

Research Article

Genetic Variability and Association of Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes in Gechi District, South West Ethiopia

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Bread wheat is the world's leading cereal grain, and more than one-third of the world's population uses it as a staple food. The bread wheat production in Ethiopia is low compared to the national average yield, mainly due to the lack of high-yielding genotypes. This study was conducted during the 2019-2020 growing season to assess genetic variability and estimate the association of traits among bread wheat genotypes. The experiment consists of 49 bread wheat genotypes and is laid out in 7×7 simple lattice designs. The results showed significant differences ($p < 0.01$) among genotypes for most of the studied traits. Moderate genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were estimated for yield plant⁻¹, thousand seed weight, and biomass yield. High heritability coupled with a high GAM was observed for thousand seed weight and yield plant⁻¹. The grain yield showed a highly significant ($p < 0.01$) correlation with many yield-related traits at the phenotypic and genotypic levels. The biomass yield and the harvest index exerted the highest positive direct effect on grain yield at the genotypic level. The highest intercluster distance was observed between clusters I and IV ($D^2 = 31.86^{**}$), followed by clusters II and IV ($D^2 = 29.21^*$), and clusters II and III ($D^2 = 28.24^*$), which indicated the chance of selecting a member of these clusters for hybridization. This experiment's result indicates sufficient genetic variability among the tested genotypes, which provides ample scope for selecting superior and desired genotypes. Best-performed genotypes should be included in the future breeding program for further yield improvement. In conclusion, attention should be given to traits with moderate to high heritability and GAM, exerting a positive direct effect on the grain yield. However, the experiment should be repeated over locations and seasons to draw a definite conclusion.

1. Introduction

Bread wheat (*Triticum aestivum* L.) is the world's leading cereal grain where more than one-third of the world's population uses it as a staple food [1]. It is a self-pollinating annual plant cultivated worldwide and domesticated 10,000 years ago. World wheat production is based almost entirely on two modern species: common or hexaploid bread wheat (*Triticum aestivum*, $2n = 6x = 42$, AABBDD) and durum or tetraploid wheat (*T. turgidum* subsp. *durum*, $2n = 4x = 28$, AABB).

It is one of the key staple crops for global food security, providing more than 35% of the cereal calorie intake in the developing world, 74% in the developed world, and 41% globally from direct consumption [2]. In Ethiopia, wheat is used for making bread, porridge (*genfo*), local beer (*tela*), roasted grain (*kolo*), and boiled grain (*nifro*) [3]. In Ethiopia, the crop is grown at an altitude ranging from 1500 to 3000 m above sea level, between 6 and 16°N latitude, and 35 and 42°E longitude. However, the most suitable agro-ecological zones are between 1900 and 2700 m.a.s.l. [4]. Soil types used for wheat production vary from well-drained, fertile soils to

waterlogged heavy vertisols [5]. The major wheat-producing areas in Ethiopia are located in Arsi, Bale, Shewa, Ilubabor, Western Hararghe, Sidamo, Tigray, Northern Gondar, and Gojam zones [4].

The development of an improved variety capable of producing a better yield under various agro-climatic conditions depends upon the amount of genotypic variability present in a population for the traits [6]. According to Rahman et al. [7], the first step in developing varieties is assessing the genetic variability of available genotypes for the characters of interest. Grain yield is a complex quantitative trait influenced by several yield-contributing traits [8]. Hence, the selection for the desirable genotypes should be based not only on the yield alone and but also on the other yield components. Direct selection for the yield is often misleading in wheat because the wheat yield is polygenically controlled. Therefore, effective utilization of genetic stock in crop improvement and knowledge about genotypic and phenotypic correlations that indicate the degree to which various characters are associated with grain yield are necessary. Correlation and path coefficient analysis could be an important tool to bring information about the appropriate cause-and-effect relationship between the yield and some yield components [9]. Several researchers indicated a positive correlation between the wheat grain yield and yield component traits, such as biomass yield and harvest index, plant height, and thousand seed weight [10–12].

Even though the productivity of wheat has increased in the last few years in Ethiopia, still its productivity in Buno Bedele as well as in Ethiopia is very low (2.85 tha^{-1} and 3.046 tha^{-1} , respectively), as compared to the world's average (3.53 tha^{-1}) [13]. This is due to many factors, including the unavailability of improved high-yielding and adapted varieties, poor management practices, and biotic and abiotic factors. Therefore, developments of high-yielding varieties resistant to different diseases and adaptable to environments with abiotic stress could be crucial for further grain yield improvement in bread wheat. In this regard, this study was conducted to answer the following questions: (1) Is there sufficient genetic variability among the tested genotypes for further grain yield improvement? (2) What is the degree of association between the grain yield and the other yield components? (3) Which genotypes are the best performed? Several studies have been conducted on bread wheat genotypes in Ethiopia's different regions and reported genetic variability [14–17]. However, this is not enough to bring effective yield improvement because the productivity of this crop was still under potential, especially in the study area, and there was limited information related to the nature and degree of genetic variability on bread wheat genotype, particularly in the study area, generally in the country. It is, therefore, of great importance to assess genetic variability and determine the association among yield and yield-related traits in bread wheat to provide basic information for further improvement of bread wheat yield. Therefore, the overall objective of the study was to assess genetic variability and determine the association among traits in bread wheat genotypes.

2. Material and Methods

2.1. Description of the Study Site. The field experiment was conducted during the 2019–2020 growing season at Gito kebele, Gechi district, Buno Bedele Zone, Southwestern Ethiopia. Geographically, the experimental site is located at $08^{\circ} 12' 0'' \text{N}$ latitude and $36^{\circ} 18' 0'' \text{E}$ longitude, at an altitude of 2132 m.a.s.l. The experimental site receives an average annual rainfall and temperature of 1850 mm and 21°C , respectively. The soil at the experimental site had a pH of 4.3, 2.56 CEC (cmolc/kg), and deep, well-drained Nitosol [18]. The field was treated with 4.22 tha^{-1} limestone, and its pH was raised to 6.5, which is ideal for wheat growth. Major crops grown in Buno Bedele and the study areas are maize, wheat, sorghum, barley, and tef.

2.2. Experimental Materials. The experimental materials comprised 47 advanced bread wheat genotypes and two released bread wheat varieties, namely, Wane and Lemu. The advanced bread wheat genotypes received for this research were originally introduced from CIMMYT by Kulumsa Agricultural Research Center (KARC) at nursery stages for variety development. These materials were received from KARC for this experiment at a national variety trial (NVT) developmental stage. The advanced genotypes are homozygous lines. The two genotypes used as checks were Lemu (ETBW 6861) and Wane (ETBW 6130), released by Kulumsa Agricultural Research Center (KARC) in 2016 (Appendix Table 1).

2.3. Experimental Design and Field Management. The experiment was laid out in a simple lattice design (7×7) with two replications. The total area of the experiment was 488 m^2 ($23.8 \text{ m} \times 20.5 \text{ m}$), and the plot size was 3 m^2 ($2.5 \text{ m} \times 1.2 \text{ m}$). The distance between blocks, replications, and plots was 0.5, 1.0, and 0.5 m, respectively. Sowing was carried out on July 2019/2020 by manual drilling in six rows, which are 20 cm apart and 2.5 meters in length. The seed rate was 150 kg ha^{-1} or (45 g plot^{-1}). Blend fertilizer (nitrogen, phosphorus, sulphur, and boron (NPSB)) with a rate of 100 kg ha^{-1} (NPSB: 18.9% N, 37.7% P_2O_5 , 6.95% S, and 0.1% B) was applied just before sowing, and 100 kg ha^{-1} of UREA was applied in the split form at the time of planting and knee stage of the crop before heading.

2.4. Data Collected. Data were collected based on the average of ten randomly selected plants and plot basis. Ten representative plants were selected from four central rows for data collection, leaving the two rows as border effect. Data were collected from the following parameters: days to 50% heading (DH), days to maturity (DM), awn length (AL) (cm), grain filling period (GFP), total tillers plant⁻¹ (TPP), fertile tillers plant⁻¹ (FPP), plant height (PH) (cm), spike length (SL) (cm), number of kernel spike⁻¹ (NKPS), grains spikelet⁻¹ (GPs), spikelets spike⁻¹ (SPS), yield plant⁻¹ (YPP)

TABLE 1: List of bread wheat genotypes used in the study during 2019/2020 cropping season in Gechi.

Entries	Genotypes	Pedigree	Source
1	ETBW 9185	KISKADEE#1/5/KAUZ * 2/MNV//KAUZ/3/MILAN/4/BAV92/6/WHEAR//2 * PRL/ 2 * PASTOR	CIMMYT
2	ETBW 9193	CHWINK/GRACKLE #1//FRNCLN	CIMMYT
3	ETBW 9086	MINO/898.97/4/2 * PFAU/SERI.1B//AMAD/3/KRONSTAD F2004	CIMMYT
4	ETBW 9087	ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CHYAK1/6/NAVJ07	CIMMYT
5	ETBW 9089	BABAX/LR42//BABAX/3/ER2000/4/BAVIS	CIMMYT
6	ETBW 9304	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2 * 2/5/ WHEAR/SOKOLL	CIMMYT
7	ETBW 9313	ROLF07/YANAC//TACUPETO F2001/BRAMBLING * 2/3/WHEAR//2 * PRL/2 * PASTOR	CIMMYT
8	ETBW 9066	PRL/2 * PASTOR/4/CHOIX/STAR/3/HE1/3 * CNO79//2 * SERI/5/KIRITATI/2 * TRCH	CIMMYT
9	ETBW 9102	CETA/AE.SQUARROSA (174)//2 * MUU	CIMMYT
10	ETBW 9315	BABAX/LR42//BABAX/3/ER2000/11/CROC_1/AE.SQUARROSA (213)//PGO/10/ATTILA * 2/ 9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA/12/BAVIS	CIMMYT
11	BW 174459	THELIN/WAXWING//ATTILA * 2/PASTOR/3/INQALAB91 * 2/TUKURU 9Y-0B	CIMMYT
12	BW 174460	PASTOR//HXL7573/2 * BAU/3/SOKOLL/WBLL1/4/SAFI-1//NS732/HER/3/SAADA,	CIMMYT
13	BW 174462	PASTOR//HXL7573/2 * BAU/3/SOKOLL/WBLL1/4/SAFI-1//NS732/HER/3/SAADA	CIMMYT
14	BW 174463	SERI.1B//KAUZ/HEVO/3/AMAD/4/ESWYT99#18/ARRIHANE/5/SITTA/BUCHIN//CHIL/ BOMB	CIMMYT
15	BW 174464	PFAU/MILAN//FUNG MAI 24/3/ATTILA * 2/CROW	CIMMYT
16	BW 174465	FLORKWA-2/85 Z 1284//ETBW 4920/3/LOULOU-18	CIMMYT
17	BW 174466	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5	CIMMYT
18	BW 174467	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR/5/HUBARA-1	CIMMYT
19	ETBW 9601	KACHU * 2/MUNAL #1	CIMMYT
20	ETBW 9233	W15.92/4/PASTOR//HXL7573/2 * BAU/3/WBLL1/6/VEE/MJI//2 * TUI/3/2 * PASTOR/4/ BERKUT/5/PFAU/MILAN	CIMMYT
21	ETBW 9594	PRL/2 * PASTOR * 2//FH6-1-7 * 2/3/PBW343 * 2/KUKUNA * 2//FRTL/PIFED	CIMMYT
22	ETBW 9605	MEX94.27.1.20/3/SOKOLL//ATTILA/3 * BCN/5/W15.92/4/PASTOR//HXL7573/2 * BAU/3/ WBLL1	CIMMYT
23	ETBW 9611	NGL//2 * WHEAR/SOKOLL	CIMMYT
24	ETBW 9613	SERI.1B//KAUZ/HEVO/3/AMAD * 2/4/KIRITATI * 2/6/BAV92//IRENA/KAUZ/3/HUITES/4/ T.SPELTA PI348764/5/BAV92//IRENA/KAUZ/3/HUITES	CIMMYT
25	ETBW 9615	SIALIA/4/PBW343 * 2/KUKUNA//SRTU/3/PBW343 * 2/KHVAKI/5/SAUAL/3/C80.1/ 3 * BATAVIA//2 * WBLL1/4/SAUAL #1	CIMMYT
26	ETBW 9616	SIALIA/4/PBW343 * 2/KUKUNA//SRTU/3/PBW343 * 2/KHVAKI/5/SAUAL/3/C80.1/ 3 * BATAVIA//2 * WBLL1/4/SAUAL #1	CIMMYT
27	ETBW 9617	SOKOLL/3/PASTOR//HXL7573/2 * BAU * 2/4/PAURAQ	CIMMYT
28	ETBW 9618	SOKOLL/3/PASTOR//HXL7573/2 * BAU/4/PARUS/PASTOR	CIMMYT
29	ETBW 9619	SUP152//PUB94.15.1.12/WBLL1	CIMMYT
30	ETBW 9623	WBLL1/KUKUNA//TACUPETO F2001/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/ YR/4/TRAP#1/7/CNO79//PF70354/MUS/3/PASTOR/4/BAV92 * 2/5/FH6-1-7	CIMMYT
31	ETBW 9624	WBLL1/KUKUNA//TACUPETO F2001/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/ YR/4/TRAP#1/7/CNO79//PF70354/MUS/3/PASTOR/4/BAV92 * 2/5/FH6-1-7	CIMMYT
32	ETBW 9626	BAV92//IRENA/KAUZ/3/HUITES * 2/4/MURGA/6/CNO79//PF70354/MUS/3/PASTOR/4/ BAV92 * 2/5/FH6-1-7/7/FRNCLN * 2/TECUE #1	CIMMYT
33	ETBW 9627	KACHU #1/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/7/KACHU/8/ KZA//WH 542/2 * PASTOR/3/BACEU #1/9/KACHU #1/KIRITATI//KACHU	CIMMYT
34	ETBW 9628	TACUPETO F2001/SAUAL//BLOUK #1/3/SAUAL/YANAC//SAUAL/4/TACUPETO F2001/ SAUAL//BLOUK #1	CIMMYT
35	ETBW 9635	REEDLING #1//KFA/2 * KACHU	CIMMYT
36	ETBW 9636	KFA/2 * KACHU/3/KINGBIRD #1//INQALAB 91 * 2/TUKURU/4/KFA/2 * KACHU	CIMMYT
37	BW 174468	KAUZ/FACT//ETBW 4920/3/MILAN/PASTOR	CIMMYT
38	BW 174469	HUW 234/REBWAH-19	CIMMYT
39	BW 174470	FLORKWA-2/85 Z 1284//ETBW 4920/3/LOULOU-18	CIMMYT
40	ETBW 9653	SHA7//PRL/VEE#6/3/FASAN/4/HAAS8446/2 * FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/ FRET2 * 2/KUKUNA/8/KINGBIRD #1	CIMMYT
41	BW 174116	CHAM-4/MUBASHIIR-9	CIMMYT
42	BW 172070	PRL/2 * PASTOR/3/2 * TRCH/SRTU//KACHU	CIMMYT
43	ETBW 6130) (Wane)	SOKOLL/EXCALIBUR	KARC

