

Variability in Ethiopian Durum Wheat under Rainfed Environment Subjected to Drought at Anthesis

Alemayehu Zemedu^{1,2}, Firew Mekbib², Kebebew Assefa¹ and Zewdie Bishaw³

¹Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia ²Harmaya University, Harmaya, Ethiopia, ³International Center for Agricultural Research Institute (ICARDA), Addis Ababa, Ethiopia

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ምርምሩ በ2016 64 የሰብል ዘመን በደብረዘይት አካባቢ በሚገኝ አሸዋማ አፈር ላይ የተደረገ ሲሆን በጥናቱም የተለያዩ የዘረመል ምንጭ የላቸው 64 የዱረም ስንዴ ዝርያዎች ሲምጥልላቲስ በሚባል የጥናት ዘዴ በሁለት ድግግሞሽ ሙከራ ተካሄደባቸዋል። የጥናቱ ዋና ዓላማ የተኮረው 15 የሚያህሉ ማሳያዎችን በመጠቀም በእድገት ዑደት ማጠናቀቂያ ወቅት ከሚያጋጥም ድርቅ ሳቢያ በዱረም ስንዴ ዝርያ ዘረመል ባህርያት ላይ ሊታዩ የሚችሉ ባህርያትን ለመለየት ነው። በጥናቱም የተሻለ ምስል ለማግኘት ሲባል በባህርያቸው የተለያዩ ባህርያት በዘረመል ዓይነቶች ላይ ጥናት ተደርጓል። ውጤቱም እንደተመለከተው ከተጠኑት 15 ማሳያዎች መካከል በ8ቱ ላይ የባህርይ ልዩነት ታይባቸዋል። በሰብል ዕድገት መጨረሻ ላይ የሚፈጠር የዝናብ አጥረት በአብዛኛዎቹ ሸፋን፣ በአፈላ ዕድገት በፍሬ ሙላት እና በምርታማነት ላይ ከፍተኛ ተጽዕኖ እንደሚፈጠር በየጥለውኑ ከተደረገው ጥናት መመልከት ተችሏል። በምርታማነት እና የገለባ መጠን በፈጣሪነት ልዩነት እና ጄኔቲክ አድቫንስ ከፍተኛ ልዩነት ማሳየቱ እንደተጠበቀ ሆኖ ምርቱ ለሰብሰባ በመደረስ ላይ በአንጻሩ አነስተኛ ተጽዕኖ ተመዘግቧል። በዝርያዎች መካከል በባህርይ መውራሪስ ረገድ የተደረገው ጥናት እንዲያሳይውም በምርት ግኝት ላይ የታወቀ ተጽዕኖ አነስተኛ ሲሆን በፍሬ ሙላት ፍጥነት እና በፍሬ ዝግጅት ማጠናቀቅ ፍጥነት (91%) ላይ የታወቀ ተጽዕኖ በአንጻሩ ከፍተኛ ሆኖ ተመዘግቧል ። ማንኛቸውም ዓይነት በጥናት የተዳሰሱት ባህርያት ከፍተኛ GCV መጠን አለመሳየታቸው ድርቅ የዝርያ ባህርይን በመቀየር ረገድ ከፍተኛ ተጽዕኖ እንደሚፈጠር ያሳያል ። የሙሉት የፍጥነት ጊዜ እና የፍሬ ሙሉት ከዝቅተኛ የጄኔቲክ አድቫንስ 5.15 እና 3.01 እንደተመለከተው የታወቀ ልዩነት ከጄን አክሽን ጋር የተያያዘ አይደለም። አምስቱ መሰረታዊ አካላት ከ eigenvalue ከ 1.1 እስከ 3.75 ሲተነተን በተደራራቢ ድምር 78.6% የሚሆነውን የፊኖታይቲክ ልዩነት መታየቱ በዱረም ስንዴ ዝርያዎች መካከል የድርቅ ተጽዕኖ ከፍተኛ መሆኑን ያሳያል። በከላላሰተር ትንታኔም የ 64ቱ ዱረም ስንዴዎች ዝርያዎቹ በአምስት ግሩፕ ከፍሏቸዋል። በዚህም መሰረት አምስቱን ዓይነቶች ከ 5 እስከ 15 ዝርያዎቹ መመልከት በውጤቱ ተስተውሏል። በተለያዩ ክፍሎች እንደተጠኑት ዝርያዎቹ (ዘረመሎቹ) በተለያየ የሰብሰባ እና ሁኔታ ሲባዙ የተለያዩ ድርቅን የመቆቋም ባህርይ ማሳታቸው ተስተውሏል። በዚህም መሰረት የዱረም ስንዴ ዘረመሎች የዕድገት ዑደት ማጠናቀቂያ ላይ የሚከሰት ድርቅን የመቆቋም ባህርያቸው በየዘረመል ዓይነት የሚለያዩ መሆኑን በጥናቱ ማረጋገጥ ተችሏል።

