Research Article

Performance Evaluation of Ethiopian Bread Wheat (*Triticum aestivum* L.) Genotypes in Southern Ethiopia

Mengistu Meskele Alambo,[1] **Mesfin Kebede Gessese** [2] **Eyasu Wada Wachamo** [1]
Belay Yebo Melo [2] **Zemach Sorsa Lakore,**[2] **Adera Sisay Wassie,**[2] **Wondimeneh Taye Haile,**[2]
and Fentanesh Chekole Kassie[2]

[1]*Wolaita Sodo University, College of Natural and Computational Sciences, Department of Biology, P.O. Box 138, Sodo, Ethiopia*
[2]*Wolaita Sodo University, College of Agriculture, Department of Plant Sciences, P.O. Box 138, Sodo, Ethiopia*

Correspondence should be addressed to Mesfin Kebede Gessese; mesfin04@yahoo.com

Ethiopia is not self-sufficient to meet its increasing wheat demand from domestic production partly due to a lack of improved seeds. Efforts are undertaken to fill the gap through off-season production of wheat using supplemental irrigation and modern cultivars adapted to arid areas. This study was carried out to evaluate the genetic variability and adaptability of 15 Ethiopian bread wheat genotypes at different agroecologies in Wolaita and Dawuro zones, Ethiopia. The field experiment was conducted at three locations using a randomized complete block design with three replications during the 2019/2020 main cropping season. Analysis of variance based on 11 morphological agronomic traits and two major wheat diseases revealed that there were highly significant differences ($P < 0.01$) among the genotypes for all the traits studied at each location and combined over locations. The top three cultivars viz. Alidoro, Galema, and Honqolo exhibited higher average grain yield (GY) of 4.54 t/ha, 4.36 t/ha, and 4.0 t/ha, respectively, combined over locations. Eight of the traits (72.73%) exhibited moderate (30–60%) to high broad-sense heritability ($h_b^2 > 60\%$) values. High h_b^2 associated with high genetic advance as percent of mean was observed for the severity of both stem and yellow rust diseases combined over locations. GY was significantly related to aboveground biomass at all locations. This study depicted that cultivar Alidoro had wider adaptability for grain yield and resistance to wheat rusts.

1. Introduction

Wheat (*Triticum aestivum* L.) is the most widely grown cereal crop in the world. It is the second major food crop next to rice [1]. It is widely cultivated for its grain for domestic consumption in various recipes and industrial uses [2–4]. It is the major staple food for 40% of the world's population [5]. The global current (2020/2021) wheat utilization was forecasted at about 758 million tons, that is, 1.5 percent higher than in 2018/19, where the increment was mostly associated with growth in food consumption [6]. To feed the world's growing population, the global demand for wheat yield should increase by 50% in 2050 as estimated by Allen et al. [7].

China and India are the world's largest wheat producers, annually producing 134,340,630 and 98,510,000 tons of wheat, respectively. Africa's average wheat production from 2014/15 to 2016/17 was 71.7 million tons, whereas that of 2017/2018 and 2018/2019 cropping seasons was 74.8 and 75.2 million tons, respectively [6]. Ethiopia is the second-largest wheat producer in Africa with annual production amounting to approximately 4.54 million tones and an average grain yield of 2.67 t/ha [8]. The annual average wheat utilization in Ethiopia in 2016/17, 2017/2018, and 2018/2019 was 5.6, 6.0, and 6.1 million tons, respectively [6], clearly showing the deficit and need for additional import to meet the domestic demand. In the Southern Nations Nationalities People Region (SNNPR) of the country, wheat covered an

area of 133,419.80 ha with a total production of 334,633.93 tons. Of which, 3,092.39 tons was obtained from Wolaita Zone on 1,630.25 ha cultivated land and about 4207 tons was obtained from Dawuro Zone on the estimated cultivated area of 2274.05 ha [9].

Wheat adapts to a wide range of environmental conditions mainly due to the complex nature of its genome, which provides great flexibility to the crop [10, 11]. In Ethiopia, wheat can grow in highlands, which are located between 6° and 16°N latitude and 35° and 42°E longitude and at altitudes ranging from 1500 to 3000 m.a.s.l. However, the most suitable altitude zones of wheat fall between 1900 and 2700 m.a.s.l [12].

Breeders are continuously working for the improvement of grain yield, with better quality (bread-making quality, seed color, seed size, protein content, etc.) and resistance to both biotic and abiotic stresses. In Mexico (CIMMYT), the segregating wheat populations, which were widely adapted, high yielding, and with stable performance, would be selected from two environments with differing disease and abiotic stresses by the shuttle breeding methods [13]. This breeding method is further corroborated by international multilocation testing of advanced lines, particularly in Kenya and Ethiopia, for screening to stem rust, leaf rust, and stripe rust diseases [14]. However, breeding for wide adaptation has not been very successful because in most areas temperatures and rainfall patterns shift annually including edaphic factors (soil acidity, salinity, alkalinity, and fertility problems) and vary from region to region. In addition, farmers could not be able to maintain the same agronomic practices consistently, since diseases and pest pressures vary from year to year.

To increase the production of crops, which adapt to diverse environmental conditions (resistant to both biotic and abiotic stresses), and to improve the quality of the product through developing more adaptive cultivars, the knowledge of the genetic diversity within a germplasm collection has a significant impact [15]. While new wheat cultivars are developed by the breeders, the new cultivars are tested for their yield performances in multilocation trials. The success of releasing a new wheat cultivar depends upon its quantity and quality of grain yield and adaptation potential in those locations. Finally, cultivars with high and stable yields are highly preferred by both farmers and breeders.

In Ethiopia, wheat production and productivity have been increasing significantly although it is still insufficient to meet the increasing demand for the ever-increasing population [7]. The wheat production of the country covers 75% of the national demand, while the remaining 25% of the wheat is imported from abroad [16]. This is due to the influence of diseases such as stem rust, yellow rust, septoria leaf spot, shortage or lack and suboptimal use of production inputs (e.g., improved seeds and fertilizers), and breakdown of disease resistance genes of the released cultivars after few years of production [17].

Therefore, evaluation of the performance of recently released improved bread wheat cultivars compared with relatively older ones and estimating their genetic variability and adaptability across diverse environmental conditions is very important to identify the most adaptable, stable, disease-resistant, and high yielder cultivar across a range of environments [18]. This requires a careful investigation to identify the most important yield and yield-related quantitative traits to select the most productive and wide range adaptable cultivar and suggest useful indexes to the wheat improvement program. Hence, this study was conceived to assess the genetic variability and adaptability of Ethiopian bread wheat (*Triticum aestivum* L.) genotypes and select the ones with higher grain yield and better adaptation across the test locations in Wolaita and Dawuro zones of southern Ethiopia.

2. Materials and Methods

2.1. Descriptions of the Study Area. The genetic variability and adaptability of Ethiopian bread wheat were assessed at farmer's field in three locations (Table 1). Two of the locations were in Wolaita Zone (in Ade Koysha Kebele, Damot Gale District, and in Sunkale Kebele, Damot Sore District). The third location is in Dawuro Zone at Wolaita Sodo University Tercha Campus Research Site (Kechi woreda).

2.2. Plant Materials and Experimental Design. Seeds of all 15 bread wheat genotypes (Table 2) were obtained from Kulumsa Agriculture Research Center (KARC), Ethiopia. The genotypes were planted in the randomized complete block design (RCBD) with three replications. Each plot was composed of six rows of 0.2 m spaced, with 2.5 m length and 1.2 m width. Therefore, the area of each experimental plot was $3 \, m^2$ ($1.2 \, m \times 2.5 \, m$).