TABLE 1: Continued.

Entries	Genotypes	Pedigree	Source
44	ETBW 6861) (Lemu)	WAXWING * /HEILO	KARC
45	ETBW 9128	FRNCLN * 2/BECARD	CIMMYT
46	ETBW 9543	KFA//PBW343/PASTOR/3/PBW343 * 2/KUKUNA/4/PBW343 * 2/KUKUNA * 2//FRTL/ PIFED/5/PBW343 * 2/KUKUNA * 2//FRTL/PIFED	CIMMYT
47	ETBW 9642	SOKOLL/3/PASTOR//HXL7573/2 * BAU/4/WHEAR/SOKOLL	CIMMYT
48	ETBW 9647	SOKOLL/3/PASTOR//HXL7573/2 * BAU/4/MEX94.2.19//SOKOLL/WBLL1	CIMMYT
49	ETBW 9651	KACHU * 2/3/ND643//2 * PRL/2 * PASTOR	CIMMYT

ETBW = Ethiopia bread wheat, BW = bread wheat.

(g), thousand seeds weight (TSW), biomass yield (BMY) (tha^{-1}), grain yield (GY) (tha^{-1}), and harvest index (HI).

2.5. Statistical Analysis

2.5.1. Analysis of Variance (ANOVA). The data collected for each quantitative trait were subjected to the analysis of variance (ANOVA). The analysis of variance (ANOVA) was performed using Proc GLM procedures of SAS version 9.3 [19].

The mathematical model for a simple lattice design is

$$Y_{ik}(j) = \mu + G_i + R_j + (Bk(j)) + \varepsilon_{il}(j), \quad (1)$$

where $Y_{ik}(j)$ is the observation of the i^{th} genotype grown in the k^{th} block of the replication j , μ is the grand mean, G_i is the effect of the i^{th} genotype, R_j is the effect of the j^{th} replicate, $Bk(j)$ is the effect of the k^{th} block in the j^{th} replicate and, and $\varepsilon_{il}(j)$ is the intrablock residual.

2.5.2. Estimation of Variance Components. The phenotypic and genotypic coefficients of variation are estimated according to the methods suggested Ref. [20]:

$$\begin{aligned} \sigma^2 g &= \frac{\text{MSg} - \text{MSe}}{r}, \\ \sigma^2 p &= \sigma^2 g + \sigma e, \\ \text{MSe} &= \sigma 2e, \\ \text{PCV} &= \frac{\sqrt{\sigma^2 p}}{\bar{x}} * 100, \\ \text{GCV} &= \frac{\sqrt{\sigma^2 g}}{\bar{x}} * 100. \end{aligned} \quad (2)$$

2.5.3. Heritability in a Broad Sense. Broad-sense heritability (H^2) was estimated as the percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and estimated on a genotype mean basis as described by Allard (1999) as $H^2 = \sigma^2 g / (\sigma^2 p) * 100$. The heritability was categorized as low (0–30%), moderate (30–60%), and high (>60%) [21].

2.5.4. Genetic Advance under Selection. Genetic advance was calculated by the assuming selection of superior 5% of the genotypes estimated following the methods illustrated in [22]:

$$GA = K * \sigma p * H^2. \quad (3)$$

2.5.5. Genetic Advance as % of the Mean (GAM). GAM was estimated according to Hanson et al. [23]. $GAM = (GA/\bar{x}) * 100$, where \bar{x} is the population mean of a character.

GAM was categorized as low (0–10%), moderate (10–20%), and high (>20%) [22].

2.6. Correlation Analysis. Correlation between variables was estimated using the R software (R version 4.1.0, 2021) package “Variability” version 0.1.0 and the method described by Miller et al. [24], and Kashiani and Saleh [25] from the corresponding variance and covariance components as follows:

$$\begin{aligned} r_{pxy} &= \frac{pcovx.y}{\sqrt{\sigma^2 px * \sigma^2 py}}, \\ r_{gxy} &= \frac{gcovx.y}{\sqrt{\sigma^2 gx * \sigma^2 gy}}. \end{aligned} \quad (4)$$

2.6.1. Path Coefficient Analysis. Using R software “Variability” package version 0.1.0, path coefficient analysis was performed as suggested in Ref. [26] with the phenotypic and genotypic correlation coefficients as $r_{ij} = P_{ij} + \Sigma r_{ik} * P_{kj}$:

$$\text{Residual can be calculated as } 1 = p2R + \Sigma p_{ij} r_{ij}. \quad (5)$$

Path coefficient was rated as very high (>1.0), high (0.30–0.99), moderate (0.2–0.29), low (0.1–0.19), and negligible (0.00–0.09) [27].

2.7. Cluster Analysis. The cluster analysis was performed by using R software. Cut points, where local peaks of the pseudo F statistic joined with small values of the pseudo t2 statistic followed by a larger pseudo t2 for the next cluster fusion, were examined to decide the number of clusters. Then, the 49 genotypes were clustered with the average linkage method.

2.8. Genetic Divergence. Genetic divergence between clusters was determined using Mahalanobis D^2 statistics [28]. The D^2 analysis was performed based on the R software program's mean values of all traits. The distance between any two groups will be estimated in matrix notation from the following relationship:

$$D_{ij}^2 = (X_i - X_j) \text{cov}^{-1} (X_i - X_j). \quad (6)$$

2.9. Principal Component Analysis. The principal component analysis was performed using R software (R version 4.1.0, 2021, package "FactoMineR" version 2.4) and computed using the formula suggested by Saporta and Niang [29]:

$$\text{Ctri}, l = \frac{f^2_{i,l}}{\lambda l} \times 100, \quad (7)$$

where $f^2_{i,l}$ is the squared factor scores of each observation and λl is the eigenvalue of the l^{th} component.

3. Results and Discussion

3.1. Analysis of Variance. The present study showed that there were highly significant differences ($p \leq 0.01$) among genotypes for days to 50% heading, days to 90% maturity, grain filling period, plant height, spike length, number of spikelets spike⁻¹, number of grains spike⁻¹, total tillers plant⁻¹, fertile tillers plant⁻¹, yield plant⁻¹, thousand seed weight, grain yield, and biomass yield. There were significant differences ($p \leq 0.05$) among genotypes for awn length and harvest index (Table 2). A complete ANOVA table is presented in Appendix Table 3. The highly significant variation among genotypes for the majority of quantitative traits indicated the presence of sufficient variability, which provides ample scope for selecting superior and desired genotypes by plant breeders for further improvement.

Similarly, Refs. [30–34] reported highly significant differences ($p < 0.01$) for days to 50% heading, days to 90% maturity, number of productive tillers plant⁻¹, number of spikelets spike⁻¹, plant height, spike length, grain yield plant⁻¹, thousand seed weight, biomass yield, and number of kernel spike⁻¹ in their previous studies on bread wheat genotypes.

3.2. Mean and Range

3.2.1. Days to Heading, Grain Filling Period, and Maturity. Days to 50% heading ranged from 61 (BW 174466) to 76 (ETBW 9066) and days to 90% maturity from 98 (BW 174466) to 119 (ETBW 9066), with a mean of 68 and 106, respectively (Table 4). The maximum days to 90% maturity was recorded for genotype ETBW 9066 (119 days), followed by BW 174467, ETBW 9594 (118 days), ETBW 9635 (116 days), ETBW 9627 (113 days), ETBW 9185 (113 days), and BW 174465 (112 days), while the minimum days to 90% maturity was recorded for BW 174466 (98 days) followed by ETBW 9653 (99 days) and ETBW 9653 (99 days). The grain

filling period ranged from 34 days (BW 174462) to 46 days (ETBW 9594). The long grain filling period was recorded for ETBW 9594 (46 days) followed by ETBW 9185, ETBW 9627, and BW 174468, which had (45 days), whereas the shortest grain filling period was recorded for BW 174462 (34 days) followed by BW 174464 (35 days) and ETBW 9304 (35 days) (Table 5). This indicates that the tested genotypes were in the early to medium maturing category. Therefore, genotypes characterized by early heading and early maturity could be promising, especially when the breeding objective is related to developing varieties resistant to drought stress. In agreement with this result, variation in days to 50% heading and days to 90% maturity has been reported by several authors [31, 35, 36].

3.2.2. Plant Height, Spike Length. Plant height ranged from 65.28 cm (BW 174465) to 87.275 cm (ETBW 9619) with a mean of 74.63 cm. The highest plant height was recorded for ETBW 9619 (87.23 cm) followed by ETBW 9626 (81.24 cm), ETBW 9615 (80.58 cm), ETBW 9594 (80.49 cm), and ETBW 9185 (80.21 cm), whereas the lowest plant height was recorded for BW 174465 (65.28 cm) followed by ETBW 9086 (66.19 cm), ETBW 6130 (67.98 cm), BW 174468 (69.55 cm), and ETBW 9128 (69.75 cm). Spike length ranged from 6.65 cm (ETBW 6130) to 9.36 cm (ETBW 9594) with a mean value of 8.29 cm. The highest spike length was recorded for ETBW 9594 (9.36 cm) followed by ETBW 9627 (9.345 cm), ETBW 9605 (9.27 cm), ETBW 9623 (9.135 cm), and ETBW 9089 (8.9 cm), whereas the lowest spike length recorded for ETBW 6130 (6.65 cm) followed by BW 174116 (6.675 cm), ETBW 9617 (7.21 cm), and BW 174460 (7.415 cm) (Table 5). In agreement with this result, several authors reported similar ranges of variation in bread wheat for spike length and plant height [16, 32].

