

Genetic Variability of Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes under Irrigation Condition in South Omo, Southern Ethiopia

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Abstract: Bread wheat (*Triticum aestivum* L.), is a self-pollinating annual plant in the true grass family Gramineae (Poaceae), and is the largest cereal crop extensively grown as staple food source in the world. The objective of this study was to assess the genetic variability and genetic diversity among genotypes using a triple lattice design in Bena-Tsema district in 2020 under irrigation conditions. The analysis of variance revealed highly significant variation ($P \leq 0.01$) among the genotypes for yield and yield components. Wide ranges of the mean values were observed for most of the traits like grain yield, plant height, days to maturity, and grain filling period, indicating the existence of variations among the tested genotypes. Moderate Phenotypic coefficient of variability and genotypic coefficient of variability was recorded for days to maturity, grain yield, and harvest index; while high heritability values were observed for plant height and days to heading. Among the studied characters grain yield showed high genetic advance. The D^2 analysis grouped the 36 genotypes into six clusters. The maximum inter-cluster distance was observed between clusters V and VI ($D^2=777.99$), followed by that between clusters III and V ($D^2=525.49$) and I and III ($D^2=310.81$), which showed that the genotypes included in these clusters are genetically more divergent from each other than those in any other clusters. Principal components (PC1 to PC6) having Eigen value greater than one, accounted for 75.6% of the total variation. The first three principal components, i.e., PC1, PC2, and PC3, with values of 22.0, 35.7, and 47.9, respectively, contributed more to the total variation. Generally, the results of this study showed the presence of variations among the studied genotypes for agro-morphology traits that could allow selection and/or hybridization of genotypes.

Keywords: Genetic advance, GCV, Heritability, PCV



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1. Introduction

Bread wheat (*Triticum aestivum* L.), a self-pollinating annual plant in the true grass family Gramineae (Poaceae), is the largest cereal crop extensively grown as staple food source in the world (Mollasadeghi and Shahryari, 2011). It is one of the most important exports and strategic cereal crops in the world and in Ethiopia in terms of production and utilization. Ethiopia is the first largest wheat producer in Sub-Saharan Africa followed by South Africa and fourth in Africa with the harvested area of 1.8 million hectares with a production of 5.3 million tons and an average yield of 2.97 t ha⁻¹ (CSA, 2021). The narrow genetic background has rendered improved varieties

less tolerant to biotic and abiotic stresses (Maqbool *et al.*, 2010).

Reduction in genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes (Aremu, 2012). Therefore, precise information on the nature and degree of genetic variability and divergence present in wheat would help to select parents for evolving superior varieties. For a successful breeding program, the presence of genetic variability plays a vital role. It is true that the more diverse plants, the greater chance of exploiting to generate productive recombinants and broad variability in segregating generations during genetic improvement (Mohammadi and Prasanna, 2003). From 1974 to 2011, the country's research efforts

resulted in the development of more than 87 bread wheat varieties: thirty varieties from 1974 to 1997 (Degewione and Alamerew, 2013), and fifty-seven varieties from 1998 to 2011, with some of them in production in various agro-ecological zones. Significant genetic variability was reported in bread wheat (Tarekegne *et al.*, 1994; Degewione *et al.*, 2013). Previous research has shown that in the study area, little information is generated about the genetic variability of yield and yield component attributes of bread wheat genotypes under irrigation. Thus, the present study was conducted to assess the extent of genetic variability of yield and yield-related traits of bread wheat genotypes under irrigation conditions.

2. Materials and Methods

2.1. Description of the study area

The genotypes were tested at Bena-Tsema Weyito Nasa Agricultural-Farm in 2019/2020 E.C. The experimental site has an altitude of 550 m a.s.l. with an annual rainfall of 750 mm with an average minimum and maximum temperature of 22 °C and 32°C, respectively. The soil type of the site is classified as vertisol and the textural class of the experimental area is sandy loam soil with a pH of 7.9-8.1 (Haileslassie *et al.*, 2015).

2.2. Experimental materials

The experimental materials consisted of 36 bread wheat (*Triticum aestivum*) genotypes including nine standard checks (Fentale, ADEL-2, Fentale-2, Atila-7, GAMBO, Amibara, Amibara-2, LUCY, and Kakaba). The genotypes were obtained from the National Wheat Research Program, specifically from Werer (WARC) Agricultural Research Center. The genotypes were selected based on adaptation to heat stress and classified under lowland type.

