (%): genotypic coefficient of variations, H<sup>2</sup> (%): broad-sense heritability, GA: genetic advance, and GAM (%): genetic advance as percent of mean.

TABLE 3: Genotypic correlation coefficients of the eleven bread wheat traits.

Traits	DH	DM	GFP	NPT	PH	SPL	NSPS	TSW	GY	BY	HI
DH	1	0.811**	-0.659**	0.646**	0.327	-0.658**	-0.766**	-0.660**	-0.679**	-0.213	0.318
DM		1	-0.506**	0.511**	0.194	-0.527**	-0.641**	-0.487*	-0.574**	-0.089	0.163
GFP			1	-0.628**	-0.014	0.681**	0.714**	0.992**	0.921**	0.467*	-0.367
NPT				1	0.360	-0.647*	-0.483*	-0.655**	0.627**	0.301	-0.130
PH					1	0.044	-0.217	-0.043	0.018	-0.148	0.309
SPL						1	0.624**	0.689**	0.748**	0.099	-0.104
NSPS							1	0.704**	0.791**	0.142	-0.479**
TSW								1	0.925**	0.495**	-0.353
GY									1	0.220**	-0.378
BY										1	-0.072
HI											1

DH: days to heading, DM: days to maturity, GFP: grain filling period, NPT: number of productive tillers, PH: plant height (cm), SPL: spike length (cm), NSPS: number of seeds per spike, TSW: thousand seed weight (g), GY: grain yield (t ha<sup>-1</sup>), BY: biomass yield (t ha<sup>-1</sup>), and HI: harvest index.

**3.7. Principal Component Analysis.** In the present investigation, only the first four principal components showed eigenvalues more than one and cumulatively they explained 73.77% of the entire variability available among accessions (Table 4). According to Chahal and Gosal [36], traits with the largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero. The first two principal components are more important as revealed by their higher eigenvalues. The principal component analysis showed that 31.96% of the total variation in the germplasm for the traits was explained by PC1. The higher contribution of PC1 was loaded by grain yield, biomass yield, thousand seed weight, number of productive tillers, number of seeds per spike, and days to heading. PC2 contributed 17.96% to the total variation of the accessions. The 17.96% contribution of PC2 was due to high variation for days to maturity, plant height, and spike length. Around 14.14% variation was accounted for by PC3, which was loaded by grain-filling period. PC4 accounted for 9.71% of total variation, which was loaded by harvest index (Table 4). Alemayehu et al. [24] found the most contributing traits were above-ground biomass, spike length, and plant height in durum wheat. Poudel et al. [37] reported that days to heading, maturity,

and grain filling period contributed more to the total diversity.

The traits far from the origin contributed more to the total diversity. Accordingly, the primary traits that contributed more to total diversity are plant height, days to maturity, days to heading, the number of seeds per spike, and grain filling period (Figure 1). In other way, the trait nearest to the  $x$ -axis contributed to PC1 and that nearest to the  $y$ -axis contributed to PC2. The traits which lie on the origin (spike length, number of productive tillers, thousand seed weight, grain yield, biomass yield, and harvest index) contributed less to total diversity.

**3.8. Cluster Mean Analysis of Major Contributing Traits to Diversity.** In the present study, cluster IV was characterized as the lowest cluster means for days to heading, which were considered to be the early heading accessions found in this cluster. The early maturing accessions were represented in cluster II, with recorded mean days to maturity of 95 days, whereas late maturing with mean days to maturity of 131 days was found in cluster VI (Table 5). Cluster II [27] exhibited the lowest grain filling period against the highest of cluster V (58.67). Cluster VI consists of the tallest accessions

TABLE 4: Eigenvectors and eigenvalues of four principal components (PCs) for eleven quantitative traits of bread wheat germplasm.

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
DH	-0.469	0.422	-0.547	0.191
DM	-0.365	0.791	0.400	0.029
GFP	-0.061	0.542	0.799	-0.100
NPT	0.692	0.306	-0.072	0.039
PH	-0.345	0.634	-0.251	-0.107
SPL	-0.052	0.635	-0.330	-0.034
NSPS	0.595	-0.040	0.259	-0.461
TSW	0.750	0.109	0.018	-0.266
GY	0.903	0.227	-0.064	0.247
BY	0.871	0.250	-0.073	0.010
HI	0.570	0.079	-0.040	0.693
Eigenvalue	3.834	2.155	1.697	1.165
Percent of total variance explained	31.96	17.96	14.14	9.71
Cumulative percent of total variance explained	31.96	49.92	64.06	73.77

DH: days to heading, DM: days to maturity, GFP: grain filling period, NPT: number of productive tillers, PH: plant height, SPL: spike length, NSPS: number of seeds per spike, TSW: thousand seed weight, GY: grain yield, BY: biomass yield, and HI: harvest index.