Abstract

Sixty-four durum wheat genotypes comprised of different sources of origin were field evaluated in a simple lattice design with two replications at Debre-Zeit sandy soil environment during the 2016 main season. The objective was to assess the extent of genetic variability for durum wheat genotypes under rain-fed terminal moisture stress using fifteen agronomic and yield related traits. There were wide ranges of variation for some of traits studied. Analysis of variance also revealed that there were significant variations among durum wheat genotypes for eight out of 15 traits studied, suggesting the possibility of improving durum wheat for these traits. Terminal drought had highly significant effect on grain yield per plot, aboveground biomass, spike length, days to heading and grain filling. Grain yield per plot and straw yield showed the highest phenotypic coefficients of variations and genetic advance, whereas days to maturity and harvest index had the lowest values, respectively. Across traits, the broad sense heritability was lowest (12 %) for harvest index and highest for days to heading (91%) followed by grain filling period (73%). None of the traits had high GCV values indicating that the effect of drought was severe for trait expressions. The existence of high heritability for days to heading and grain filling period along with low genetic advance of 5.15 and 3.01 suggested that the variation observed may not indicate the expression of additive gene action. Five principal components (PCs) with eigenvalue between 1.1 and 3.73 explained a cumulative of about 78.6% of the total phenotypic variability observed among the durum wheat genotypes. Cluster analysis also classified

the 64 durum wheat genotypes into five groups. The genotypes found in to five clusters ranged from seven to 15. The genotypes maintained under different groups had specific characters and it may give desirable genetic recombinants in developing drought tolerant varieties. Overall, the present study revealed that there is sufficient variability existed in durum wheat genotypes tested under terminal drought environment.

Introduction

Wheat is the fourth most important cereal crop after maize, tef, and sorghum in terms of area coverage and production in Ethiopia. Both bread and durum are grown extensively in the country, although separate area coverage and production is not known. They are cultivated over an area of 1.69 million hectares with annual production of about 4.5 million tons (CSA, 2017). However, average productivity in the country is low (1800 kg/ha). Drought stress globally, particularly under rain-fed based crop production system of Ethiopia is one of the largest causes of wheat yield reduction. Apart from in the lowland light textured soils, terminal moisture stress is common across most of the traditional highland pellic-vertisol durum wheat growing areas of the country due to late planting. Research efforts made in the country led to the development of 39 durum wheat varieties from 1982 to 2017 (MoALR, 2017), but none of them were targeted and confidentially released for moisture stress environments. Lack of methodology and proper screening environments which minimize the challenges associated to screening to drought stress breeding such as drought intensity, uniformity and timing of stresses and the difficulty to control the amount of water applied to the field environment while using irrigation are among the challenging ones to be considered in breeding for drought stress tolerance. Most of the current drought screening research attempt to control soil moisture by controlling rainfall or simulated rainfall, not through maximum capacity limitation on soil moisture. Campos *et al.* (2004) indicated that field-testing is the only true way to screen for drought tolerance. Field screening under rain-fed environment following late planting using site with little soil moisture capacity and there by exposing genotypes uniformly to terminal moisture stress during their reproductive stages would be among the alternative methods to screen large number of genotypes to identify drought tolerance ones. In line with breeding for drought tolerance, information on the extent of variability for terminal moisture stress would be useful and is a pre requisite for varietal development of durum wheat through hybridization.

Although several previous genetic variability studies were reported in Ethiopian bread wheat (Tarekegne *et al.*, 1994; Degewione *et al.*, 2013) and on durum wheat (Mohammed *et al.*, 2016; Birhanu *et al.*; Yonas *et al.* 2016, Tesgaye *et al.*, 2012), little information is generated about genetic variability of wheat germplasm under drought environments. Therefore, the present study was undertaken to assess the variation in durum wheat germplasm for terminal moisture stress and to identify lines for use in the future breeding program.

Materials and Methods

Sixty-four durum wheat genotypes of different origin were used in the study. Twenty of the materials were released cultivars over different era and half of the materials were introduced breeding lines obtained from CIMMYT and ICARDA, while the remainder ones were landraces (Table 1). The materials were grown in the field during the main rainy season in 2016 at Debre-Zeit experimental station located at 8° 41'36" latitude and 39° 03'17" longitude with altitude 1880 m. According to the data obtained from the Agricultural and Nutritional Research Laboratory of Debre-Zeit Agricultural Research Center (2018), the soil of the experimental site is characterized by clay loam texture with pH of 7.3, and organic carbon, total N, electrical conductivity (EC) and soil Cation Exchange Capacity (CEC) of 1%, 0.08%, 0.12 Ds/m and c100 meq/100 g of soil, respectively.