2.3. Sowing and Crop Management. The experimental field was well tilled (ploughed three times before sowing), and planting rows were prepared using hand-pulled row marker. Seeds were sown by hand drilling method at a planting depth of ~5 cm and 10 cm intra-raw spacing between plants. Planting was carried out at the appropriate planting time for each location (at Damot Gale on July 23, 2019, Kechi on July 26, 2019, and Damot Sore on July 31, 2019). For all plots, inorganic fertilizer was uniformly applied at the rate of $100 \, kg \, ha^{-1}$ di-ammonium phosphate (DAP) and 150 kg urea ha^{-1} as recommended for bread wheat by KARC. The whole rate of DAP and half of the urea were applied at planting time, and the remained half was added at the mid-tillering stages. The seed rate was 150 kg/ha. Hand weeding was done to control weeds in the experimental fields in all the three locations. However, neither herbicides nor fungicides were applied to control weeds and diseases, respectively.

2.4. Data Collection for Agronomic Traits. All necessary data were collected from the four middle rows of each plot. Data were collected on the plant and plot bases. For the data collected on a plant basis, 10 plants per plot were randomly selected for each of the traits; that is, number of tillers per plant, number of kernels per spike, number of spikelets per

TABLE 1: Specific descriptions of the study area's experimental sites.

Zone	Districts	Study location (Kebele)	Geographic coordinates		Average annual temperature		Average annual rainfall		Altitudes in m.a.s.l
			Latitude	Longitude	Min	Max	Min	Max	
Wolaita	Damot Gale	Ade Koysha	6°83″N	37°73″E	13.4°C	26°C	1200 mm	1300 mm	1907
	Damot Sore	Sunkale	7°35″N	38°01″E	14°C	27.5°C	1150 mm	1250 mm	2070
Dawuro	Kechi	Kechi	6°35″N	36°04″E	11.5°C	25.5°C	1230 mm	1320 mm	2215

TABLE 2: Details of bread wheat genotypes used in the field experiment.

S. N	Genotypes	Origin	Released by	Pedigree	Year of release
1	ETBW 8070	NA	NA	NA	Candidate
2	Wane	NA	Kulumsa	SOKOLL/EXCALIBUR 2016	2016
3	Hidasse	CIMMYT	Kulumsa	YANAC/3/PRL/SARA//TSI/VEE#5/4/CRC	2012
4	Ogolcho	CIMMYT	Kulumsa	WORRAKATTA/2*PASTOR 2012	2011
5	Lemu	NA	Kulumsa	WAXWING*2/HEILO 2016	2012
6	Honqolo	NA	Kulumsa	NA	2016
7	Alidoro	USA	Holetta	HK-14-R251	2007
8	Danda'a	CIMMYT	Kulumsa	KIRITATI//2*PBW65/2*SERI.1B	2007
9	Huluka	ICARDA	Kulumsa	UTQUE96/3/PYN/BAU//MILAN 2012	1995
10	Galama	CIMMYT	Kulumsa	4777(2)//FKN/GB/3/PVN"S"	1982
11	Hawi	CIMMYT	Kulumsa	CHIL/PRL 1999	1999
12	Pavone-76	CIMMYT	Werer	VCM//CNO"S"/7C/3/KAL/BB	1999
13	Shorima	ICARDA	Kulumsa	UTQUE96/3/PYN/BAU//MILAN 2011	2010
14	Hoggena	ICARDA	Kulumsa	PYN/BAU//MILAN 2011	2011
15	Biqa	NA	Kulumsa	NA	2014

KARC = Kulumsa Agricultural Research Center, CIMMYT = International Maize and Wheat Improvement Center. ICARDA = International Center for Agricultural Research in the Dry Areas. NA = not available.

spike, plant height (cm), peduncle length (cm), and spike length (cm). The data for number of days to heading (75%), number of days to maturity (90%), grain filling period, number of productive tillers per meter square, thousand-kernel weight (gm), aboveground biomass (kg), grain yield (t/ha), and harvest index (%) were collected on a plot basis.

2.5. Data on Disease Parameters.
Disease severity data were recorded for stem rust and stripe rust when the disease severity reached between 60% and 100% in the field on susceptible cultivars. The data were recorded every week until the susceptible plants showed 100% susceptibility. The 1–9 scoring scale was adopted to record the data as described in Bariana et al. [19].

2.6. Data Analysis

2.6.1. Analysis of Variance. The agro-morphological data including disease parameters of the three locations were subjected to the variance analysis using GenStat 16th edition statistical software package (VSN International Ltd., London, UK) following the standard procedures described by Gomez and Gomez [20] to evaluate the performance of genotypes for each trait and location and calculate the error variances for each of the environments. For combined analysis of variance over locations, the homogeneity of error variance was tested using Bartlett's test for homogeneity of variances using the same software. The difference between treatment means was compared using the least significant difference

(LSD) test at 5% level of significance when the ANOVA showed a significant difference among genotypes.

2.6.2. Genetic Parameters. The estimation of genetic parameters was done to identify and ascertain genetic variability among the bread wheat genotypes and to determine the extent of environmental effect on various traits. By considering all the genotypes tested in the uniform environment, the mean square for error (MSe) for each trait was assumed to be purely a random environmental variance ($\sigma^2 e$). The genotypic variance ($\sigma^2 g$) was calculated from the ANOVA table for each trait by adopting the formula described in Singh and Chaudhary [21], and the phenotypic variance ($\sigma^2 p$) was computed by adopting the following formula as suggested below by Burton and Devane [22].

Genotypic variance ($\sigma^2 g$) = (MSg − MS$e/r$) and phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$, where MSg—mean squares of genotypes, MSe—mean square due to error, and r—number of replications.

Genotypic and phenotypic coefficients of variations were calculated using the formula described in Singh and Chaudhary [21] as follows.

Genotypic coefficients of variations (GCV) = ($\sqrt{\sigma^2 g}/X$) × 100 and phenotypic coefficients of variations (PCV) = ($\sqrt{\sigma^2 p}/X$) × 100, where $\delta^2 g$ is genotypic variance, $\delta^2 p$ is phenotypic variance, and x is the grand mean value of the trait.

The combined genetic variance components across locations were computed using a similar approach as for

individual locations using the following formula adopted from Allard [23].

Environmental variance $(\sigma^2 e) = MSe$, genotype variance $(\sigma^2 g) = (MSg - MSe/lr)$, genotype-by-location interaction variance $(\sigma^2 gl) = (Mgl - MSe/r)$, and phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e + \sigma^2 gl$, where $MSe =$ mean square for error, $MSgl =$ mean square of genotype-by-location interaction, $MSg =$ mean square of genotype, $r =$ replication, and $l =$ location.

2.6.3. Estimation of Heritability and Genetic Advance.
Heritability in broad sense (h_b^2) for all traits was computed using the formula adopted by Allard [23]. Heritability in a broad sense $(h_b^2\%) = (\delta^2 g/\delta^2 p) * 100$, where $\delta^2 g$ is genotypic variance and $\delta^2 p$ is phenotypic variance. Genetic advance was computed using the formula adopted from Johnson et al. [24] and Allard [23]. Genetic advance $(GA) = (k)$ $(\sigma_p) \times (h_b^2)$, where $\delta^2 g$ is genotypic variance, $\delta^2 p$ is phenotypic variance, δp is the standard deviation of phenotypic variance, and k is the selection differential at a particular selection intensity, i.e., 2.06, suggested by Falconer at 10% selection intensity. Genetic advance as percent of mean was calculated to compare the extent of predicted advances of different traits under selection using the formula given by Falconer and Mackey [25]. $GAM = (GA/X) \times 100$, where $GAM =$ genetic advance as percent of mean, $GA =$ genetic advance, and $x =$ mean value of the trait.