3.2.3. Number of Spikelets Spike⁻¹, Kernel Spike⁻¹, and Grains Spikelets⁻¹. The number of spikelets spike⁻¹ ranged from 12.6 (ETBW 9647) to 16.95 (BW 174465) with a mean of 14.57. The highest number of spikelets spike⁻¹ was recorded from BW 174465 (26.95) followed by ETBW 9613 (16.8), ETBW 9615 (16.7), ETBW 9185 (15.95), and ETBW 9313 (15.85), whereas the lowest number of spikelets spike⁻¹ was recorded from ETBW 9647 (12.6) followed by ETBW 9623 (12.75), BW 174116 (12.9), and ETBW 9128 (13.1). Kernel spike⁻¹ ranged from 30.95 (BW 174116) to 50.45 (ETBW 9185) with a mean of 42.69. The highest number of kernel spike⁻¹ was recorded for genotypes ETBW 9185 (50), BW 174468 (50), and ETBW 9626 (49), whereas the lowest number of kernel spike⁻¹ was recorded for BW 174116 (31) followed by ETBW 9647 (34) and ETBW 9623 (35). The number of grains spikelet⁻¹ ranged from 2.5 (ETBW 9128) to 3.75 (ETBW 9613) with a mean of 3.257. The highest number of grains spikelets⁻¹ was recorded for ETBW 9613 (3.75) followed by ETBW 9617 (3.675), BW 172070 (3.6), and BW 174469 (3.55), whereas the lowest number of grains spikelets⁻¹ recorded for ETBW 9128 (2.5) followed by BW 174463 (2.65), ETBW 9651, and ETBW 9089 (2.9) (Table 5).

TABLE 2: Mean square from analysis of variance for 16 traits of bread wheat genotypes tested in Gechi during 2019/2020.

Traits	Rep(df= 1)	Genotype(df= 48) (adj.)	Blocks(adj) (df= 12)	Error(df= 36)	CV (%)
DH	0.25	21.66**	2.20	2.32	2.23
DM	0.01	50.25**	5.5	4.48	1.98
GFP	4.08	17.64**	5.15	3.66	4.96
PH	115.6	30.97**	18.36	10.56	4.35
SL	0.026	0.66**	0.15	0.18	5.19
AL	0.003	0.67*	0.27	0.37	8.5
NsPS	5.83	2.33**	0.5	0.42	4.44
NGPs	0.12	0.11**	0.048	0.05	6.91
NTPP	2.64	0.199**	0.147	0.065	10.99
NFPP	1.37	0.21**	0.16	0.06	12.83
NKPS	44.04	38.6**	7.3	10.83	7.7
YPP	0.56	0.11**	0.027	0.025	10.73
TSW	100.4	44.56**	8.84	5.25	7.65
GY	1.99	0.82**	0.39	0.288	16.1
BMY	28.5	3.98**	1.67	1.60	14.36
HI	0.0016	0.0049*	0.0027	0.0026	13.7

DH = days to 50% heading, DM = days to 90% maturity, GFP = grain filling period, NTPP = number of total tillers per plant, NFPP = number of fertile tillers per plant, PH = plant height(cm), SL = spike length(cm), AL = awn length (cm), NGPs = number of grains per spikelet, NKPS = number kernel per spike, NsPS = number of spikelets per spike, YPP = yield per plant (g), TSW = thousand seeds weight (g), BMY = biomass yield (tha⁻¹), HI = harvest index, GY = grain yield (tha⁻¹), ** = highly significant at probability level of 0.01), * = significant at probability level of 0.05), df = degree of freedom.

TABLE 3: Mean square from analysis of variance for 16 traits of bread wheat genotypes tested in Gechi during 2019/2020.

Character	Rep(df= 1)	Genotype(df= 48)		Blocks (adj) (12)	Error		Re to RCBD	CV%
		Un-adj	Adj		Intra(36)	RCBD(48)		
Days to heading	0.25	23.83	21.66**	2.20	2.32	2.29	98.72	2.23
Days to maturity	0.01	55.5	50.25**	5.5	4.48	4.73	100.99	1.98
Grain filling period	4.08	20.2	17.64**	5.15	3.66	4.04	102.72	4.96
Plant height	115.57	35.58	30.97**	18.36	10.56	12.51	107.09	4.35
Spike length	0.026	0.74	0.66**	0.15	0.18	0.17	96.21	5.19
Awn length	0.003	0.70	0.67*	0.27	0.37	0.34	93.11	8.5
Number spikelet spike ⁻¹	5.83	2.36	2.33**	0.5	0.42	0.44	100.95	4.44
Number grain spikelet ⁻¹	0.12	0.12	0.11**	0.048	0.05	0.05	98.68	6.91
Total tiller plant ⁻¹	2.64	0.26	0.199**	0.147	0.065	0.086	115.04	10.99
Fertile tiller	1.37	0.27	0.21**	0.16	0.06	0.088	119.48	12.83
Number of kernel spike ⁻¹	44.04	41.16	38.6**	7.3	10.83	9.94	91.83	7.7
Yield plant ⁻¹	0.56	0.115	0.11**	0.027	0.025	0.026	100.06	10.73
Thousand seed weight	100.41	47.56	44.56**	8.84	5.25	6.15	106.29	7.65
Grain yield (t/ha)	1.99	0.87	0.82**	0.39	0.288	0.31	102.24	16.1
Biomass yield (t/ha)	28.5	4.42	3.98**	1.67	1.60	1.62	100.04	14.36
Harvest index	0.0016	0.005	0.0049*	0.0027	0.0026	0.0027	100.04	13.7

DH = days to heading, DM = days to maturity, GFP = grain filling period, NTPP = number of total tiller per plant, NFPP = number of fertile tiller per plant, PH = plant height (cm), SL = spike length (cm), length (cm), NGPs = number of grain per spikelet, NKPS = number kernel per spike, NsPS = number of spikelet per spike, YPP = yield per plant (g), TSW = thousand seed weight (g), BMY = biomass yield, HI = harvest index, GY = grain yield (tha⁻¹).

3.2.4. Grain Yield, Yield Plant⁻¹, Biomass Yield, and Harvest Index. Grain yield ranged from 2.435 tha⁻¹ (ETBW 9102) to 5.0915 tha⁻¹ (ETBW 9613) with a mean value of 3.33 tha⁻¹. In line with this result, Refs. [16, 31] reported a wide variation in the grain yield per hectare, which ranged from 2.115 tha⁻¹ (Menze) to 5.955 tha⁻¹ (Alidoro) and 2.5883 tha⁻¹ (ETBW 8511) to 4.6833 tha⁻¹ (ETBW 7871) in bread wheat. The highest grain yield was recorded for genotypes ETBW 9613 (5.0915 tha⁻¹) followed by ETBW 9605 (4.8857 tha⁻¹), ETBW 9626 (4.8846 tha⁻¹), ETBW 9594 (4.8018 tha⁻¹), ETBW 9185 (4.6444 tha⁻¹), BW 172070 (4.1782 tha⁻¹), ETBW 9619 (4.1243 tha⁻¹), ETBW 9304 (3.9992 tha⁻¹), ETBW 9636 (3.8383 tha⁻¹), and BW 174116 (3.7198 tha⁻¹). The above genotypes were high yielders than the other

genotypes including checks (Wane (3.2644 tha⁻¹) and Lemu (3.511 tha⁻¹)). The lowest grain yield was recorded for ETBW 9102 (2.435 tha⁻¹) followed by ETBW 9635 (2.6213 tha⁻¹), BW 174467 (2.622 tha⁻¹), and ETBW 9624 (2.6567 tha⁻¹) (Table 5). Therefore, the above genotypes performed better than all other genotypes including check varieties could be selected for further evaluation to develop high-yielding varieties. Generally, the difference in the mean performance of genotypes for yield and yield-related traits indicates the difference in genetic potential of the genotypes, which confirms the presence of a wide range of genetic variability among genotypes.

Yield plant⁻¹ ranged from 1.02 g (BW 174116) to 1.885 g (ETBW 9185) with a mean of 1.496 g. The highest yield

TABLE 4: Estimation of components of variance and genetic parameters for 16 quantitative traits.

Traits	Ranges	Mean \pm SD	$\sigma^2 p$	$\sigma^2 g$	PCV	GCV	(h^2)	GA	GAM
DH	61–76	68.21 \pm 3.59	11.98	9.66	5.07	4.55	80.6	5.748	8.427
DM	98–119	106.56 \pm 5.46	27.36	22.88	4.91	4.48	83.6	9.01	8.455
GFP	34–46	38.61 \pm 3.46	10.65	6.98	8.45	6.84	65.5	4.4	11.4
PH	65.28–87.275	74.63 \pm 4.99	20.76	10.20	6.1	4.28	49.13	4.61	6.17
SL	6.65–9.36	8.29 \pm 0.677	0.426	0.24	7.87	5.91	56.37	0.757	9.13
AL	6.57–8.87	7.58 \pm 0.72	0.52	0.1488	9.52	5.01	28.54	0.425	5.6
NsPS	12.6–16.95	14.57 \pm 1.2	1.37	0.955	8.04	6.7	69.48	1.678	11.51
NGPs	2.5–3.75	3.257 \pm 0.295	0.083	0.032	8.84	5.54	38.97	0.213	7.1
NTPP	1.5–2.95	2.33 \pm 0.448	0.13	0.066	15.6	11.07	50.32	0.377	16.18
NFPP	1.3–2.9	1.975 \pm 0.44	0.138	0.074	18.8	13.77	53.62	0.41	20.76
NKPS	30.95–50.45	42.69 \pm 5.07	24.71	13.88	11.64	8.73	56.2	5.755	13.48
YPP	1.02–1.885	1.496 \pm 0.275	0.067	0.042	17.4	13.72	62.1	0.333	22.26
TSW	20.75–38.55	29.93 \pm 5.25	24.90	19.65	16.67	14.8	78.92	8.11	27.1
GY	2.435–5.0915	3.33 \pm 0.78	0.554	2.657	22.35	15.48	47.94	0.73	22.03
BMV	6.138–12.407	8.819 \pm 1.8	2.787	1.182	18.93	12.32	42.4	1.458	16.53
HI	0.28–0.48	0.377 \pm 0.06	0.0038	0.00116	16.43	9.042	30.27	0.0386	10.24

DH = days to 50% heading, DM = days to 90% maturity, GFP = grain filling period, NTPP = number of total tillers per plant, NFPP = number of fertile tillers per plant, PH = plant height(cm), SL = spike length(cm), AL = awn length (cm), NGPs = number of grains per spikelet, NKPS = number kernel per spike, NsPS = number of spikelets per spike, YPP = yield per plant (g), TSW = thousand seeds weight (g), BMV = biomass yield (tha⁻¹), HI = harvest index, GY = grain yield (tha⁻¹).

plant⁻¹ was recorded for ETBW 9185 (1.885 g) followed by ETBW 9615 (1.865 g), ETBW 9613 (1.83 g), ETBW 9651 (1.825 g), and ETBW 9594 (1.8), whereas the lowest yield plant⁻¹ was recorded for BW 174116 (1.02 g) followed by ETBW 9647 (1.03 g) and ETBW 9653 (1.11 g). Biomass yield showed a wide range of variation from 6.138 tha⁻¹ (ETBW 9647) to 12.407 tha⁻¹ (ETBW 9185) with a mean of 8.819 tha⁻¹. The highest biomass yield was observed for ETBW 8185 (12.407 tha⁻¹), ETBW 9613 (11.563 tha⁻¹), BW 172070 (11.563 tha⁻¹), ETBW 9605 (11.238), ETBW 9601 (11.063 tha⁻¹), and ETBW 9618 (10.188 tha⁻¹), whereas the lowest biomass yield was observed for ETBW 9647(6.138 tha⁻¹) followed by ETBW 9624 (6.39 t ha⁻¹), BW 174470 (6.662 tha⁻¹), BW 174470 (6.728 tha⁻¹), and BW 174464 (6.99 tha⁻¹). The harvest index ranged from 0.28 (ETBW 9635) to 0.48 (ETBW 9626) with mean of 0.377. The highest harvest index was recorded for ETBW 9624 (0.48) followed by BW 174116 (0.475), ETBW 9595 (0.45), ETBW 9613 (0.44), and ETBW 9605 (0.4385), while the lowest harvest index was recorded for ETBW 9635 (0.28), ETBW 9618 (0.2935), ETBW 9601 (0.295), ETBW 9233 (0.298), and ETBW 9623 (0.305) (Table 5).