The genotypes were planted late in the season on August first, 2016 on clay loam soil to expose them to terminal moisture stresses uniformly since the date of heading and anthesis which is common to lowland wheat growing areas of Ethiopia. The planting date was selected based on the consistency of the incidence of drought and targeted timing to match on heading to anthesis stages for most of the genotypes included in the study.

The genotypes were evaluated in 8 x 8 simple lattice design field experiments with two replications on plots consisting of two rows 2 meter in length and 20 cm between rows spacing. In the experiment, 100 kg of Di-ammonium Phosphate was applied at planting and split application of 100 kg of urea where two third at planting and one-third at time of tillering was used. The plots were hand weeded and fungicides applied twice in the season to protect the genotypes from stem rust infection.

Observation for plant height, spike length, spikelet number per spike, and grain yield per spike and kernel number per spike were recorded from ten randomly spikes of the selected plants. Days to heading, days to maturity, grain filling period, 1000 seed weight, aboveground biomass, straw yield and grain yield were recorded on plot basis. Protein content was determined based on Mininfra Smart T Grain Analyzer (Mininfra Smar T Grain Analyzer Operating Manual, 2013).

The SAS GLM procedure (SAS Institute, Inc. 2002) was employed for the analysis of variance. Fisher's protected least significant difference (LSD) test at 5% level of significance was used for mean comparisons, whenever genotype differences were significant. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were analyzed with Meta R software. Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance according to Singh and Ciccarelli (1996). Genetic advance as percent of the mean assuming selection of the superior 5% of the genotypes was also estimated following the procedure elaborated by Singh and Chaudhary (2004). Principal component and cluster analysis were carried out using Ward linkage and correlation coefficient distance matrices in Mintab version 16.

Table 1. Names and sources of durum wheat varieties and breeding lines used in the study

Name	Source	No	Name	Source
Arendato	Released variety	33	IL-PV-6	CIMMYT
Cocorit	Released variety	34	LRPL-86	CIMMYT
Boohai	Released variety	35	LRPL-215	Landrace
Quamy	Released variety	36	IL-PV-20	Landrace
Assasa	Released variety	37	IL-PV-17	CIMMYT
Ginchie	Released variety	38	IL-ID-2	CIMMYT
Ude	Released variety	39	IL-ID-3	CIMMYT
Yerer	Released variety	40	IL-ID-4	CIMMYT
Denbi	Released variety	41	IL-ID-5	CIMMYT
Hitosa	Released variety	42	IL-ID-6	CIMMYT
Werer	Released variety	43	IL-ID-7	CIMMYT
Mangudo	Released variety	44	IL-ID-8	CIMMYT
Mangudo	Released variety	45	IL-ID-9	CIMMYT
Tob-66	Released variety	46	IL-ID-10	CIMMYT
Gerado	Released variety	47	IL-ID-11	CIMMYT
Ejersa	Released variety	48	IL-ID-12	CIMMYT
Utuba	Released variety	49	IL-ID-13	CIMMYT
Toletu	Released variety	50	IL-N-8	CIMMYT
Kilinto	Released variety	51	ID-N-11	CIMMYT
Bichena	Released variety	52	IL-IDO-2	CIMMYT
Flakit	Released variety	53	IL-IDO-3	CIMMYT
LRPL-1	landrace	54	IL-IDO-4	CIMMYT
LRPL-6	landrace	55	IL-IDO-5	CIMMYT
LRPL-2	landraces	56	IL-IDO-6	CIMMYT
LRPL-8	landraces	57	IL-IDO-7	CIMMYT
LRPL-18	landraces	58	IL-IDO-8	CIMMYT
LRPL-14	landraces	59	IL-IDO-9	CIMMYT
LRPL-9	landraces	60	IL-IDO-10	CIMMYT
LRPL-11	landraces	61	IL-IDO-11	CIMMYT
LRPL-3	landraces	62	IL-IDO-12	CIMMYT
LRPL-7	landraces	63	IL-NLM-3	CIMMYT
LRPL-4	landraces	64	IL-NLM-13	CIMMYT

Results and Discussions

The maximum and minimum daily temperatures and daily rainfall received during the growing period are presented on Table 2. The genotypes received only 195.1mm of rainfall during the growing season (August 1 to end of September). No rainfall was received then after creating moisture stress after flowering and the beginning of moisture stress coincides with anthesis stage (Table 2). The average maximum and minimum temperatures were within the expected conditions regardless of plant development stage. Thus differences in genotypes performance are probably mainly due to moisture stress.