3. Results and Discussion

3.1. Analysis of Variance.
The analyses of variance showed significant differences among the tested genotypes. Except stem rust, which was nonsignificant, all other traits showed significant differences between genotypes when subjected to the combined analysis of variance over the three locations (Table 3). Similar findings have been reported by other authors that bread wheat exhibited significant differences among genotypes for number of days to maturity, number of days to heading, plant height, spike length, number of seeds per spike, thousand seed weight, harvest index, and grain yield per plant as reviewed by Majumder et al. [26]. The nonsignificant difference obtained in the combined ANOVA (for location and genotype-by-location interaction effect) for stem rust disease severity data (Table 3) could be the presence of major genes (all stage resistance gene/seedling resistance gene) in the majority of the Ethiopian bread wheat cultivars, which are less influenced by environmental effects compared with adult plant resistance (slow rusting resistance) genes [27]. These findings encourage carrying out additional genetic studies to improve the cultivars through hybridization and selection programs.

The interaction between locations and genotypes was significant for the majority (61.5%) of the traits such as plant height, number of tillers per plant, number of effective tillers per plant, number of seeds per spike, biomass yield (t/ha), grain yield (t/ha), thousand seed weight (g), and harvest index. Desalegn and Dinesh [28] reported a significant genotype-by-environment (location) (GxE) effect for days to

heading, days to maturity, plant height, grain filling period, spike length, aboveground biomass yield, thousand seed weight, and harvest index, most of which were in agreement with the present findings. Traits such as days to maturity, resistance to both stem and yellow rust diseases, thousand-seed weight, and spike length were less influenced by the effect of environmental differences indicating that such traits could contribute to the genotypes for wider adaptation or uniform performance of genotypes across environments. Traits that showed nonsignificant differences for GxE effect (Table 3) indicated that there was less influence on environment compared with the genotype effect. Such traits would have high heritability value and could contribute to the successful selection of genotypes for wider adaptation areas [29].

3.2. Mean Performance of Genotypes.
The mean performance of 15 bread wheat genotypes for 13 agro-morphological traits at Damot Gale, Damot Sore, and Kechi locations is presented in Tables 4–6, respectively. The result showed the presence of significant differences for all studied traits at all locations ($P < 0.05$). The number of days to heading (DH) was the highest at Kechi (78) as compared to Damot Gale (73) and Damot Sore (69). Days to maturity (DM) followed a similar fashion as DH where Kechi exhibited the highest DM (127.5), followed by Damot Gale (110) and Damot Sore (105), respectively. The genotypes grouped as early and late heading corresponded with the respective early and late maturity characteristics of each location. In a similar study, Birhanu et al. [30] and Mollasadeghi et al. [31] reported that the days to heading and maturity of bread wheat genotypes corresponded with each other. However, a recent study on bread wheat traits showed the absence of significant association between number of days to heading and days to maturity [32]. Days to maturity (DM) data showed that nearly similar genotypes were grouped uniformly as early maturing, intermediate maturing, and late maturing types across locations, implying genetic factors contributed to the lions' share for the variations in DH and DM among the genotypes. The causes of variations in DH could be the differences in the number of days that the genotypes have taken at the three locations as there were variations in average rainfall, temperature, and light intensity at the three locations. The maturity date is an important trait for farmers of the study areas in which they are interested in identifying early and late maturing wheat varieties. *Hidase* variety was among the early maturing bread wheat genotypes at all locations. This result agrees with the study result reported by Bekele et al. [33] in which the Hidasse variety was preferred by farmers because of its early maturity.

The mean value of bread wheat genotypes for plant height (PH) showed that the genotypes evaluated at Damot Sore location (79.8 cm) were shorter than those evaluated at Damot Gale (91.6 cm) and Kechi (96.6 cm) locations. This could be related to higher rainfall and relatively lower temperature at Damot Gale and Kechi sites that might have increased the height of bread wheat plants at these locations. It was reported that the performance of bread wheat genotypes for PH was significantly and uniformly influenced

TABLE 3: Mean squares of the combined ANOVA for grain yield, components of yield, stem rust, and yellow rust disease severity for the 15 bread wheat genotypes tested across three locations.

Traits	MS of replication (df = 2)	MS of genotypes (df = 14)	MS of location (df = 2)	MS of $G \times L$ (df = 28)	MS of error (df = 84)	CV (%)
DH	17.5	104.1**	992.3**	15.8 ns	12	4.7
DM	8.5	95.8**	8686**	12.4 ns	12	3.1
PH	11.3	232.6**	3362**	38.5**	11.7	3.8
TNT	0.4	0.7*	147.3**	1.2**	0.3	9.7
ENT	0.4	0.6*	135.2**	1.1**	0.3	10
SL	0.4	3.8**	10.3**	0.4 ns	0.4	7.4
SPS	62.6	51.4**	975.0**	65.4**	21.9	10.1
SR	1.9	15.9**	2.5 ns	0.6 ns	0.9	40.5
YR	2	5.5**	8.8**	1.1 ns	0.8	47.8
ABM	2.3	9.5**	203.7**	5.6**	2	6.4
GY	0.1	1.4**	37.3**	0.8**	0.3	15.2
TSW	34	68.3**	215.5**	23.9**	12.1	8.9
HI	15.8	134.8**	1034**	87.2**	22.9	10.7

MS—mean square, df—degree of freedom, CV—coefficient of variation, $G \times L$—genotype-by-location interaction effect, ** significant at $P < 0.01$, * significant at $P < 0.05$, ns—nonsignificant, DH—days to heading, DM—days to maturity, PH—plant height (cm), TNT—number of tillers/plant, ENT—number of effective tillers/plant, SL—spike length (cm), SPS—number of seeds/spike, SR—stem rust (scale), YR—yellow rust (scale), ABM—aboveground biomass (t/ha), GY—grain yield (t/ha), TSW—thousand seed weight (g), HI—harvest index.

by average temperature, altitude, and precipitation of the environment they were evaluated [34]. Similar trends were also observed for traits such as number of tillers/plant, effective number of tillers/plant, spike length, aboveground biomass (g), and grain yield (g). These traits were best performed at Damot Gale location. Two traits namely number of seeds/spike and thousand seed weight were best performed at Kechi location. The highest mean value of harvest index (49.2%) was obtained at Damot Sore location, while the lowest harvest index (39.7%) was obtained at Kechi location. The maximum and minimum grain yields per hectare were recorded from genotype Galema (6.25 t/ha) at Damot Gale location and from Pavon-76 (2.45 t/ha) at Kechi location, respectively.

Analysis of combined data of the three locations showed that the genotype Alidoro exhibited the highest average grain yield (4.54 t/ha) (Table 7), indicating its wider adaptability and resistance to the rusts. The mean score values of stem rust and yellow rust severity data showed little variation across locations, which could be attributed to the specificity of genes possessed by genotypes. Qualitative genes are less likely influenced by environmental effect [35]. In general, the mean performance of genotypes with respect to grain yield, plant height, and aboveground biomass indicated that bread wheat genotypes were better performed at Damot Gale (4.8 t/ha of grain yield) compared with those at Kechi (3.24 t/ha of grain yield) (Tables 4–6). This result is similar to the findings of Allison et al. [36], who reported that wheat grain yield was low at high elevations where temperatures were too low to allow the crops to mature. The highest yields occurred at intermediate elevations with sufficient precipitation and mild temperatures.

