

Full Length Research Paper

Genetic diversity of Ethiopian durum wheat (*Triticum durum* Desf) landrace collections as revealed by morphological markers

Meseret Asmamaw Wondifaw^{1*}, Gemechu Keneni² and Kassahun Tesfaye³

¹Holeta Agricultural Research Center, Ethiopian Institute of Agricultural Research, Ethiopia.

²Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia.

³Institute of Biotechnology, Addis Ababa University, Ethiopia.

Received 5 January, 2020; Accepted 7 July, 2020

Knowledge of the extent and pattern of genetic diversity within and among populations is crucial to identify useful breeding materials and design appropriate collection and conservation strategies. Genetic diversity of 160 durum wheat (*Triticum durum* Desf) accessions was studied using 15 morpho-agronomic traits. The field studies for morphological characterization were undertaken at Adadi Maryam and Ginchi locations using randomized complete block design with two replications. The average linkage technique of clustering produced a more understandable portrayal of the 160 durum wheat accessions and released varieties by grouping them into seven clusters with inter-cluster D2 values ranged from 13.72 to 235. The highest genetic distances (253) was observed between cluster five (improved varieties) and cluster three accessions. The minimum genetic distance (13.72) was observed between cluster one and two both are landrace collections. Five of the 15 principal components accounted for more than 76.98% of the total variation in the Ethiopian durum wheat genotypes. The first principal components accounted for 32% of the total differences. In this study, there is a moderate genetic diversity between landraces collected from Tigray, Gonder, and Wello. Landraces from these areas can be used as a source of important pre-breeding material for future breeding programs.

Key words: Landraces, durum wheat varieties, genetic distances, correlation, genetic diversity, morphological characters.

INTRODUCTION

Durum wheat (*Triticum durum*, $2n=4x=28$) is a monocotyledonous crop of the Gramineae family grown in Ethiopia since antiquity (Feldman, 2001). Zohary (1970) considered Ethiopia as the center of origin for the crop, whereas Purseglove (1975) reported the existence of adequate genetic diversity in landraces of durum wheat grown in the country. However, it is controversial

that Ethiopia is the center of origin for durum wheat because of the absence of ancestral forms and wild relatives, which rule-out the proposition that Ethiopia is the center of origin (Pecetti et al., 1992). In Ethiopia, durum wheat (*T. durum* Desf.) is mostly planted on heavy black clay soils (vertisols) of the highlands between 1800 and 2800 m above sea level (masl) (Tesemma et al.,

*Corresponding author. E-mail: mameseret45@gmail.com.

1991). It is the main source of semolina for the production of pasta, couscous, burghul, and other local end-use products, but also provides many beneficial traits, including resistance to rust diseases, environmental stability, yield potential, and high quality for bread wheat improvement.

Durum wheat is predominantly grown in central, northwestern and northeastern parts of Ethiopia (Tesemma et al., 1991; Bechere et al., 2000; Gashaw et al., 2007) for different purposes, mainly for its resistance to biotic and abiotic stresses, and better flour and food quality, competitive ability to weeds and straw production. Durum wheat was once the only crop grown in most of the wheat-producing areas of Ethiopia until very recently when it was overtaken by the adoption of improved bread wheat varieties (Tsegaye and Berg, 2007).

There is no doubt that plant breeding is considered one way to confront the challenge of bridging the widening gap between the demand and supply of food grain crops in Ethiopia. The inception of wheat (*Triticum aestivum* and *T. durum*) breeding in Ethiopia dated back to the early 1960s, and, as a result of the efforts made hitherto, many improved varieties have been developed and released to farmers. Ethiopia, as a center of diversity for durum wheat, has plenty amount of germplasm resources, which are essential for breeding programs as a source of genes for different traits. Assessment of the genetic diversity and identify the area with the highest genetic diversity, therefore, the crucial step to use the genetic resources in the breeding program.

Wheat is grown dominantly grown in Ethiopia since antiquity. Even though durum wheat is grown in many areas of the country, the production is very low compared with other crops due to biotic and abiotic stresses (Faris, 2011). To overcome these stresses, using improved resistant varieties and agronomic practices are the major ones. Most of the improved varieties become out of production in a very short time after release due to the low level of resistance to frequent disease Stem rust because of the appearance of new aggressive pathogen races (Singh et al., 2011) and drought. To increase the tolerance of durum wheat varieties to biotic and abiotic stresses crossing of genotypes distant genetic backgrounds is the major and safe option. Mostly genotypes selected from distant parents can resist stresses. Assessment of extent and pattern of genetic diversity is, therefore, a crucial step to equip wheat breeding programs. Therefore, this study aims to assess the genetic diversity of Ethiopian durum wheat landraces and identifying regions with high genetic diversity.

MATERIALS AND METHODS

One hundred and forty-one durum wheat germplasm accessions collected from various eco-geographical zones of Ethiopia and nineteen released varieties were evaluated in this study. The genotypes were all received from the Ethiopian Biodiversity Institute, whereas the released varieties were obtained from Debre

Zeit Agricultural Research Center. The germplasm accessions were initially collected from the major durum wheat producing zones of Oromia, Tigray and Amhara regions including Arsi, Bale, West Shewa, East Shewa, Harergie, Semen Shewa, North Gonder, South Gondar, South Wello, North Gojam, South Gojam, Northern Tigray, Central Tigray, and Eastern Tigray (Table 1). The germplasm accessions and released varieties tested in this study are, hereafter, treated as genotypes for experimental purposes.

F Test locations

The genotypes were evaluated at two locations, Ginchi and Adadi, in Ethiopia during the year 2015. The locations were assumed to represent the major durum wheat production areas of Ethiopia. The detailed descriptions of the test locations in terms of geographical position, mean annual rainfall, mean annual temperature, and soil characteristics are shown in Table 2.