Table 2. Rainfall, maximum and minimum temperature during growing season (August 1, 2016 to November 16, 2016)

Time interval	Total rainfall (mm)	Average max. temp. (°C)	Average min. temp. (°C)	Crop development stages
August 1-10, 2016	39.4	23.9	15.2	Planting-emergence
August 11-20, 2016	58.9	24.4	14.7	Emmer.-four leaf
August 21-31, 2016	30.6	24.5	14.1	Four leaf-tillering
Sept. 1-10, 2016	38.6	24.3	13.9	Tillering-Booting
Sept. 11-20, 2016	13.9	25	13.4	Booting-Heading
Sep. 21-30, 2016	13.7	25.5	13.3	Heading-Anthesis
Oct. 1-10, 2016	No rain	27.6	9.7	Early grain filling
Oct. 11-20, 2016	No rain	28.2	9.8	Late grain filling
Oct. 21-31, 2016	No rain	27.7	9.5	Physiological maturity
Nov. 1-10, 2016	No rain			
Total in the season	195.1			

Table 3 summarizes some descriptive statistics for each traits based on the average data of the 64 genotypes in sandy clay soil environment at Debre-Zeit. Considerable variations were observed for all characters. The mean for days to heading were (58 days). The earliest line to heading was entry 59 (49 days) and the latest line to reach heading was entry 15 (62 days). For days to maturity, a narrow range (93-100 days) was observed. The differences between maximum and minimum mean values in biological yield per plot, grain yield per plot, straw yield, harvest index, grain yield per spike and spike harvest index were 639.9(g), 217.9(g), 562.5(g), 21.4%, and 35%, respectively. Plant height ranged from 58.0 to 90.3 cm with a mean of 72.4 cm. The range of kernel number /spike and number of spikelet/spike varied from 23 to 40 and from 11 to 18 with overall mean 30 and 15, respectively. Genotypes with long spikes and with low number of spikes per plant and with more spikelets per spike may produce a greater number of seeds per spike. Entry 10 had maximum number of spikelets per spike (18) followed by entry 16 (17 spikelet per spike). Entry 16 and 18 produced high number of kernels per spike of 40 and 38 kernels per spike, respectively. Those genotypes are useful in hybridization program where long spikes, more spikelet number and high number of kernels are to be combined. Hence, entry 16 that produced a greater number of kernels per spike with relatively high number of spikelets per spike could be used for hybridization. Length of spike had variation of 4.1 to 7.8 cm with an overall mean of 5.3 cm long. There was enough variation in seed size among the genotypes (21.8- 44.1g/1000seeds). The mean thousand-kernel weight was 30.8 g. Entry 50 had the largest seeds (44.1g/1000seeds) followed by entry 13 (40.1g/1000seeds). Grain yield ranged from 1321 kg/ha to 4045 kg/ha with a mean of 2656 kg/ha. The wide range for grain yield and seed size offers the possibility of developing large seeded and high yielding genotypes.

The results of this study showed differences in both phenology yield and yield related traits among durum wheat genotypes. The variations in the ranges and mean values for most of the traits in this study were smaller compared with values reported earlier from evaluation of wheat genotypes (Rathwa *et.al.* 2018; Fellahi *et.al.*, 2013; Sentayehu *et.al.*2016) and comparable to study conducted under stress on some yield component traits (Junior *et al.*, 2015). The differences in the ranges and mean values of traits between this study and the previous studies can be associated to the variation in the genotypes and

the environment and/ or conditions in which the genotypes were tested. Besides, the terminal moisture stress environment that occurred in the current study might also have effect on the crop phenology and yield related traits.