3.3. Genotypic and Phenotypic Coefficients of Variations.
Most of the traits considered in this study had a high phenotypic and genotypic coefficient of variation (>20%) according to the categorization given by Deshmuk et al. [37] as low (<10%), moderate (10–20%), and high (>20%). The

combined analysis of variance over three locations revealed that the majority of traits showed a significant difference among locations and genotypes. Higher values of GCV were recorded from stem rust (55.9%) and yellow rust (38%), indicating that the traits are controlled by genetic factor, and hence, there is a higher chance of improvement of the crop through selection. Only stem rust (56.7%) and yellow rust (37.2%) showed moderate values of GCV (Table 8). The rest of the traits displayed lower-to-moderate values of GCV that ranged from 2.7% (days to maturity) to 10.7% (aboveground biomass). This study's result agrees with Ibrahim et al. [38], suggesting that there may also be some chance of improving traits with moderate GCV through phenotypic selection. However, the selection is practically impossible in traits with low genotypic coefficient of variation. Higher values of PCV were recorded by stem rust (68.7%), yellow rust (62.3%), aboveground biomass (23.5%), and grain yield (22.1%). Moderate values of PCV were shown by the major components of yield, whereas the growth (plant height) and phenological traits exhibited low value of PCV (Table 8). The traits that exhibited low estimates of GCV and PCV are difficult or virtually impractical to improve through selection due to the masking effect of environment on the genotypic effect [39]. In our study, the PCV values were also higher than the corresponding GCV values for all the traits. This indicates the observed variations between the genotypes for each trait were not only due to genotypic effect but also due to environmental influences.

3.4. Broad-Sense Heritability (h_b^2).
Estimates of heritability in broad sense (h_b^2) were calculated for all the traits studied. The value of heritability calculated for each trait was grouped into high heritability (>60%), moderate heritability (30–60%), and low heritability (<0–30%) as per the classification suggested by Robinson et al. [40]. Accordingly, high estimates of heritability were recorded only for stem rust (68%), whereas moderate heritability was obtained for spike length (49%), number of days to maturity (43%), number of

Table 4: Mean values for different agronomic traits for 15 treatments at Damot Gale site in 2019/2020.

Traits	DH	DM	PH	TNT	ENT	SL	SPS	SR	YR	ABM	GY	TSW	HI
ETBW8070	73bcde	110abcd	84.6ab	7.4abcd	6.7a	7.93abcd	42.1a	1.0ab	1.0ab	9.76abc	4.35abc	36.7abcd	44.7ab
Wane	74.7bcde	111.67bcde	84.6ab	7.2ab	7.1abc	7.1a	58.5d	1.7abc	1.7abc	11.34bcde	5.47cd	38.7cd	48.7b
Hidasse	68.33ab	105.3a	86.4bc	7.3abc	7abc	8abcd	41.6a	5.3e	2.2abc	12.1cde	5.14cd	34ab	42.45ab
Ogolcho	74cdef	110.7abcde	101.3gh	7.1ab	6.9ab	9.1de	41.53a	3.3d	4.5d	11.3bcde	4.49abc	40d	40.25a
Lemu	78efg	115de	92.23de	7.7abcd	7.5abcd	8.83cde	39.4a	1.0ab	1.0ab	11.91cde	4.98c	36.3abcd	41.8ab
Honqolo	79.67g	116.3e	89.53cd	8.5de	8.3de	7.8abcd	44.6a	1.83abc	2.2abc	7.48a	5.52c	34.7abc	74.14c
Alidoro	73bcde	113cde	102.97h	6.6a	6.5a	9.8e	52.27a	1.3ab	2.7bc	12.24cde	4.95c	34.7abc	40.2a
Danada'a	76efg	112.7cde	97.77fg	6.77a	7.97bcd	8.7cde	47.13a	1.3ab	1.0ab	10.87bcde	4.49abc	37bcd	41.11ab
Huluka	79fg	116de	95.77ef	8.4cde	7.13abcd	8.63cde	46a	1.0ab	2.7bc	7.67a	3.42a	33a	44.56ab
Galema	67a	107abc	81.3a	7.4abcd	7.1abc	7.5abc	55a	3.0cd	3.3cd	13.04e	6.25d	37.7bcd	48.29b
Hawi	69abc	105.33a	83.43ab	7.3abcd	7.1abc	8.53bcde	44.47a	2.3bcd	2.7bc	10.04abc	4.5abc	37.7bcd	44.75ab
Pavon-76	70abcd	107abc	92.2de	6.9a	6.93abc	8.7cde	41.93a	3.3d	2.2abc	8.96ab	3.57ab	35.7abcd	40.17a
Shorima	70abcd	107.33abc	95.6ef	8.3bcde	8.1cd	7.3ab	39.4a	1.8abc	1.83a	10.4bcd	4.66bc	37.67bcd	44.8ab
Hoggena	75.33efg	112bcde	91.9de	9.4e	9.2e	8.53bcde	42.67a	1.83a	2.3abc	12.9de	5.08cd	33a	39.4a
Biqa	69abc	106ab	93.6def	7.7abcd	7.5abcd	8.93de	47.4a	3.5d	2.0abc	11.45bcde	5.05cd	39cd	44.1ab
Range	67–79.67	105.3–116.3	81.3–102.97	6.6–9.4	6.5–9.2	7.1–9.8	39.4–58.5	1.0–5.3	1.0–4.5	7.48–13.04	3.42–6.25	33–40	39.4–74.14
Mean	73.07	110.4	91.55	7.61	7.36	8.36	45.6	2.18	2.14	10.8	4.795	36.38	45.27
LSD 5%	5.26	6.083	4.496	1.225	1.154	1.338	9.037	1.362	1.732	2.605	1.194	3.999	7.286
CV	4.3	3.3	2.9	9.6	9.4	9.6	11.8	37.4	48.3	14.5	14.9	6.6	9.6

DH—days to heading, DM—days to maturity, PH—plant height (cm), TNT—number of tillers/plant, ENT—number of effective tillers/plant, SL—spike length (cm), SPS—number of seeds/spike, SR—stem rust (scale), YR—yellow rust (scale), ABM—biomass yield (scale), ABM—biomass yield (t/ha), GY—grain yield (t/ha), TSW—thousand seed weight (g), HI—harvest index, and mean followed by the same letter(s) within a column is not significantly different from each other at 5%.

TABLE 5: Mean values for different agronomic traits for 15 treatments at Damot Sore site in 2019/2020.