3.3. Estimation of Components of Variation. In the present study, the genotypic coefficient of variation (GCV) ranged from 4.28 for plant height to 15.48 for the grain yield. In contrast, the phenotypic coefficient of variation (PCV) values ranged from 4.91 for days to 90% maturity to 22.35 for the grain yield (Table 4). The GCV and PCV values were categorized as low (<10%), moderate (10 to 20%), and high (>20%) [37, 38]. The estimates of GCV and PCV values were moderate for the number of total tillers plant⁻¹ (11.07 and 15.6), the number of fertile tillers plant⁻¹ (13.77 and 18.8), yield plant⁻¹ (13.72 and 17.4), thousand seed weight (14.8 and 16.67), and biomass yield (12.32 and 18.93) and moderate GCV and high PCV (15.48 and 22.35) for grain

yield (Table 4), respectively. This indicates that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance of these characters. On the other hand, it indicates the existence of substantial variability, ensuring ample scope for their improvement through selection. In agreement with this result, Refs. [31, 34] reported moderate GCV and PCV for the grain yield and above-ground biomass yield.

The lowest GCV and PCV were estimated for days to 50% heading (4.55 and 5.07), day 90% maturity (4.49 and 4.91), grain filling period (6.84 and 8.45), plant height (4.28 and 6.1), spike length (5.91 and 7.87), awn length(5.01 and 9.52), and number spikelets spike⁻¹ (6.7 and 8.04), respectively. This indicates the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for improvement of these traits through direct selection for better-performing genotypes.

3.3.1. Estimation of Broad-Sense Heritability and Genetic Advance. The estimated values of heritability in the present study ranged from 28.54% for awn length to 83.6% for days to maturity (Table 4). Robinson et al. [21] classified heritability values as low (0–30%), moderate ((30–60%), and high (>60%). Based on this, high heritability was observed for days to 90% maturity (83.6%), days to 50% heading (80.6%), thousand seed weight (78.92%), number of spikelets spike⁻¹ (69.48%), grain filling period (65.5%), and yield plant⁻¹ (62.1%) (Table 4). This indicated that the variation observed was mainly under genetic control and was less influenced by the environment, and there will be the possibility of progress from the selection. However, only high broad-sense heritability does not always provide a high prediction of genetic gain to ensure effective selection for improvement. Rather, higher heritability coupled with a higher estimate of GCV and GAM [39].

TABLE 5: Mean values of the sixteen traits of 49 bread wheat genotypes tested in Gechi during 2019/2020.

Code	Genotypes	Traits							
		DH	DM	GF	NTPP	NFTPP	PH	SL	AL
1	ETBW 9185	67.5 ⁱ⁻ⁿ	113 ^{bc}	45.5 ^{ab}	2.85 ^{a-c}	2.45 ^{a-d}	80.21 ^{b-d}	8.65 ^{a-h}	7.75 ^{a-n}
2	ETBW 9193	67 ^{j-o}	104 ^{i-m}	37 ^{f-k}	2.5 ^{a-i}	2.1 ^{b-g}	71.47 ^{h-p}	8.36 ^{c-m}	7.81 ^{a-m}
3	ETBW 9086	72 ^{b-f}	108.5 ^{d-h}	36.5 ^{g-k}	2.35 ^{c-j}	1.95 ^{d-i}	66.195 ^{op}	7.71 ^{j-o}	7.23 ^{f-n}
4	ETBW 9087	68 ^{h-m}	103.5 ⁱ⁻ⁿ	35.5 ^{i-k}	2.6 ^{a-h}	2.05 ^{c-h}	74.38 ^{c-m}	8.31 ^{c-m}	8.375 ^{a-f}
5	ETBW 9089	63 ^{qr}	101.5 ^{l-o}	38.5 ^{g-j}	2.1 ^{h-m}	1.6 ^{g-j}	76.555 ^{b-j}	8.9 ^{a-e}	8.87 ^a
6	ETBW 9304	66 ^{l-q}	101 ^{m-o}	35 ^{jk}	2.45 ^{a-i}	2.1 ^{b-g}	77.97 ^{b-h}	8.21 ^{d-n}	8.19 ^{a-g}
7	ETBW 9313	70.5 ^{d-i}	112 ^{b-d}	44 ^{a-c}	2.6 ^{a-h}	2.45 ^{a-d}	75.76 ^{b-k}	8.855 ^{a-e}	7.61 ^{d-n}
8	ETBW 9066	76 ^a	119a	43 ^{a-d}	2.5 ^{a-i}	2.35 ^{b-e}	75.21 ^{b-l}	8.21 ^{d-n}	7.65 ^{a-n}
9	ETBW 9102	67 ^{j-o}	104.5 ^{h-m}	37.5 ^{f-k}	2.35 ^{c-j}	1.9 ^{e-i}	75.11 ^{b-l}	8.04 ^{e-n}	7.94 ^{a-j}
10	ETBW 9315	67.5 ⁱ⁻ⁿ	101.5 ^{l-o}	36 ^{h-k}	2 ⁱ⁻ⁿ	1.9 ^{e-i}	74.5 ^{5c-m}	7.835 ^{g-o}	7.45 ^{d-n}
11	BW 174459	67.5 ⁱ⁻ⁿ	108.5 ^{d-h}	44 ^{a-c}	2.5 ^{a-i}	2 ^{c-i}	74.16 ^{c-m}	8.91 ^{a-e}	7.78 ^{a-n}
12	BW 174460	67.5 ⁱ⁻ⁿ	106 ^{f-k}	38.5 ^{e-j}	2.4 ^{b-j}	2.15 ^{b-f}	75.205 ^{b-l}	7.415 ^{n-p}	7.175 ^{f-n}
13	BW 174462	70 ^{e-j}	104.5 ^{h-m}	34.5 ^k	2.4 ^{b-j}	2.1 ^{b-g}	77.52 ^{b-i}	7.55 ^{no}	7.395 ^{d-n}
14	BW 174463	69.5 ^{f-k}	106 ^{f-k}	36.5 ^{g-k}	2.2 ^{e-n}	1.55 ^{h-j}	70.04 ^{j-p}	7.695 ^{k-o}	7.23 ^{f-n}
15	BW 174464	66 ^{l-q}	101 ^{m-o}	35 ^{kj}	2.25 ^{e-l}	1.7 ^{f-j}	72.76 ^{e-o}	7.82 ^{i-o}	7.26 ^{f-n}
16	BW 174465	73 ^{a-e}	112.5 ^{b-d}	39.5 ^{d-h}	1.75 ^{l-n}	1.75 ^{f-j}	65.28 ^p	8.44 ^{b-l}	6.67 ^{mn}
17	BW 174466	61.5 ^r	98 ^o	37 ^{f-k}	2.4 ^{b-j}	1.9 ^{e-i}	71.335 ^{i-p}	8.175 ^{d-n}	8.54 ^{a-d}
18	BW 174467	74.5 ^{ab}	118.5 ^a	44 ^{a-c}	2.4 ^{b-j}	1.75 ^{f-j}	77.045 ^{b-i}	8.59 ^{a-i}	7.435 ^{d-n}
19	ETBW 9601	69.5 ^{f-k}	107 ^{e-i}	37.5 ^{f-k}	2.4 ^{b-j}	1.9 ^{d-i}	75.935 ^{b-k}	8.26 ^{5c-n}	8.03 ^{a-h}
20	ETBW 9233	70 ^{e-j}	105.5 ^{g-l}	35.5 ^{i-k}	2.8 ^{a-d}	2.5 ^{a-c}	79.12 ^{b-f}	8.59 ^{a-i}	7.655 ^{a-n}
21	ETBW 9594	73.5 ^{a-d}	118.5 ^a	46.5 ^a	2.6 ^{a-h}	2.1 ^{b-g}	80.49 ^{bc}	9.36 ^a	7.59 ^{c-n}
22	ETBW 9605	65.5 ^{m-q}	101 ^{m-o}	35.5 ^{i-k}	2.15 ^{g-l}	2 ^{c-i}	79.31 ^{b-e}	9.27 ^{ab}	7.4 ^{d-n}
23	ETBW 9611	63.5 ^{p-r}	102.5 ^{j-o}	39 ^{e-g}	1.9 ^{j-n}	1.7 ^{f-j}	75.89 ^{b-k}	8.28 ^{e-n}	7.745 ^{a-n}
24	ETBW 9613	69 ^{f-l}	107.5 ^{e-i}	38.5 ^{e-j}	2.4 ^{b-j}	2.2 ^{b-f}	73.68 ^{d-m}	8.32 ^{c-m}	6.635 ^{mn}
25	ETBW 9615	66.5 ^{k-p}	106.5 ^{e-j}	40 ^{d-g}	2.75 ^{a-e}	2.15 ^{b-f}	80.58 ^{bc}	8.695 ^{a-g}	7.9 ^{a-l}
26	ETBW 9616	66.5 ^{k-p}	102 ^{k-o}	35.5 ^{i-k}	2.3 ^{d-k}	1.9 ^{e-i}	76.54 ^{b-j}	8.68 ^{a-h}	7.3 ^{e-n}
27	ETBW 9617	66.5 ^{k-p}	107 ^{e-i}	40.5 ^{e-f}	2.1 ^{h-m}	1.6 ^{g-j}	73.835 ^{d-m}	7.21 ^{o-p}	7.155 ^{f-n}
28	ETBW 9618	72 ^{b-f}	109.5 ^{c-g}	39.5 ^{d-h}	2.675 ^{a-f}	2.4 ^{b-e}	78.365 ^{b-g}	8.8185 ^{d-n}	8.725 ^{a-c}
29	ETBW 9619	69.5 ^{f-k}	107 ^{e-i}	37.5 ^{f-k}	2.7 ^{a-f}	2.05 ^{c-h}	87.275 ^a	8.73 ^{a-f}	8.75 ^{a-c}
30	ETBW 9623	69 ^{f-l}	102.5 ^{j-o}	36 ^{h-k}	2.65 ^{a-g}	2.5 ^{a-c}	75.835 ^{b-k}	9.135 ^{a-c}	7.285 ^{e-n}
31	ETBW 9624	64.5 ^{n-r}	101 ^{m-o}	36.5 ^{g-k}	2.4 ^{b-j}	2 ^{c-i}	75.12 ^{b-l}	8.965 ^{a-d}	6.925 ^{h-n}
32	ETBW 9626	67.5 ⁱ⁻ⁿ	107 ^{e-i}	39.5 ^{d-h}	2.7 ^{a-f}	2.4 ^{b-e}	81.24 ^{ab}	8.85 ^{a-e}	6.57 ⁿ
33	ETBW 9627	68.5 ^{g-m}	113.5 ^{bc}	45 ^{ab}	1.9 ^{j-n}	1.5 ^{ij}	77.24 ^{b-i}	9.345 ^a	7.35 ^{d-n}
34	ETBW 9628	70 ^{e-j}	110 ^{c-f}	40 ^{d-g}	2.45 ^{a-i}	2.05 ^{c-h}	73.14 ^{e-n}	7.61 ^{k-o}	8.5 ^{a-e}
35	ETBW 9635	74 ^{a-c}	116 ^{ab}	42 ^{b-e}	2.2 ^{f-l}	2 ^{c-i}	73.43 ^{e-m}	8.355 ^{c-m}	7.7 ^{a-n}
36	ETBW 9636	68 ^{h-m}	106.5 ^{e-j}	38.5 ^{e-j}	2.65 ^{a-g}	2.2 ^{b-f}	74.208 ^{c-m}	8.225 ^{d-n}	6.725 ^{j-n}
37	BW 174468	67 ^{j-o}	112 ^{b-d}	45 ^{ab}	2.25 ^{e-l}	1.9 ^{e-i}	69.555 ^{k-p}	8.7 ^{a-g}	7.34 ^{e-n}
38	BW 174469	71.5 ^{b-g}	110.5 ^{c-e}	39 ^{e-i}	2.85 ^{a-c}	2.95 ^a	73.49 ^{e-m}	8.36 ^{c-m}	6.97 ^{g-n}
39	BW 174470	63.5 ^{p-r}	99.5 ^{no}	36 ^{h-k}	1.5 ⁿ	1.3 ^j	66.57 ^{n-p}	7.657 ^{k-o}	7.63 ^{c-n}
40	ETBW 9653	63 ^{qr}	99 ^o	36 ^{h-k}	2.6 ^{a-h}	2.15 ^{b-f}	72.02 ^{h-o}	8.575 ^{a-j}	7.97 ^{a-i}
41	BW 174116	63 ^{qr}	101.5 ^{l-o}	38.5 ^{i-j}	1.6 ^{mn}	1.3 ^j	68.875 ^{l-p}	6.675 ^p	6.685 ^{k-n}
42	BW 172070	68.5 ^{g-m}	106.5 ^{e-j}	37 ^{f-k}	2.9 ^{ab}	2.6 ^{ab}	78.26 ^{b-g}	8.99 ^{a-d}	7.25 ^{f-n}
43	ETBW 6130(Wane)	69.5 ^{f-k}	109.5 ^{c-g}	40 ^{d-g}	2.15 ^{g-l}	1.5 ^{ij}	67.98 ^{m-p}	6.65 ^p	8.84 ^{ab}
44	ETBW 6861(Lemu)	74.5 ^{ab}	112 ^{b-d}	37.5 ^{f-k}	2.925 ^a	2.4 ^{b-e}	77.04 ^{b-i}	8.64 ^{a-i}	7.64 ^{a-n}
45	ETBW 9128	65.5 ^{m-q}	102 ^{k-o}	36.5 ^{g-k}	2.1 ^{h-m}	1.8 ^{f-j}	69.755 ^{k-p}	7.92 ^{f-o}	7.92 ^{a-k}
46	ETBW 9543	71 ^{c-h}	106 ^{f-k}	35.5 ^{i-k}	1.5 ⁿ	1.3 ^j	74.97 ^{b-l}	8.51 ^{a-k}	7.725 ^{a-n}
47	ETBW 9642	64 ^{o-r}	100.5 ^{m-o}	36.5 ^{g-k}	1.8 ^{k-n}	1.55 ^{h-j}	71.96 ^{g-o}	7.97 ^{f-o}	7.48 ^{d-n}
48	ETBW 9647	63 ^{qr}	101.5 ^{l-o}	38.5 ^{e-j}	1.75 ^{l-n}	1.35 ^j	72.625 ^{f-o}	8.12 ^{d-n}	6.94 ^{h-n}
49	ETBW 9651	71 ^{c-h}	106.5 ^{e-j}	35.5 ^{i-k}	2.1 ^{h-m}	1.75 ^{f-j}	71.975 ^{g-o}	7.775 ^{i-o}	6.79 ⁱ⁻ⁿ
	Mean	68.2	105.56	38.6	2.33	1.97	74.63	8.29	7.58
	CV (%)	2.23	1.198	1.91	10.99	12.83	4.35	5.197	8.048
	LSD (1%)	4.09	5.68	5.1376	0.7439	0.7392	9.2963	1.1559	1.637
Code	Genotype	Traits							
		NGPs	NKPS	NsPS	Ypp	TSW	BMY	HI	GY
1	ETBW 9185	3.25 ^{b-j}	50.45 ^a	15.95 ^{a-d}	1.885 ^a	36.3 ^{a-e}	12.407 ^a	0.37 ^{c-j}	4.6444 ^{a-d}
2	ETBW 9193	3g-k	42.1 ^{d-l}	14.4 ^{g-n}	1.58 ^{a-j}	29.7 ^{i-q}	7.781 ^{h-m}	0.3545 ^{c-j}	2.8011 ^{h-j}
3	ETBW 9086	3.36 ^{a-h}	44.8 ^{a-g}	14.15 ^{h-o}	1.635 ^{a-i}	28.45 ^{k-s}	6.875 ^{k-m}	0.385 ^{a-i}	2.6834 ^{h-j}
4	ETBW 9087	3.3 ^{a-j}	41.4 ^{e-m}	13.4 ^{h-q}	1.42 ^{d-n}	31.7 ^{e-m}	8.219 ^{d-m}	0.345 ^{d-j}	2.9181 ^{f-j}
5	ETBW 9089	2.9 ^{i-l}	36.7 ^{k-o}	13.3 ^{m-q}	1.45 ^{d-m}	36.2 ^{a-e}	7.531 ^{i-m}	0.415 ^{a-f}	3.17 ^{e-j}