Experimental design and layout

The seed rate for a plot of one row 1 m long was 6 g. The spacing between rows was 30 cm. A blanket basal application of nitrogen and phosphorus fertilizer has applied to all plots at the recommended rate of the Ethiopian wheat research program N₂: P₂O₅ Ginchi (64:46) and Adadi (60:69), respectively. All other crop management practices were applied uniformly to all plots as required so that the test genotypes could express their full genetic potential for the traits under consideration. The experiment was laid down in a randomized complete block design (RCBD) with two replications. The genotypes were assigned to plots at random within each block. The data will be collected for fifteen agro-morphological traits (Table 3).

Data analysis

The magnitude of genetic distances

Genetic distance analyses: Genetic distances between clusters as standardized Mahalanobis's D² statistics was calculated as:

$$D_{ij}^2 = (x_i - x_j)' \text{cov}^{-1}(x_i - x_j)$$

where D²_{ij} = the distance between cases i and j; x_i and x_j = vectors of the values of the variables for cases i and j; and cov⁻¹ = the pooled within-groups variance-covariance matrix. Principal components based on the correlation matrix will be calculated using the same software as in clustering.

The D² values obtained for pairs of clusters were considered as the calculated values of Chi-square (χ²) and were tested for significance both at 1 and 5% probability levels against the tabulated values of χ² for 'P' degree of freedom, where P is the number of characters considered (Singh and Chaudhary, 1985).

Patterns of genetic distances

Cluster analysis: The data on quantitative measurements were standardized to a mean of zero and a variance of unity before clustering and principal component analysis to avoid differences in scales used to measure different traits. The grouping of the genotypes into different homogeneous groups based on multiple characteristics was conducted following the average linkage method. Genetic diversity between clusters based on a correlation matrix was calculated based on Mahalanobis's D² statistic (Mahalanobis, 1936) using the SAS system software package (SAS Institute, 2002). The important traits in each principal component

Table 1. Description of the test genotypes and released varieties.

Region	Zone	No. of genotypes	Name of genotypes/accession number
Amhara	South Wello	10 (1-10)	Acc. No 231623, 231597, 231600, 222855, 226094, 8185, 8186, 214590, 214550, 213149
Amhara	South Gonder	11 (11-21)	Acc. No. 206573, 222621, 222641, 216614, 222655, 222608, 222613, 7412, 216474, 226951, 222616
Amhara	West Gojam	6 (22-27)	Acc. No. 203750, 203922, 203893, 5487, 208212, 203757
Amhara	East Gojam	11 (28-38)	Acc. No. 208189, 208195, 210821, 226833, 226844, 231617, 231618, 214515, 8333, 8328, 214517
Amhara	North Gonder	10 (39-48)	Acc. No. 222515, 203840, 5217, 204340, 6856, 216492, 216545, 226207, 226208, 216440
Oromia	North Shewa	11 (49-59)	Acc. No. 208265, 208278, 208286, 208310, 208312, 208317, 208491, 226375, 5679, 5739, 226892
Oromia	Arsi	11 (60-70)	Acc. No. 222421, 222422, 222428, 226868, 226356, 7073, 214498, 7022, 226273, 5927
Oromia	Bale	7 (71-77)	Acc. No. 231467, 222324, 222338, 204349, 204370, 227060, 204357
Oromia	Harergie	14 (78-91)	Acc. No. 214503, 203695, 203886, 226180, 226183, 222708, 231471, 203690, 231603, 5730, 203854, 226179, 231606, 231613
Oromia	East Shewa	11 (92-102)	Acc. No. 210808, 5429, 216651, 5314, 203748, 5300, 5248, 5180, 5736, 214313, 226959
Oromia	West Shewa	11 (103-113)	Acc. No. 231528, 222457, 222461, 231557, 231526, 214328, 5454, 5144, 6101, 7206, 227020
Tigray	Southern Tigray	10 (114-123)	Acc. No. 214343, 7956, 207854, 206551, 206554, 223257, 226199, 206558, 238113, 226245
Tigray	Central Tigray	10 (124-133)	Acc. No. 238114, 238118, 238121, 238122, 238123, 238124, 238125, 238126, 238136, 238137
Tigray	Eastern Tigray	8 (134-141)	Acc. No. 238127, 238128, 238129, 238130, 238131, 238133, 238134, 238135
Improved varieties		19 (142-160)	Ginchi, Yerer, Worer, Mangudo, Arendato, Assasa, Denbi, Tob, LD-357, Hitosa, Mukye, Killinto, Quamy, Gerardo, Foka, Cocorit, Boohie, Bichena, Meteyaya

that significantly contributed to the variation observed were identified as suggested by Johnson and Wichern (1988).

The clustering of the genotypes was performed by the average linkage method of SAS system software (SAS Institute, 2002). Points, where local peaks of the pseudo F statistic join with small values of the pseudo t2 statistic followed by a larger pseudo t2 for the next cluster fusion, were examined to decide the number of clusters (SAS Institute, 2002). The dendrogram was built using MINITAB 14.

RESULTS AND DISCUSSION

The magnitude of phenotypic diversity

Genetic distances

Genetic distances (D^2) between the clusters of 160 durum wheat genotypes are presented in Table 4. Inter-cluster D^2 values ranged from 13.72 (between clusters C1 and C2) to 253.89 (between clusters C3 and C6) (Table 4). The maximum

pairwise generalized squared distances (D^2) were found between clusters C3 and C6. Cluster C3 constituted landraces collected from Tigray and Amhara, whereas cluster C6 constituted of released varieties from (DZARC).