Traits	DH	DM	PH	TNT	ENT	SL	SPS	SR	YR	ABM	GY	TSW	HI
ETBW8070	71.00abcde	102.00abcd	78.30abc	4.53ef	4.43de	7.700cde	36.73a	1.0ab	1.0ab	5.89de	2.63ab	37.3abc	44.74a
Wane	65.00a	96.67a	76.73abc	3.77ab	3.73ab	6.700a	46.73d	1.67abc	1.67abc	6.3bc	2.96abc	40.3abcde	47.05abc
Hidasse	68.00abc	99.00abc	76.37abc	4.2bcde	4.1bcd	7.5bcd	37.6ab	5.33e	2.17abc	6.9bc	3.45cd	44e	50.15bcd
Ogolcho	67.33abc	99.00abc	88.23d	4.03bcd	3.87abc	8.7fg	46.57bcd	3.33d	4.5d	6.78bc	3.85de	44e	58.1d
Lemu	67.67abc	99.67abcd	77.00abc	4.1bcde	4.03bcd	8.8fg	43.1bcd	1.0ab	1.0ab	6.4bc	3.23bcd	43de	50.4bcd
Honqolo	68.67abcd	99.abcd	76.27abc	3.97abc	3.93bcd	7.3abc	40.13ab	1.8abc	2.2abc	6.2b	3.1abc	39.3abcde	49.9bcd
Alidoro	72.00bcde	102.67bcd	90.97d	3.83abc	3.8ab	9.4g	47.2d	1.33ab	2.67bc	9.1e	4.333e	42cde	47.99abc
Danada'a	75.67e	104.67cd	89.73d	3.53a	3.4a	8.1def	43.6bcd	1.33ab	1.0ab	7.1bcd	3.34bcd	41.3bcde	46.73abc
Huluka	65.33de	105.33d	86.23d	4.47def	4.4de	8.2def	43.6bcd	1.0ab	2.67bc	7.4cde	3.29bcd	36.4ab	44.88abc
Galema	65.00a	96.67a	73.80a	4.13def	4.1de	6.9ab	42.2abcd	3.0cd	3.33cd	5.98b	3.15bcd	38.3abcd	52.7cd
Hawi	66.00ab	97.67ab	74.97abc	4.17bcde	4.13bcde	7.9ef	44.3cd	2.33bcd	2.67bc	6.1b	2.95abc	40.4abcde	48.7bc
Pavon-76	65.00a	97.67ab	79.77c	4.67f	4.63e	8.2def	42.5abcd	3.33d	2.17abc	6.34bc	3.35bcd	38abc	52.6cd
Shorima	66.67ab	98.00ab	79.00bc	4.27cdef	4.33cde	8.8fg	42.5abcd	1.83abc	1.83a	6.8bc	2.92cde	40abcde	42.7ab
Hoggena	74.00cde	104.00cd	74.07ab	3.97abc	3.97bcd	7.5bcd	36.9a	1.83a	2.33abc	4.6a	2.39a	36.3a	51.8cd
Biqa	65.00a	97.00ab	74.83abc	3.93abc	3.93bcd	8.3ef	42.03abcd	3.5d	2abc	5.99b	3abc	40.3abcde	50.2bcd
Range	65–75.67	96.67–105.33	73.8–90.97	3.53–4.67	3.4–4.63	6.7–9.4	36.73–47.2	1.0–5.33	1.0–4.5	4.6–9.1	2.39–4.33	36.3–44	42.7–58.1
Mean	68.82	99.98	79.75	4.1	4.05	8.01	42.37	2.18	2.14	6.523	3.196	40.11	49.24
LSD 5%	6.89	5.727	5.12	0.4453	0.5074	0.743	6.122	1.362	1.732	1.367	0.7222	4.7	7.264
CV	6	3.4	3.8	6.5	7.5	5.5	8.6	37.4	48.3	12.5	13.5	7	8.8

DH—days to heading, DM—days to maturity, PH—plant height (cm), TNT-number of tillers/plant, ENT—number of effective tillers/plant, SL—spike length (cm), SPS—number of seeds/spike, SR—stem rust (scale), YR—yellow rust (scale), ABM—biomass yield (t/ha), GY—grain yield (t/ha), TSW—thousand seed weight (g), HI—harvest index, and mean followed by the same letter(s) within a column is not significantly different from each other at 5%.

TABLE 6: Mean values for different agronomic traits for 15 treatments at Kechi site in 2019/2020.

Traits	DH	DM	PH	TT	Et	SL	SPS	SR	YR	ABM	GY	TSW	HI
ETBW8070	80bcd	129.7bc	92.87bc	6.03e	5.73f	8.33ab	54.33bcd	1.67a	1.0a	10.53bc	3.59def	39abcd	34.25ab
Wane	77.67abcd	127abc	96.67bcde	5.07cd	4.83cde	7.77a	47.87abc	2.5bcde	1.67def	7.69a	2.74abc	48.33ef	35.44abcd
Hidasse	75ab	124ab	98.33cde	5.3cd	5cde	8.87bcd	54.93cd	5.0h	2.33f	7.99a	3.34cdef	42.67cde	41.91bcdef
Ogolcho	77.67abcd	126.7bc	108.83f	5cd	4.7cd	9.03bcd	51.21abc	4.17fgh	2.33f	7.7a	3.31bcde	46.33def	43.05def
Lemu	80.33d	130.3c	94.10bcd	5.57de	5.4def	9.34cde	52.87bcd	2.0abcde	1.33cde	7.5a	3.37cdef	36.33abc	44.63ef
Honqolo	80bcd	129.3bc	86.57a	5.23cd	4.87cde	9.13bcd	55.33cd	2.67cdef	2.0ef	7.54a	3.35cdef	37.67abc	44.52ef
Alidoro	81.33d	130.7d	101.7e	4.97cd	4.63bc	10.05e	46.8ab	1.67abcd	1.0bcd	11.9c	4.33g	51f	37.47abcde
Danada'a	76abc	125abc	95.63bcde	6.23e	5.5ef	9.07bcd	60.6d	3.17defg	2.0ef	12.03c	4.05fg	39.33abcd	34.45abc
Huluka	88.67e	138.7d	96.47bcde	5cd	4.93cde	9.67de	51.6abc	1.17abc	1.67abc	8.03a	3.12abcde	34ab	39.08abcdef
Galema	75ab	124ab	95.23bcd	4.83bc	4.77cd	7.64a	44a	2.0abcde	1.0bcd	8.42ab	3.68efg	42.67cde	45.56f
Hawi	74a	123a	95.83bcde	5.07cd	4.6abc	8.49abc	51.4abc	3.33efg	1.67def	7a	2.79abc	40abcd	39.94abcdef
Pavon-76	75.33abc	124.3ab	99de	4.2ab	3.97ab	9.3cde	52.67bcd	3.33efg	2.0ef	6.43a	2.45a	34.33ab	38.93abcdef
Shorima	76abc	125abc	99.27de	5.1cd	4.9cde	9.44de	49.53abc	1.33abc	1.33ab	7.08a	2.99abcde	38.33abc	42.45cdef
Hoggena	80bcd	129.7bc	91.1ab	4a	3.9a	8.93bcd	46.73ab	1.0ab	1.33ab	7.87a	2.6ab	32.67a	33.06a
Biqa	76abc	125abc	97.27cde	4.7bc	4.37abc	9.25cde	53.3bcd	4.33g	2.0ef	7.13a	2.88abcd	40.67abcdef	40.76abcdef
Range	74–88.67	123–138.7	86.57–108.8	4–6.23	3.9–5.73	7.64–10.05	44–60.6	1.0–5.0	1.0–2.33	6.43–12.03	2.45–4.33	32.67–51	33.06–45.56
Mean	78.2	127.49	96.59	5.1	4.8	9	51.6	2.6	1.4	8.3	3.24	40.22	39.7
LSD 5%	5.189	5.7	6.089	0.671	0.702	0.866	8.027	1.703	0.909	2.431	0.74	7.946	8.066
CV	4	2.7	3.8	7.9	8.7	5.8	9.3	35.5	40	17.5	13.7	11.8	12.1

DH—days to heading, DM—days to maturity, PH—plant height (cm), TNT—number of tillers/plant, ENT—number of effective tillers/plant, SL—spike length (cm), SPS—number of seeds/spike, SR—stem rust (scale), YR—yellow rust (scale), ABM—biomass yield (t/ha), GY—grain yield (t/ha), TSW—thousand seed weight (g), HI—harvest index, and mean within followed by the same letter(s) within a column is not significantly different from each other at 5%.

Table 7: Mean values for different agronomic traits for 15 treatments over location in 2019/2020.