TABLE 5: Continued.

Code	Genotypes	Traits							
		DH	DM	GF	NTPP	NFTPP	PH	SL	AL
6	ETBW 9304	3.61 ^{a-c}	47.7 ^{a-f}	15.1 ^{c-i}	1.67 ^{a-e}	28.25 ^{k-t}	9.419 ^{b-k}	0.415 ^{a-f}	3.9992 ^{b-f}
7	ETBW 9313	3.35 ^{a-i}	45.6 ^{a-g}	15.85 ^{a-e}	1.4 ^{d-n}	28.65 ^{j-r}	8.844 ^{c-l}	0.305 ^{g-j}	2.6815 ^{h-j}
8	ETBW 9066	3.15 ^{d-j}	44.1 ^{a-h}	14.85 ^{d-k}	1.44 ^{d-m}	28.1 ^{l-t}	8.938 ^{c-l}	0.405 ^{a-g}	3.6567 ^{d-i}
9	ETBW 9102	3.5 ^{a-f}	48.5 ^{a-d}	13.45 ^{l-q}	1.565 ^{a-j}	27.2 ^{m-t}	7.949 ^{h-m}	0.4 ^{a-h}	2.435 ^j
10	ETBW 9315	2.85 ^{j-l}	37.7 ^{g-n}	13.3 ^{m-q}	1.35 ^{e-o}	30.3 ^{i-p}	8.295 ^{d-m}	0.41 ^{a-f}	3.4197 ^{e-j}
11	BW 174459	3.465 ^{a-f}	45.7 ^{a-g}	15.7 ^{a-g}	1.61 ^{a-i}	32.05 ^{e-l}	9.438 ^{b-k}	0.33 ^{f-j}	3.1643 ^{e-j}
12	BW 174460	3.3 ^{a-j}	40.4 ^{g-n}	13.7 ^{i-q}	1.59 ^{a-j}	31.55 ^{g-o}	8.344 ^{d-m}	0.34 ^{e-j}	2.8845 ^{g-j}
13	BW 174462	3.425 ^{a-g}	41.9 ^{d-l}	13.9 ^{i-q}	1.66 ^{a-f}	31 ^{h-o}	8.325 ^{d-m}	0.325 ^{f-j}	2.7136 ^{h-j}
14	BW 174463	2.65 ^{kl}	48 ^{a-e}	14.8 ^{d-k}	1.39 ^{d-n}	26.3 ^{q-t}	8.113 ^{e-m}	0.38 ^{a-j}	3.1144 ^{e-j}
15	BW 174464	3.4 ^{a-g}	41.1 ^{f-m}	13.15 ^{n-q}	1.265 ^{j-p}	23.95 ^{s-u}	6.994 ^{k-m}	0.41 ^{a-f}	2.8853 ^{g-j}
16	BW 174465	3.35 ^{a-i}	49 ^{a-c}	16.95 ^a	1.325 ^{g-p}	21.05 ^u	8.344 ^{d-m}	0.365 ^{c-j}	3.0993 ^{e-j}
17	BW 174466	3.26 ^{b-j}	41.1 ^{f-m}	14.8 ^{d-k}	1.41 ^{d-n}	32.55 ^{c-l}	10.398 ^{a-g}	0.3435 ^{d-j}	3.5748 ^{d-j}
18	BW 174467	3 ^{g-k}	45.8 ^{a-g}	15.1 ^{c-i}	1.42 ^{d-n}	28.2 ^{k-t}	7.313 ^{j-m}	0.355 ^{c-j}	2.622 ^{ij}
19	ETBW 9601	3.2 ^{c-j}	42.2 ^{d-l}	15.85 ^{a-e}	1.86 ^a	34.8 ^{a-h}	11063 ^{a-c}	0.295 ^{ij}	3.3117 ^{e-j}
20	ETBW 9233	3.25 ^{b-j}	40.7 ^{g-m}	14.8 ^{d-k}	1.5 ^{c-k}	31.6 ^{f-n}	10.646 ^{a-e}	0.298 ^{h-j}	3.1875 ^{e-i}
21	ETBW 9594	3.4 ^{a-g}	41.3 ^{c-k}	14.5 ^{f-m}	1.8 ^{ab}	36.7 ^{a-d}	10.697 ^{a-d}	0.45 ^{a-c}	4.801 ^{a-c}
22	ETBW 9605	3.5 ^{a-f}	41.6 ^{f-l}	13.85 ^{i-q}	1.67 ^{a-e}	37.05 ^{a-c}	11.238 ^{a-c}	0.4385 ^{a-j}	4.8857 ^{ab}
23	ETBW 9611	3.3 ^{a-j}	48.4 ^{a-d}	15.25 ^{c-g}	1.65 ^{a-g}	30 ^{i-p}	7.563 ^{i-m}	0.385 ^{a-i}	2.9188 ^{f-g}
24	ETBW 9613	3.75 ^a	48.5 ^{a-d}	16.8 ^{ab}	1.83 ^a	38.55 ^a	11.563 ^{ab}	0.44 ^{a-d}	5.0915 ^a
25	ETBW 9615	3.1 ^{e-k}	46.2 ^{a-g}	16.7 ^{ab}	1.865 ^a	35.8 ^{a-g}	10.532 ^{a-f}	0.344 ^{d-j}	3.649 ^{d-i}
26	ETBW 9616	3.4 ^{a-g}	48 ^{a-e}	15.8 ^{a-f}	1.8 ^{ab}	33.7 ^{b-i}	8.738 ^{c-l}	0.335 ^{e-j}	2.9459 ^{f-j}
27	ETBW 9617	3.675 ^{ab}	37.3 ^{i-o}	13.6 ^{k-q}	1.2 ^{k-p}	27.65 ^{tu}	8.746 ^{c-l}	0.37 ^{c-j}	3.3154 ^{e-j}
28	ETBW 9618	3.3 ^{a-j}	45.5 ^{a-g}	13.4 ^{l-q}	1.695 ^{a-d}	30.5 ^{h-p}	10.188 ^{a-h}	0.2935 ^{ij}	3.0029 ^{f-j}
29	ETBW 9619	3.45 ^{a-g}	40 ^{g-n}	13.9 ^{i-q}	1.42 ^{d-n}	33.25 ^{c-j}	9.938 ^{a-i}	0.41 ^{a-f}	4.1243 ^{a-e}
30	ETBW 9623	3.35 ^{a-i}	34.9 ^{m-o}	12.75 ^{p-q}	1.33 ^{g-p}	26.95 ^{o-t}	9.412 ^{b-k}	0.305 ^{g-j}	2.9131 ^{f-j}
31	ETBW 9624	3.25 ^{b-j}	43.9 ^{a-i}	14.4 ^{g-n}	1.47 ^{c-l}	28.65 ^{j-r}	6.394 ^{lm}	0.42 ^{a-f}	2.6567 ^{h-j}
32	ETBW 9626	3.5 ^{a-f}	49 ^{a-c}	14.7 ^{d-l}	1.78 ^{a-c}	38.15 ^{ab}	10.038 ^{a-i}	0.48 ^a	4.8846 ^{ab}
33	ETBW 9627	2.92 ^{h-l}	43.7 ^{b-j}	15 ^{c-j}	1.71 ^{a-d}	37.9 ^{ab}	9.844 ^{a-j}	0.358 ^{c-j}	3.4527 ^{e-j}
34	ETBW 9628	3.35 ^{a-i}	44.15 ^{a-h}	14.25 ^{h-n}	1.315 ^{h-p}	25.3 ^{q-u}	8.313 ^{d-m}	0.405 ^{a-h}	3.3745 ^{e-j}
35	ETBW 9635	3.1 ^{e-k}	44.65 ^{a-g}	14.9 ^{c-k}	1.66 ^{a-f}	31 ^{h-o}	9.313 ^{b-k}	0.28 ^j	2.6213 ^{i-j}
36	ETBW 9636	3 ^{g-k}	44.8 ^{a-g}	15.1 ^{c-i}	1.68 ^{a-d}	33.65 ^{b-i}	10.386 ^{a-g}	0.374 ^{b-j}	3.8383 ^{b-g}
37	BW 174468	3.2 ^{c-j}	50.2 ^{ab}	16.2 ^{a-c}	1.64 ^{a-h}	28.85 ^{j-r}	8.438 ^{d-m}	0.4 ^{a-h}	3.422 ^{e-j}
38	BW 174469	3.55 ^{a-e}	40.1 ^{g-n}	14.85 ^{d-k}	1.19 ^{k-p}	21.4 ^u	7.525 ^{i-m}	0.3935 ^{a-i}	2.9506 ^{f-j}
39	BW 174470	3.3 ^{a-j}	37.3 ^{i-o}	14.15 ^{h-o}	1.13 ^{m-p}	24.5 ^{r-u}	6.728 ^{lm}	0.44 ^{a-d}	3.0091 ^{f-j}
40	ETBW 9653	3.2 ^{c-j}	37.9 ^{h-n}	13.9 ^{i-q}	1.11 ^{n-p}	27 ^{n-t}	7.367 ^{j-m}	0.407 ^{a-g}	3.0153 ^{f-j}
41	BW 174116	3.25 ^{b-j}	30.9 ^s	12.9 ^{o-q}	102 ^p	20.75 ^u	6.662 ^{lm}	0.475 ^{ab}	3.7198 ^{a-h}
42	BW 172070	3.6 ^{a-d}	42.2 ^{d-l}	15.6 ^{b-g}	1.79 ^{a-c}	33.6 ^{e-l}	11.563 ^{ab}	0.36 ^{c-j}	4.1782 ^{a-e}
43	ETBW 6130(Wane)	3.4 ^{a-g}	41.35 ^{e-m}	14.6 ^{e-m}	1.16 ^{n-p}	20.85 ^u	7.966 ^{g-m}	0.415 ^{a-f}	3.2644 ^{e-j}
44	ETBW 6861(Lemu)	3.3 ^{a-j}	37.65 ^{h-n}	14.95 ^{c-j}	1.34 ^{f-p}	32.2 ^{d-l}	8.906 ^{c-l}	0.385 ^{a-i}	3.511 ^{e-j}
45	ETBW 9128	2.5 ^l	36.2 ^{l-o}	13.1 ^{o-q}	1.19 ^{k-p}	28.2 ^{k-t}	8.32 ^{d-m}	0.355 ^{c-j}	2.9535 ^{f-j}
46	ETBW 9543	3.135 ^{e-j}	37.05 ^{j-o}	13.8 ^{i-q}	1.275 ^{j-p}	32.1 ^{d-l}	8 ^{g-m}	0.36 ^{c-j}	2.9243 ^{f-j}
47	ETBW 9642	3.3 ^{a-j}	41 ^{g-m}	14 ^{h-p}	1.31 ^{i-p}	25.15 ^{q-u}	7.661 ^{h-m}	0.435 ^{a-e}	3.2988 ^{e-j}
48	ETBW 9647	3.05 ^{f-k}	34 ^{no}	12.6 ^q	1.03 ^{op}	20.75 ^u	6.138 ^m	0.435 ^{a-e}	2.7241 ^{h-j}
49	ETBW 9651	2.9 ^{i-l}	45.3 ^{a-g}	15.8 ^{a-f}	1.825 ^{ab}	32.75 ^{c-k}	8.75 ^{c-l}	0.304 ^{g-j}	2.7034 ^{h-j}
	Mean	3.257	42.69	14.57	1.496	29.93	8.82	0.3775	3.329
	CV (%)	6.9	7.71	4.44	10.73	7.65	14.36	13.7	16.13
	LSD (1%)	0.604	8.827	1.7372	0.4306	6.5415	3.3986	0.1387	1.4406