The first most divergent cluster group were clusters C3 and C6 ($D^2 = 253.89$), which constituted local landraces collected from Amhara and Tigray regions and released varieties (DZARC), respectively. Landraces collected from Amhara (south Gonder and Wello) and Tigray (central and eastern) showed high genetic diversity within the location, and landraces fall into distant clusters 1 and 3. On the other hand, the least divergent groups were clusters C1 and C2 ($D^2 = 13.72$). Most of the landraces collected from the three regions (Amhara, Oromia, and Tigray) were included in the first and second clusters; they have the lowest genetic diversity between them. Within landraces, the highest genetic diversity was observed between cluster three

(from south Gonder and central Tigray) and cluster four (Central Tigray). This result showed that all landraces except accession no. 238134 were grouped in the first three clusters, and only it remains accession 238134 solitary at cluster four, and it was the most distantly related to the other genotypes. The landraces/accessions obtained from Tigray, Wello, and south Gonder did not group closer with each other while other accessions from Oromia and the rest of Amhara were group closer.

Patterns of genetic diversity

Cluster analysis

Cluster analysis of the 160 genotypes distinguished them into seven different clusters (Figure 1 and Table 5). Members within a single cluster or in clusters with non-significant distances have closer

Table 2. Description of the test locations in terms of geographical position and Physico-chemical properties of the soils.

Descriptor	Location	
	Ginchi	Adadi Maryam
Latitude	09°30' N	08°31' N
Longitude	38°30' E	38°13' E
Altitude (m a. s. l.)	2200	2383
Mean annual rainfall (mm)	1139	1105
Mean annual temperature (°C)	16.3	16.9
Soil type	Black Vertisol	Light brown
Soil drainage	Poorly drained	Well-drained
Soil pH	6.18	7.62
% clay	65.83	61.19
% silt	20.42	25.91
% sand	13.75	12.66
Organic C(%)	1.30 (low)	1.16
N (%)	0.103 (low)	0.15
P (ppm*)	4.49 (low)	8.70
K (ppm)	2.483 (high)	39.75
PH (H ₂ O)	6.18	6.32
EC (µs)	547.33	405.63

Source: Keneni et al. (2012).

relationships than genotypes from significantly distant groups. The first cluster (C1, n = 113) had the largest number of genotypes collected from three regions in Ethiopia. Followed by the second cluster (C2, n = 25) was the second-largest in the number of genotypes constituted from all over the areas, the fourth and six clusters, with only a single genotype each, being the least in terms of the number of genotypes (n=1, 1), respectively. The fifth and seventh clusters were taking the third and fourth ranks in terms of numbers of genotypes (n =10 and 8), respectively. Data in the table revealed the following.

Cluster I: The first cluster consisted of 113 landraces collected from the entire regions of collection. Members exhibited medium plant height (107.25 cm) and late mature (126.27) than other clusters. This cluster was relatively better in the number of tillers (7.9) and relatively better in thousand kernels weights (29.83). From the first four clusters made by landraces, cluster three was the highest in harvest index, grain yield, and biomass yield (78.53, 103.67, 129.32), respectively, followed by cluster one (77.29, 96.36, 122.88). In all clusters, cluster one showed medium performance from other clusters.

Cluster II: This cluster had consisted of 25 landraces collected from all regions of collection, which were medium in plant height and relatively late matured (127.22 days) than genotypes of other clusters (Table 6). Genotypes in this cluster were characterized by low harvest index (60.19), grain yield, and biomass yield

(46.51, 75.58), respectively. They were medium in grain filling duration (64.55), but they showed the lowest efficiency in grain production (59.61) and had a low rate of biomass production and economic growth (72.01).

Cluster III: Consisted of two landraces collected from the Amhara and Tigray region. It was characterized by the latest maturing (127.83) days, and it needs a more extended grain filling period than others (Table 6). It has disease severity (36.8%) for stem rust disease. Genotypes in this cluster showed the lowest thousand kernel weight (19.93, 103.67, 129.32), respectively, medium in grain yield, and biomass yield. From the clusters made by landraces, this cluster had shown the highest production biomass production (101.51) and economic growth rate (146.87).

Cluster IV: Had only one landrace which was collected from the Tigray region. When we compare its value with the mean of the landraces of other clusters, it had the most extended plant height (117.5), late-maturing (125.75), largest leaf area index (147.75), for stem rust had 39.46% disease severity, the number of tillers per plant (5.25), and harvest index (67.43). This cluster was the least performance cluster in terms of yield, and yield components had a lower rate of biomass production (64.68) and economic growth rate (88.68) than the other clusters.

Cluster V: Consisted of 10 released varieties. They were characterized by the shortest plant height (85.91),

Table 3. Measurements and their description were taken to all genotypes.

S/N	Traits	Description
1	Plant height (PH)	The average height of the plants in cm from the ground level to the tip at maturity excluding the awn
2	Heading date (HD)	The number of days from planting to a stage when 50% of the plants in a plot have produced spikes
3	Maturity date (MD)	The number of days from planting to a stage when 50% of the plants in a plot have reached maturity
4	Stem rust scoring (SR)	Incidence and severity of the disease scored at two times
5	Number of tillers/plant (TPP)	The average number of effective tillers per plant
6	Number of spikelets/spike (SPPS)	The average number of spikes lets per spike from five randomly selected spikes from a genotype
7	Grain yield/plant (GLD)	The weight (in grams of grain yield obtained from randomly selected five plants in a genotype
8	Harvest index (HI%)	The ratio of dried grain yield to the biomass yield and multiplied by 100;
9	Biomass/Plant (BMP)	The total above-ground biological yield (grains and all other parts) in grams per plant
10	Leaf area index at maturity (LAI)	It is defined as the one-sided green leaf area per unit ground surface area (LAI = leaf area /ground area, m ² /m ²)
11	Grain filling period (GFP)	The number of days from the heading to maturity
12	Grain production efficiency (GPE)	Grain filling duration divided by duration of vegetative; period and then multiplied by grain yield
13	Economic growth rate (EGR)	Grain weight divided by grain filling duration and then multiplied by 100);
14	Thousand kernel weight (TKW)	The weight in a gram of 1000 seeds
15	Spike length (SL)	The average length of a spike, in cm from its base to the tip, excluding awns.