2.3. Experimental design and trial management

The experiment was carried out in a 6 x 6 triple Lattice design comprising six incomplete blocks where each block contains 6 test entries and 4 checks (randomly allocated) with a total of 36 genotypes in each block. The genotypes were grown under irrigation conditions. Each genotype was sown in six rows of 1.8 m long and 30 cm apart, with a seed rate of 7.5g, 120 kg/h. Weeds were controlled manually by hand weeding. Planting was done by hand drilling on July 05, 2011, EC. Recommended fertilizer rate of

100kg/ha NPSB in (19% N, 38%P: 7% S, and 2.5% B) at the rate of 50 kg ha⁻¹ in the shallow furrow depths and mixed with soil at the same time during sowing.

2.4. Statistical analysis

2.4.1. Analysis of variance

The analysis of variance (ANOVA) was carried out to dissect total variability of the entries into sources attributable to genotype and error using the SAS software version (9.2) (SAS, 2008). The statistical model for the augmented design was the same as that of the randomized complete block design (Federer, 1956) as indicated below [1].

$$y_{ij} = \mu + g_i + c_j + \beta_j + \varepsilon_{ij} \quad [1]$$

Where

- y_{ij} = observation of treatment i in j th block
- μ = general mean,
- g = effect of test treatment,
- c_j = effect of control treatments in a j th block
- β_j = block effects
- ε = error

2.4.2. Estimation of variance components

The phenotypic, genotypic, and environmental variances were calculated as indicated below.

$$\sigma^2 p = \sigma^2 g + \sigma^2 e \quad [2]$$

Where

- $\sigma^2 p$ = phenotype variance
- $\sigma^2 g$ = genotypic variance
- $\sigma^2 e$ = environmental variance

$$\sigma^2 g = \frac{[Msg - Mse]}{r} \quad [3]$$

Where

- $\sigma^2 g$ = genotypic variance
- MTS = MST mean square treatment
- $\sigma^2 e$ = environmental variance
- Msg = mean square of genotype,
- Mse = mean square of error,
- r = number of replications

$$PCV = \left(\frac{(\sigma^2 p)}{\bar{x}} \right) * 100 \quad [4]$$

$$GCV = \left(\frac{(\sigma^2 g)}{\bar{x}} \right) * 100 \quad [5]$$

Where

- $\bar{x}$ = Grand mean of the character studied
- PCV = phenotypic coefficient of variability
- GCV = genotypic coefficient of variability

PCV and GCV values were categorized as low (0-10), moderate (10-20), and high (>20) as indicated by Burton and de vane (1953).

2.5. Broad sense heritability

Broad sense heritability (H^2B) for all characters was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage [6] according to the methods suggested by Falconer *et al.* (1996).

$$H^2B = \left(\frac{\sigma^2_g}{\sigma^2_p} \right) * 100 \quad [6]$$

Broad sense heritability values were categorized as High (>60%), Moderate (30-60%), and Low (0-30%) as described by Johnson *et al.* (1955).

2.6. Genetic advance under selection

The expected genetic advance expressed under selection (GA) in a broad sense, assuming selection intensity of 5% of the superior progeny was estimated in accordance with the methodology methods illustrated by Johnson *et al.* (1955).

$$GA = K * SDp * H2 \quad [7]$$

Where

- GA = Genetic advance
- SDp = Phenotypic standard deviation on mean basis
- H2 = Heritability in the broad sense.
- K = the standardized selection differential at 5% selection intensity (K = 2.063).

2.7. Genetic advance as percent of mean

Genetic advance as percent of mean (GAM) was estimated following the formula described by (reference), which is indicated below [8].

$$GAM = \left(\frac{GA}{\bar{x}} \right) * 100 \quad [8]$$

Where

- GAM = Genetic advance as percent of mean,

- GA = Genetic advance

Genetic advance as percent of mean was categorized as low (0 - 10%), moderate (10 – 20%) and high (>20%) as suggested by Johnson *et al.* (1955).