Traits	DH	DM	PH	TNT	ENT	SL	SPS	SR	YR	ABM	GY	TSW	HI
ETBW8070	74.67def	113.9cde	85.27abc	6e	5.622bcde	8abc	44.38abc	1.9a	1.7a	8.729cde	3.527abcd	37.7bcd	41.22ab
Wane	72.44bcd	111.8abcd	86abcd	5.333ab	5.211abcd	7abcd	51.01e	1.9bc	1.7bcd	8.444bcd	3.722bcd	42.4efg	43.6abc
Hidasse	70.44abc	109.4ab	87.03bcd	5.589abcde	5.37abcde	8.1bcd	44.71abc	5.2g	2.2de	8.999cde	3.979de	40.2defg	44.84abcd
Ogolcho	73cde	112.1bcd	99.46i	5.389abc	5.144ab	8.9i	46.4abcd	3.6ef	3.8f	8.596cd	3.886cde	43.4g	47.14cd
Lemu	75.33def	115cde	87.78cde	5.789bcde	5.656cde	9cde	45.1abc	1.3ab	1.1ab	8.608cd	3.858cde	38.6cd	45.61bcd
Honqolo	76.11ef	115.1de	84.12ab	5.911de	5.689de	8.1ab	46.7bcde	2.1bc	2.1cde	7.066a	4de	37.2abcd	56.19e
Alidoro	75.4ef	115.4e	98.54i	5.144a	4.978a	9.7i	48.74cde	1.4ab	2.1cde	11.068f	4.54f	42.6fg	41.9ab
Danada'a	75.9ef	114.1cde	94.38h	5.511abcde	5.144ab	8.6g	50.4de	1.9bc	1.3abc	7.688abc	3.961de	36.2cde	40.76a
Huluka	81e	120f	92.82gh	5.956de	5.767e	8.8gh	47.1bcde	1.1a	2cde	9.147de	3.277ab	34.6ab	42.84abc
Galema	69a	109.2ab	83.44a	5.456abcd	5.33abcde	7.4a	47.1bcde	2.7cd	2.6e	7.713abc	4.36ef	39.6def	48.9d
Hawi	69.67ab	108.7a	84.74abc	5.522abcde	5.27abcde	8.3abc	46.7bcde	2.8cde	2.33de	7.241ab	3.414abc	39.4def	44.46abcd
Pavon-76	70.11abc	109.7ab	90.32efg	5.267a	5.178abc	8.7efg	45.7abc	3.3def	2.1cde	8.104abcd	3.12a	36abc	43.9abc
Shorima	70.89abc	110.1ab	91.29fgh	5.9cde	5.767e	8.5fgh	43.81ab	1.7ab	1.7a	8.451bcd	3.522abcd	38.7cd	43.3abc
Hoggena	76.44f	115.2de	85.69abcd	5.789bcde	5.7de	8abcd	42.1a	1.9a	1.7bcd	8.451bcd	3.354abc	34a	41.4ab
Biqa	70abc	109.3ab	88.57def	5.456abcd	5.27abcde	8.8def	47.8bcde	3.8f	2cde	8.19abcd	3.642abcd	40def	45abcd
Range	69–81	108.7–120	83.44–99.46	5.144–6.0	4.978–5.767	7.2–9.7	42.1–51.01	1.0–5.2	1.0–3.8	7.07–11.068	3.12–4.54	34–43.4	40.76–56.19
Mean	73.36	112.6	89.3	5.6	5.41	8.44	46.5	2.3	1.9	8.5	3.5	38.9	44.7
LSD 5%	3.239	3.25	3.198	0.511	0.505	0.583	4.391	0.8782	0.8452	1.313	0.531	3.26	4.479
CV	4.7	3.1	3.8	9.7	10	7.4	10.1	40.5	47.8	16.4	15.2	8.9	10.7

DH—days to heading, DM—days to maturity, PH—plant height (cm), TNT—number of tillers/plant, ENT—number of effective tillers/plant, SL—spike length (cm), SPS—number of seeds/spike, SR—stem rust (scale), YR—yellow rust (scale), ABM—biomass yield (t/ha), GY—grain yield (t/ha), TSW—thousand seed weight (g), HI—harvest index, and mean within followed by the same letter(s) within a column is not significantly different from each other at 5%.

TABLE 8: Estimates of variance components calculated from the combined data over location.

Traits	Mean	$\delta^2 e$	MSgxl	$\delta^2 g$	$\delta^2 g\, l$	$\delta^2 p$	PCV (%)	GCV (%)	h_b^2 (%)	GA	GAM (%)
DH	73.4	12.0	15.8	10.2	1.3	23.5	6.6	4.4	0.43	4.3	5.9
DM	112.6	12.0	12.4	9.3	0.1	21.4	4.1	2.7	0.43	4.1	3.7
PH	89.3	11.7	38.5	24.5	8.9	45.1	7.5	5.5	0.54	7.5	8.4
TNT	5.6	0.3	1.2	0.0	0.3	0.6	14.3	3.6	0.06	0.1	1.8
ENT	5.4	0.3	1.1	0.0	0.3	0.6	14.8	3.7	0.06	0.1	1.9
SL	8.4	0.4	0.4	0.4	0.0	0.8	10.7	7.5	0.49	0.9	10.9
SPS	46.5	21.9	65.4	3.3	14.5	39.7	13.6	3.9	0.08	1.1	2.3
SR	2.3	0.9	0.6	1.7	−0.1	2.5	68.7	56.7	0.68	2.2	96.3
YR	1.9	0.8	1.1	0.5	0.1	1.4	62.3	37.2	0.36	0.9	45.8
ABM	8.5	2.0	5.6	0.8	1.2	4.0	23.5	10.5	0.20	0.8	9.7
GY	3.5	0.3	0.8	0.1	0.2	0.6	22.1	9.0	0.17	0.3	7.6
TSW	38.9	12.1	23.9	6.2	3.9	22.2	12.1	6.4	0.28	2.7	7.0
HI	44.7	22.9	87.2	12.4	21.4	56.7	16.8	7.9	0.22	3.4	7.6

$\delta^2 g$ = genotypic variance, $\delta^2 p$ = phenotypic variance, $\delta^2 e$ = environmental variance, GVC = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, DH = days to heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), SPS = number of seeds spike^{-1}, TNT = number of tillers plant^{-1}, ENT = number of effective tillers plant^{-1}, SR = stem rust (scale), YR = yellow rust (scale), GY = grain yield (t/ha), ABM = biomass yield (t/ha), HI = harvest index, TSW = thousand seed weight (g).

TABLE 9: Estimates of variance components at Damot Gale experimental site.

Traits	Mean	$\delta^2 g$	$\delta^2 p$	$\delta^2 e$	GCV (%)	PCV (%)	h_b^2 (%)	GA	GAM (%)
DH	73.70	13.22	23.11	9.89	4.93	6.52	0.57	5.67	7.69
DM	110.40	10.39	23.62	13.23	2.92	4.40	0.44	4.40	3.99
PH	91.55	40.53	47.76	7.23	6.95	7.55	0.85	12.08	13.20
TNT	7.61	0.39	0.93	0.54	8.24	12.70	0.42	0.84	11.02
ENT	7.36	0.40	0.88	0.48	8.59	12.75	0.45	0.88	11.93
SL	8.36	0.33	0.97	0.64	6.91	11.80	0.34	0.70	8.33
SPS	45.60	22.56	51.75	29.19	10.42	15.78	0.44	6.46	14.17
SR	2.18	1.42	2.08	0.66	54.66	66.16	0.68	2.03	93.04
YR	2.14	0.62	1.69	1.07	36.89	60.81	0.37	0.99	46.11
ABM	10.76	2.14	4.57	2.43	13.60	19.87	0.47	2.06	19.17
GY	4.80	0.35	0.86	0.51	12.33	19.32	0.41	0.78	16.20
TSW	36.38	2.89	8.61	5.72	4.68	8.07	0.34	2.03	5.58
HI	45.27	65.32	84.29	18.97	17.85	20.28	0.77	14.66	32.38

TABLE 10: Estimates of variance components at Damot Sore experimental site.