DH = days to heading, DM = days to maturity, GFP = grain filling period, NTPP = number of total tiller per plant, NFTPP = number of fertile tiller per plant, PH = plant height (cm), SL = spike length (cm), length (cm), NGPs = number of grain per spikelet, NKPS = number kernel per spike, NsPS = number of spikelet per spike, YPP = yield per plant(g), TSW = thousand seed weight (g), BMY = biomass yield, HI = harvest index, GY = grain yield (tha⁻¹), mean followed by the same letter(s) within a column is not significantly different from each other at 5%. DH = days to heading, DM = days to maturity, GFP = grain filling period, NTPP = number of total tiller per plant, NFTPP = number of fertile tiller per plant, PH = plant height(cm), SL = spike length (cm), length(cm), NGPs = number of grain per spikelet, NKPS = number kernel per spike, NsPS = number of spikelet per spike, YPP = yield per plant (g), TSW = thousand seed weight (g), BMY = biomass yield, HI = harvest index, GY = grain yield (tha⁻¹), and mean followed by the same letter(s) within a column is not significantly different from each other at 5%.

This indicates that for these traits to be effective for selection to ensure grain yield improvement, they must be supported with higher GCV and GAM estimates. This result

was in close agreement with the finding of Ref. [40], which reported high heritability for days to 90% maturity, days to 50% heading, number of spikelets spike⁻¹, number of kernel

spike⁻¹, and thousand seed weight in bread wheat. Moderate broad-sense heritability was estimated for spike length (56.37%), number of kernel spike⁻¹ (56.2%), number of fertile tillers plant⁻¹ (53.62%), plant height (49.13%), grain yield (47.94%), biomass yield (42.4%), number of grains spikelet⁻¹ (38.97%), harvest index (30.27%), and number of total tillers plant⁻¹ (50.32%) (Table 4). This indicates that the variation observed was mainly due to the influence of the environment. In line with this result, Refs. [10, 41] reported moderate heritability for grain yield, plant height, spike length, number of kernel spike⁻¹, number of spikelets spike⁻¹, and biomass yield.

In this study, genetic advance as percent of the mean (GAM) ranged from 5.6% (awn length) to 27.1% for (thousand seed weight), which indicates that selecting the top 5% of the base population could result in advance of 5.6% to 27.1% percent over the base population mean (Table 4). In the present study, high heritability coupled with high genetic advance as a percent of the mean was observed for thousand seed weight (78.92% and 27.1%) and yield plant⁻¹ (62.1% and 22.26%), respectively (Table 4). This suggests that environmental factors do not much influence these traits, and substantial improvement for these traits could also be achieved through direct selection. These traits are considered to be governed by additive genes. In conformity with this result, Refs. [30, 32] reported high heritability coupled with high genetic advance as a percentage of the mean for thousand seed weight and yield plant⁻¹. Moderate heritability coupled with high genetic advance as a percent of the mean was observed for the grain yield (47.94%, 22.03), and the number of fertile tiller plant⁻¹ (53.62%, 20.76) indicates that improving these traits through selection would be effective (Table 4). High heritability values associated with low genetic advances as a percentage of mean were observed for days to 50% heading (80.6% and 8.427) and days to 90% maturity (83.6% and 8.455), indicating nonadditive gene expression of these traits (Table 4). Therefore, selection based on these traits may not be effective, but heterosis breeding might be necessary for improving these traits. Similar reports of high heritability coupled with low genetic advances as a mean percentage for days to 50% heading and days to 90% maturity [42].

3.4. Association Analysis

3.4.1. Correlation of Grain Yield with Other Traits at the Genotypic and Phenotypic Level. Grain yield showed a positive and highly significant correlation with plant height, the number of grains spikelet⁻¹, yield plant⁻¹, thousand seed weight, and biomass yield at both phenotypic and genotypic levels. It also exhibited a positive and significant correlation with total tillers and the number of productive tillers at the phenotypic and genotypic levels (Table 6). It showed a highly significant positive correlation with the number of spikelet spike⁻¹, spike length, and harvest index at phenotypic and genotypic levels, respectively (Table 6).

A significant positive correlation of these traits with grain yield suggests that any improvement would result in a

substantial increment in grain yield. Likewise, [42] reported that plant height, thousand seed weight, biomass yield, and harvest index showed a significant positive correlation with grain yield at the genotypic and phenotypic levels. Grain yield exhibited a nonsignificant correlation with days to heading, days to maturity, and awn length at both the genotypic and phenotypic levels. In contrast, the grain filling period shows a significant correlation with grain yield at a phenotypic level only, which suggests that an increase in days to 50% heading, days to 90% maturity, awn length, and grain filling period had no significant effect on grain yield increment (Table 6). In agreement with this result, Refs. [42, 43] reported a nonsignificant correlation of grain yield with days to 50% heading and days to 90% maturity.

3.4.2. Correlation between Major Traits at the Genotypic and Phenotypic Level.

Days to 50% heading had a significant positive correlation with days to 90% maturity, grain filling period, number of total tillers plant⁻¹, and number of fertile tillers plant⁻¹ at both the genotypic and phenotypic level and a significant positive correlation with the number of grains spike⁻¹, number of spikelet spike⁻¹, and biomass yield at the genotypic level. In agreement with this result, Refs. [44–46] reported a positive and highly significant correlation of days to 50% heading with days to 90% maturity, while a negative and significant correlation with harvest index at both genotypic and phenotypic levels. Days to 90% maturity showed positive and highly significant correlation with grain filling period, number of total tillers, number of fertile tillers, number of grains spike⁻¹, and number of spikelet spike⁻¹, and significant positive correlation with biomass yield and yield plant⁻¹ at both genotypic and phenotypic levels. Similar to this result, Ref. [47] reported a highly significant and positive correlation between days to 90% maturity and the number of spikelets spike⁻¹, number of kernel spike⁻¹, and number of grains spikelet⁻¹ at both the genotypic and phenotypic levels.

Plant height showed a positive and highly significant correlation with spike length, yield plant⁻¹, biomass yield, thousand seed weight, and grain yield at both the genotypic and phenotypic levels. This indicates that an increase in plant height leads to increase spike length, yield plant⁻¹, biomass yield, thousand seed weight, and grain yield. The number of grains spikelet⁻¹ showed a positive and highly significant correlation with grain yield at the genotypic and phenotypic levels. The number of grains spikelet⁻¹ showed a positive and highly significant association with biomass yield and a significant positive association with harvest index at the genotypic and phenotypic levels, respectively. The number of kernel spike⁻¹ showed a positive and highly significant association with the number of spikelets spike⁻¹, yield plant⁻¹, thousand seed weight, and biomass yield at both the phenotypic and genotypic levels (Table 6). In agreement with the present findings, Refs. [48, 49] reported that the number of kernel spike⁻¹ showed a significant positive correlation with spike length and thousand seed weight at both the genotypic and phenotypic levels.

TABLE 6: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of 16 traits in bread wheat genotypes tested in Gechi during the 2019/2020 cropping season.

Traits	DH	DM	GF	NTPP	NFPP	PH	SL	NGPs	NKPS	NsPS	YPP	TSW	BMY	HI	GY
DH		0.86**	0.40**	0.40**	0.46**	0.19	0.11	0.07	0.32*	0.32*	0.26	0.07	0.30*	-0.57**	-0.02
DM	0.81**		0.81**	0.33*	0.33*	0.2	0.22	-0.01	0.45**	0.50**	0.31*	0.13	0.33*	-0.34*	0.13
GF	0.28**	0.76**		0.16	0.12	0.16	0.32*	-0.1	0.42**	0.49**	0.23	0.16	0.28*	-0.04	0.24
NTPP	0.27**	0.25*	0.13		0.98**	0.67**	0.47**	0.42**	0.42**	0.39**	0.61**	0.42**	0.76**	-0.55**	0.336*
NFPP	0.33**	0.25*	0.09	0.86**		0.48**	0.52**	0.63**	0.35*	0.41**	0.49**	0.31*	0.70**	-0.55**	0.306*
PH	0.11	0.14	0.13	0.5**	0.44**		0.52**	0.3*	0.1	0.01	0.59**	0.71**	0.70**	-0.21	0.472**
SL	0.12	0.20*	0.25*	0.34**	0.35**	0.57**		0.04	0.29*	0.35*	0.6**	0.7**	0.56**	-0.29*	0.293*
NGPs	0.01	0.03	0.04	0.23	0.21*	0.19	0.05		0.2	0.14	0.24	-0.05	0.53**	0.35*	0.458**
NKPS	0.24*	0.35**	0.30**	0.17	0.20*	0.16	0.22*	0.14		0.77**	0.73**	0.40**	0.42**	0.34*	0.132
NsPS	0.27**	0.39**	0.31**	0.15	0.18	0.06	0.26**	0.15	0.67**		0.66**	0.4**	0.61**	0.47**	0.284*
YPP	0.19	0.25*	0.207*	0.3**	0.32**	0.42**	0.33**	0.09	0.66**	0.51**		0.87**	0.86**	-0.46**	0.478**
TSW	0.08	0.13	0.13	0.36**	0.3**	0.59**	0.53**	0.01	0.28**	0.29***	0.73**		0.87**	0.26*	0.624**
BMY	0.17	0.25*	0.23*	0.40**	0.42**	0.50**	0.37**	0.10	0.32**	0.39**	0.59**	0.62**		-0.33*	0.772**
HI	-0.25*	-0.13	0.01	-0.15	-0.17	-0.04	-0.05	0.25*	0.34*	0.22*	-0.23*	0.32**	-0.24*		0.348*
GY	-0.022	0.14	0.212*	0.229*	0.23*	0.42**	0.285**	0.286**	0.212*	0.262**	0.329**	0.467**	0.663**	0.526**	

DH = days to heading, DM = days to maturity, GFP = grain filling period, NTPP = number of total tiller per plant, NFPP = number of fertile tiller per plant, PH = plant height (cm), SL = spike length (cm), length(cm), NGPs = number of grain per spikelet, NKPS = number kernel per spike, NsPS = number of spikelet per spike, YPP = yield per plant(g), TSW = thousand seed weight (g), BMY = biomass yield, HI = harvest index, GY = grain yield (tha^{-1}), ** = highly significance ($p \leq 0.01$), * = significance ($p \leq 0.05$).