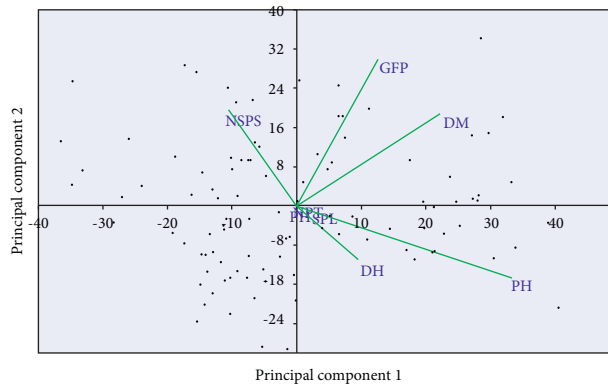


FIGURE 1: Principal component’s biplot of all studied traits of bread wheat germplasm. DH: days to heading, DM: days to maturity, GFP: grain filling period, PH: plant height, NSPS: number of seeds per spike, and dot symbol = accession code.

TABLE 5: Cluster mean values for eleven traits in bread wheat accessions.

Traits	Clusters						
	I	II	III	IV	V	VI	VII
DH	67.10	68.21	76.36	61.40	63.44	73.00	71.22
DM	110.61	95.00	124.05	101.40	122.11	131.50	107.78
GFP	43.52	26.00	47.68	40.00	58.67	58.50	36.56
NPT	4.75	4.09	4.23	6.00	4.89	5.50	4.69
PH	115.01	114.88	135.13	87.68	105.64	139.00	98.91
SPL	9.95	9.38	11.42	9.72	9.80	12.70	10.62
NSPS	46.42	35.09	31.46	56.24	43.91	51.80	29.16
TSW	2.58	2.10	1.83	2.77	2.48	2.00	1.85
GY	3.61	3.11	2.82	3.59	3.64	2.69	3.15
BY	4.87	4.06	3.87	4.49	4.65	3.63	4.18
HI	0.74	0.76	0.72	0.79	0.77	0.75	0.75

DH: days to heading, DM: days to maturity, GFP: grain filling period, NPT: number of productive tillers, PH: plant height (cm), SPL: spike length (cm), NSPS: number of seeds per spike, TSW: thousand seed weight (g), GY: grain yield (t ha<sup>-1</sup>), BY: biomass yield (t ha<sup>-1</sup>), and HI: harvest index.

with a mean plant height of (139 cm), whereas the shortest with a mean height of 98.91 cm was found in cluster VII. The highest mean performances of the number of seeds per spike were recorded for cluster IV (56.24), while the smallest numbers of seeds per spike were for cluster VII (29.16). This

result implies sufficient scope for genotypic improvement through hybridization between the accessions from divergent clusters. In general, cluster IV exhibited the highest cluster mean value for the number of productive tillers, number of seeds per spike, and thousand seed weight,



TABLE 6: Average intra- (bold) and inter-cluster divergence value for bread wheat accessions

Cluster	I	II	III	IV	V	VI	VII
I	<b>2.401</b>	18.212 <sup>ns</sup>	19.745*	27.198**	16.825 <sup>ns</sup>	51.029**	18.390*
II		<b>2.913</b>	46.320**	31.983**	52.980**	103.880**	14.912 <sup>ns</sup>
III			<b>3.087</b>	74.423**	24.390**	26.179**	44.821**
IV				<b>6.050</b>	39.416**	104.775**	21.226**
V					<b>4.875</b>	38.322**	35.618**
VI						<b>7.883</b>	92.492**
VII							<b>4.875</b>

whereas cluster V exhibited the highest grain yield which indicates the accessions present in clusters IV and V may be used as parents in hybridization programs for developing high-yielding wheat varieties.

**3.9. Intra- and Inter-Cluster Distances.** The highest average intercluster  $D^2$  was recorded between cluster IV and cluster VI ( $D^2 = 104.77$ ) followed by between cluster II and cluster VI ( $D^2 = 103.880$ ), cluster IV and cluster VII ( $D^2 = 92.492$ ), and cluster III and cluster IV ( $D^2 = 74.423$ ) (Table 6). This revealed that these clusters were genetically more divergent from each other and had the tendency of obtaining promising parents for crossing. The minimum intercluster distance was observed between cluster II and cluster VII ( $D^2 = 14.91223$ ) (Table 6), indicating that accessions of these two clusters were closely related, which suggests the presence of gene flow. Thus, the crossing of accessions belonging to the same cluster is not expected to yield superior hybrids.

#### 4. Conclusion

The present study indicated the presence of variability among the tested accessions that can be exploited in the wheat improvement program. The existence of variability among accessions for quantitative traits shows the direction for the direct selection of parental genotypes to develop hybrids. The top five accessions that performed better than the released check varieties for grain yield were 29812, 29811, 29813, 242427, 242429, and 243702. Therefore, for grain yield production, direct selection of those accessions can be possible. In general, the presence of genetic variability creates enormous opportunities for the improvement of bread wheat genotypes. Therefore, the information generated from this study can be used by breeders who are interested in different traits. However, the present result is only an indication and cannot draw a definite conclusion. Since the experiment was carried out at one location and in one season, it is recommended to further evaluate high-yielding accessions over locations and seasons to check the stability of the accession.

#### Data Availability

The data supporting the findings of this study are available on request from the corresponding author.

#### Conflicts of Interest

The authors declare that they have no conflicts of interest regarding the publication of this paper.

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