3. Results and Discussion

3.1. Analysis of variance

Mean squares of the 13 yield and yield-related traits from the analysis of variance (ANOVA) showed highly significant differences among genotypes ($P \leq 0.01$) for days to heading, days to maturity, grain filling period, 1000 kernel weight, kernel number, plant height, spike length, number of spikelet's per spike and grains yield (Table1). Significant differences were observed in the number of productive tillers per plant, biomass yield, and seeds per spike. In line with the present results, many scholars also reported highly significant differences among all the wheat genotypes for all the traits (Mohammed *et al.*, 2011; Dergicho *et al.*, 2015; Gezahegn *et al.*, 2015). Significant differences among genotypes for all traits except for plant height and number of spike lets per plant were reported by Adhiena *et.al.* 2016. Similarly, moderate values for the phenotypic and genotypic coefficients of variation in wheat were reported by Kolakar *et al.* (2012), Mohammed *et al.* (2011), and Berhanu *et al.* (2017) for grain yield, biomass yield, plant height, spike length, number of productive tillers per plant, number of spikelets per spike, number of grains per spike and 1000-grain weight.

Table 1: Mean squares of thirty six bread wheat genotypes evaluated at Bena-Tsemay weyito during the 2020 growing season

Traits	Replication	Block within rep. (Adj.)(d.f=15)	Treatment		Intra block error (DF = 55)	RCBD error	RE (%)	CV (%)
			(df=35) unadj.)	(Adj.)				
Days to heading	13.12*	0.78**	140.76	109.11***	0.82	0.8	98.9323	2.272
Grain filling period	0.25ns	2.751*	297.14	248.67***	1.42	1.70	108.78	1.727
Days to maturity	2.56ns	1.08ns	1469.03	1098.59***	0.97	0.99	100.22	1.720
Plant height (Ph)	4.014ns	5.21ns	45.69	131.08***	7.11	6.7060	94.26	4.721
No. of fertile tillers/plant	3.45**	0.59ns	1.064	0.96*	0.58	0.5880	100.00	23.658
Spike length (cm)	0.031ns	2.36ns	4.40	4.32 **	2.21	2.2484	100.09	14.676
No. of spikelet/spike	0.703ns	0.55ns	3.02	2.49***	0.38	0.4180	102.91	18.712
No. of kernels/ spike	90.19**	16.34ns	35.85	31.41**	11.66	12.6690	102.32	19.888
Seeds/spike	0.70ns	0.55ns	3.02	60.51*	0.38	0.41	102.00	6.01
1000-kernel weight (g)	46.001*	13.61ns	25.71	20.91**	8.39	9.5129	104.71	14.521
Grain yield (kg/ha)	971899	1202694	32942	1421576***	1165619	1173564	100.02	6.086
Biomass yield (t/ha)	3.91**	0.42ns	1.4995	1.23*	0.49	0.4800	97.20	29.881

Note: ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively, DF = degree freedom, RE = relative efficiency, RCBD = completely randomized block design, CV= coefficient of variations, adj. = adjusted treatment, unadj. = unadjusted treatment

3.2. Phenotypic and genotypic coefficient of variability

The PCV of traits ranged from 15.87% for grain filling period to 92.85% for Plant height whereas GCV ranged from 8.25% for the spike length to 85.76% for plant height (Table 4). In the present study, high PCV coupled with high GCV of traits were observed for days to maturity, grain yield, and biomass yield and harvest index. Considering the GCV estimates, number of fertile tillers per plant, thousand-kernel weight, and kernel number and seeds per spike exhibited moderate values. Moderate GCV with moderate PCV was observed for a number of grain filling periods, thousand-kernel weight, and spike length. Accordingly, the genotypes coefficient of variation (GCV) ranged from 5.67% for the plant height to 14.74% for a number of fertile tillers plant-1, whereas the phenotypic variation (PCV) ranged from 7.06% for days to maturity to 19.08% for a number of fertile tillers plant-1 (Table 4).

Moderate GCV coupled with moderate PCV was observed for the grain filling period and thousand seed weight. Considering the GCV estimates, days to heading, fertile tiller per plant, and seeds per spike exhibited moderate values. The studied characters that had high GCV coupled with high PCV values were days to maturity, plant height, spikelet's number per spike, grain yield, biomass yield, and harvest index.