Table 4. Pairwise generalized squared distances between seven clusters constituting 160 durum wheat genotypes.

Cluster	Clusters						
	C1	C2	C3	C4	C5	C6	C7
C1	0.00	13.72 ^{NS}	128.80**	33.35**	60.26**	71.62**	57.35**
C2		0.00	149.94**	35.17**	73.20**	104.32**	45.88**
C3			0.00	149.69**	235.51**	253.89**	231.05**
C4				0.00	101.83**	135.74**	100.55**
C5					0.00	40.54**	29.55*
C6						0.00	75.95**
C7							0.00

* =Significant, **= highly significant and NS = Non significant.

relatively early maturing (124.41), and it required the shortest time for grain filling (60.02). It has exhibited (18.85) for stem rust disease severity. It was the second cluster in grain yield (103.27)

performance next to cluster six. This cluster had better performance in harvest index (83.82), grain production efficiency (95.26), biomass production rate (99.61), and economic growth rate (175.56).

Cluster VI: This cluster consisted of only one released variety, characterized by best performance in terms of thousand kernel weight (43.23), harvest index (89.10), grain yield (163.99),

Table 5. Clustering of 160 durum wheat genotypes from different origins into seven clusters using 15 morpho-agronomic characters.

Cluster	No. of genotypes	Sources of genotypes	Origins of genotypes
1	113	Collection	Tigray, Amhara and Oromiya
C2	25	Collection	Tigray, Amhara and Oromiya
C3	2	Collection	Amhara and Tigray
C4	1	Collection	Tigray
C5	10	Released varieties	DZARC
C6	1	Released varieties	DZARC
C7	8	Released varieties	DZARC

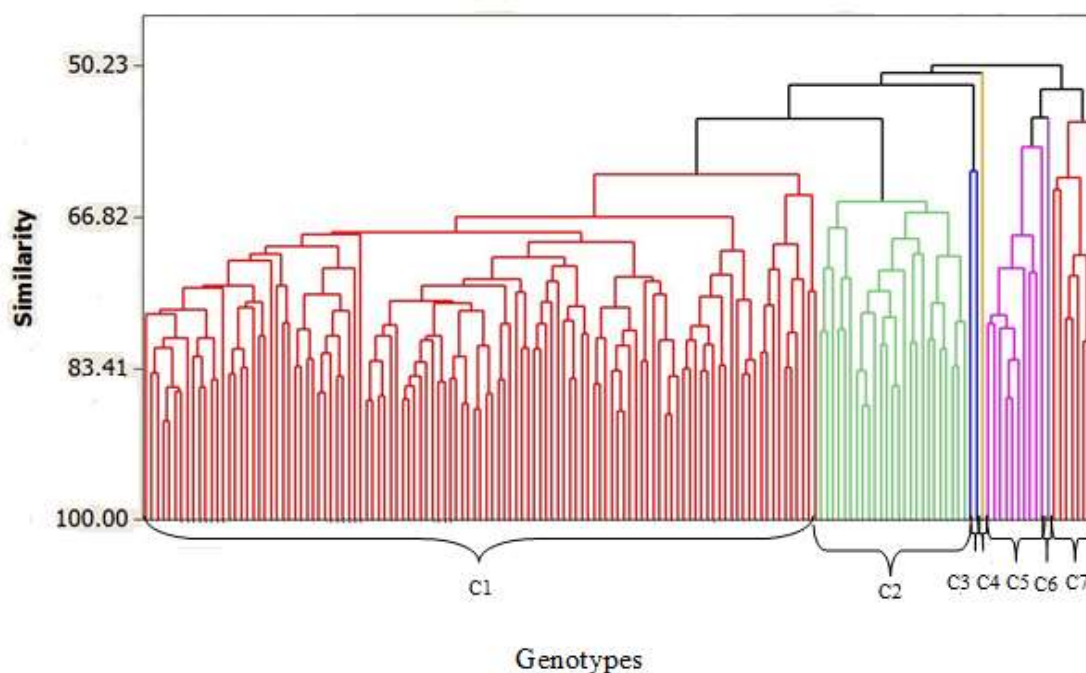


Figure 1. A dendrogram of 160 durum wheat genotypes developed by average linkage method based on Euclidean distance using 15 morpho-agronomic characters.

and biomass yield (183.87). It was resistant to stem rust disease severity (10.80%). It matured early (124.25), and it required a shorter grain-filling period (62.00). It had a relatively short spike length (6.50) with dense spike type. It was also characterized by high grain yield (163.99) and biomass yield production (148.57). The only member included in this cluster, variety Mangudo was better in yield and yield components than other released varieties and landrace collections as well. It was better efficient in grain production, and it had high biomass production and economic growth rate.

Cluster VII: This was the last cluster, which consisted of 8 released varieties. They were small in yield performance than other clusters except cluster two. They were

characterized by early maturing (125.86) and short plant height (100.86). They also showed that smaller spike length (8.19) with dense spike shape. It has 26.09% for stem rust disease severity, but it was lower in grain yield and biomass yield (114.17) and also harvest-index. The grain production efficiency, biomass production rate (91.21), and economic growth rate were also lower for this cluster (141.56).