Table 3. Ranges, lines showing extreme values, means, standard error (SE) of means for 15 traits of 64 durum wheat genotypes tested at Debre-Zeit sandy clay soil environment

Trait	Minimum	line	maximum	lines	mean	SE
Days to heading (days)	49	51	62	11	58	2.8
Days to maturity (days)	93	51	100	11	96	1.4
Grain filling period (days)	36	15	47	41	41	2.6
Protein content (%)	13.6	38	20.6	3	18.3	0.18
Grain yield (kg/ha)	1321	42	4045	30	2656	54.4
Grain yield per spike(g)	0.59	2	1.4	13	0.9	0.02
Straw yield (kg/ha)	38.1	61	108.4	24	68.0	0.14
Biological yield (tons/ha)	57.2	61	136.4	24	94.6	0.17
1000 kernel weight (gram)	21.8	55	44.1	50	30.8	0.57
Number of spikelets/spike	10	7	18	10	14	0.14
Kernel number /spike	23	2	40	16	30	0.5
Plant height (cm)	58.1	61	90.3	14	72.4	1.1
Spike length (cm)	4.1	33	7.8	32	5.3	0.9
Harvest index (%)	16.4	42	37.8	36	28.5	0.5
Spike harvest index	41.1	42	76.1	21	60.1	0.6

The mean squares of the 15 traits from analysis of variance (ANOVA) are presented on Table 4. Highly significant differences among genotypes were found on grain yield per plot, above ground biomass yield, spike length, days to heading and grain filling duration, while straw yield, protein content and number of spikelets per spike showed significant variation ($p < 0.05$) between genotypes. No significant variations existed among the genotypes in most important production traits such as days to maturity, plant height, thousand kernel weight, and number of kernels per spike, harvest indices, spike harvest indices, and grain yield per spike.

In the analysis of variance, the variation among durum wheat genotypes were highly significant ($p < 0.01$) and significant for 5 and 3 out of the 15 traits evaluated, respectively indicating that terminal drought had significant effect on grain yield per spike, plant height, and thousand kernel weight and kernel number per spike (Liu *et al.*, 2017). Lack of variation among genotypes on thousand kernel traits and number of kernels per spike recorded after stress period were contrary to other similar studies (Mohammed *et al.*, 2011; Danghco A. *et al.*, 2016; Tsegaye *et al.* 2012), suggesting that the intensity or severity of the stress that occurred in the current was very high.

Table 4. Mean squares from the combined analysis of variance for 15 traits of 64 genotypes tested at Debre-Zeit sandy clay soil in 2016 main season.

Trait	Error df=49	Genotypes df=63	CV (%)
Grain yield	1675.1	3351.5**	19.3
Grain yield per spike	0.038	0.05 ^{ns}	21.4
Above-ground biomass	12314.7	28809**	14.7
Straw yield	10560.6	18563.7*	18.9
Thousands kernel weight	27.3	40.4 ^{ns}	16.9
Plant height	87.9	112.2 ^{ns}	12.9
Spike length	0.42	0.81**	12.3
Number of spikelets per spike	1.33	2.21*	7.9
Number of kernels per spike	22.9	24.7 ^{ns}	16.2
Harvest index	0.003	0.004 ^{ns}	18.9
Spike harvest index	0.006	0.0064 ^{ns}	12.7
Protein content	2.01	3.63*	7.8
Days to head	2.01	18.8**	5.9
Days to mature	2.02	2.98 ^{ns}	1.7
Grain filling duration	3.99	13.4**	7.2

** Highly significant, * significant, ns =non-significant

Estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variations, broad sense heritability (H) and genetic advances expected from selection of the best 5% of the genotypes are presented on Table 5. The estimates of genotypic and phenotypic coefficients of variability in the study area indicated that the values of phenotypic coefficients of variation were relatively higher than the genotypic coefficients of variation for most of the traits. None of the traits had high GCV values in the present study indicating that the effect of drought was severe for trait expressions. All the traits had low GCV value, except grain yield per plot, protein content, aboveground biomass and straw yield, which showed moderate GCV values. High PCV was observed for kernel weight per spike followed by grain yield per plot. The majority of the traits showed moderate values of PVC (Table 5). Phenotypic coefficient of variation for protein content and number of spikelets per spike remains low under terminal drought. Across traits, the broad sense heritability estimates were lowest (12 %) for harvest index and highest for days to heading (91%) followed by grain filling period (73%). Intermediate heritability values of 30-60% were observed for grain yield per plot (55.9%), days to maturity (43.9%), protein content (55.6%), above ground biomass yield (55.4%), straw yield (36.9%), spike length (52.5%), and number of spikelet per spike (51.9%), 1000 grain weight (29.3%), number of kernel per spike (25.2%), plant height (23.6%), and harvest index (11.5). Spike harvest index (21.8%), and, grain yield per spike (26.5%) had low heritability. Genetic advance as percentage of mean ranged from 2.11 % in days to maturity to 28.4 grain yield per plot.