The high PCV and GCV indicate that selection may be effective based on these traits. In support of such a study, several workers reported high PCV and GCV for grain yield, biomass, harvest index, 1000 grain weight, and plant height in wheat. Medium PCV and GCV values were recorded for the rest of the characters. The high and medium PCV and GCV indicate that selection may be effective based on these traits. In support of this study, Tarekegne et al. (1994) reported high PCV and GCV for grain yield, biomass, harvest index, 1000 grain weight, and plant height in wheat. In addition, the findings of Ali and Shakor (2012) reported medium PCV and GCV for grain yield per plot in 20 bread wheat genotypes. Degewione *et al.* (2013) reported medium PCV and GCV for 1000-grain weight, plant height, and days to heading in twenty-six bread wheat genotypes. Similar to the current finding, Berhanu *et al.* (2004) reported

that higher GCV and PCV values were observed for grain yield, thousand-kernel weight, harvest index, tillers per plant, spikes per plant, spike length, kernels per spike, and grain protein yield while lowest GCV and PCV values (<5%) were observed for days to maturity in bread wheat. Similar results of PCV to GCV estimates for most characters were also reported by Dawit et al. (2012) and Adhiena et al. (2016).

Similar observations showed moderate values for the PCV and GCV in wheat were reported by Kolakar et al. (2012), Mohammed et al. (2011), and Berhanu et al. (2017) for grain yield, biomass yield, plant height, number of productive tillers per plant, spike length, number of spikelets per spike, number of grains per spike and 1000-grain weight. Similar to the current finding, Berhanu et al. (2004) reported that higher GCV and PCV values for grain yield, thousand kernel weight, harvest index, tillers per plant, spikes per plant, spike length, kernels per spike, and grain protein yield while contrary lowest GCV and PCV values (< 5 %) were observed for spike length in bread wheat.

Adhiena (2015) reported high heritability for days to heading which supports this finding. Similarly, Kyosev and Desheva (2015) and Desheva and Cholakov (2014) reported a high heritability value for spike length. Kyosev and Desheva (2015) also reported high estimates of heritability for spike length with awns (74.93%), spike length without awns (80.48%), spikelets per spike (63.96%), grain weight per spike (67.47)% and thousand-grain weight (73.51%) in their study on variability, heritability, genetic advance.

3.3. Estimates of heritability In Broad Sense

In the present study, the heritability in broad sense (H^2_B) estimates ranged from 19.56 % for days to heading to 100.2% for grain yield (Table 2). High heritability was noticed for days to maturity (99.87%) followed by grain filling period (98.30%), plant height (85.31), grain yield (97.67%), and the number of spikelet's per spike (64.91). Moderate heritability values were also recorded for No. of kernels/ spike, 1000-kernel weight, and biomass yield. The remaining traits like fertile tiller per plant, spike length, and seeds per spike had low heritability. High

heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from the selection. This may be attributed due to uniform environmental conditions during the conduct of the experiment. The results of the present study were in agreement with the results of El-Mohsen *et al.* (2012) who noticed higher heritability values for plant height, days to 50 percent flowering, number of productive tillers per plant, grain yield per plot, and number of grains per spike. Further, Salem *et al.* (2008), and Ali *et al.* (2008) recorded high heritability estimates for grain yield, the number of kernels per the main spike, plant height, thousand kernel weights, and the number of tillers per plant.

The results obtained in the present study are similar to that of results reported by El-Mohsen *et al.*, (2012) and Farshadfar and Mohammed (2012). Rahim *et al.* (2010) noticed higher heritability value for plant height, days to 50% flowering, the number of productive tillers per meter length, grain yield per plot, and the number of grains per spike. Awale *et al.* (2013) also reported high heritability values for plant height, tillers per meter, and spike length. In contrary with the current result, Berhanu *et al.* (2017) reported moderate heritability for grain filling period, kernels per spike, plant height, biomass, thousand-kernel weight in bread wheat genotypes. The present results were also in line with the results of Dergicho *et al.* (2015) who reported high heritability was observed for, days to heading, thousand-grain weight, grain filling period, days to maturity, spike length, and the number of spikelets per spike in 68 bread wheat genotypes. Jericho *et al.* (2015) reported similar findings for high heritability associated with high genetic advance for grain yield per plot and harvest index which supports the present findings. Mohammed *et al.* (2011) and Berhanu *et al.* (2017) also reported similar results, showing relatively high estimates of genetic advance (as a percentage of mean) for grain yield and yield-related traits like the number of fertile tiller per m², plant height, thousand-kernel weight, kernel number per spike and harvest index.