The local landraces were distributed over clusters C1-C4 but mostly fell into clusters C1 and C2, whereas the released varieties fell into three clusters C5, C6, and C7. Generally, the pattern of distribution of the genotypes from different origins over different clusters was random, showing that there was no clear association between

Table 6. Differences among the seven clusters of 160 durum wheat genotypes for mean performance of 15 characters.

Character	Cluster							Grand mean
	C1	C2	C3	C4	C5	C6	C7	
Plant Height (PHT)	107.25	107.72	108.75	117.5	85.91	90.00	88.89	100.86
Heading Date (HD)	62.86	62.39	56.83	62.00	63.95	62.25	63.19	61.92
Maturity Date (MD)	126.97	127.22	127.83	125.75	124.41	124.25	124.56	125.86
Leaf Area Index (LAI)	96.95	92.86	101.50	147.75	77.87	72.33	84.98	96.32
Stem Rust first score (SR)	30.43	30.73	36.80	39.46	18.85	10.80	15.56	26.09
Number of tillers/ plant (TIL)	7.9	8.18	8.92	5.25	7.61	7.00	8.56	7.63
Thousand Kernel Weight (TKW)	29.83	25.42	19.93	24.54	27.21	34.23	30.3	27.35
Harvest Index (HI)	77.29	60.19	78.53	67.43	83.82	89.10	64.34	74.39
Grain Yield (GLD)	96.36	46.51	103.67	56.88	103.27	163.99	55.7	89.48
Biomass Yield (BM)	122.88	75.58	129.32	81	123.27	183.77	83.36	114.17
Grain Filling Duration (GFD)	64.1	64.55	71	63.75	60.02	62.00	60.61	63.72
Spike length (SL)	9.71	9.82	10.33	9.75	5.64	6.50	5.61	8.19
Spike lets Per Spike (SLPS)	20.25	20.08	18.83	16	17.07	17.75	19.75	18.53
Grain Production Efficiency (GPE)	99.89	49.06	159.75	60.45	95.26	165.03	53.75	97.60
Biomass Production Rate (BPR)	97.23	59.61	101.51	64.68	99.61	148.57	67.29	91.21
Economic Growth Rate (EGR)	151.37	72.01	146.87	88.68	175.56	264.88	91.57	141.56

Table 7. Clustering pattern of Durum wheat genotypes from different locations over seven clusters based on the mean performance of 15 response characters at two locations.

Origin	No. of genotypes	No. of genotypes in each cluster						
		C1	C2	C3	C4	C5	C6	C7
North Shewa	11	9	2	-	-	-	-	-
Arsi	11	8	3	-	-	-	-	-
Bale	7	5	2	-	-	-	-	-
West Harergie	3	3	-	-	-	-	-	-
East Harergie	11	9	2	-	-	-	-	-
East Shewa	11	10	1	-	-	-	-	-
West Shewa	11	11	-	-	-	-	-	-
South Wello	11	8	-	3	-	-	-	-
South Gonder	11	10	-	1	-	-	-	-
West Gojam	6	6	-	-	-	-	-	-
East Gojam	11	9	2	-	-	-	-	-
North Gonder	9	8	1	-	-	-	-	-
Southern Tigray	10	5	5	-	-	-	-	-
Central Tigray	10	9	-	1	-	-	-	-
Eastern Tigray	8	4	3	-	1	-	-	-
Released Varieties	19	-	-	-	-	10	1	8

geographic sources of origin and genetic diversity.

Landraces collected from West Shewa, West Harergie, and West Gojam zones showed limited phenotypic diversity in that their members were entirely grouped only into cluster C1. The landraces collected from the other zones, except for genotypes from Central Tigray, Eastern Tigray, South Gondar, and South Wello, which were either distributed over distantly divergent or more than

two clusters, fell into the first two clusters (C1 and C2) with a non-significant distance. The detailed distribution of the genotypes over the clusters is shown in Table 7.

Principal component analysis

Five of the 15 principal components accounted for more

Table 8. The Eigenvalues and vectors of the correlation matrix for 17 traits of 160 *Triticum turgidum* L. landraces of Ethiopia.

Parameter	PRIN1	PRIN2	PRIN3	PRIN4	PRIN5
Eigen value	5.60	3.19	1.67	1.31	1.14
% variance	32.91	20	9.7	8	6.2
Cumulative	32.91	52.93	62.71	70.77	76.98
Character	Eigenvectors				
Plant Height (PHT)	-0.069	0.358	0.141	0.124	-0.156
Heading Date (HD)	-0.003	-0.222	0.497	0.248	0.413
Maturity Date (MD)	-0.072	0.315	-0.237	0.027	0.434
Leaf Area Index (LAI)	-0.054	0.303	0.201	0.231	-0.026
Stem Rust score (SR)	-0.119	0.353	0.291	-0.247	-0.089
Tillering (TIL)	-0.062	0.037	0.014	-0.302	0.560
Thousand Kernel Weight (TKW)	0.116	-0.060	-0.143	0.558	-0.255
Harvest Index (HI)	0.348	0.053	0.009	-0.073	0.115
Grain Yield (GLD)	0.416	0.083	0.037	-0.027	0.047
Biomass Yield (BM)	0.403	0.094	0.062	-0.008	0.016
Grain Filling Duration (GFD)	-0.048	0.377	-0.517	-0.156	0.012
Spike length (SL)	-0.075	0.418	0.102	0.294	-0.087
Spike lets Per Spike (SLPS)	-0.017	0.150	-0.137	0.505	0.443
Grain Production Efficiency (GPE)	0.384	0.184	-0.129	-0.080	-0.038
Biomass Production Rate (BPR)	0.405	0.069	0.076	-0.013	-0.018
Economic Growth Rate (EGR)	0.414	0.014	0.124	-0.012	0.061