Traits	Mean	$\delta^2 g$	$\delta^2 p$	$\delta^2 e$	GCV (%)	PCV (%)	h_b^2 (%)	GA	GAM (%)
DH	68.82	9.07	26.04	16.97	4.38	7.41	0.35	3.66	5.32
DM	99.98	5.07	16.80	11.73	2.25	4.10	0.30	2.55	2.55
PH	79.75	32.39	41.76	9.37	7.14	8.10	0.78	10.33	12.95
TNT	4.10	0.07	0.14	0.07	6.45	9.13	0.50	0.39	9.40
ENT	4.05	0.07	0.16	0.09	6.53	9.88	0.44	0.36	8.90
SL	8.01	0.49	0.69	0.20	8.74	10.37	0.71	1.22	15.17
SPS	42.37	6.70	20.10	13.40	6.11	10.58	0.33	3.08	7.27
SR	2.18	1.42	2.08	0.66	54.66	66.16	0.68	2.03	93.04
YR	2.14	0.62	1.69	1.07	36.79	60.75	0.37	0.98	45.91
ABM	6.52	0.69	1.36	0.67	12.74	17.89	0.51	1.22	18.69
GY	3.20	0.16	0.35	0.19	12.50	18.49	0.46	0.56	17.41
TSW	40.11	3.52	11.42	7.90	4.68	8.43	0.31	2.15	5.35
HI	49.24	8.52	27.38	18.86	5.93	10.63	0.31	3.35	6.81

days to heading (43%), yellow rust (36%), and plant height (51%) (Table 8). Studies conducted by Gergana and Bozhidar [41] showed high heritability values for spike length. Singh [39] stated that for a character with high heritability (≥80%), the selection is fairly easy, because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environmental factors to the expression of the phenotype. However, very low

TABLE 11: Estimates of variance components at Kechi experimental site.

Traits	Mean	$\delta^2 g$	$\delta^2 p$	$\delta^2 e$	GCV (%)	PCV (%)	h_b^2 (%)	GA	GAM (%)
DH	78.20	10.73	20.35	9.62	4.19	5.77	0.53	4.90	6.27
DM	127.49	12.60	24.21	11.61	2.78	3.86	0.52	5.28	4.14
PH	96.59	20.33	33.59	13.26	4.67	6.00	0.61	7.23	7.48
TNT	5.09	0.33	0.49	0.16	11.29	13.75	0.67	0.97	19.08
ENT	4.81	0.20	0.38	0.18	9.30	12.82	0.53	0.67	13.90
SL	8.95	0.35	0.62	0.27	6.61	8.80	0.56	0.92	10.23
SPS	51.55	9.61	32.65	23.04	6.01	11.08	0.29	3.46	6.72
SR	2.60	1.47	2.51	1.04	46.63	60.93	0.59	1.91	73.51
YR	1.38	0.50	0.80	0.30	51.24	64.81	0.63	1.15	83.45
ABM	8.32	2.31	4.42	2.11	18.27	25.27	0.52	2.26	27.20
GY	3.24	0.22	0.42	0.20	14.48	20.00	0.52	0.70	21.58
TSW	40.22	20.30	42.87	22.57	11.20	16.28	0.47	6.39	15.88
HI	39.70	8.83	32.09	23.26	7.48	14.27	0.28	3.21	8.09

$\delta^2 g$ = genotypic variance, $\delta^2 p$ = phenotypic variance, $\delta^2 e$ = environmental variance, GVC = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, DH = days to heading, DM = days to maturity, PH = plant height (cm), SL = spike length (cm), SPS = number of seeds spike^{-1}, TNT = number of tillers plant^{-1}, ENT = number of effective tillers plant^{-1}, SR = stem rust (scale), YR = yellow rust (scale), GY = grain yield (t/ha), ABM = biomass yield (t/ha), HI = harvest index, TSW = thousand seed weight (g).

heritability estimates were recorded for number of seeds spike^{-1} (8%), total number of tillers plant^{-1} (6%), and effective number of tillers plant^{-1} (6%) (Table 8).

3.5. Genetic Advance. It is important to find out the genetic gains likely to be achieved in the next generation that is classified as high (>20%), medium (10 to 20%), and low (<10%) as suggested by Johnson et al. [24]. The genetic advance as percent of means (GAM) expressed ranged from 2.55% (number of days to maturity) to 93.04% (stem rust) at Damot Gale and Damot Sore sites, respectively (Tables 9–11). This refers to the improvement of the traits in genotypic value for the new population compared with the base population in one cycle of selection that is within the range of 2.55% (for number of days to maturity) to 93.04% (stem rust resistance) at 5% selection intensity.

High heritability (h_b^2) accompanied by high genetic advance as percent of means (GAM) was exhibited from stem rust (68%, 96.3%) and moderate h_b^2 accompanied by high GAM was obtained from yellow rust (36%, 45.8%), respectively. In addition, spike length (49%, 10.9%) exhibited moderate heritability (h_b^2) and moderate genetic advance as percent of means (GAM), respectively (Table 8). Gezahegn et al. [42] also reported that high heritability coupled with moderate GAM for spike length (63.66%, 10.34%), which was in line with this study.

Even though heritability estimates provide the basis for the success of selection on the phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously, since high heritability alone will not always be associated with high genetic advance [24]. The estimates of GA help in understanding the type of gene action involved in the expression of various polygenic traits. High values of genetic advance are indicative of the involvement of additive gene action, whereas low values are indicative of nonadditive gene action [43]. Thus, the heritability estimates will be reliable if accompanied by a high genetic advance.

4. Conclusion and Suggestions

The research results indicated the presence of significant variations among bread wheat genotypes for yield and yield-related traits. This variability can potentially be exploited in future improvement of bread wheat breeding programs. However, it was evident that cultivar "Alidoro" showed outstanding performance in terms of grain yield and other components of yield including resistance to both stem and yellow rust diseases. Hence, we recommend cultivar "Alidoro" for wider cultivation across Wolaita and Dawuro zones and similar agroecologies.

Data Availability

All the necessary data are included in the manuscript. If additional data are required, the corresponding author can be contacted.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

References

[1] R. Bousba, B. Michael, D. Abdelhamid et al., "Screening for drought tolerance using molecular markers and phenotypic diversity in durum wheat accessions," World Applied Sciences Journal, vol. 16, no. 9, pp. 1219–1226, 2012.

[2] R. B. Belderok, H. Mesdag, and A. D. Donner, Bread-Making Quality of Wheat, Springer, Berlin, Germany, 2000.

[3] J. D. Mauseth, "Perhaps the simplest of fruits are those of grasses (all cereals such as corn and wheat): these fruits are caryopses," *Botany*, Jones and Bartlett Publishers, Burlington, MA, USA, 2014.

[4] P. R. Shewry, "Wheat," *Journal of Experimental Botany*, vol. 60, no. 6, pp. 1537–1553, 2009.

[5] J. Peng, D. Sun, and E. Nevo, "Wild emmer wheat, *Triticum dicoccoides*, occupies a pivotal position in wheat domestication," *Agricultural Journal of Crop Science*, vol. 5, pp. 1127–1143, 2011.

[6] FAO, "Food and agriculture organization of the united nations)," *FAO Cereal Supply and Demand*, FAO, Rome, Italy, 2019.

[7] A. M. Allen, M. O. Winfield, A. J. Burridge et al., "Characterization of a wheat breeders' array suitable for high-throughput SNP genotyping of global accessions of hexaploids bread wheat (*Triticum aestivum*)," *Plant Biotechnology Journal*, vol. 15, no. 3, pp. 390–401, 2017.

[8] Faostat, *Food and Agriculture Organization of the United Nations. Provisional, 2016 Production and Production Indices Data*, Crop Primary, Rome, Italy, 2018.

[9] CSA (Central Statistical Authority of Ethiopia), *Report on Area and Production of Major Crops, Private Peasant Holdings*, Meher Season, Addis Ababa, Ethiopia, 2016.

[10] E. Acevedo, P. Silva, and H. Silva, "Bread wheat production and improvement. wheat in the world," in *Curtis: FAO Plant Production and Protection Series*FAO, Rome, Italy, 2002.

[11] M. Kamali, "Review on wheat status in the past, present and future," in *Proceedings of the 10th Conference on Sciences of Breeding*, pp. 23–45, Yezin, Iran, April 2008.