The contrasting results as compared to the present investigation, Berhanu *et al.* (2017) reported as high

heritability is coupled with moderate genetic advance as percent of the mean for days to heading and days to maturity in bread wheat genotypes. This finding is in part similar to those reported by Gezahegn *et al.* (2015). Rehman *et al.* (2015) report explained that high heritability is coupled with high genetic advance. Contrasting results as compared to the present investigation, high heritability associated with high genetic advance noticed for days to heading, grain filling period, fertile productive tillers, spikelet per spike, spike length, kernel per spike, thousand-grain weight, and biomass yield per plot respectively by Dergicho *et al.* (2015); moderate heritability coupled with high genetic advance observed for grain yield (41.71%, 63.05%) whereas high heritability coupled with moderate genetic advance as percent of mean was observed for 1000 kernel weight (74.28%, 20.13%), and plant height (69.43%, 10.27%), respectively (Gezahegn *et al.*, 2015).

3.4. Estimates of expected genetic advance

Genetic advance (GAM %) as a percentage of the mean was high for grain yield (92.08%) followed by the number of days to maturity (62.50%), the number of spikelets per spike (42.35%), biomass yield (33.92), and grain filling period (32.20%) as indicated in Table 2. plant height, spike length, days to heading, thousand-kernel weight, number of kernels per spike, seeds per spike, and harvest index showed moderate GAM. It was also moderate for seeds per spike (18.79%) and the number of kernels per spike (18.31%), harvest index (14.50%), and seeds per spike (10.12).

Accordingly, high heritability with high genetic advance as a percent of mean shows for grain yield (97.67%, 92.08%), spikelet's number per spike (64.91%, 42.35%), grain filling periods (98.30 %, 32.20%) and days to maturity (99.87%, 62.50%). High heritability coupled with moderate genetic advance as percent of mean were noticed for grain filling periods, and spike lets per spike. Moderate heritability associated with high genetic advance was observed for the number of kernels per spike, biomass yield, and harvest index, whereas moderate heritability coupled with moderate genetic advance as percent of mean was observed for seeds per spike, and harvest index.

The estimates of genetic advances help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh 2009). Accordingly, Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.*, 1955). high heritability associated with high genetic advance was observed for days to heading, grain

filling period, fertile productive tillers, spikelet per spike, spike length, kernel per spike, thousand-grain weight, grain yield per plot, biomass yield per plot, and harvest index respectively. These are simply inherited traits indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Kalimullah *et al.* (2012) reported similar findings for plant height, biomass yield per plot, and 1000 grain weight, which supports the present studies.

Table 2: Estimates of Ranges, Mean, Phenotypic (PV) and Genotypic (GV) Coefficient of Variation, Broad Sense Heritability and Genetic Advance as Percent of Mean of traits

Traits	Range	Mean± SE	PCV (%)	GCV (%)	H ² B (%)	GA	GAM (%)
Days to heading (days)	17-65	38.79 ± 1.16	82.89	16.21	19.56	3.67	9.46
Grain filling period(days)	42-83	57.66 ± 1.02	15.87	15.74	98.30	18.56	32.20
Days to maturity (days)	23-107	63.22 ± 2.17	30.29	30.25	99.87	39.51	62.50
Plant height (cm)	41.6-74	56.17± 0.66	92.85	85.76	85.31	1.63	2.90
fertile tillers/plant (no)	1.2-5.8	2.31 ± 0.08	30.77	12.57	17.65	0.11	4.84
spikelets/spike (no.)	2-6	3.29 ±0.16	31.62	25.60	64.91	1.39	42.35
Spike length(cm)	0.2-12.8	10.16 ±0.10	16.81	8.25	24.11	0.85	8.36
kernels/ spike (no)	10.2-41.4	17.35±0.50	24.61	14.78	46.07	3.75	18.31
Seeds per spike(no)	12-46.2	24.90±0.66	26.71	11.46	18.36	2.52	10.12
1000-kernel weight (g)	11.8-32.5	19.95 ±0.66	19.77	13.41	46.07	3.75	18.79
Grain yield (kg/ha)	183.3-1333.3	691.38±0.08	45.44	45.04	97.67	636.62	92.08
Biomass yield (kg/plot)	0.4-4.8	1.75 ±0.37	49.21	28.44	33.41	0.59	33.92

Note: PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; H²b = Broad sense heritability; GA = Genetic advance and GAM = Genetic advance as percent of mean

3.5. Clustering of genotypes

The D2 values based on the pooled mean of genotypes resulted in classifying the 36 bread wheat genotypes into six clusters (eight groups and one solitary). It was indicated that the tested bread wheat genotypes were moderately divergent. The genotypes were clustered in such a way that 40% genotypes in cluster I (38.88%), 10% in cluster II (27%), 6% genotypes in III (16.67%), 3% genotypes in cluster IV (8.33%) whereas another 2% genotypes in cluster V (5.56%) and 1% genotypes in cluster VI (2.78), respectively (Table 3). This indicates that the crossing between superior genotypes of the above diverse cluster pairs might provide desirable recombinants for developing high-yielding bread wheat varieties.