PRIN1, PRIN2, PRIN3, PRIN4 and PRIN5 = Principal components 1, 2, 3, 4 and 5 respectively.

than 76.98% of the total variation in the Ethiopian durum wheat genotypes. The first principal component accounted for 32% of the overall differences, and the corresponding value for the second principal component was 20% (Table 8). The first two principal components (PRIN1 and PRIN2) contributed about 52.93% of the total variation. Generally, the traits included in the first principal component had small effects of individual contribution (-0.089 to 0.416) to the difference in PRIN1, but characters with relatively higher positive weights of eigenvectors in PRIN1 include grain yield, economic growth rate, biomass production rate, biomass yield, and harvest index. Selection based on these characters may be effective because of the higher comparative variability. Other characters like days to heading and the number of spikelets per spike had smaller negative/ positive eigenvector values contributed the least share to the total variation of genotypes in the first principal component. Spike length, grain filling duration, plant height, stem rust scores, and leaf area index had a relatively higher positive contribution to the second principal component. Different characters also contributed to the variation in the third fourth and five principal components (PRIN3 PRIN4, and PRIN5), but the component accounted for relatively smaller total differences of 9.7, 8, and 6.2%, respectively.

Characters with relatively higher positive weights of Eigenvectors in PRIN1 include Grain yield, Economic

growth rate, biomass production rate, biomass yield, and harvest index. Breeding programs should target those characters to improve the yield and its components as well. Besides this, Eigenvectors of stem rust scores, maturity date, spike length, and plant height had relatively large negative weights on this component. Breeding efforts may need to simultaneously focus on the genetic manipulation of these characters to reduce the disease infection and length of maturity time. Heading date and spikelets per spike with smaller negative and positive effects respectively were contributing the least to the variation of genotypes in the first principal component.

Spike length, grain filling duration, plant height, stem rust scores, and leaf area index had a relatively significant positive effect on the differentiation of the population in the second principal component. Heading date and thousand kernel weight had negative effects, but others were positive effects. Two characters, namely economic growth and thousand kernel weight with small positive and negative effects respectively, contributed least to the variation of genotypes in this component.

DISCUSSION

The magnitude of genetic diversity

The minimum inter-cluster distance was observed

between clusters C1 and C2. It indicated that members of these clusters were closely related and, therefore, the crossing of genotypes from these two clusters may not produce a high level of heterotic expression in the F1's with broad-spectrum of variability in segregating (F2) populations (Allard, 1960). On the other hand, the maximum inter-cluster distance between clusters C3 and C6 indicated that the members of these clusters were most divergent. Hence, the crossing of genotypes from these clusters may be successful in terms of producing higher heterotic expression in the first filial generation and better variability in the segregating generations thereof. Parents for hybridization could be selected based on the large inter-cluster distance for isolating useful recombinants in the segregating generations (Allard, 1960). Increasing parental distance implies a greater number of constraining alleles at the desired loci, and then to the extent that these loci recombine in the F2 and F3 generations following a cross of distantly related parents, the greater will be the opportunities for successful selection for any character of yield interest (Ghaderi et al., 1984; Gashaw et al., 2007).

The first most divergent cluster group were clusters C3 and C6 ($D^2 = 253.89$), which constituted local landraces collected from Amhara and Tigray regions and released varieties, respectively. Maximum genetic recombination and variation in the subsequent generation are expected from crosses that involve parents from the clusters characterized by maximum distances. Crosses between the landraces and introduced genotypes constituted in different clusters are expected to provide relatively better genetic recombination and segregation in their progenies (Singh et al., 2014). On the other hand, the least divergent groups were clusters C1 and C2 ($D^2 = 13.72$). Therefore, crossing from those parents with small genetic distance will not give us higher segregation.

Patterns of genetic diversity

Clustering

Genetic diversity using cluster mean analysis by Euclidean dissimilarity dendrogram has also been reported previously in other studies by (Ali et al., 2013; Shahryari et al., 2011; Aharizad et al., 2012; Ahmadi et al., 2012; Degwoine and Alamrew, 2013; Mengistu and Pè, 2016). The dendrogram elaborates on the relative magnitude of resemblance among the genotypes as well as the clusters (Singh et al., 2014). Based on agromorphological traits, the tetraploid wheat landraces and improved varieties were clustered into seven cluster groups consisting of 1 up to 113 accessions. Most of the landraces collected from the three regions were grouped into cluster one, which contained 113 landraces. This indicated that the genetic diversity of Ethiopian durum wheat shows some reduction, or there is a duplication of

germplasms in Ethiopian collection. This may be due to the fast rate of replacement of landraces with new, improved bread and durum wheat varieties in the country to overcome the yield loss caused by frequent wheat rust disease epidemics. Faris (2011) reported similar results on the reduction of genetic diversity of Ethiopian tetraploid wheat landraces.

On the other hand, the current result is contrary to the previous studies conducted by Yifru et al. (2006), Negassa (1986), Teklu and Hammer (2008) and Mengistu et al. (2015). Who reported the presence of high genetic diversity in Ethiopian durum wheat landrace collections, and they found similar patterns repeatedly in their study. Besides, Hamrick and Godt (1989) indicated that self-pollinating species maintain high genetic diversity at their polymorphic loci and that most of the variation is found among accessions of landrace collections. Additionally, Mengistu et al. (2015) analyzed the genetic diversity of 274 landraces by using eight qualitative and three quantitative traits scored for 2740 plants and analyzed for genetic diversity and reported that Ethiopian durum wheat landraces are very diverse both within and among districts of origin and altitude classes. Also, Mengistu and Pè (2016) reported higher genetic diversity in EBI collections of durum wheat landraces.