3.4.3. Path Coefficient Analysis of Different Traits on Grain Yield at the Genotypic Level. Genotypic path coefficient analysis revealed that biomass yield ($rg = 0.88$; $p \leq 0.01$) exerted the highest positive direct effect on grain yield, followed by harvest index ($rg = 0.70$; $p \leq 0.01$) and thousand seed weight ($rg = 0.56$; $p \leq 0.01$), which showed a good relationship between these traits and grain yield (Table 7). This result indicates that the positive and significant correlation of the biomass yield and the harvest index with grain yield at the genotypic level was due to the direct effect of these characters on the grain yield. Therefore, these traits could be considered the main components of the breeding program, and selection based on these traits may be effective in improving the grain yield of bread wheat. This result is in agreement with the findings of Refs. [36, 42, 43], which reported the highest and most positive direct effect of the biomass yield and the harvest index on the grain yield. The residual genotypic value was low (0.0271), indicating that traits included in the genotypic path analysis explained 97.29% of the variation in the grain yield.

3.4.4. Path Coefficient Analysis of Different Traits on Grain Yield at the Phenotypic Level. Direct effects of one character on the grain yield showed that this character directly affected the grain yield and might be helpful in selection for the improvement of yield. Indirect effects on the grain yield indicated that such traits affected the yield via other component characters. The relationship between yield and yield-related characters through the phenotypic path coefficient reveals that the biomass yield ($rp = 0.77$; $p \leq 0.01$) and the harvest index ($rp = 0.72$; $p \leq 0.01$) exerted the highest positive direct effect on the grain yield at the phenotypic level. In contrast, other traits exert a negligible direct effect on the grain yield (Table 8). These highest direct effects of the biomass yield and the harvest index on the grain yield suggest a true relationship, and selection based on these

traits may give better response for the improvement of grain yield. In agreement with the present findings, Refs. [15, 43, 50] reported the biomass yield and the harvest index exerted the highest positive direct effect on the grain yield at the phenotypic level.

Plant height (0.39), spike length (0.28), number of spikelet's spike $^{-1}$ (0.3), number of kernel spike $^{-1}$ (0.25), and thousand seed weight (0.48) exerted a moderate to high indirect effect via the biomass yield and negligible direct effect on the grain yield (Table 8). This indicates that the significant positive correlation of these traits with the grain yield at the phenotypic level was due to the indirect effect of these traits via the biomass yield. In agreement with this result, Ref. [43] reported positive indirect effects of plant height and the number of kernel spike $^{-1}$ on the grain yield. The residual phenotypic value was low (0.0759), which indicated that traits included in phenotypic analysis explained 92.41% of the variation in the grain yield.

3.5. Principal Component Analysis. In the present study, the principal component analysis revealed five principal components with eigenvalues greater than 1 (Table 9). The first five principal components accounted for about 76.7% of the total variation for sixteen studied traits, which showed the presence of genetic variability among the studied bread wheat genotypes.

The first principal component alone explains about 34.41% of total variation due to high positive load from the biomass yield (0.82), yield plant $^{-1}$ (0.82), thousand seed weight (0.75), number of total tillers (0.68), spike length (0.65), number of fertile tillers plant $^{-1}$ (0.65), plant height (0.64), number of spikelets spike $^{-1}$ (0.63), number of kernel spike $^{-1}$ (0.61), days to 90% maturity (0.54), and grain yield (0.53). This indicates their significant importance for this component. On the other hand, other traits are less important to PC1. PC2 accounted for 14.46% of total variation

TABLE 7: Genotypic path coefficients of direct (diagonal) and indirect (off-diagonal) effects of ten traits of bread wheat genotypes tested in Gechi during 2019/2020.

Traits	PH	NTPP	NFPP	SL	NsPS	NGPs	TSW	YPP	BMY	HI	rg	p value
PH	-0.22	0.08	0.08	-0.11	0.00	0.00	0.40	-0.23	0.62	-0.14	0.47**	$p \leq 0.01$
NTPP	-0.12	0.12	0.15	-0.10	0.03	0.00	0.24	-0.24	0.67	-0.38	0.34*	$p \leq 0.05$
NFPP	-0.11	0.12	0.16	-0.11	0.04	0.00	0.17	-0.19	0.62	-0.38	0.31*	$p \leq 0.05$
SL	-0.12	0.06	0.08	-0.21	0.03	0.00	0.39	-0.24	0.50	-0.20	0.29*	$p \leq 0.05$
NsPS	0.00	0.05	0.06	-0.07	0.09	0.00	0.22	-0.27	0.54	-0.33	0.28*	$p \leq 0.05$
NGPs	-0.07	0.05	0.09	-0.01	0.01	0.00	-0.03	-0.10	0.47	0.03	0.46**	$p \leq 0.01$
TSW	-0.16	0.05	0.05	-0.15	0.03	0.00	0.56	-0.35	0.76	-0.18	0.62**	$p \leq 0.01$
YPP	-0.13	0.08	0.08	-0.13	0.06	0.00	0.49	-0.40	0.75	-0.32	0.48**	$p \leq 0.01$
BMY	-0.16	0.09	0.11	-0.12	0.05	0.00	0.49	-0.34	0.88	-0.23	0.77**	$p \leq 0.01$
HI	0.05	-0.07	-0.09	0.06	-0.04	0.00	-0.15	0.18	-0.30	0.70	0.35**	$p \leq 0.01$

Residual = 0.0271

NTPP = number of total tiller per plant, NFPP = number of fertile tiller per plant, PH = plant height(cm), SL = spike length(cm), NGPs = number of grain per spikelet, NsPS = number of spikelet per spike, YPP = yield per plant(g), TSW = thousand seed weight(g), BMY = biomass yield, HI = harvest index, *, ** indicate significance at the 0.05 and 0.01 probability levels, respectively, rg = genotypic correlation coefficients.

TABLE 8: Phenotypic path coefficients of direct (diagonal) and indirect (off-diagonal) effects of twelve traits of bread wheat genotypes tested in Gechi during 2019/2020.

Traits	PH	SL	GFP	NsPS	NKPS	TSW	BMY	HI	rp	p value
PH	0.05	-0.02	0.00	0.01	-0.01	0.04	0.39	-0.03	0.43**	$p \leq 0.01$
SL	0.03	-0.03	0.01	0.02	-0.02	0.04	0.28	-0.03	0.3**	$p \leq 0.01$
GFP	0.01	-0.01	0.03	0.03	-0.03	0.01	0.18	0.00	0.22*	$p \leq 0.05$
NsPS	0.00	-0.01	0.01	0.09	-0.06	0.02	0.30	-0.08	0.27**	$p \leq 0.01$
NKPS	0.01	-0.01	0.01	0.06	-0.09	0.02	0.25	-0.03	0.22*	$p \leq 0.05$
TSW	0.03	-0.02	0.00	0.03	-0.03	0.07	0.48	-0.09	0.47**	$p \leq 0.01$
BMY	0.02	-0.01	0.00	0.03	-0.03	0.04	0.77	-0.17	0.66**	$p \leq 0.01$
HI	0.00	0.00	0.00	-0.01	0.00	-0.01	-0.19	0.72	0.51**	$p \leq 0.01$

Residual = 0.0759

GFP = grain filling period, PH = plant height (cm), SL = spike length(cm), NKPS = number grain per spike, NsPS = number of spikelet per spike, TSW = thousand seed weight(g), BMY = biomass yield, HI = harvest index, *, ** indicate significance at the 0.05 and 0.01 probability levels, respectively, rg = phenotypic correlation coefficients.

TABLE 9: Eigenvectors and eigenvalues of five principal components (PCs) for 16 traits of bread wheat genotypes tested in Gechi during 2019/2020.

Traits	Eigenvectors				
	PC1	PC2	PC3	PC4	PC5
DH	0.45	-0.63	-0.22	0.30	0.03
DM	0.54	-0.72	0.04	0.29	0.28
GFP	0.44	-0.53	0.25	0.18	0.47
NTPP	0.68	0.20	-0.42	0.36	-0.19
NFPP	0.65	0.12	-0.39	0.39	-0.34
PH	0.64	0.47	-0.18	0.10	0.25
SL	0.65	0.21	-0.07	-0.07	0.23
AL	0.02	0.18	-0.47	0.01	0.38
NGPs	0.25	0.22	0.30	0.50	-0.47
NKPS	0.61	-0.34	0.27	-0.30	-0.29
NsPS	0.63	-0.37	0.29	-0.27	-0.29
YPP	0.82	0.05	0.10	-0.41	-0.14
TSW	0.75	0.38	-0.01	-0.36	0.22
BMY	0.82	0.23	0.08	-0.07	0.05
HI	-0.28	0.30	0.70	0.37	0.17
GY	0.53	0.40	0.60	0.21	0.18
Eigenvalue	5.51	2.31	1.83	1.41	1.22
% Of total variance explained	34.41	14.46	11.42	8.79	7.63
Cumulative % of total variance explained	34.41	48.9	60.3	69.1	76.7

due to high negative load from days to 90% maturity (-0.72), days to 50% heading (-0.63), and grain filling period (-0.53) and positive load from plant height (0.47) and grain yield (0.4). The third PC accounted for about 11.42% of total variation due to a high positive load from the harvest index (0.7) and the grain yield (0.6) and negative load from awn length (-0.47), the number of total tillers plant⁻¹ (-0.42), and number fertile tillers plant⁻¹ (-0.39). The fourth PC accounts for about 8.79% due to a positive load from the number of grains per spikelets (0.50), fertile tillers plant⁻¹ (0.39), harvest index (0.37), number of total tiller plant⁻¹ (0.36), and negative load from yield plant⁻¹ (-0.41). Lastly, PC5 contributed 7.63% for total variability due to load positive from grain filling period (0.47) and awn length (0.38), and negative load from grains spikelets⁻¹ (-0.47) (Table 9).

The first three PCs accounted for a cumulative 60.3% of the total variation, which indicates much of the variability that occurred originated from traits included in these PCs. The most important yield and yield attributing traits were present in the first three PCs. Generally, maximum contributions toward the variability of genotypes were due to days to 90% maturity, days to 50% heading, grain filling period, biomass yield, yield plant⁻¹, thousand seed weight, and grain yield. Similar works have also been reported by Dargicho et al. [14], who found that three principal components (PCs) out of 12 contributed 63.2% of the variation. Ref. [51] studied 26 genotypes and reported that five PCs contributed 91% of the variation. The traits far from the PCA biplot origin contributed more to the total variability. Accordingly, the primary traits contributing more to total variability were days to maturity, days to heading, plant height, thousand seed weight, biomass yield, grain yield, and yield plant⁻¹.

And the traits close to the biplot origin that contributed less to total variability were awn length, harvest index, grain filling period, number of grains spike⁻¹, number of grains spikelet⁻¹, and number of fertile tillers plant⁻¹. In addition, the traits nearest to the x-axis contributed more for PC1, whereas those nearest to the y-axis contributed more for PC2 (Figure 1).