3.6. Average intra and inter-cluster distance (D2)

The average inter-cluster distance (D2) values are presented in (Table no.10). Maximum inter-cluster distance was observed between clusters V and VI (D2 = 777.98770), followed by that between clusters III and IV (D2 = 525.49337). The lowest inter-cluster distance D2 was recorded in clusters III and VI (D2=62.04524) (Table 3). According to Rahim *et al.* (2010) Hybrid of genotypes with maximum distance resulted in high yield; the crosses between those genotypes can be used in a breeding program to achieve maximum heterosis. Therefore, more emphasis should be on clusters V and VI for selecting genotypes as parent for crossing with the genotype of the cluster, which may produce new recombinants with desired traits. This indicates that the crossing

between superior germ plasm of above diverse cluster pair's might provide desirable recombinants for developing high-yielding bread wheat varieties. Similarly, Degewione and Alamerew (2013) grouped

26 bread wheat genotypes into six clusters; Shashikala (2006) grouped 169 wheat genotypes into 11 clusters.

Table 3: Average intra (bold) and inter-cluster (off-diagonal) distance values (D2) among six clusters in 36 bread wheat genotypes

	I	II	III	IV	V	VI
I	31.14	109.67856**	310.81179**	19.80514ns	36.66184*	506.65355**
II		22.00	70.91886**	63.07811**	251.71101**	205.14023**
III			7.41	243.29602**	525.49337 **	62.04524*
IV				24.04	78.46869**	436.79455**
V					0.01	777.98770**
VI						13.23

$\chi^2 = 82.529$ at 5% probability level and $\chi^2 = 92.010$ at 1% probability level, * = Significant at 0.05 probability level, ** = Highly significant at 0.01 probability level., where χ^2 is Chi-square.

3.7. Genetic divergence

Genetic divergence analysis quantifies the genetic distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence. Divergence analysis is a technique used to categorize genotypes that are as similar as possible into one group and others into a different. D-square statistics (D2) developed by Mahalanobis (1936). It has been used to classify the divergent genotypes into different groups. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization.

The lowest intra cluster distance D2 was recorded in cluster IV (19.80514), which shows the presence of less genetic variability or diversity within this cluster. The diversity among clusters or inter cluster distance D2 ranged from 85.15 to 174.32. Cluster V and VI showed maximum inter cluster distance of (D2 = 777.98770), followed by that between clusters III and IV (D2 = 525.49337) and I and VI (D2 = 506.65355). The lowest inter cluster distance was noticed between clusters I and IV (19.80514), followed by that

between clusters I and V (36.66184). Evaluation of genetic diversity can be useful for the selection of the most efficient genotypes. The results of this study showed the presence of a high genetic divergence among wheat genotypes, which is similar to the findings of Ali et al. (2008) who reported that cluster analysis can be useful for finding high yielding wheat genotypes. According to Rahim et al. (2010) hybrids genotypes with maximum distance resulted in high yield. Thus the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. Therefore, more emphasis should be given on cluster V and VI for selecting genotypes as parents for crossing with the genotypes of cluster, which may produce new recombinants with desired traits.

The chi-square test for the clusters indicated that there was a statistically significant difference in all characters (Table 7). The χ^2 - test for the six clusters indicated that there was a statistically significant difference in all characters.

Table 4: Bread wheat genotypes in six clusters tested based on D2 analysis

Clusters	Number and (%) of Genotypes	Genotypes (G*)
I	14 (38.88%)	G13,G16,G22,G14,G15,G10,G11,G25,G7,G8,G26,G28,D5,G33
II	10 (27%)	G30, G32, G3 ,G19, G34, G36, G17, G18, G2, G9
III	6 (16.67%)	G27, G31, G21, G29, G1,G24
IV	3(8.33%)	G12 , G23, G4 (Atila-7)
V	2 (5.56%)	G6 (ETBW5957), G35(kakaba)
VI	1 (2.38%)	G20 (ANGI-2/HUBARA-3)