Based on the cluster analysis, some landraces from the same places of origin fell into different clusters and *vice versa*. There was no correspondence between geographic and genetic distances, that is, germplasms, collected from the same geographic area were placed into different cluster groups, and those obtained from different geographic regions were placed into the same cluster. Similar results were found from previous works by Gashaw et al. (2007). Landraces and improved varieties formed different cluster groups; this may be due to the distant genetic background between the improved varieties and landraces. Most of the improved varieties used for this study have CIMMYT and ICARDA backgrounds. Similar results were found by Mengistu and Pè (2016), who analyzed Durum wheat genotypes consisting of 265 farmers' varieties and 24 improved varieties. These analyses displayed larger genetic diversity than in those improved varieties.

On the other hand, Mengistu et al. (2015) also reported that separate cluster formation of improved varieties from the landraces. Landraces collected from Wello, South Gonder, and Eastern Tigray showed better genetic diversity than others, this might be due to low gene flow because of slow seed exchange in these areas. Landraces of these three locations (Wello, South Gonder, and Eastern Tigray) showed much similarity than others. They fell into clusters 1 and 3 similarly. On the other hand, landraces collected from Shewa, Arsi, and Bale failed to separate into different clusters. They were grouped in the first and second clusters without showing significant genetic distances. It might be due to the

highest rate of reduction of durum wheat production in these areas, and there is a high chance of replacement of durum wheat by improving bread wheat varieties because of the proximity of the national wheat research coordinating center. Similar findings of the low level of genetic diversity of Arsi and Bale and Shewa locations were reported by the previous studies (Tessema et al., 1991, Bechere et al., 2000; Mengistu et al., 2015).

The clustering of various districts of origins appeared to follow a propinquity-based trend, representing a higher probability of germplasm exchange among farmers in neighboring regions than among those in the distant areas (Faris, 2011). This trend may explain the clustering of North Gonder with West Gojam and of West Shewa with North Shewa in the same cluster. However, the clustering of mutually distant districts could be due to the introduction of germplasm from one to the other, either formally or informally, sometimes long ago. For instance, the clustering of Arsi and East Tigray landraces in one sub-cluster and Bale and South Gonder in the other sub-cluster may be due to such movements. Faris (2011) also suggested germplasm exchange among non-proximal farmers as an explanation for the clustering of landraces from Arsi and Wollo, mutually distant regions, in their study. Bayush et al. (2007) reported that lumping of species together from larger areas not only affects the clustering pattern but may bias estimates of diversity.

Principal components

The first two principal components (PRIN1 and PRIN2) contributed about 52.93% of the total variation. Therefore, characters with relatively larger absolute values of eigenvector weights in PRIN1 had the highest contribution to the difference of the genotypes into clusters. As it is normally assumed that characters with larger absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002). In consequence, the traits included in the first principal component had small effects of individual contribution (-0.089 to 0.416) to the variation in PRIN1. Therefore, the differentiation of the accessions into different clusters was dictated by the cumulative effects of many characters (Keneni et al., 2013). Landraces grouped in similar clusters showed the same pattern in the principal component analysis by failing in a similar quadrant. Similar results were found by Mengistu et al. (2015) and Ratiba et al. (2012).

Conclusion

Based on the results of this study, we can conclude that there is a moderate genetic diversity between landraces collected from Tigray, Gonder, and Wello. Landraces of

these areas can be used as a source of essential genes for future breeding programs.

On the other hand, minimum genetic diversity was found between landraces of Shewa, Arsi, and Bale, and this might be due to high gene flow between these areas as they are nearby geographically. Moreover, improved varieties showed high genetic diversity with landraces, but they have profound differences between them. In general, the selection of parent materials from germplasms collected from areas that have wider genetic diversity would be useful to incorporate essential genes underlying different traits like yield and resistance for biotic and abiotic stresses.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