In the current study, higher phenotypic coefficients of variation compared to that of genotypic coefficients of variation were observed for most traits, and this was probably associated to high environmental effect due to moisture stress on the expression of traits. The current study disagreed with those previous experiments conducted in relatively stress free environments (Rathwa *et. al.*, 2018; Berihanu *et. al.*, 2017; Mohammed *et. al.*, 2011; Dargicho *et.al.*, 2016; Gezahegn, 2015). The observed low genotypic and phenotypic coefficients of variation for days to heading and grain filling period in the study resulted in high heritability values. This result is in line with the work of Eid (2009)

and contrary to the findings reported by Khan and Naqvi (2011). High heritability values were observed only for days to heading and grain filling duration, and this could be due to higher contribution of genotypic components. The existence of high heritability for days to heading and grain filling period in this study along with low genetic advance of 5.15 and 3.01 suggested that the variation observed may not indicate the expression of additive gene action Eid, (2009). Low heritability values for the traits were associated to high phenotypic variances indicating the growing season effect. This result is supported by Ciccarelli (1994), Mevlut (2009) and Eid, (2009) who reported low heritability values for yield and yield related trait under drought stress. This was further illustrated by Ciccarelli about the importance of screening and the selection of genotypes in optimum environment for drought tolerance and low yielding environment is associated to low heritability. The lowest genetic advance as percentage of mean for days to maturity was about 2.11% and the highest of 28.4 % was for grain yield. This suggested that selecting 5% of the base population could result in an advance of 2.11 to 28.4 percent over the respective population means.

Table 5. Phenotypic (PCV) and genotypic (GCV) coefficient of variations, broad sense heritability (H) genetic advance expected (GA) and genetic advance as percent of mean (GAM %) of 15 traits of 64 genotypes tested at Debre-Zeit sandy clay soil environment

Trait	GCV (%)	PCV (%)	H (%)	GA	GAM	Mean
Grain yield per plot	15.33	24.6	55.95	60.34	28.39	212.53
Grain yield per spike	9.11	23.3	26.5	0.12	12.75	0.91
Above-ground biomass	12.37	19.98	55.41	172.8	22.83	756.71
Straw yield per plot	10.88	22.85	36.95	94.81	17.42	544.18
Thousand kernel weight	7.89	19.06	29.26	3.55	11.51	30.8
Plant height	5.7	24.1	23.6	8.5	11.7	72.37
Spike length	9.11	15.27	52.51	0.87	16.54	5.26
Number of spikelets per spike	5.5	9.29	51.87	1.45	9.94	14.59
Number of kernels per spike	6.3	16.61	25.18	2.56	8.63	29.65
Harvest index	4.72	19.13	11.48	0.01	4.53	0.29
Spike harvest index	4.58	13.08	21.82	0.04	5.89	0.6
Protein content	5.91	9.53	55.62	2	10.93	18.27
Days to head	4.99	5.44	91	5.15	9.42	54.7
Days to mature	1.03	2.34	43.9	2.02	2.11	96
Grain filling duration	5.05	6.84	71	3.01	7.34	41

Five principal components (PCs) with eigenvalue between 1.1 and 3.73 explained a cumulative of about 78.6% of the total phenotypic variability observed among the durum wheat genotypes (Table 6). Of these, about one third (24.9 %) of the total variance was explained by the first PC alone, and this was due mainly to variations in above ground biomass yield, straw yield per plot, Spike length , plant height and grain yield per plot. Similarly, the second PC captured about 21.9 % of the variation and the major traits were days to heading and protein content. The proportion of the total phenotypic variance of the genotypes accounted for by third, fourth, and fifth PCs were 13.3, 11.3 and 7.3 respectively. Variations in grain filling period, number of spikelets per spike, spike length, and number of kernels per spike accounted for the third PC. Grain filling period contributed the maximum variation for the fourth PC while thousand kernel weights and grain yield per spike brought the highest variation in the fifth PC respectively.

Principal component analysis further confirmed the existence of sufficient variability between the genotypes based on the traits under study. That the first two principal components explained 24.9 and 21.9 percent of the total variations indicated that about 50 % of differences captured by the traits included in the first two PCs. Grain yield per plot , above ground biomass, spike length and plant height found in the first PC and days to flowering and grain protein content were the most important traits included in the first two PCs that captured most of the variations and should be considered as a selection traits for drought stress breeding. This finding was in line with the work of Gezahegn *et al.* (2015): who found that grain yield and days to heading were among the most important trait explaining much of the variation in bread wheat. Similar results have also been found in the study of Dargicho *et. al.* (2016) using 68 bread wheat genotypes.

Table 6. Eigenvectors and eigenvalues of the six five principal components (PC) for 15 traits of 64 durum wheat genotypes

Trait	PC1	PC2	PC3	PC4	PC5
Grain yield per plot	0.329	-0.342	-0.124	-0.025	-0.291
Grain yield per spike	0.015	-0.442	-0.100	-0.218	0.442
Above-ground biomass	0.482	-0.054	-0.002	0.183	-0.007
Straw yield per plot	0.462	0.066	0.045	0.233	0.104
Thousand kernel weight	-0.054	-0.371	-0.280	0.203	0.450
Plant height	0.361	-0.109	-0.046	0.112	0.262
Spike length	0.375	0.071	0.204	0.006	-0.166
Number of spikelets per spike	0.375	-0.063	0.309	-0.363	-0.018
Number of kernels per spike	0.066	-0.194	0.201	-0.586	0.079
Harvest index	-0.130	-0.392	-0.146	-0.257	-0.364
Spike harvest index	0.097	-0.221	-0.368	0.018	-0.456
Protein content	0.052	0.298	0.054	-0.269	0.003
Days to head	0.145	0.300	-0.479	-0.278	0.105
Days to mature	0.060	0.148	-0.449	0.033	-0.133
Grain filling duration	-0.142	-0.284	0.351	0.345	-0.187
Eigenvalue	3.728	3.279	1.988	1.700	1.091
Proportion	0.249	0.219	0.133	0.113	0.073
Cumulative	0.249	0.467	0.600	0.713	0.786

Cluster analysis based on 15 standardized traits of 64 durum wheat genotypes from different sources resulted in the formation of five clusters comprised of 4 to 35 genotypes. Comparable results were also reported by Dargicho *et al.* (2016) using 68 bread wheat genotypes that grouped in to six clusters. In the current study, cluster I, II, III, IV and V comprised of 7, 4, 35, 8 and 10 genotypes respectively (Table 7 and figure 1). The first cluster comprised of those genotypes which had highest in grain yield associated to high number of kernels and long spike and maximum spike harvest. The second cluster included four genotypes produced relatively low grain, biomass and straw yield. Cluster III comprised of 35 genotypes, of which more than half were exotic breeding lines. This cluster included the first two high yielding landraces having long spikes and good straw yield. The remaining genotypes were medium to low in most yield related traits. The majority of genotypes found in cluster IV are recently released cultivars and exotic lines, characterized by high biomass and straw yield and late to head resulted in short grain filling period. Ten genotypes are exotic in their origin, were found in cluster V which had shortest in their height associated with low biomass and straw yield resulted in high

harvest index. Furthermore, cluster distance confirmed the existence of high genetic variability for developing drought tolerance varieties through hybridization between cluster IV and cluster V, followed by cluster I and V, and Cluster II and IV respectively (Table 8). The differences in clusters could imply their being originated from different sources, while the genotypes grouped together would mean affinity among individuals in the same group. The genotypes maintained under different groups had specific characters and it may give desirable genetic recombinants in developing drought tolerant varieties if they are used in hybridization.

Overall, the present study revealed that sufficient variability existed in durum wheat genotypes tested under terminal drought environment, and this offers many opportunities for genetic improvement through direct selection for future utilization and hybridization program.

Table 7. Cluster numbers and lines grouped in each clusters for the 64 genotypes tested at Debre-Zeit

Cluster number	No of lines	(%)	Lines in the clusters
I	7	10.9	Arendato, Boohai, LRP-1, LRP-6, LRP-2, LRPL-8 and LRPL-18
II	4	6.3	Cocorit, LRP-14, IL-ID-6, IL-ID-9
III	15	23.4	Quamy, Assasa, Ginchi, Ude, Werer, Mangudo, Mukiye, Gerardo, Utuba, Kilinto, Bichena, LRPL-9, LRPL-11, LRPL-3, LRPL-7, LRPL-4, IL-PV-6, LRPL-215, IL-PV-17, IL-ID-2, IL-ID-3, IL-ID-4, IL-ID-5, IL-ID-7, IL-ID-8, IL-ID-10, IL-ID-11, IL-ID-12, ID-N-11, IL-IDO-2, IL-IDO-3, IL-IDO-5, IL-IDO-6, IL-IDO-9 and IL-NLM-3
IV	8	12.5	Yerer, Denbi, Tob-66, Ejersa, Toletu, Flakit, LRPL-86, IL-PV-20
V	10	15.6	Hitosa, IL-ID-13, IL-N-8, IL-IDO-4, IL-IDO-7, IL-IDO-8, IL-IDO-10, IL-IDO-11, IL-IDO-12 and IL-NLM-13

Table 8. Distance among five clusters of the 64 durum wheat genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	0.0				
Cluster II	426.5				
Cluster III	228.2	198.5			
Cluster IV	199.2	611.6	414.9		
Cluster V	655.5	229.2	427.7	840.1	0.0

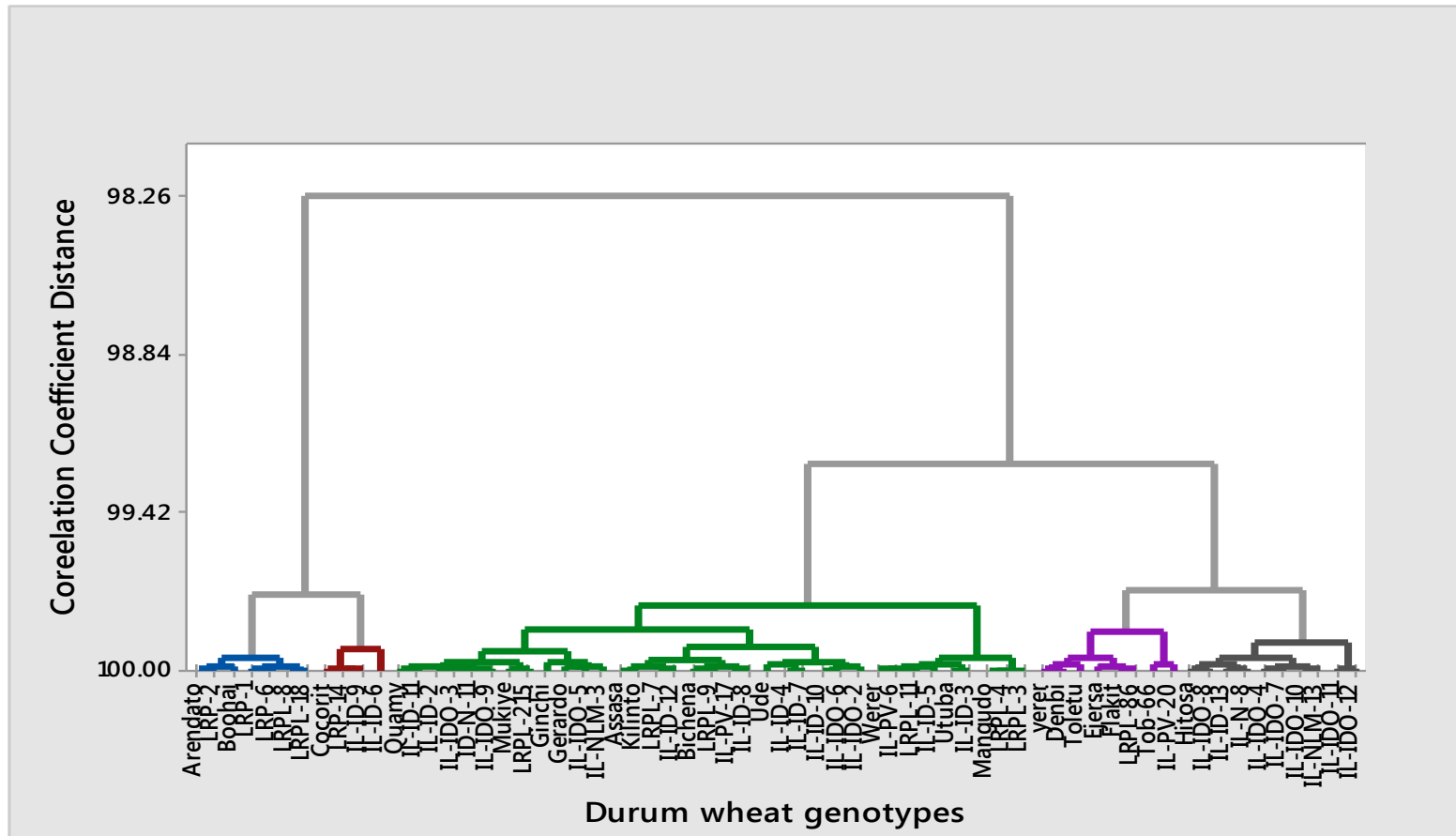


Figure 1: Dendrogram showing clustering of 64 durum wheat genotypes based on evaluation of 15 traits.

Acknowledgments

The authors would like to thank the Ethiopian Institute of Agricultural Research (EIAR), Agricultural Growth Program II, (AGP II) and International Center for Agricultural Research Institute (ICARDA) for providing technical and financial supports for the execution of the field experiment. The authors also acknowledged the support provided by Wondo-Genet Research Center and Debre-Zeit Research Center. Research and technical staff members of the crop research process of Debre-Zeit Research Center are highly acknowledged for assisting us on field activities.

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