G*=genotype number

3.8. Principal component (PC) analysis

The eigenvalues are often used to determine how many factors to retain. The first four components together accounted for about 75.6% of the total variation among the genotypes with respect to all the 13 traits evaluated and showed the presence of considerable genetic diversity among the genotypes for most of the traits under consideration. Individually, PC1, PC2, PC3, PC4, PC5, and PC6 in that order accounted for about 22%, 13%, 12%, 11%, 9% and 7% of the gross variation among the 36 bread wheat genotypes evaluated for 13 traits. The traits, which contributed more to PC1, were days to heading, plant height, grain filling period, and Spike

length. Whereas for second PC grain yield, days to maturity, fertile tiller/plant, 1000-kernel weight, and harvest index. For the third PC, biomass yield, No. of kernels/ spike, and harvest index while for the fourth PC, Fertile tiller/plant and The first two principal components PC1 and PC2 with values of 22% and 13% respectively, contributed more than half to the total variation. Therefore, the present study confirmed that the bread wheat genotypes showed significant variations for the characters studied and it suggested the many opportunities for genetic improvement through selection. Similar results were reported by Sajjad et al (2011), El-Mohsen et al. (2012) and Degewione and Alamerew (2013).

Table 5: Eigenvalues and Eigenvectors of the first six principal components (PCs) for 13 traits of 36 bread wheat genotypes tested at Benatsemay weyito kebele during the 2020 growing season

Characters	PC1	PC2	PC3	PC4	PC5	PC6
Days to heading(days)	0.744	0.189	-0.135	-0.185	0.384	0.120
Grain filling period (days)	0.594	0.163	0.177	-0.020	-0.167	-0.408
Days to maturity (days)	0.028	0.498	0.056	0.766	-0.171	0.025
Plant height(cm)	0.783	0.171	0.237	0.246	0.004	0.160
Fertile tiller (no)	0.198	0.509	-0.149	-0.247	-0.110	0.606
No. of spikelet/spike (no.)	0.088	0.259	-0.631	0.204	-0.110	0.297
Spike length (cm)	0.594	0.204	-0.268	-0.009	0.202	-0.465
No. of kernels/ spike (no.)	-0.320	0.753	0.559	0.452	-0.365	0.208
Thousand-kernel weight (g)	-0.320	0.753	0.187	-0.129	0.221	-0.160
Grain yield (t/ha)	-0.135	0.536	-0.131	-0.208	-0.630	-0.208
Biomass yield (t/ha)	0.077	-0.111	0.569	-0.435	0.184	0.168
Eigen value	3.083	1.926	1.698	1.548	1.311	1.028
Variance explained (%)	22	13.7	12.1	11	9.3	7.3
Cumulative variance explained (%)	22	35.7	47.9	58.9	68.3	75.6
Difference	1.156	0.227	0.150	0.237	0.282	0.112

4. Conclusion

The present study comprises thirty-six bread wheat germplasm that were evaluated at weyito Nasa agricultural farm with the objective of assessing the genetic variability of yield and yield-related traits. Analysis of variance revealed that highly significant differences were obtained among the treatments for all thirteen traits. Selected quantitative characters indicated adequate variability among the germplasm considered in this study. The estimates of ranges of mean values revealed that bread wheat germplasm possesses a good amount of genetic variability. Productive tillers per plant, spike length, kernel per spike, thousand-grain weights, biomass yield per plot, and grain yield per plot showed a high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values. Heading date, maturity date, grain filling period, and plant height showed a medium phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The high to a medium phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values of characters suggest the possibility of improving the desired traits through selection. The values of heritability for all the quantitative characters were high. The expected genetic advance as a percentage of the mean ranged from 0.11% No of fertile tiller per plant to 636.62% 5% for grain yield(GY) Characters with high genetic advance as a percent of mean allow the improvement of the characters through selection. The cluster analysis based on D2 analysis on the pooled mean of genotypes classified the thirty-six genotypes into six clusters, which makes them moderately divergent. There was a statistically approved difference between all the clusters. It was obvious from the analysis that three PCs out of thirteen were selected having >1 Eigenvalues and contributed 75.6 % variation among thirty-six bread wheat genotypes for all parameters. It was noted that the principal component first contributed 22%, the principal component second 13%, and the principal component third 12%, of the total genetic variability for all the genotypes Productive tillers per plant, spikelet per spike, spike length, kernel per spike thousand-grain weight and harvest index showed high heritability with the high genetic advance of percent mean, these traits may be included as components of indirect selection.

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Conflict of interest

The authors declare no conflict of interest

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