- Aharizad S, Sabzi M, Abolghasem SA, Kohadadadi E (2012). Multivariate analysis of genetic diversity in wheat (*Triticum aestivum* L.) recombinant inbred lines using agronomic traits. *Annals of Biological Research* 3(5):2118-2126.
- Ahmadi M, Farshadfar E, Veisi S (2012). Evaluation of genetic diversity in landraces of bread wheat under irrigated and rainfed conditions. *International Journal of Agriculture and Crop Science* 4:1627-1636.
- Ali S, Khan G, Zia Kumar B, Yousuf M, Roomi T, Ahmad MF (2013). Estimation of Genetic Diversity in Genetic Stocks of Common Wheat (*Triticum aestivum* L.) Using SDS-PAGE, *European Academic Research* 1:1861- 1871.
- Allard R (1960) *Principles of Plant Breeding*. New York, USA: John Wiley and Sons.
- Bayush T (2007). Incentives for on-farm conservation in a center of diversity: A case study of durum wheat (*Triticum turgidum* L.) landraces from East Shewa, Central Ethiopia. Norwegian University of Life Sciences (UMB), Norway.
- Bechere E, Kebede H, Belay G (2000). Durum wheat in Ethiopia. An old crop in an ancient land. IBCR, Addis Ababa, Ethiopia.
- Chahal GS, Gosal SS (2002). *Principles and procedures of plant breeding: biotechnological and conventional approaches*. Narosa Publishing House, New Delhi.
- Degwoine A, Alamrew S (2013). Genetic diversity in bread wheat genotypes (*Triticum aestivum* L.) genotypes. *Pakistan Journal of Biological Science* 10:3923-3929.
- Faris H (2011). Genetic Diversity and Grain Protein Composition of Tetraploid Wheat (*Triticum durum* Desf.) Germplasm from Ethiopia. *Alnarp*. https://pub.epsilon.slu.se/8485/1/hailu_f_111202%20%281%29.pdf
- Feldman M (2001). "Origin of cultivated wheat," in *The World Wheat Book: A History of Wheat Breeding*, eds A. P. Dans Bonjean and W. J. Angus (Andover: Intercept Limited) pp. 3-58.
- Gashaw A, Mohammed H, Singh H (2007). The selection criterion for improved grain yields in Ethiopian durum wheat genotypes. *African Crop Science Journal* 15:25-31.
- Keneni G, Bekele E, Getu E, Asefa F (2012). Genetic diversity for attributes of biological nitrogen fixation in Abyssinian field pea (*Pisum sativum* var. *Abyssinicum*) germplasm accessions *Ethiopian Journal of Applied Science and Technology* 4(2):1-20
- Keneni G, Bekele, E, Assefa F, Imtiaz M, Debele T, Dagne K, Getu, E (2013). Evaluation of Ethiopian chickpea (*Cicer arietinum* L.) germplasm accessions for symbio-agronomic performance. *Renewable Agriculture and Food Systems* 28(4):338-349.
- Ghaderi A, Adams MW, Nassib AM (1984). Relationship between genetic distance and Heterosis for yield and morphological traits in

- dry edible bean and fababean. *Crop Science* 24:37-24.
- Hamrick JL, Godt MJW (1989). Allozyme diversity in plant species. In: Brown, A.H.D., Clegg, MT, Kahler, AL, & Weir, B.S. (eds.), Sunderland, MA: Sinauer pp. 43-63.
- Johnson A, Wichern B (1988). Biological nitrogen fixation. In: A Revolution in biotechnology, (Marx, J.L., ed). Cambridge University Press, Cambridge, New York pp. 103-118.
- Mahalanobis PC (1936). On the generalized distance in statistics. *Proceedings on National Science. India B.* 2:49-55.
- Mengistu D, Pè M (2016) Revisiting the ignored Ethiopian durum wheat (*Triticum turgidum* var. durum) landraces for genetic diversity exploitation in future wheat breeding programs. *Journal of Plant Breeding and Crop Science* 8:45-59.
- Mengistu D, Afeworki Y, Fadda, C, & Pè, M (2015). Ethiopian durum wheat landraces harbor resistant genotypes for terminal drought adaptation. In *Improving Food Security in the Face of Climate Change in Africa. Proceeding of the international conference* (pp. 13-15).
- Negassa M (1986). Patterns of diversity of Ethiopian wheat (*Triticum* spp.) and a gene Center for quality breeding. *Plant Breeding* 97:47-162.
- Pecetti L, Annicchiarico P, Damania AB (1992). Biodiversity in a germplasm collection of durum wheat. *Euphytica* 60:229-238.
- Purseglove JW (1975). *Tropical Crops; monocotyledons.* John Wiley and Sons, Inc., New York pp. 287-291.
- Ratiba B, Michael B, Abdelhamid D, Samer L, Abdulkader D, Kadour B, Mustapha L, Fatima G, Nadia Y (2012). Screening for Drought Tolerance Using Molecular Markers and Phenotypic Diversity in Durum Wheat Genotypes. *World Applied Sciences Journal* 16(9):1219-1226.
- SAS Institute (2002) *SAS/STAT system guide for personal computers, version 9.0 edition.* SAS Institute Inc., Cary, North Carolina, USA.
- Shahryari R, Mahfoofi B, Mollasadeghi V, Khayatnezhad M (2011). Genetic diversity in bread Wheat for phenological and morphological traits under terminal drought stress condition. *Journal of Advanced Environmental Biology* 5:169-173.
- Singh RK, Chaudhary BD (1985). *Biometrical methods in quantitative genetic analysis.* Kalyani Publishers, New Delhi P 318.
- Singh RP, Hodson DP, Huerta-Espino J, Jin Y, Bhavani S, Njau P, Govindan V (2011). The emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. *Annual Review of Phytopathology* 49:465-481.
- Singh G, Kulshreshtha N, Singh BN, Setter TL, Singh MK, Saharan MS, Sharma I (2014). Germplasm characterization, association and clustering for salinity and waterlogging tolerance in bread wheat (*Triticum aestivum*). *Indian Journal of Agricultural Sciences* 84(9):1102-1110.
- Teklu Y, Hammer K (2008). Diversity of Ethiopian tetraploid wheat germplasm: breeding Opportunities for improving grain yield potential and quality traits. *Plant Genetic Resources* 7:1- 8.
- Tesemma T, Belay G, Worede M (1991). Morphological diversity in tetraploid wheat Landrace populations from the central highlands of Ethiopia. *Hereditas* 114:171-176.
- Tsegaye B, Berg T (2007). Genetic erosion of Ethiopian tetraploid wheat landraces in Eastern Shewa, central Ethiopia. *Genetic Resources and Crop Evolution* 54:715-726.
- Yifru T, Hammer K, Huang XQ, Röder MS (2006). Regional patterns of microsatellite Diversity in Ethiopian tetraploid wheat accessions. *Plant Breeding* 125:125-130.
- Zohary D (1970). Centers of Diversity and centers of Origin: In: O.H. Frankel and E. Bennett (Eds. *Genetic Resources in Plants. Their Exploration and Conservation.* I. B. P. Handbook 11:33-42.