3.6. Cluster Analysis. The cluster analysis based on the unweighted pair group method with arithmetic means (UPGMA) clustering method from the Euclidean distance matrix grouped 49 bread wheat genotypes into five major clusters of 2 to 21 genotypes (Figure 2). Cluster II (42.857%) was the largest cluster of 21 genotypes. Cluster I (20.408%) was the second-largest cluster and consisted of 10 genotypes. Cluster IV (18.367%) was the third largest cluster containing nine genotypes, whereas cluster V (4.0816%) was the least and followed by cluster III (14.285%), consisting of 2 and 7 genotypes, respectively (Table 10).

3.6.1. Cluster Means Analysis of the Major Contributed Traits for Variability. In the current study, cluster IV was characterized by having the lowest cluster means for days to 50% heading (64.28) and days to 90% maturity (100.7),

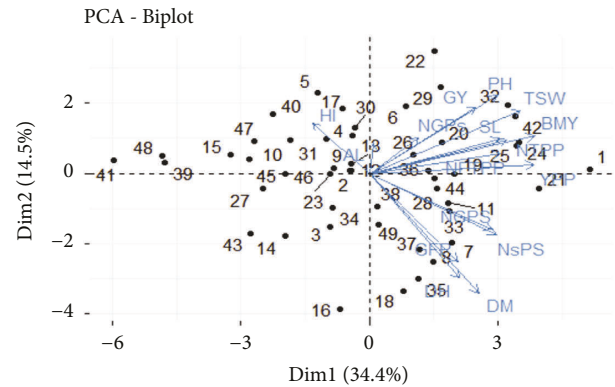


FIGURE 1: Principal component's biplot of all studied traits of bread wheat genotypes. DH= days to heading, DM= days to maturity, GFP = grain filling period, NTPP = number of total tiller per plant, NFPP = number of fertile tiller per plant, PH = plant height(cm), SL = spike length(cm), length(cm), NGPs = number of grain per spikelet, NKPS = number kernel per spike, NsPS = number of spikelet per spike, YPP = yield per plant(g), TSW = thousand seed weight(g), BMY = biomass yield, HI = harvest index, GY = grain yield(th⁻¹), Number = genotypes code.

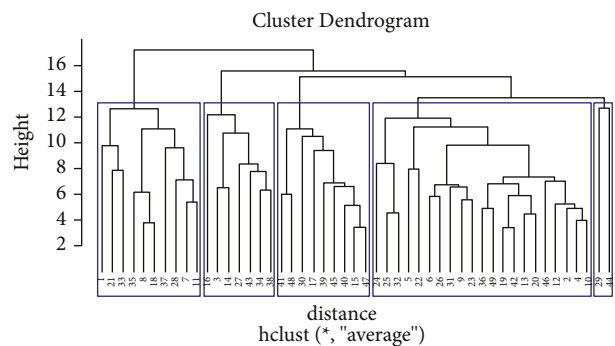


FIGURE 2: Hierarchical dendrogram generalized from Euclidean distance using a cluster method of the paired group. Numbers = genotype codes.

which indicates the presence of early heading and early maturing genotypes, which were represented in this cluster (Table 11). Thus, further evaluation of members of this cluster is needed to develop promising early maturing genotypes. Cluster I exhibited the lowest grain filling period (36.67), whereas the highest mean for the grain filling period (43.85) was from cluster I. The highest mean for the number of grains spike⁻¹ (45.88) and the number of spikelets spike⁻¹ (15.15) was recorded from cluster I, whereas the highest mean for the grain yield (3.82) and the biomass yield (9.542) was recorded from clusters V and I, respectively.

This result indicates sufficient scope for genotypic improvement through hybridization between the genotypes from divergent clusters. The genotypes in clusters III and IV might not be selected for further evaluation due to the undesirable character of low yield comparably, while the members of these clusters can be selected for the traits with greater mean values. Generally, cluster I was characterized by having the highest mean values for spike length, number

TABLE 10: Distribution of genotypes into five clusters based on squared distance analysis for 49 bread wheat genotypes.

Clusters	Number of genotypes	%age	Genotypes
I	10	20.408	ETBW 9185, BW 174459, BW 174467, ETBW 9594, ETBW 9618, ETBW 9627, ETBW 9635, BW 174468, ETBW 9313, ETBW 9066
II	21	42.857	ETBW 9315, BW 174460, BW 174462, ETBW 9193, ETBW 9601, ETBW 9233, ETBW 9605, ETBW 9611, ETBW 9613, ETBW 9615, ETBW 9616, ETBW 9624, ETBW 9626, ETBW 9636, BW 172070, ETBW 9087, ETBW 9651, ETBW 9543, ETBW 9089, ETBW 9304, ETBW 9102
III	7	14.285	BW 174463, BW 174465, ETBW 9617, ETBW 9086, ETBW 9628, BW 174469, Wane
IV	9	18.367	BW 174464, BW 174466, ETBW 9623, BW 174470, ETBW 9653, BW 174116, ETBW 9128, ETBW 9642, ETBW 9647
V	2	4.0816	ETBW 9619, Lemu

BW = Bread wheat, ETBW = Ethiopian bread wheat, %age = percentage.

TABLE 11: Cluster mean values for sixteen traits in forty-nine (49) bread wheat genotypes.

Traits	Cluster				
	I	II	III	IV	V
DH	71.1 ± 3.34	67.5 ± 2.22	70.3 ± 2.14	64.28 ± 2.24	72 ± 3.54
DM	114.1 ± 3.79	104 ± 2.33	109 ± 2.19	100.7 ± 1.39	110 ± 3.54
GFP	43.85 ± 1.99	37 ± 1.64	38.9 ± 1.68	36.67 ± 1.17	37.5 ± 0.5
NTPP	2.433 ± 0.26	2.38 ± 0.31	2.21 ± 0.37	2.085 ± 0.4	2.82 ± 0.19
NFPP	2.069 ± 0.31	2.03 ± 0.28	1.89 ± 0.53	1.753 ± 0.41	2.19 ± 0.33
PH	75.71 ± 3.16	76.4 ± 2.53	69.8 ± 3.53	71.41 ± 2.82	82 ± 7.18
SL	8.716 ± 0.42	8.38 ± 0.49	7.67 ± 0.62	8.007 ± 0.67	8.69 ± 0.06
AL	7.693 ± 0.39	7.52 ± 0.60	7.51 ± 0.82	7.523 ± 0.57	8.2 ± 0.78
NGPs	3.214 ± 0.17	3.27 ± 0.26	3.33 ± 0.33	3.179 ± 0.27	3.38 ± 0.11
NKPS	45.88 ± 2.52	43.6 ± 3.81	43.5 ± 4.23	37.16 ± 3.55	38.8 ± 1.66
NsPS	15.15 ± 0.83	14.7 ± 1.10	14.7 ± 1.07	13.48 ± 0.75	14.4 ± 0.74
YPP	1.626 ± 0.16	1.63 ± 0.17	1.32 ± 0.16	1.199 ± 0.14	1.38 ± 0.06
TSW	31.62 ± 3.83	32.8 ± 3.28	23.8 ± 3.02	25.36 ± 3.77	32.9 ± 0.52
BMV	9.542 ± 1.38	9.16 ± 1.53	7.98 ± 0.62	7.742 ± 1.40	9.42 ± 0.73
HI	0.355 ± 0.05	0.37 ± 0.05	0.39 ± 0.02	0.401 ± 0.05	0.4 ± 0.02
GY	3.407 ± 0.78	3.41 ± 0.79	3.11 ± 0.24	3.122 ± 0.34	3.82 ± 0.43

DH = days to 50% heading, DM = days to 90% maturity, GFP = grain filling period, NTPP = number of total tillers plant⁻¹, NFPP = number of fertile tillers plant⁻¹, PH = plant height (cm), SL = spike length (cm), AL = awn length (cm), NGPs = number of grains spikelet⁻¹, NKPS = number kernel spike⁻¹, NsPS = number of spikelets spike⁻¹, YPP = yield plant⁻¹ (g), TSW = thousand seed weight (g), BMV = biomass yield (tha⁻¹), HI = harvest index, GY = grain yield (tha⁻¹).

of grains spike⁻¹, number of spikelets spike⁻¹, and biomass yield. In contrast, cluster V was characterized by having the highest mean values for the number of total tillers plant⁻¹, number of fertile tillers plant⁻¹, number of kernel spikelet⁻¹, thousand seed weight, harvest index, and grain yield (Table 11). Therefore, genotypes in these clusters could be used as a parent for crossing to develop high-yielding bread wheat varieties.

3.7. Analysis of the Genetic Divergence

3.7.1. Intra- and Intercluster Distances. The average intra- and intercluster distance D^2 values are presented in Table 12. The maximum intracluster distance was recorded in cluster V (12.77), whereas the minimum intracluster distance was recorded in cluster IV (9.2). However, the chi-square test for within (intra) clusters was insignificant for all clusters. This indicates that genotypes within the cluster are less diverged than genotypes of different clusters. On the other hand, the chi-square values for intercluster distances showed that

TABLE 12: Average intra- and intercluster distance value for bread wheat genotypes.

Cluster	I	II	III	IV	V
I	10.9	25.57*	23.93 ^{ns}	31.86**	26.32*
II		9.56	28.24*	29.21*	18.58 ^{ns}
III			10.13	24.10 ^{ns}	27.92*
IV				9.2	26.15*
V					12.77

χ^2 at 5% = 24.996; χ^2 at 1% = 30.578, ** = highly significant, * = significant, ns = nonsignificant.

there was a significant acceptable difference between clusters I and IV, clusters III and V, clusters II and III, clusters I and V, and clusters IV and V. The highest intercluster distance was observed between clusters I and IV ($D^2 = 31.86^{**}$) and followed by clusters II and IV ($D^2 = 29.21^*$), clusters II and III ($D^2 = 28.24^*$), clusters III and V ($D^2 = 27.92^*$), clusters I and V (26.32*), and clusters IV and V ($D^2 = 26.15^*$) (Table 12). This result indicated the presence of genetically distant genotypes, which could be used in hybridization

programs to combine the most desirable traits to develop varieties. Among these, cluster V had a significant distance from cluster I, which was divergent for the grain yield and yield-related traits, indicating crossing members of these clusters could be used for yield improvement. The members of clusters III and IV may not be used due to undesirable lower yields, but they could be used for other traits. Refs. [14, 41, 52, 53] reported that the selection of wheat parents for hybridization should be carried out from two clusters having wider intercluster distances to get maximum variability in segregating generations. The lowest and nonsignificant intercluster distance was observed between clusters II and V ($D^2 = 18.58$ ns), followed by clusters I and III ($D^2 = 23.93$ ns) and clusters III and IV ($D^2 = 24.10$ ns) (Table 12). This indicated that genotypes of these clusters were closely related and crossing of genotypes from those clusters might not give a higher heterotic value.

4. Conclusions

The present study showed highly significant differences ($p < 0.01$) among genotypes for all the traits except awn length and harvest index, which can be exploited to develop high-yielding varieties. The existence of genetic variability among the studied genotypes for quantitative traits shows the possibility of direct selection of parental genotypes to develop hybrid varieties. Based on the mean performance of genotypes, genotypes ETBW 9613, ETBW 9605, ETBW 9624, ETBW 9594, ETBW 9185, BW 172070, ETBW 9304, BW 174116, ETBW 9066, ETBW 9615, and BW 174466 were performed better than all genotypes including check varieties. Therefore, for grain yield improvement, direct selection of these genotypes can be rewarding. In general, the presence of sufficient variability creates opportunities for further improvement of bread wheat genotypes. The biomass yield followed by the harvest index and thousand seed weight exerted the highest positive direct effect on grain yield indicating that these traits are effective for selection. Therefore, the information generated from this study can be used by breeders to improve their traits of interest. Therefore, it is recommended to evaluate the genotypes for high yielding over location and season to know the stability of the genotypes and to draw a definite conclusion.

Appendix

Planting materials used in the study.

Mean square values from ANOVA.

Mean values of forty-nine bread wheat genotypes for sixteen traits.

Data Availability

The data supporting the findings of this study can be obtained from the corresponding author upon request.

Conflicts of Interest

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

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