[12] H. K. Bekele, H. Varkuijl, W. Mwangi, and D. G. Tanner, *Adaptation of Improved Wheat Technologies in Adaba and Dodola Woredas of the Bale Highlands, Ethiopia*, Mexico D.F: International Maize and Wheat Improvement Centre (CIMMYT) and Ethiopian Agricultural Research Organization (EARO), Addis Ababa, Ethiopia, 2000.

[13] R. Ortiz, R. Trethowan, G. O. Ferrara et al., "High yield potential, shuttle breeding, genetic diversity, and a new international wheat improvement strategy," *Euphytica*, vol. 157, pp. 365–384, 2007.

[14] H. J. Dubin and J. P. Brennan, *Combating Stem and Leaf Rust of Wheat Historical Perspective, Impacts, and Lessons Learned*, International Food Policy Research Institute, Washington, DC, USA, 2009.

[15] G. Desheva and B. Kyosev, "Genetic diversity assessment of common winter wheat (*Triticum aestivum* L.) genotypes," *Emirates Journal of Food and Agriculture*, vol. 27, no. 3, p. 283, 2015.

[16] USDA, "United states department of agriculture," *World Agricultural Production*, vol. 22, p. 3, 2016.

[17] E. Hailu and G. Woldeab, "Survey of rust and septoria leaf blotch diseases of wheat in central Ethiopia and virulence diversity of stem rust *Puccinia graminis* f.sp. *tritici*," *Advances in Crop Science and Technology*, vol. 3, p. 166, 2015.

[18] Z. Kadi, F. Adje, and H. Bouzerzour, "Analysis of the genotype by environment interaction of barley grain yield (*Hordeum vulgare* L.) under semi-arid conditions," *Advances in Environmental Biology*, vol. 4, no. 1, pp. 34–40, 2010.

[19] H. S. Bariana, H. Miah, G. N. Brown, N. Willey, and A. Lehmensiek, "Molecular mapping of implication in breeding," in *Proceedings of the Proceedings of the 7th International Wheat Conference*, H. T. buck, J. E. Nisi, and N. salomon, Eds., Springer, Mar Del plata, Argentina, December 2007.

[20] K. A. Gomez and A. A. Gomez, *Statistical Procedures for Agricultural Research*, John Wiley & Sons, New York, NY, USA, 2nd edition, 1984.

[21] R. K. Singh and B. D. Choudhary, *Biometrical Methods in Quantitative Genetics Analysis*, Kalyani Publishers, New Delhi, India, 1996.

[22] G. W. Burton and E. H. Devence, "Estimating heritability in tall fenscue (*Festeca arundinaceae*) from replicated clonally material," *Agronomic Journal*, vol. 45, pp. 478–481, 1953.

[23] R. W. Allard, *Principles of Plant Breeding*, John Wiley & Sons, New York, NY, USA, 1960.

[24] H. W. Johnson, H. F. Robinson, and R. E. Comstock, "Genotypic and phenotypic correlations and their implication in selection," *Agronomic Journal*, vol. 47, pp. 477–483, 1955.

[25] D. S. Falconer and T. F. C. Mackay, *Introduction to Quantitative Genetics*, Longman Group Limited, Kuala Lumpur, Malaysia, 4th edition, 1996.

[26] D. A. N. Majumder, A. K. M. Shamsuddin, M. A. Kabir, and L. Hassan, "Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat," *Journal of the Bangladesh Agricultural University*, vol. 6, no. 2, pp. 227–234, 2008.

[27] B. H. Ayele, "Breeding wheat with multiple disease resistance and high yield for the Ethiopian highlands: broadening the genetic basis of yellow rust and tan spot resistance," Doctoral Dissertation, Cuvlier Verlag Gottingen, Göttingen, Germany, 2020.

[28] N. Desalegn and K. C. Dinesh, "Variability, heritability and genetic advances in wheat (*Triticum aestivum* L) breeding lines grown at horro guduru wollega zone, western Ethiopia," *International Journal of Advanced Scientific Research and Management*, vol. 1, no. 1, p. 25, 2016.

[29] Y. Kaya and M. Akcura, "Effects of genotype and environment on grain yield and quality traits in bread wheat (*T. aestivum* L.)," *Food Science and Technology*, vol. 34, no. 2, pp. 386–393, 2014.

[30] M. Birhanu, A. Sentayehu, A. Alemayehu, A. Ermias, and D. Dargicho, "Genetic variability, heritability and genetic advance for yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes," *Global Journal Of Science Frontier Research: D. Agriculture and Veterinary*, vol. 16, no. 7, pp. 975–5896, 2016.

[31] V. Mollasadeghi, S. Elyasi, and B. Mirzamasoumzadeh, "Genetic variation of 12 bread wheat genotypes based on number of phonological and morphological traits," *Annals of Biological Research*, vol. 3, no. 10, pp. 4734–4740, 2012.

[32] M. I. Ullah, S. Mahpara, R. Bibi et al., "Grain yield and correlated traits of bread wheat lines: implications for yield improvement," *Saudi Journal of Biological Sciences*, vol. 28, no. 10, pp. 5714–5719, 2021.

[33] G. Bekele, E. Ayana, M. Seyoum, S. Feyera, and T. Degefa, *Best Fit Practice Manual for Wheat Production in Central Oromia*BFM_AAU, Umarpada, India, 2015.

[34] N. Muhder, M. K. Gessese, and Z. Sorsa, "Assessment of genetic variability among agronomic traits and grain protein content of elite bread wheat (*Triticum aestivum* L.) genotypes in the central highlands of Ethiopia," *Asian Journal of Agricultural Research*, vol. 14, pp. 1–12, 2020.

[35] H. S. Bariana, "Breeding for disease resistance," in *Encyclopedia of Applied Plant Sciences*, B. Thomas, D. J. Murphy, and B. G. Murray, Eds., pp. 244–253, Academic Press, Harcourt, Nigeria, 2003.

[36] M. Allison, R. A. Thomson, S. J. Brown et al., "Elevation dependence of winter wheat production in eastern 61

Washington state with climate change," *A Methodological Study*, vol. 54, no. 1-2, pp. 141–164, 2002.

[37] S. N. Deshmuk, M. S. Basu, and P. S. Reddy, "Genetic variability character association and path coefficient analysis of quantitative traits in virgina bunch varieties in plant breeding," *Indian Journal of Agricultural Sciences*, vol. 56, pp. 816–821, 1986.

[38] H. Ibrahim, M. Shailesh, and G. M. Lal, "Inter-relationship studies among grain yield and its component traits in wheat," *Journal of Pharmacognosy and Phytochemistry*, vol. 6, no. 4, pp. 186–191, 2017.

[39] B. D. Singh, *Plant Breeding*, Kalyani Publishers, New Delhi, India, 1990.

[40] H. Robinson, R. Comstock, and P. Harvey, "Estimates of heritability and the degree of dominance in corn," *Agronomy Journal*, vol. 41, pp. 353–359, 1949.

[41] D. Gergana and K. Bozhidar, "Study on variability, heritability, genetic advance and associations among traits in emmer wheat genotypes (*Triticum dicoccon Schrank*)," *Journal of Biological Science and Biotechnology*, pp. 221–228, 2015.

[42] F. Gezahegn, A. Sentayehu, and T. Zerihun, "Genetic variability studies in bread wheat (*Triticum aestivum L.*) genotypes at kulumsa agricultural research center, south east Ethiopia," *Journal of Biology, Agriculture and Healthcare*, vol. 5, pp. 2224–3208, 2016.

[43] P. Singh and S. S. Narayanan, *Biometrical Techniques in Plant Breeding*, Kalyani Publishers, New Delhi, India, 1993.