Genetic Variation in Durum Wheat Genotypes *(Triticum durum* L.) Under Waterlogging Condition

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Abstract

Durum wheat is mostly cultivated on vertisol, which is characterized by high water holding capacity and poor drainage due to heavy clays that inhibit infiltration, resulting in water logging during the peak rainy season. As a result of this, the crop is highly affected by waterlogging stress. *This study was conducted to assess the genetic variability of durum wheat genotypes under waterlogging conditions. The experiment was laid out in 10 x 10 simple lattice design and conducted during the 2018 cropping season at the Debre Zeit research center on station and Chefe Donsa sub site. The result revealed that the genotypes had significant variations in grain yield with the range between 3515.25 kg/ha to 7539.25 kg/ha with an overall mean value of 5788.98 kg/ha. The maximum grain starch percentage of the genotypes was 68.13% (CD15DZ-ELT/1094/2015), while the minimum was 64.53% for (CD15DZ-ELT/off/1144/2015). The total grain protein content varied from 11.43% for (CD15DZ-ELT/off/1035/2015) to 15.38% for genotype (CD15DZ_ELT/off/943/2015). The traits that had high PCV and GCV were grain yield, thousand-grain weight, number of kernels per spike, and harvest index. The estimated values of H^2B and GAM ranged from* 61.82% *to* 92.48%, *and 3.92% to 78.35%, respectively; the maximum and the minimum values being associated with grain starch percentage, plant height, and gluten index, respectively, in both cases. In this study, seven significant Principal Components which explained cumulatively 83.7% of the total variation were extracted. Generally, the present study revealed high genetic variation among the tested durum wheat genotypes and hence, can serve as a source of germplasm for durum wheat improvement under waterlogging conditions, where durum wheat is dominantly growing.*

Keywords: Durum Wheat, Waterlogging, Genetic Variability, Principal Component

Introduction

Bread wheat (*Triticum aestivum*) and durum wheat (*Triticum turgidum L. durum*) are the two cultivated species of wheat widely grown in the world as well as in Ethiopia. In Ethiopia, wheat is one of the major staple and strategic food security crops. At a national level, 1,696,907.05 hectares of land was covered by both bread and durum wheat with a total production of 4,642,965.7 tons during the 2017/18 cropping season with average productivity of 2.7 tons/ha (CSA, 2018) which was below world average yield of 3.1 t ha^{-1} in 2016/2017 (FAOSTAT, 2017). It has been well established in durum wheat that protein quantity and gluten quality are widely responsible for the so-called al dente pasta cooking characteristics. In addition to color and protein characteristics, kernel size and vitreousness are also important in durum wheat quality, as they are strongly related to semolina yield, the bright yellow appearance of semolina, and the cooking properties of pasta products (Hoseney, 1994; Bushuk, 1998; Troccoli *et al*., 2000; Dziki and Laskowski, 2005). Ethiopia is considered one of the centers of genetic diversity of durum wheat (Vavilov, 1951), with important sources of rust and drought resistance, waterlogging tolerance, and early maturity (Payne *et al*., 2001). The crop is widely grown in the central highlands of Ethiopia and is one of the most important crops for food and cash income. It is mostly grown on black clay soils (*Vertisols)*, which are characterized by high water holding capacity and poor drainage due to heavy clays that inhibit infiltration, which results in water logging during the peak rainy season when the crop is usually in its vegetative development phase.

Water logging' is defined as a condition of the soil where excess water limits gas diffusion; while 'water-logging tolerance' is defined as survival or the maintenance of high growth rates, biomass accumulation, or grain yield under water logging relative to non-waterlogged (usually drained soil) conditions (Setter and Waters, 2003). Waterlogging occurs when the soil is fully saturated, and standing water replaces the air in the soil pore spaces.

Many agricultural soils of the world destined for wheat and barley cultivation are frequently exposed to waterlogging (Sayre *et al*., 1994; Samad*et al*., 2001; Reussi Calvo and Echeverria, 2006; Shaw *et al*., 2013; de San Celedonio *et al*., 2014a) affecting crop yield, and causing economical yield losses. Waterlogged plants are affected by oxygen and mineral nutrient deficiencies and microelement toxicities (Setter *et al.*, 2009). In addition, waterlogging can also reduce the availability of some essential nutrients, e.g., Fe and Mn (Ponnamperuma, 1972). As a consequence, an increase in micronutrients in the soil and subsequently in shoots may affect plants both during waterlogging and during recovery. Higher micronutrient concentrations in shoots have been reported during the recovery period when soils have returned to fully aerated conditions (Setter and Waters, 2003). Waterlogging has a significant impact on the growth of wheat, leading to a decrease in biomass accumulation. This is due to the negative effects on the development and growth of tillers, resulting in a reduction in the number of spikes per plant. As a result, the length of the spikes and the overall yield of wheat are also affected. According to McDonald and Gardner (1987) report, the effect of water logging during tillering and stem elongation leads to fewer tillers, more floral sterility, fewer grains per spike, reduced kernel weight, and a final yield loss of 50% or more.

Delayed planting has been traditionally exercised to overcome the problem associated to waterlogging stress. However, planting late in the season has a yield penalty as the crop would be exposed to terminal drought due to soil moisture deficit and frost damage (Jutzi and Mesfin, 1987; Teklu *et al.,* 2005). Thus, an alternative complementary approach to manage the challenges of waterlogging is the prior research topic.

It was hypothesized that the use of a large number of genotypes from different sources and evaluation for waterlogged stress to be among the alternatives for the identification of tolerant genotypes for high moisture stress for improving the productivity of durum wheat in the vertisol environment of Ethiopia. However, there is no sufficient information about the genetic variability of durum wheat genotypes under waterlogging conduction. Therefore, this investigation was designed to assess the extent of genetic variability in durum wheat genotypes exposed to excess moisture stress and identify lines to be used for future breeding using morph-agronomic traits.

Materials and Methods

The experiment was conducted at Debre-Zeit Agricultural Research Center's (DZARC) research field and Chefe Donsa sub site of Debre-Zeit Agricultural Research Center, in Ethiopia during 2018 main cropping season under rainfed condition. The test locations represent the major durum wheat production areas of Ethiopia with the dominant soils being Vertisols and known for their long histories of frequent waterlogging. A total of 100 durum wheat materials, including advanced lines and released varieties were used for this study. The advanced lines are materials introduced from ICARDA and CIMMYT, whereas the released varieties were collected from DZARC.

The durum wheat genotypes were planted on flat bed plots of four rows and the row lengths were 2.5m with spacing of 20 cm between rows and 30 cm between plots. The trials were laid out in a 10 x10 simple lattice design. All crop management practices were applied uniformly to all plots as required to allow the test genotypes express their full genetic potential. Seed rate and fertilizer dose were applied as per the recommendations.

Table 1. Description of the study areas.

Location	Altitude	Soil Type	Latitude	Longitude	Temperature		Rainfall (mm)
					Min	Max	
Debre Zeit	1900	heavy clay	8°41'36" N	39° 03'17" E	15°C	27°C	700-900 mm
Chefe Donsa	2444	Clay	8°57'60" N	39°06'28" E	12°C	25°C	>1000 mm

Source Hailu *et al.* 2015

Table 2. Names and Sources of Durum Wheat Varieties and Breeding lines used for this study.

No	Name	Source	No	Name	Source
1	CD15DZ_ELT/off/1084/2015	CIMMYT	51	CD15DZ_ELT/off/1025/2015	CIMMYT
2	CD15DZ_ELT/off/1024/2015	CIMMYT	52	CD15DZ_ELT/off/980/2015	CIMMYT
3	CD15DZ_ELT/off/994/2015	CIMMYT	53	CD15DZ-ELT/off/973/2015	CIMMYT
4	CD15DZ_ELT/off/253/2015	CIMMYT	54	CD15DZ-ELT/off/1117/2015	CIMMYT
5	CD15DZ_ELT/off/943/2015	CIMMYT	55	CD15DZ-ELT/off/849/2015	CIMMYT
6	CD15DZ_ELT/off/950/2015	CIMMYT	56	CD15DZ-ELT/off/306/2015	CIMMYT
7	CD15DZ_ELT/off//248/2015	CIMMYT	57	CD15DZ-ELT/off/846/2015	CIMMYT
8	CD15DZ_ELT/off/275/2015	CIMMYT	58	CD15DZ-ELT/off/1239/2015	CIMMYT
9	CD15DZ_ELT/off/982/2015	CIMMYT	59	CD15DZ-ELT/off/889/2015	CIMMYT
10	CD15DZ_ELT/off/1029/2015	CIMMYT	60	CD15DZ-ELT/off/891/2015	CIMMYT
11	CDSS09B00191T-099Y-020M-6Y00M	CIMMYT	61	CD15DZ-ELT/off/1235/2015	CIMMYT
12	CDSS09B00067S-099Y-035M-3Y-0M	CIMMYT	62	CD15DZ-ELT/off/1072/2015	CIMMYT
13	CDSS09B00203T-099Y-066M-2Y-0M	CIMMYT	63	CD15DZ-ELT/off/661/2015	CIMMYT
14	ICD08-291-0AP	CIMMYT	64	CD15DZ-ELT/off/664/2015	CIMMYT
15	CDSS09B00190T-099Y-036M-18Y-0M	CIMMYT	65	CD15DZ-ELT/off/745/2015	CIMMYT
16	CD15DZ_ELT/off/1103/2015	CIMMYT	66	CD15DZ-ELT/off/790/2015	CIMMYT
17	CD15DZ_ELT/off/1116/2015	CIMMYT	67	CD15DZ-ELT/off/792/2015	CIMMYT
18	CD15DZ_ELT/Off/1102/2015	CIMMYT	68	CD15DZ-ELT/off/801/2015	CIMMYT
19	CD15DZ_ELT/off//1057/2015	CIMMYT	69	CD15DZ-ELT/off/802/2015	CIMMYT
20	CD15DZ_ELT/off/999/2015	CIMMYT	70	CD15DZ-ELT/off/935/2015	CIMMYT
21	CD15DZ_ELT/off/1112/2015	CIMMYT	71	CD15DZ-ELT/off/981/2015	CIMMYT
22	CD15DZ_ELT/off/1067/2015	CIMMYT	72	CD15DZ-ELT/off/995/2015	CIMMYT
23	CD15DZ_ELT/off/1094/2015	CIMMYT	73	CD15DZ-ELT/off/1032/2015	CIMMYT
24	CD13DZOS F6SR 2013 MS DZLS/22	CIMMYT	74	CD15DZ-ELT/off/1081/2015	CIMMYT
25	CD13DZOS F6SR 2013 MS DZLS/93	CIMMYT	75	CD15DZ-ELT/off/1082/2015	CIMMYT
26	CD13DZOS F6SR 2013 MS DZLS/106	CIMMYT	76	CD15DZ-ELT/off/1087/2015	CIMMYT
27	CD13DZOS F6SR 2013 MS DZLS/81	CIMMYT	77	CD15DZ-ELT/off/1129/2015	CIMMYT
28	CD13DZOS F6SR 2013 MS DZLS/105	CIMMYT	78	CD15DZ-ELT/off/1131/2015	CIMMYT
29	CD13DZOS F6SR 2013 MS DZLS/84	CIMMYT	79	CD15DZ-ELT/off/1144/2015	CIMMYT
30	CD13DZOS F6SR 2013 MS DZLS/111	CIMMYT	80	CD15DZ-ELT/off/1152/2015	CIMMYT
31	CD13DZOS F6SR 2013 MS DZLS/83	CIMMYT	81	CD15DZ-ELT/off/1159/2015	CIMMYT
32	CD13DZOS F6SR 2013 MS DZLS/87	CIMMYT	82	CD15DZ-ELT/off/1164/2015	CIMMYT
33	CD13DZOS F6SR 2013 MS DZLS/80	CIMMYT	83	CD15DZ-ELT/off/1176/2015	CIMMYT
34	CD13DZOS F6SR 2013 MS DZLS/97	CIMMYT	84	CD15DZ-ELT/off/1193/2015	CIMMYT
35	CD15DZ_ELT/off/251/2015	CIMMYT	85	CD15DZ-ELT/off/1516/2015	CIMMYT
36	CD15DZ_ELT/off//1086/2015	CIMMYT	86	CD15DZ-ELT/off/1244/2015	CIMMYT
37	CD15DZ_ELT/off/1006/2015	CIMMYT	87	CD15DZ-ELT/off/305/2015	CIMMYT
38	CD15DZ_ELT/off/989/2015	CIMMYT	88	Ude	CIMMYT
39	CD15DZ_ELT/off/303/2015	CIMMYT	89	Tesfaye	CIMMYT
40	CD15DZ_ELT/off/1113/2015	CIMMYT	90	Tob-66 (Arsi-Robe)	CIMMYT
41	CD15DZ_ELT/off/1035/2015	CIMMYT	91	Bichena	CIMMYT
42	CD15DZ_ELT/off/1034/2015	CIMMYT	92	Foka	CIMMYT
43	CD15DZ_ELT/off/1038/2015	CIMMYT	93	Utuba	CIMMYT
44	CD15DZ_ELT/off/1115/2015	CIMMYT	94	Ginchi (DZ 1050)	CIMMYT
45	CD15DZ_ELT/off/1037/2015	CIMMYT	95	Yerer	CIMMYT
46	CD15DZ_ELT/off/1069/2015	CIMMYT	96	Mukiye	ICARDA
47	CD15DZ_ELT/off/1079/2015	CIMMYT	97	Robe (DZ 1640)	CIMMYT
48	CD15DZ_ELT/off/998/2015	CIMMYT	98	Hitosa	CIMMYT
49	CD15DZ_ELT/off/1083/2015	CIMMYT	99	Mangudo	ICARDA
50	CD15DZ_ELT/off/1000/2015	CIMMYT	100	Werer	ICARDA

Data collection

Data were collected both on plot and plant basis, plant basis data were collected from randomly selected five plants from each plot and the mean values were used to estimate the performance of each genotype for the trait under consideration.

Soil moisture content: Was determined by taking the soil sample from 30 cm soil depth at four crop stages (at planting, seedling, tillering and booting) based on the gravimetric method.

$$\text{Moisture content of the soil (\%)} = \frac{\text{WW}-\text{DW}}{\text{DW}} \text{ X } 100$$

Where, WW is wet weight of the soil and DW is dry weight of the soil.

The following agronomic traits were included in the investigation.

(1) Days to heading.
(2) Days to maturity.
(3) Grain filling period.
(4) Plant height.
(5) Spike length.
(6) Number of productive tillers per plant.
(7) Number of spikelets per spike.
(8) Grain yield.
(9) Harvest index.
(10) The number of kernels per spike.
(11) Thousand kernel weight.
(12) Biomass yield per plot.

Data analysis

All measured parameters at each location and the combined locations were subjected to analysis of variance as per the simple lattice anova model and the relative efficiency (RE) of the lattice design relative to RCBD was checked. As the RE values were less than 104% for all traits at both locations, RCBD was used for the final analysis reported herein since it provides larger error degrees of freedom, thus more precision than the lattice model under such conditions. The analysis with the RCBD model was performed following the standard procedure (Gomez and Gomez, 1984) using the appropriate statistical software.

Phenotypic and genotypic variability

The variance components and coefficients of variations for the data combined over locations were estimated according to the methods suggested by Johnson *et al. (*1955)

Heritability (H^2) in the broad sense for all traits was computed using the formula adopted from Allard (1960) and for each trait, genetic advance (GA) was computed using the formula adopted from Johnson *et al*. (1955) and Allard (1960).

Results and Discussions

Analysis of variance

Analysis of variance for 21 quantitative traits revealed the presence of significant differences among 100 durum wheat genotypes for all traits at Debre Zeit and Chefe Donsa (Tables 3). The observed variations among the genotypes provided valuable information for grain yield and nutritional quality improvement in the studied durum wheat genotypes under waterlogging condition. Similarly, the research finding of Tesfaye *et al.* (2016) also reported highly significant differences among durum wheat genotypes for days to heading, days to maturity, grain filling period, number of productive tillers per plant, plant height, kernels per spike, number of spikelets per spike, spike length, thousand-grain weight, biological yield, grain yield, and harvest index.

The result showed highly significant ($P \leq 0.01$) variations among the genotypes for all traits considered. Location effects were also highly significant ($P \leq 0.01$) for all traits except for biological yield, harvest index, grain yield, and number of kernels per spike; while location by genotype interactions were highly significant ($P \leq 0.01$) for all studied traits. The observed significant differences among genotypes for the traits under study indicated the presence of genetic variations among the genotypes, which in turn suggested that the selection of genotypes can be effective in improving both yield and quality traits of durum wheat. Mohammed *et al.* (2011) also reported considerable genetic variability for quantitative and qualitative traits in durum wheat genotypes. Generally, this finding indicated the existence of great variability among the test genotypes under water-logging conditions for all characters measured, which could be exploited through selection, as variability within populations is a basic requirement for plant breeding programs.

Table 3. Analysis of variance for the 21 characters of 100 durum wheat genotypes grown at Debre Zeit and Chefe Donsa (2018) under water-logging conditions

Traits	Location (df=1)	Replication (df=2)	Genotype (df=99)	Gen x Loc. (df=99)	Error (df=198)	CV (%)
Days to heading	5677.62**	0.12	38.11**	12.86**	5.12	3.30
Days to maturity	78344.01**	5.76	13.47**	10.92**	5.65	2.22
Grain filling period	41840.70**	7.56	27.77**	18.84**	7.68	7.21
Plant height (cm)	58.52**	103.02	66.60**	10.41**	6.23	3.25
Number of effective tillers/m2	2916.00**	1176.49	614.81**	323.16**	149.61	9.63
Spike length (cm)	15.44**	2.86	1.55**	1.20**	0.67	12.20
Number of spikelet per spike	119.95**	9.78	5.86**	4.55**	2.62	7.70
Harvest index (%)	3.09	5.62	27.51**	19.40**	12.88	15.08
Grain Yield kg/ha	144628	2140954	3670292**	2432374.**	1410263	20.51
Number of kernels per spike	102.62	0.61	226.36**	120.97**	28.43	9.51
Thousands kernel weight (g)	2827.26**	3.01	110.78**	83.85**	13.41	10.76
Biological yield (kg/ha)	16933225	3.93	17944449**	14662720.**	7408524.00	11.44
Ash Content	4.63**	68.62	0.01**	0.01**	0.00	7.82
Grain starch percentage	52.20**	668.89	2.52**	2.75**	1.84	2.05
Grain protein Content (%)	525.10**	1.44	2.30**	1.66**	0.44	4.95
Grain gluten Content (%)	1515.47**	4.99	38.11**	18.84**	10.08	9.42
Wet gluten Content (g)	876.16**	1.67	31.77**	18.65**	9.50	10.45
Dry gluten Content (%)	114.19**	97.20	23.59**	2.56**	1.09	9.03
Gluten index	1896.60**	40.30	4.87**	287.54**	26.52	8.69
Sedimentation Volume	778.41**	1327.89	695.29**	32.44**	11.32	8.69
Vitreousness	1335.17**	32.20	86.99**	71.49**	12.19	3.85

** shows highly significant at ($p \leq 0.01$) probability level, df= degree of freedom,
Gen = genotype, Loc. = Location, CV= coefficient of variation

Phenotypic and genotypic variances

The result showed that estimates of phenotypic coefficients of variation were higher than their corresponding genotypic coefficients of variation, indicating the influence of environment on the expression of these traits. According to Deshmukh *et al.* (1986), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% were considered to be low and values between 10% and 20% as medium.

Higher GCV and PCV value (>20%) were observed for gluten index (38.67, 38.91), followed by grain yield (30.95, 32.56), thousand-grain weight (28.17, 28.69), number of kernels per spike (25.39, 25.82), sedimentation volume (22.63, 23.02) and harvest index

(20.45,21.77) (Table 4). Similar results were also reported by Krasimira *et al.* (2019) for sedimentation volume and grain yield and by Yonas *et al.* (2016) for thousand kernels weight and grain yield. The high values for both PCV and GCV along with the small difference between the two values might be an indication of the little influence of environmental factors for the phenotypic expression of these traits which implies selection on phenotypic bases of these traits may be effective for genetic improvement of the crop. The traits which showed moderate GCV and PCV (10%-20%) were number of effective tillers (18.12, 18.74), spike length (16.59, 17.62), dry gluten content (16.59, 17.53), biological yield (15.91, 16.94), grain gluten content (15.48, 16.46), wet gluten content (14.96, 15.79) and ash content (12.28, 12.89). Lowest GCV and PCV (<10%) values were observed for grain starch percentage (2.15, 2.35), days to maturity (3.29, 3.46), days to heading (8.43, 8.58), plant height (8.88, 9.03), and vitreousness (9.27, 9.46). However, lower GCV (9.89) and moderate PCV (10.2) was observed for grain protein content.

Heritability and genetic advance

Pramoda and Gangaprasad (2007) generally classified heritability estimates as low (<40%), medium (40-59%), moderately high (60-79%) and very high (≥80%), whereas genetic advance as percent of mean was classified as low (0-10%), moderate (10-20%) and high (>20%) (Johnson *et al.*, 1955). In this study, the estimated values of H^2 ranged from 61.82% to 92.48%, while the GAM ranged from 3.92% to78.35%. Relatively very high (≥80) H^2 was observed for four traits; namely plant height (92.48), days to heading (84.44), gluten index (81.26), and sedimentation volume (84.15) (Table 4). However, number of effective tillers (76.77), number of kernels per spike (76.43), grain gluten content (74.18), ash content (72.83), grain yield (71.57), harvest index (70.02), grain filling period (71.00), grain protein content (69.40), thousand grain weight (68.17), number of spikelets per spike and spike length (67.5), wet gluten content (66.99) , days to maturity (66.31), biological yield (66.01), vitreousness (65.91), grain starch percentage (61.82) resulted in moderately high H^2 (Table 4) .

Higher GAM (>20%) were observed for gluten index (78.35), grain yield (52.76), thousand grain weight (47.43), sedimentation volume (45.33), number of kernels per spike (45.05), harvest index (34.53), number of kernels per spike (32.90), dry gluten content (32.09), spike length (28.26), grain gluten content (27.42), biological yield (26.62), wet gluten content (24.91), ash content (24.02), grain filling period (21.71), and plant highest (20.68). However, grain starch percentage (3.92) and days to maturity (5.14) resulted in lower GAM. Among the studied traits, high H^2 associated with high GAM were observed for grain yield, thousand grain weight, dry gluten content, wet gluten content, harvest index, grain gluten content, ash content, biological yield, number of kernels per spike, spike length, number of effective tillers, plant height, gluten index and grain filling period. This shows that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Berhanu *et al.* (2019) also reported high heritability and high genetic advance as percent of mean for grain yield, harvest index and biomass yield. High H^2 and moderate GAM were recorded for days to heading, number of spikelets per spike, gran protein content and vitreousness.

High H^2 values for those traits indicated that the characters were less influenced by the environmental factors and the variation observed was mainly under genetic control and selection for such characters could be fairly easy. Similarly, maturity dates and grain starch percentage had high broad sense heritability and low genetic advance as percent of mean. Low values of PCV and high estimated values of H^2 lead those traits to have low GAM. So, improvements of these traits are difficult because selection and improvement is the result of variability, heritability, and genetic advance as percent of mean. Therefore, grain yield, thousand grain weight, dry gluten content, wet gluten content, harvest index, grain gluten content, ash content, biological yield, number of kernels per spike, spike length, number of effective tillers, plant height, gluten index and grain filling period are important traits to select durum wheat genotypes for yield and quality underwater logging condition.

Principal Component Analysis

The principal component analysis (PCA) for 21 traits was computed to identify the critical traits that are important for the improvement of the crop and the traits that explained more of the variation in durum wheat (Table 5). As a result, seven significant principal components (PC) with an eigenvalue greater than one and component loading greater than ± 0.3, which accounted for 83.7% of the total variation among the genotypes were identified. Accordingly, the first principal component had an eigenvalue of 3.46 and accounted for 26.5% of the total variation. