

Research Article

Genetic Distance of Selected Durum Wheat (*Triticum turgidum* L.) Landraces in Ethiopia

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Abstract

Wheat especially, durum wheat is one of the most important cereal crops and there is huge diversity of this in Ethiopia. Knowledge on identification of important characters and their interrelationship is a prerequisite for the development of high yielding. The present study was carried out to cluster selected durum wheat landraces. Forty-nine durum wheat genotypes were studied for 20 traits at Sinana and Selka Ethiopia locations using simple lattice design. The experiment was conducted during 2018/19 main season under rainfed condition. The studied traits were analyzed and grouped into ten clusters and the genotypes maintained under different groups had specific characters that contributed durum wheat variation. On average D^2 values accessions Obsa had the maximum value (16.1) while, Acc7210 had minimum value (2.2) and thus found to be the minimum divergent. Among the clustered groups, highest intra cluster distance was observed in cluster IV, VI, VII, VIII and IX ($D^2 = 6.4$). The highest inter cluster distance was observed between cluster V and VI ($D^2 = 774.3$), indicating there is divergence among clustered groups. The principal component analysis showed about 74.22% of the total variation explained by the first six principal components with eigenvalues greater than unity among 49 durum wheat accessions evaluated for 20 traits. The first principal component accounted for about 20.18% of the total variation. DH, PLH, GY, GPC, KPS and HI had high contribution effect to PC 1. This study provides further insights into population structure and genetic relationships in a diverse set of durum wheat germplasm, which could be further used in wheat breeding programs.

Keywords

Durum Wheat, Mean, Cluster, Genetic Distance, Principal Component

1. Introduction

Durum wheat is one of industrial crop growing over the world. Durum wheat (*Triticum turgidum* L.) growing areas are situated in the Mediterranean Basin, North America, North and East Africa and South West Asia [1]. Out of these regions, durum wheat is the oldest traditional crop produced

in Ethiopia and farmers' varieties which, are often referred to as 'landraces', are characterized by significant phenotypic variability [2]. Ethiopia is known as a "secondary center of durum wheat diversity" [3]. Landraces from Ethiopia have unique morphology and represent a separate subspecies un-

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der the name *Triticum durum. abyssinicum* or *T. a ethiopicum* [2]. Ethiopian durum wheat landraces attracted the world wheat community because of their uniqueness for morphological aspects, wide adaptation and resistance to biotic and abiotic stresses [4]. Around 79,000 tetraploid and 253,000 unspecified *Triticum* accessions are currently available in gene bank collections around the world [5] and Ethiopia is a center of diversity for tetraploid wheat and more than 7,000 local durum wheat accessions are available at the national gene bank of Ethiopia [6].

Wheat landraces may contribute traits including biotic resistance [7], abiotic stress resistance [8] and gluten quality and composition [9]. Therefore, the Ethiopian durum wheat is a source of several adaptive traits of breeding relevance, including disease resistance alleles to rusts and septoria tritici blotch [10]. The efficient utilization of landraces in breeding programs requires understanding of their genetic diversity and population structure [11]. Even though, Ethiopia is endowed with huge durum wheat genetic diversity, the breeding program in the country did not exploit these genetic resources in the wheat improvement program [12]. This is mainly due to the fact that, the available durum wheat landraces are not well characterized for the major agronomic and quality traits. To achieve this goal, the identification of durum wheat genotypes that have exploitable variation for the traits of interest is the first step in durum wheat breeding programs. Genetic diversity contributes to the understanding of genetic relationships among populations and consequently leads to specific heterogeneous groups of parents for hybridization [13]. Estimates of genetic parameters such as variances and heritability allow understanding the nature and magnitude of genetic variability in a population [14], whereas cluster and principal component analysis are convenient methods for identifying homogeneous groups of genotypes and reducing variables [15].

Genetic divergence is genetic distance among the genotypes under consideration. The resulting clusters of individuals within a group are more similar to one another and different from the individual in other groups. D-square statistics (D^2) is one of statistical technique developed by Mahalanobis, P. C. [16] used to classify the different genotypes into different groups. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization. Principal component analysis (PCA) is a standard tool in modern data analysis used to extract relevant information from confusing data sets by identifying directions, called principal components [17]. Therefore, PCA used to identify and minimize the number of traits for effective selection and improvement of yield and its related trait. The presence of genetic variability of durum wheat and divergence analysis is essential for a broadening the gene pool and therefore for success of plant breeding programs. However, no such studies divergence analyses on diversity of durum wheat collections were carried out under Bale highland condition. Therefore, the objective of this study was to assess

potential genetic distance of Ethiopian durum wheat landraces which could be used as parent in future breeding program.

2. Materials and Methods

2.1. Description of the Study Sites

The field experiment was conducted at two locations in Southeastern Ethiopia namely, Sinana with geographical coordinate units of 07°07'N, 40°10'E and Selka with geographical coordinate 07°04'28''N, 040°12'18''E during 2018/19 cropping season. Both experimental sites are characterized by pellic vertisol with a slightly acidic soil and its pH ranges from 6.3 to 6.8. Altitude 2400 m and 2509 m above sea level for both locations representing the potential durum wheat production area in the zone. Sinana Agricultural Research Center (SARC) is located 463 km South-East of Addis Ababa in the highlands of Bale Zone, South-Eastern Oromia and it founds at a distance of 33 km in East of Robe town, the capital city of the Zone. Selka site is on the way to Sinana Agricultural Research Center (SARC) 7 km away from the SARC. Both areas are characterized by bi-modal rainfall pattern and receive annual total rainfall ranging from 750 to 1400 mm. The main season receives 270 to 842 mm rainfall, while the short season receives from 250 to 562 mm rainfall annually. Mean annual minimum and maximum temperatures are 9.6 and 20.7 °C, respectively. The experiment at both locations was conducted during the main cropping season 'which extends from August to December.

2.2. Plant Materials

The experimental materials comprised 49 durum wheat accessions including three checks viz. Bulala, Dire and Obsa and 46 landraces. These land-races were developed into pure lines by SARC from collections introduced from Ethiopian Biodiversity Institute (EBI). The details of durum wheat accessions along with checks used in this study are summarized in Table 1.

Table 1. Names and origin of 49 durum wheat germplasm used in the study.

No.	Name	Origin	S/N	Name	Origin
1	Acc 5152	SNNP	26	Acc 5586	Oromia
2	Acc 5373	Oromia	27	Acc 5428	Oromia
3	Acc 243733	Amahara	28	Acc 6933	Oromia
4	Acc 242791	Oromia	29	Obsa	Oromia
5	Acc 5457,	Oromia	30	Acc 242780	Oromia
6	Acc 242787	Oromia	31	Acc 2211	Oromia

No.	Name	Origin	S/N	Name	Origin
7	Acc 5344	Oromia	32	Acc 226879	Oromia
8	Acc 7576	Amahara	33	Acc 5141	Tigray
9	Acc 7010,	B/Gumz	34	Acc 7665	Amahara
10	Acc 5760	Oromia	35	Acc 5354	Oromia
11	Acc 7580	Amahara	36	Acc 7673	Amahara
12	Dire	Oromia	37	Acc 5198	Amahara
13	Acc 243401,	Oromia	38	Acc 243706	Oromia
14	Acc 5472	Amahara	39	Acc 5510	Oromia
15	Acc 230678	Oromia	40	Acc 242783	Oromia
16	Bulala	Oromia	41	Acc 242782	Oromia
17	Acc 6988	Oromia	42	Acc 226694	Oromia
18	Acc 5473,	Amahara	43	Acc 235051	Amhara
19	Acc 5149	Oromia	44	Acc 7210	Oromia
20	Acc 222393	Oromia	45	Acc 7647	Amahara
21	Acc 7295,	Amhara	46	Acc 6974	Amahara
22	Acc 6978	Amahara	47	Acc 5591	Oromia
23	Acc 8072	Oromia	48	Acc 242790	Oromia
24	Acc 5020	Oromia	49	Acc 243403,	Oromia
25	Acc 5342,	Amahara			

Acc = Accession, SNNP = South Nation and Nationalities and People, SARC = Sinana Agricultural Research Center

2.3. Experimental Design and Trial Management

The experiment was laid out in 7x7 simple lattice design with two replications having plot size of four rows 20 cm spacing and 2.5 m length. Seed and fertilizer rate 150kg/ha and 100 Urea/100 DAP were applied. Urea (N) was applied in split application where 1/3rd was applied at planting and the remaining 2/3rd was applied at tillering stage and all agronomic practices were followed uniformly according to the recommendation for the area. Planting was done by hand drilling; weed was controlled by using hand weeding and as well as by using herbicide Pallas 45 OD at the recommended rate and time of application.

2.4. Data Collection

All agronomic, yield and yield related traits and quality traits both on plant and plot basis were recorded from the two middle rows of each experimental unit. Plant-based data were collected from randomly selected and representative ten plants in the plot while, the plot-based data were collected from the whole harvestable plot (Table 2).

Table 2. Plot-based and plant-based data collected.

SNO.	Plot Based Data	Plant Based Data
1	Grain yield (GY) (kg ha ⁻¹)	Plant height (PLH) (cm)
2	Days to physiological maturity (DM)	Spike length (SPL) (cm)
3	Biomass Yield (BM) (kg ha ⁻¹)	Number of spikelets per spike (SPS)
4	Thousand kernel weight (TKW) (g)	Productive tillers per plant (PTL)
5	Vitreous (VTR) (%)	Number of grains per spike (KPS)
6	Hectoliter weight (HLW) (kg/L)	
7	Days to heading (DH)	
8	Grain Filling Period (GFP)	
9	Grain protein content (GPT) (%)	
10	Grain gluten content (GGL) (%)	
11	Zeleny Index (ZI) (ml)	
12	Wet gluten content (WGL) (%)	
13	Harvest Index (HI) (%)	
14	Sodium dodecyl sulfate (SDS) sedimentation (ml)	
15	Ash content (ASC)	

Traits were assessed as follows:

Plant height (cm): Ten plants were randomly sampled and tagged from harvest-able rows and measured at physiological maturity in centimeter from ground level of the plant to the base of the spike excluding awns.

Spike length (cm): This was randomly sampled and tagged 10 plants from central two rows and recorded from the base of the spike to the tip and measured in centimeters.

Number of spikelets/spike (number): Total number of spikelets on main spike of all ten plants that was randomly sampled from central two rows of each plot was counted at maturity and the average was recorded.

Number of productive tillers/plant (number): Total effective tillers were counted on 10 randomly sampled plants from central rows of each plot and the average of the 10 observations was used for analysis.

Number of grains per spike (number): The spikes of the randomly sampled of 10 plants selected from central two rows were threshed manually and numbers of kernels/spike was counted for each accession during harvesting time and the average of the 10 observations was used for analysis.

Days to heading: Days to 50% booting (number of days from sowing to the stage at which fifty percent of the plants within a plot boot, Zadoks stage 45).

Days to physiological maturity: Physiological maturity occurs when the kernel has accumulated its highest content of dry matter has become hardened and changed colour. The most important change is the loss of moisture from 30 to 35% in mature grain to 12 to 13% in ripe grain [18].

Grain Filling Period (GFP): This was computed by subtracting the number of days to heading from the number of days to physiological maturity.

Grain yield (kg ha⁻¹): Grain yield in kilo gram per hectare was calculated from the yield harvested from the harvestable rows at 12.5% moisture content and calculated as follow:

$$\text{Grain yield} = \text{Grain yield obtained (kg ha}^{-1}\text{)} \times \frac{(100 - \text{MC}\%) }{(100 - 2.5)}$$

Biomass Yield (BM) (kg ha⁻¹): The above ground biomass was measured using hanging balance in the field during harvesting from harvestable two rows.

Harvest Index (HI) (%): On a plot basis, is the ratio of dried grain weight to the dried above ground biomass weight multiplied by 100 and is indicated as follow:

$$\text{HI} (\%) = \frac{\text{GY}(\text{Kg ha}^{-1})}{\text{BY}(\text{Kg ha}^{-1})} \times 100$$

Note: HI = harvest index, GY = grain yield (at 12.5% moisture content) and BY = total biomass yield at harvest.

Seeds of randomly homogeneous sample of each harvested accessions was used for laboratory analysis. Seeds samples from each accession was harvested and analyzed for quality traits separately. For some of quality traits a representative grain sample (500gm) from each plot for each accession was sampled and milled at Addis Ababa, Oroimia Agricultural Research Institute (Head Office) food science laboratory using laboratory grain milling machine. Then, data on the following quality traits were analyzed and recorded on plot basis for each experimental units as follow:

Thousand kernel weight (g): Counted 1000 grains on an analytical balance.

Vitreous (%): Kernel Vitreous was estimated by using transmitted light according to ICC standard number 129 (ICC, 2000). The percentage of vitreous kernels was determined by carefully examined the translucent and non-translucent (opaque and non-opaque) kernels by using the transmitted light. Vitreous grains appear translucent, while opaque grains appear dark and starchy (AACC, 1983).

Hectoliter weight (kg/L): The flour density (kg/l) produced from a hectoliter of seed as measured by a Moisture and Hectoliter Analyzer according to AACC, 1983 procedure.

Grain protein content (%): Protein content was determined based on Mininfra Smart T Grain Analyzer (Mininfra Smart T Grain Analyzer Operating Manual, 2013). About 100 gm

grain samples were poured into the hopper and took the measurement that displayed on the screen or print out the values.

Grain gluten content (%): Also the gluten content was determined using Mininfra Smart Grain Analyzer. About 100 gm grain samples were poured into the hopper and the measurement displayed on the screen was taken for each experimental unit.

Zeleny Index (ml): Zeleny index was also measured using the same equipment that used for gluten and protein content analysis. About 100 gm grain samples were poured into the hopper and take the measurement that displayed on the screen or print out the values for each experimental unit.

Wet gluten content (%): Ten gram of the flour was weighted and washed. Sodium chloride and distilled water (20 g/l) solution was prepared and used for washing starch from the meal by dispenser. Wet Gluten Content (WGC) = Total wet gluten (g) x 10.

Sodium dodecyl sulfate (SDS) sedimentation test (ml): The SDS volume was measured according to AACC Method No. 56-70. Whole meal (10 gm) was put into measuring cylinder with lid. Then a 50 ml of distilled water, 1.2% SDS and 1ml lactic acid (85%) solution was prepared and added to 100 ml graduated tube, and then immediately shaken for 15 seconds quickly about 11 times, and then it was allowed to rest for about 2 minutes and again shaken 4 times. Then the value of the sedimentation volume was recorded to the nearest 50 ml after 10 minutes at room temperature. Results was expressed in height (ml) of the interface line between solid or ground samples and liquid or solution in a measuring cylinder according to the AACC, 1983 procedure.

Ash content: Ash content was determined using Mininfra Smart Ash Analyzer. About ten gram flour was poured into the hopper and took the measurement that displayed on the screen or print out the values.

2.5. Data Analysis

Inter-cluster distances, D² and cluster mean values for each trait were used to compute genetic divergence, as described in Mahalanobis [16]. Significance of the squared distances of each cluster was validated using the chi-square (χ²) test at (t-1) degrees of freedom at alpha level of 5%, where t' represents the number of traits used for clustering genotypes.

Genetic distance Euclidean distance (ED) calculated from quantitative and qualitative traits after standardization as established by Singh, R. K. and Choudhary, B. D. [19]. Mean ED was calculated for each genotype by averaging of a particular genotype to the other forty nine accessions. The calculated average distance (ED) was used to estimate which accession(s) is closest or distant to others. The formula to calculate genetic distance is as follows:

$$ED_{jk} = \sqrt{\sum_{i=1}^n (X_{ij} - X_{ik})^2}$$

Note; ED_{jk} = distance between genotypes j and k ; x_{ij} and x_{ik} = phenotype traits values of the i^{th} character for genotypes j and k , respectively and n = number of phenotype traits used to calculate the distance. The distance matrix from phenotype traits was used to construct dendrogram based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA).

Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation [20]. The data was standardized to mean zero and variance of one before computing principal component analysis. Only principal components with Eigenvalues greater than one were considered in this analysis according to Chahal and Gosal [21].

3. Results and Discussions

3.1. Cluster Analysis

The Euclidean distance matrix of 1,176 pair of genotypes estimated from agronomic traits and quality traits was used to construct dendrograms based on the Unweighted Pair-group methods with Arithmetic Means (UPGMA). Based on the pooled mean of accessions resulted in classifying the 49 durum wheat genotypes into ten distinct clusters (Table 3). Also it indicated by Figure 1, of Dendrogram that used 49 durum wheat landraces used in the study. The number of accessions per cluster ranged from a minimum of one to a maximum of twenty nine.

The results of the hierarchical cluster analysis are presented in Figure 1. The cluster analysis was performed on the average data of two locations. The bigger cluster (C II) covers exclusively the material from different regions of the

countries and it composed of just 29 (59.18%) genotypes. It indicates that, the accessions in this cluster had narrow genetic divergence among them. This may be due to the similarity in the base population from which they had been involved. For instance, most of accessions in this cluster were originated from Oromia and Amahara regions while the remaining was from SNNPR, Tigray and Somali region. This indicates that genetic divergences were used as the basis of grouping rather than geographical location. The dendrogram shows one big cluster in the first level of division. As indicated in Table 3, the numbers of accessions in cluster I, V and X each of them consisted of a single accession that constituted a total of 6.12% accessions. The low intra-cluster distance indicated that the accessions in the clusters were closely related due to the heterogeneous nature of the genotypes within a cluster and the presence of less genetic diversity within the cluster [22]. Therefore, the selection of suitable parental material for hybridization based on genetic divergence analysis more likely rewarding than based on materials sources for a successful durum wheat improvement. This cluster also exhibit high internal (within cluster) homogeneity and high external (between clusters) heterogeneity. These similarities within the same cluster might be due to different seed exchange through different social interaction as well as for research purpose among different organizations. Clusters VI, VII, VIII and IX each of them consists a pair of accessions with a total proportion of 16.32% accessions and most of them were originated from Amahara region and the sixth cluster (VI) contain the two checks durum wheat while, cluster VIII brings together one check (Bulala) and a single accession (Acc242780). The fourth cluster (CL IV) also captures 12.24% and most of them originated from Oromia while, three of the accessions with proportion of 6.12% made a third cluster (CL III). Comparable results were also reported by Alemayehu *et al.* [23] using 64 durum wheat genotypes that grouped in to five clusters. Again Bantewalu H. *et al.* [24] studying 104 durum wheat landraces and grouped into six clusters.

Table 3. Pattern of clustering of forty nine durum wheat accessions based on twenty traits.

Clusters	No. of accessions	Proportion (%)	Name of accessions in the clusters
Cluster I	1	2.04	Acc5152
Cluster II	29	59.18	Acc5373, Acc243733, Acc5760, Acc6988, Acc5473, Acc5149, Acc222393, Acc7295, Acc6978, Acc8072, Acc 5020, Acc5342, Acc5586, Acc5428, Acc6933, Acc2211, Acc226879, Acc7665, Acc5354, Acc7673, Acc243706, Acc5510, Acc242782, Acc226694, Acc235051, Acc7210, Acc6974, Acc5591, Acc243703
Cluster III	3	6.12	Acc242791, Acc7580, Acc243701
Cluster IV	6	12.24	Acc5457, Acc242787, Acc5344, Acc7576, Acc5472, Acc7647
Cluster V	1	2.04	Acc 7010
Cluster VI	2	4.08	Dire, Obsa

Table 4. Average intra (bold) and inter cluster divergence (D^2) values in 49 accessions.

CLR	I	II	III	IV	V	VI	VII	VIII	IX	X
I	0.0	63.5**	101.8**	81.4**	654.5**	272.2**	216.1**	270.2**	148.5**	178.3**
II		1.0	90.7**	32.4*	567.4**	191.0**	101.7**	161.0**	71.9**	165.7**
III			5.5	86.1**	667.4**	241.8**	308.1**	342.2**	177.4**	150.7**
IV				4.2	592.7**	223.5**	115.4**	225.7**	109.7**	147.3**
V					0.0	774.3**	705.6**	701.3**	558.5**	759.1**
VI						6.4	285.6**	124.8**	181.9**	203.5**
VII							6.4	226.6**	136.0**	282.2**
VIII								6.4	160.5**	342.2**
IX									6.4	254.2**
X										0.0

Note: *, ** = represents significant at 5 and 1%, $\chi^2 = 30.14$ and 36.19 at 5 and 1% significance level, respectively, CL = Clusters

The minimum inter distance was found between clusters II and IV that followed by cluster I and III suggesting that, accessions in this cluster were not genetically diverse or there was little genetic diversity among these clusters. This signifies that, crossing of accessions from these two clusters might not give higher heterotic value in F₁ and narrow range of variability in the segregating F₂ population. Maximum genetic recombination is expected from the hybridization of the parents selected from highly divergent cluster groups. Therefore, maximum recombination and segregation of the progenies is expected from crosses involving parents selected from between clusters V and VI, between V and X and between V and VII and between V and VIII, however the breeder must specify his objectives in order to make best use of the characters where traits are divergent. Several approaches and analyses of cluster distances among and between groups of cultivars studied based on morphological and growth attributes have been suggested by many researchers for the estimation of genetic diversity [25-27].

According to Ghaderi *et al.* [28] increasing parental distance implies a great number of contrasting alleles at the desired loci and then to the extent that these loci recombine in the F₂ and F₃ generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors. Therefore selection in segregating generations of these crosses seems to give promising results.

3.1.2. Mean Values of Clusters

The mean performances of accessions in each cluster for the twenty agronomic and quality characters are presented in

Table 5. The first cluster (CL I) was characterized by late days to heading, the tallest plant height, high harvest index, high thousand kernel weight, low vitreous, low protein content and minimum SDS- sedimentation value. The second cluster (CLII) is where most of accessions were concentrated and it showed moderate mean values for all of traits studied. The third cluster (CL III) was described by minimum thousand kernel weight and test weight while, the fourth cluster (CL IV) was characterized by minimum productive tillers/plant, low grain gluten and wet gluten content and it showed moderate values for the remaining traits. The fifth cluster (CLV) was characterized by moderate values for all of studied characters. The sixth cluster (CLVI) was consisted of the two checks and characterized by late mature, high test weight, short plant height, long grain filling period, high grain and biomass yield, minimum harvest index, short spike length, high number of spikelets/spike, maximum kernels/spike and maximum productive tillers/plant. The seventh cluster (CLVII) was illustrated by early days to heading, long spike length, low kernels/spike, minimum number of spikelets/spike, high protein content, high grain gluten, low wet gluten and less ash content. Cluster eight was also (CLVIII) characterized by high vitreous, maximum Zeleny index and higher ash content while, the ninth (CL IX) cluster described by earlier mature, earlier grain filling period, minimum biomass yield and less productive tillers/plant. The last but not the least, tenth cluster (CL X) cluster described by maximum SDS- sedimentation. Similarly, Mengistu *et al.* [2] reported huge genetic diversity in durum wheat landraces from Ethiopia with unique morphologies.

Table 5. Combined mean value of twenty characters for ten clusters of 49 durum wheat accessions tested in 2018/19.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Min	Max
DH	62.5	63.8	66.2	64.8	63.5	61.8	59.9	61.0	64.4	63.0	59.9	66.2
DM	116.4	117.2	117.0	119.3	119.0	124.0	121.4	122.5	113.7	121.3	113.7	124.0
PLH	111.3	107.3	107.1	108.5	109.0	84.8	108.1	88.7	103.9	104.3	84.8	111.3
GFP	53.9	53.5	50.8	54.5	55.5	62.2	61.5	61.5	49.3	58.3	49.3	62.2
BM	10275.0	12705.2	14433.3	13985.4	12700.0	16162.5	11587.5	12537.5	9537.5	10475.0	9537.5	16162.5
GY	4211.8	4082.0	5113.9	4127.7	4260.1	5516.3	3380.0	4185.6	2756.9	4141.5	2756.9	5516.3
HI	41.0	33.4	36.7	30.9	34.8	36.3	30.5	34.7	29.5	39.6	29.5	41.0
SPL	7.7	7.5	7.3	6.9	6.8	5.7	7.9	7.1	5.2	7.4	5.2	7.9
SPS	15.7	16.6	19.5	15.8	15.0	20.6	15.6	15.9	16.5	16.5	15.0	20.6
KPS	28.1	30.2	34.9	30.7	33.0	44.0	26.3	40.0	32.9	26.9	26.3	44.0
PTL	2.8	2.7	3.2	2.4	2.7	4.5	2.6	2.5	2.4	2.9	2.4	4.5
TKW	52.4	39.0	36.3	38.0	37.4	43.8	40.9	47.7	38.6	42.1	36.3	52.4
HLW	78.0	79.5	76.9	77.5	77.2	84.2	81.2	82.5	78.1	80.4	76.9	84.2
VTR	62.3	87.4	93.0	85.2	73.8	96.1	88.8	97.0	88.9	96.4	62.3	97.0
GPC	11.1	13.8	13.2	12.4	12.5	12.4	14.8	13.7	13.0	13.8	11.1	14.8
ZI	45.1	62.3	59.0	53.3	48.3	66.3	64.0	68.7	61.0	58.3	45.1	68.7
GGL	30.4	34.4	31.7	29.3	31.2	32.2	36.2	34.3	30.7	35.7	29.3	36.2
WGL	33.9	33.8	30.9	28.4	30.2	33.4	34.1	33.2	33.9	33.6	28.4	34.1
ASC	0.8	1.1	1.3	1.2	1.0	1.1	0.6	1.4	1.2	1.0	0.6	1.4
SDS	40.5	46.1	50.8	48.0	42.0	55.3	49.6	46.3	50.3	56.3	40.5	56.3

Note: DH = Days to heading, DM = Days to mature, PLH = Plant height, GFP = Grain filling period, BM = Biomass, GY = Grain yield, HI = Harvest Index, SPL = Spike length, SPS = Number of spike per spike, KPS = Number of kernel per spike, PTL = Productive tiller, TKW = Thousand kernel weight, HLW = Hecto liter weight, VTR = Vitreous, PC = Grain protein content, ZI = Zeleny Index, GGL = Grain gluten, WGL = Wet gluten, ASC = Ash content and SDS = Sodium Dodecyl Sulphate.

3.2. Genetic Distance Analysis

The genetic distances of 1,176 pair of accessions estimated from 20 quantitative and qualitative traits of durum wheat genotypes evaluated from combined over locations data are presented in Supplementary Table 1 and the mean euclidean distance of each genotype to other 48 genotypes is presented in Table 6. The genetic distance for all possible pairs of 49 durum wheat genotypes ranged from 2.2 to 16.1 ED with the overall mean, standard deviation and coefficient of variation of 6.1, 1.6 and 27.3% respectively. The highest genetic distance (16.1) (Euclidean distance) was computed between Obsa (check) and Acc7010 while, the lowest genetic distance (2.2 ED) was estimated between Acc7210 and Acc5428 (Supplementary Table 1; Figure 3). Among pair of accessions, 166 (14.1%), 552 (46.9%), 402 (34.2%) and 56 (4.8%) pair of acces-

sions had Euclidean distances of 2.2 to 4, 4.01 to 6, 6.01 to 10 and greater than 10 respectively. From possible paired 438 (37.2%) pair of accessions had euclidean distances values greater than 6.1 (overall means ED of accessions). This suggested that there are a considerable number of accessions which had genetic distances above the average genetic distance of the durum wheat accessions that could be considered for crossing programs to combine the desirable traits. The genotypes with high genetic distances between them also have the potential to produce heterotic hybrids through crossing. Obsa variety (standard check) had the highest mean Euclidean distance of 16.1 compared to other durum wheat accessions which was also significantly higher than the overall mean ED values of accessions. The Acc7210 had the lowest mean ED of 2.2 compared to other 48 accessions (Appendix Table 1; Figure 3). Similarly, Soriano *et al.* [29] reported wide genetic distance between modern cultivars and landrace populations of durum wheat.

Table 6. Range and mean Euclidean distance of 49 durum wheat accessions estimated from twenty quantitative and qualitative traits based on mean values of accessions based on combined over the two locations data 2018/19.

S/N	Accessions	Mean	Max	Min	SEM	CV%	S/N	Accessions	Mean	Max	Min	SEM	CV%
1	Acc 5152	7.3	15.3	5.0	1.6	22.6	26	Acc 5586	5.2	12.5	2.5	1.7	33.5
2	Acc 5373	5.1	12.8	2.7	1.9	36.8	27	Acc 5428	5.0	11.3	2.2	1.7	33.9
3	Acc 243733	4.7	11.7	2.4	1.6	34.1	28	Acc 6933	5.7	11.6	2.4	1.7	29.8
4	Acc 242791	6.5	13.3	4.5	1.5	23.2	29	Obsa	8.7	16.1	4.8	1.5	17.5
5	Acc 5457	5.4	13.3	3.4	1.7	31.9	30	Acc 242780	6.5	12.4	3.9	1.3	20.4
6	Acc 242787	6.3	13.5	3.4	1.8	28.0	31	Acc 2211	6.1	11.6	2.4	1.6	27.1
7	Acc 5344	6.0	12.2	3.4	1.7	28.7	32	Acc 226879	5.2	11.4	2.6	1.7	32.9
8	Acc 7576	5.8	11.3	3.5	1.7	29.8	33	Acc 5141	6.7	13.3	3.7	1.8	26.7
9	Acc 7010	12.5	16.1	10.6	1.1	8.4	34	Acc 7665	5.0	11.8	2.7	1.5	30.9
10	Acc 5760	5.4	12.0	3.1	1.5	27.5	35	Acc 5354	5.5	13.4	2.8	1.9	34.5
11	Acc 7580	6.6	12.7	4.8	1.3	19.6	36	Acc 7673	5.4	12.3	3.0	1.8	32.5
12	Dire	8.9	14.4	4.8	1.4	15.9	37	Acc 5198	6.2	11.3	3.5	1.6	26.0
13	Acc 243701	5.7	12.7	3.6	1.6	28.7	38	Acc 243706	5.2	11.9	3.1	1.6	31.2
14	Acc 5472	6.2	11.7	4.0	1.5	23.5	39	Acc 5510	5.5	12.7	3.5	1.6	28.9
15	Acc 230678	6.5	12.6	3.5	1.5	23.0	40	Acc 242783	7.9	13.4	5.9	1.1	14.3
16	Bulala	6.8	14.3	3.9	1.5	21.6	41	Acc 242782	5.8	12.0	3.7	1.6	28.2
17	Acc 6988	5.6	11.4	3.3	1.3	23.6	42	Acc 226694	5.0	12.7	2.7	1.6	32.7
18	Acc 5473	4.8	11.8	2.6	1.7	35.5	43	Acc 235051	5.9	12.1	3.6	1.4	23.5
19	Acc 5149	4.7	12.3	2.7	1.6	35.1	44	Acc 7210	4.9	11.2	2.2	1.7	35.7
20	Acc 222393	5.4	10.6	2.8	1.5	27.1	45	Acc 7647	6.3	13.3	3.4	1.6	26.3
21	Acc 7295	5.2	12.1	3.0	1.7	33.0	46	Acc 6974	5.3	13.0	3.3	1.7	32.0
22	Acc 6978	4.8	12.3	2.4	1.7	35.8	47	Acc 5591	6.7	12.6	3.9	1.5	23.0
23	Acc 8072	5.8	11.4	2.8	1.5	26.5	48	Acc 242790	6.0	12.4	3.9	1.6	26.4
24	Acc 5020	5.2	12.6	3.2	1.6	30.2	49	Acc 243703	5.1	13.3	2.7	1.8	35.5
25	Acc 5342	5.2	12.2	3.1	1.7	33.0	Overall		6.1	12.7	3.7	1.6	27.3

Note; SD = Standard Deviation, Max = Maximum, Mini = Minimum, Acc = Accessions, CV = Coefficient of Variation

3.3. Principal Component Analysis

Based on twenties agro-morphological features of 49 wheat accessions, the principal components (PCs) were presented in Table 7. The component with an eigenvalue of less than one had no significant contribution to the total variation [21] while, PCs with eigenvalue greater than one and component loadings greater than 10% have a meaningful and significant contribution to the total variations among accessions. According to Chahal and Gosal [21], characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with

lower absolute values closer to zero.

The PC analysis is represented graphically in Figure 2 and Figure 3. The two main components PC-1 and PC-2 account for 20.18% of the total variation for all genotypic traits. This variation is large enough to perform the analysis. Figure 2 shows the points and vectors of the traits investigated in the experiment. From the angles between the vectors of the traits, can be explained the correlation between them. From the magnitude of the angle we can judge the magnitude of the correlation. The smaller the angle, the stronger the correlation between the traits is. At an angle of 90 degrees the correlation is zero. At angles greater than 90 degrees, the correlation is negative, increasing with the increase in the angle.

According to the corners of [Figure 2](#), the correlation relationships are close to the correlation coefficients. This [Figure 2](#) should be viewed in conjunction with [Figure 3](#). [Figure 3](#) shows the distribution of genotype points in the coordinate system the PC-1 to PC-2. According to the quadrant in which the genotyping points and passing vectors of the traits are located, [Figure 2](#) can be judged for the corresponding stronger influence of the particular trait on the genotype. [Figure 3](#) shows a significant similarity between the genotype distribution in the PC analysis ([Figure 2](#)) and the data from dendrogram ([Figure 1](#)). Golabadi and Arzani [30] suggest that cluster analysis was similar to factor analysis in grouping the characters. In general, it can be assumed that the separation by cluster analysis gives the best estimate of the genetic distance of the genotypes. Therefore, in studying genetic diversity related to genetic proximity and distance, it is preferable to use cluster analysis [13, 31].

The first six components together accounted for about 74.22% of the total variation among the forty nine durum wheat accessions with respect to all the twenty traits studied. The first principal component (PC 1) accounted for about 20.18% of the total variations of accessions, while PC 2, PC 3, PC 4, PC 5 and PC 6 accounts for about 18.99%, 12.98%, 8.86%, 7.74% and 5.48% of the gross variations, respective-

ly. Days for heading, Plant height, Grain yield, Grain protein content, Number of kernels per spike and Harvest index are the most significant traits contributing to PC1. The second component accounting for about 18.99% and the most variation contributors' traits were Days for mature, Grain gluten and Zeleny Index. Similarly, the third principal component (PC 3) accounted for 12.98% of the total variation and it was chiefly accounted by variation in Days for heading, Ash content, Wet gluten and Biomass. The fourth PC captured about 8.86% of the variation and the major variation contributor traits were number of kernels per spike, vitreous and biomass, variations in grain filling period, thousand kernels weight and days for heading accounted for the fifth principal component (PC 5). In the last but not the least sixth principal component (PC 6) the five traits contributing high variation were; biomass, vitreous, productive tillers, hectoliter weight and SDS-sedimentation. Generally, principal component analysis revealed that differentiation of the accessions into different cluster was due to relatively high contribution of a number of characters rather than smaller contribution of all characters. Thus characters such as days to heading, plant height, grain yield, grain protein content, number of kernels per spike and harvest index in the first principal component contribute more for clustering ([Figure 1](#); [Table 7](#)).

Table 7. Characters loading among 49 durum wheat landraces for 20 traits.

Traits	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Days to heading	0.36	0.05	-0.32	-0.05	-0.03	-0.20
Days to mature	0.14	0.32	-0.21	0.23	0.37	-0.15
Plant height	0.32	-0.07	-0.05	-0.28	0.22	0.03
Grain filling period	-0.19	0.29	0.08	0.29	0.40	0.03
Biomass yield	-0.07	0.26	-0.33	-0.31	0.13	0.36
Grain yield	-0.34	0.18	-0.15	-0.29	-0.01	0.21
Harvest Index	-0.30	-0.09	0.22	0.06	-0.17	-0.28
Spike length	0.23	0.13	0.17	-0.38	0.05	-0.05
No. Spikelet's/spike	-0.21	0.25	-0.21	-0.25	-0.23	-0.11
Kernels/spike	-0.30	0.19	-0.17	0.01	-0.07	0.10
Productive tillers/plant	-0.20	0.29	-0.06	-0.23	-0.15	-0.32
Thousand kernel weight	-0.17	0.16	0.23	0.14	0.43	-0.01
Hecto-liter weight	-0.11	0.28	0.17	0.08	-0.08	-0.37
Vitreous	-0.02	0.07	-0.15	0.42	-0.25	0.42
Grain protein content	0.32	0.28	0.18	-0.05	-0.14	0.06
Zeleny Index	0.19	0.38	0.06	0.21	-0.24	0.19
Grain gluten	0.26	0.33	0.24	0.01	-0.12	0.13
Wet gluten	0.00	0.16	0.39	-0.03	-0.30	0.03
Ash content	0.05	-0.09	-0.37	0.27	-0.29	-0.12

Traits	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
SDS-sedimentation	0.15	0.18	-0.28	0.15	0.00	-0.40
Eigenvalue	4.04	3.80	2.60	1.77	1.55	1.10
Variability (%)	20.18	18.99	12.98	8.86	7.74	5.48
CTVE%	20.18	39.17	52.15	61.01	68.74	74.22

Note; PC = Principal Component, CTVE = Cumulative percent of total variance explained

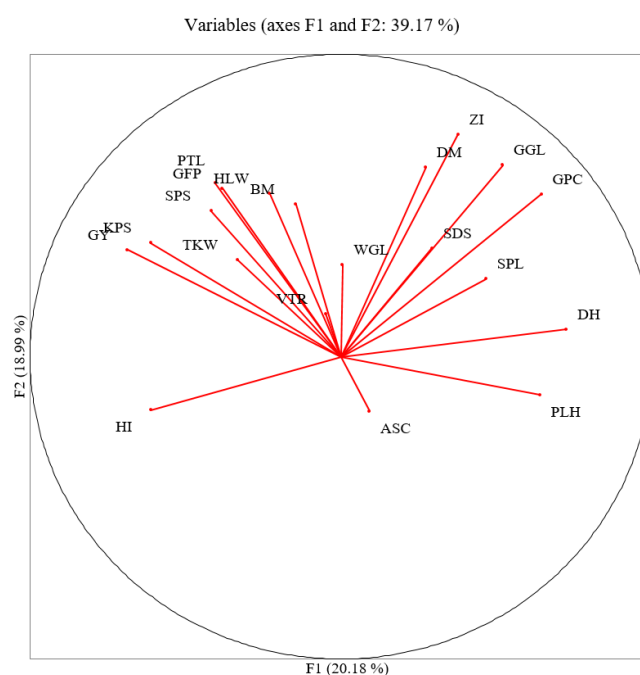


Figure 2. Biplot PC - analysis of traits.

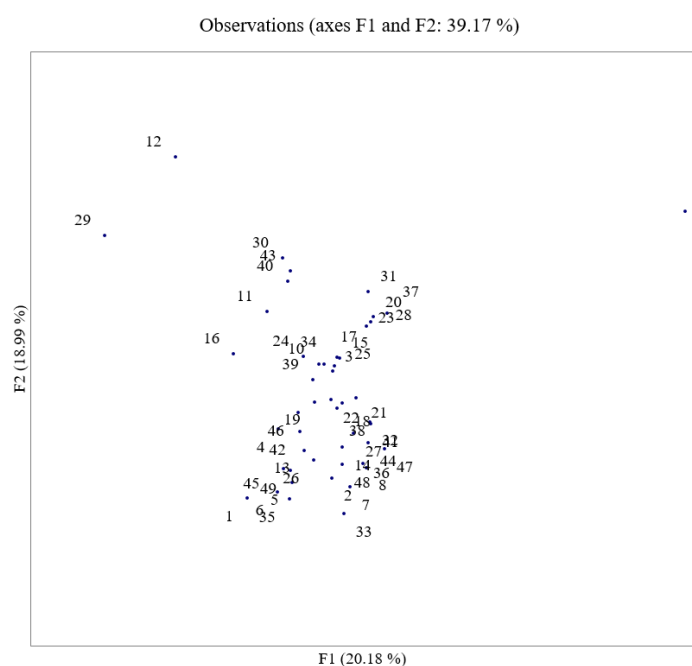


Figure 3. Biplot PC – analysis of genotypes.



Figure 4. Field performance and character of durum wheat landraces.

4. Conclusions

Based on the findings in the present study, the forty nine durum wheat landraces are found more diversified landraces that can be employed in wheat breeding programs. Established correlation relationships between the studied traits can be successfully used in the breeding of durum wheat. Using of cluster analysis provides a reliable estimation of the genetic distance of genotypes in our breeding program. The established genetic distance of genotypes allows optimization of the breeding schemes when choosing its strategy. Despite the possibility of PC analysis to show clustering of genotypes by genetic proximity and distance, it is preferable to apply cluster analysis for this purpose because its more precision. In conclusion, the existence of wide range of genetic variation in the study paves high possibility for durum wheat improvement through selection and hybridization for improving grain yield. Moreover, these findings should be supported by marker assisted selection for identification of gens of interest in durum wheat breeding.

Abbreviations

Acc	Accession
CL	Cluster
CTVE	Cumulative Percent of Total Variance Explained
D ²	Euclidian Distance
EBI	Ethiopian Biodiversity Institute
ED	Euclidean Distance
PC	Principal Component

PCA	Principal Component Analysis
SAR	Sinana Agricultural Research Center
SNNP	South Nation and Nationalities and People
UPGMA	Unweighted Pair-Group Methods with Arithmetic Means
χ^2	Chi-Square

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Public Interest Statement

Updating better yielding varieties and using recommended managements can improve productivity of the crops. Varieties should be evaluated under different environments and confirmed for their adaptation by National Variety Releasing Committee before disseminating to a large community, which is a usual practice that has been conducted in the research ethics. This is due to varying environment affecting crop adaptation. In this study, therefore, different accessions were evaluated and characters were identified for specific objective which will be used for crossing purpose for the improvement of durum wheat.

Conflicts of Interest

The authors declare no conflicts of interest.

Appendix

Table 8. Euclidean distances of 49 durum wheat accessions estimated from mean values of accessions for 20 quantitative traits and qualitative of combined over location in 2018/19.

Acc.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1		6.2	5.9	7.6	5.0	6.9	7.4	7.6	15.3	6.0	9.0	11.2	6.9	7.4	6.8	7.3	6.5	6.4	6.2	8.8	6.8	5.6	7.3	6.6	6.2
2			4.3	6.0	3.8	4.9	4.0	4.0	12.8	4.7	6.7	9.6	4.2	5.8	6.1	6.2	5.2	3.7	3.0	4.6	4.0	3.7	5.8	4.2	3.9
3				5.0	4.5	5.7	5.4	5.4	11.7	3.6	6.0	8.3	4.9	5.4	5.2	5.5	4.0	2.6	3.5	3.9	3.0	2.4	2.8	3.4	3.5
4					5.1	5.7	5.9	6.0	13.3	6.6	5.6	8.4	4.5	5.9	8.8	8.1	5.9	5.4	6.2	6.0	6.1	5.7	6.9	5.1	7.1
5						4.2	4.3	4.2	13.3	5.0	6.9	9.6	4.5	4.4	5.7	6.4	4.8	4.4	4.6	6.1	5.1	4.1	6.4	4.6	5.4
6							5.1	3.7	13.5	6.6	7.0	9.1	5.4	5.4	7.5	7.3	5.8	6.1	4.8	6.6	6.9	5.3	7.0	5.8	7.0
7								3.5	12.2	5.7	6.8	10.2	4.5	4.0	7.1	6.9	5.3	5.4	4.7	5.9	4.8	5.4	6.9	6.4	5.9
8									11.3	5.8	6.2	9.8	4.5	4.0	7.0	7.5	5.2	5.4	4.0	5.2	6.0	5.1	6.5	5.6	6.2
9										12.0	12.7	14.4	12.7	11.7	12.6	14.3	11.4	11.8	12.3	10.6	12.1	12.3	11.4	12.6	12.2
10											6.4	8.2	5.2	5.5	4.1	5.1	5.5	3.1	4.1	5.2	3.8	4.7	4.9	4.9	3.9
11												6.4	4.8	6.9	8.7	8.0	5.9	6.0	5.2	5.6	6.9	6.1	7.1	5.7	6.3
12													8.9	9.8	9.6	8.0	8.4	8.8	8.2	7.5	9.4	8.8	8.8	7.5	8.7
13														5.5	7.7	7.7	5.7	4.2	4.6	5.4	5.5	5.4	7.2	4.8	5.5
14															6.5	6.3	5.6	5.5	5.4	6.3	5.8	6.1	6.6	6.7	7.0
15																6.0	6.4	5.2	5.4	6.5	5.4	5.5	5.7	5.8	5.1
16																	6.6	5.8	5.4	6.7	5.7	6.1	6.1	6.7	5.8
17																		5.4	4.2	4.9	5.0	3.3	5.0	4.4	4.6
18																			3.7	4.2	3.1	3.7	4.6	3.9	3.3
19																				3.9	4.2	2.9	4.3	3.7	3.2
20																					4.3	4.2	4.4	3.5	4.6
21																						3.6	4.2	4.8	3.4
22																							3.4	3.2	3.1
23																								4.8	4.6
24																									4.1
25																									

Table 8. Continued.

S/ N	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
1	6.6	7.4	8.0	9.3	8.6	8.6	7.5	8.1	7.3	6.2	6.8	7.7	6.2	5.8	8.4	5.7	5.4	7.3	7.1	6.5	7.0	6.8	6.8	6.3
2	3.9	4.0	5.5	9.3	6.6	5.8	3.3	4.8	3.7	3.5	3.8	5.9	3.9	4.8	8.2	4.5	3.5	6.5	3.2	5.3	3.9	5.3	5.1	2.7
3	4.2	3.7	3.7	8.1	5.1	4.5	4.1	6.0	3.5	4.6	4.4	4.2	3.9	3.6	7.1	4.6	3.8	3.6	3.7	5.2	4.0	6.1	4.5	4.7
4	5.3	5.1	6.9	8.9	7.8	7.0	6.0	6.8	5.4	5.4	6.2	8.2	6.3	6.3	7.9	7.6	6.0	6.2	5.7	4.5	5.4	8.1	5.8	5.5

S/ N	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
5	4.3	4.3	6.0	8.6	7.1	6.8	5.3	6.5	4.6	4.1	4.5	6.4	4.2	5.6	7.2	5.2	4.1	5.8	4.2	3.8	4.0	6.0	4.9	3.4
6	4.3	4.1	7.9	8.8	7.8	8.5	5.9	6.4	4.7	4.4	6.5	7.6	5.0	6.7	8.4	7.0	5.5	7.2	4.8	3.4	5.2	8.0	5.2	4.3
7	5.4	4.4	6.6	9.6	7.3	7.1	4.5	6.0	4.9	4.4	5.3	7.4	5.4	6.5	8.8	6.1	5.4	7.1	3.4	5.8	4.9	6.8	5.7	3.6
8	4.4	3.5	6.9	9.8	7.4	7.2	4.8	6.7	4.0	4.9	5.3	6.8	4.0	6.3	8.1	5.8	5.3	6.8	3.7	4.6	4.6	6.7	5.8	3.8
9	12.5	11.3	11.6	16.1	12.4	11.6	11.4	13.3	11.8	13.4	12.3	11.3	11.9	12.7	13.4	12.0	12.7	12.1	11.2	13.3	13.0	12.6	12.4	13.3
10	4.9	4.7	4.9	7.4	5.7	5.8	4.2	6.6	4.7	5.0	4.9	4.5	5.0	4.0	7.8	5.5	3.1	4.2	4.2	6.6	5.8	6.1	5.8	5.3
11	5.7	5.5	6.8	6.8	6.7	6.0	6.2	7.9	5.4	6.2	6.8	8.1	5.7	5.6	7.3	7.3	6.2	5.3	6.4	7.1	5.5	8.2	7.9	5.6
12	8.8	8.7	8.9	4.8	6.6	8.5	9.1	10.4	7.4	9.4	10.2	9.2	9.2	8.5	8.0	10.3	8.5	7.0	9.2	9.1	8.7	10.9	9.6	8.9
13	4.5	4.3	6.6	8.6	7.3	6.3	4.6	5.9	5.1	4.2	4.7	7.5	4.3	4.5	7.6	5.8	4.3	6.3	4.8	5.3	4.8	6.9	6.6	3.6
14	5.0	4.7	7.0	9.2	6.9	7.8	6.0	7.5	5.7	5.5	5.4	7.2	5.8	6.9	8.7	6.7	5.4	6.2	4.3	4.9	5.6	7.4	5.3	5.3
15	6.5	6.2	5.1	8.8	6.6	6.4	6.0	8.0	5.8	7.1	5.7	3.5	6.0	5.9	7.8	5.9	5.3	5.8	5.6	7.4	6.8	6.5	6.0	6.4
16	6.0	6.8	6.7	6.5	3.9	7.7	6.7	7.9	6.0	6.2	6.8	6.9	7.0	6.9	9.4	7.1	5.2	5.8	5.9	7.3	6.0	8.1	6.3	6.3
17	5.5	5.2	4.9	8.3	6.0	4.8	5.7	7.3	4.5	5.7	5.7	5.4	3.8	4.7	6.9	4.8	5.5	5.0	5.1	5.5	4.4	7.0	5.9	4.8
18	3.4	3.3	3.8	8.4	5.6	4.7	3.2	5.1	4.2	3.9	3.0	4.9	4.2	3.8	7.8	4.7	2.7	4.5	3.3	5.9	4.2	5.6	4.8	4.4
19	3.5	3.6	4.9	7.9	5.1	5.1	3.4	5.6	2.7	4.2	4.2	5.0	3.1	3.8	7.2	4.1	3.7	5.1	3.4	5.4	3.4	5.5	5.0	2.9
20	5.2	4.3	4.0	9.0	5.1	3.8	4.1	6.6	2.8	6.1	5.1	4.7	4.6	5.2	6.9	5.5	5.3	5.0	4.2	6.4	4.4	6.4	6.1	5.1
21	5.2	4.4	3.2	9.0	5.7	4.3	3.2	5.5	4.3	4.6	4.2	4.8	5.2	4.6	8.1	5.0	4.2	5.0	3.3	6.8	4.6	5.5	5.3	4.7
22	4.2	3.9	3.9	8.6	5.8	4.3	4.2	5.9	3.3	4.5	4.4	4.4	3.3	3.7	6.8	3.7	4.2	4.6	3.8	5.2	3.3	5.4	4.7	4.0
23	5.5	5.0	4.3	9.1	5.4	5.2	5.1	7.3	4.0	6.4	5.9	4.0	5.4	5.2	7.8	5.5	5.7	4.4	4.7	6.7	5.3	6.4	5.3	6.4
24	4.9	4.8	4.3	8.1	5.7	4.1	4.7	6.8	3.2	5.6	4.8	4.6	3.6	4.0	5.9	5.0	4.6	4.7	5.1	5.0	4.0	6.3	5.6	4.4
25	5.0	4.9	3.6	8.1	5.1	3.7	3.8	6.0	4.4	5.0	4.2	4.5	4.2	3.5	7.7	3.9	3.9	4.8	4.4	7.0	4.4	5.5	5.9	4.5

Table 8. Continued.

Acc.	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
26		2.5	5.9	8.4	6.4	6.6	4.2	4.4	4.5	2.8	3.7	6.5	4.4	4.9	8.4	5.2	3.0	5.9	3.3	4.8	4.2	6.1	4.0	3.8
27			5.1	8.8	6.6	5.9	3.3	4.6	3.5	3.2	4.2	5.9	4.2	5.0	7.8	5.4	3.8	5.4	2.2	5.0	4.1	6.1	4.4	3.7
28				9.0	5.5	2.4	4.5	6.6	4.8	6.2	4.5	4.0	5.3	4.9	7.5	5.2	5.3	4.7	4.9	7.5	4.8	6.3	5.9	5.7
29					6.5	9.1	9.2	10.3	8.0	8.3	9.9	9.6	8.9	8.3	8.9	9.9	7.7	6.5	9.1	9.1	8.3	10.8	9.6	8.3
30						5.9	6.2	8.4	5.2	7.1	6.6	6.4	6.4	6.7	8.2	6.9	6.0	4.7	6.1	7.4	5.2	8.3	6.8	6.4
31							5.1	7.3	5.0	6.9	5.2	4.8	5.2	4.5	6.9	5.2	6.0	5.1	5.8	8.0	5.1	6.6	7.2	5.8
32								4.5	3.6	4.1	3.9	5.5	5.1	4.9	8.4	5.5	4.2	6.0	2.6	6.2	4.7	5.5	4.8	3.9
33									6.4	3.7	5.1	7.9	6.9	6.1	9.8	6.3	4.7	8.6	4.3	7.3	6.6	6.5	5.1	4.9
34										5.1	5.3	4.9	4.0	5.2	6.5	5.4	4.8	4.7	3.5	5.0	3.5	6.1	5.3	3.8
35											4.5	7.3	5.0	5.0	8.9	5.6	3.0	6.5	3.4	5.5	4.5	6.4	5.0	3.4
36												5.7	4.6	4.7	8.6	4.6	3.8	6.3	3.9	5.8	4.4	5.5	4.5	4.1
37													5.4	5.0	7.7	5.7	5.8	5.2	5.5	7.3	6.4	6.6	6.0	6.7
38														3.9	7.0	3.9	4.5	5.1	4.8	5.3	3.5	6.5	6.3	3.9

Acc.	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
39															7.1	4.2	3.7	5.1	5.2	6.6	5.5	6.0	6.3	5.0
40																6.6	7.6	7.1	8.1	8.0	7.7	6.9	9.0	7.2
41																	4.3	6.5	4.9	7.1	5.1	3.9	6.3	4.6
42																		5.4	3.6	5.8	5.0	5.2	5.0	3.9
43																			5.8	6.7	4.9	7.8	6.9	6.4
44																				5.5	4.4	5.1	3.9	3.6
45																					5.2	7.9	4.5	5.0
46																						6.8	5.7	3.3
47																							6.4	5.7
48																								5.3
49																								

Note Acc. = Accessions

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Biography

Mulatu Aberra is research staff of crop improvement specifically cereal research department at Sinana Agricultural Research Center of Oromia Agricultural Research Institute, Ethiopia. He has undertaken applied research to enhance cereal crop productivity and production. Additionally, he has designed and conducted many experimental studies on field crops. He appreciates crop production under different agro-ecologies and encourages farmers to exploit the integrated potential of cultural practices to manage climate change and sustain productivity. He is involved in many national and international projects focusing on crop improvement along with different stakeholders.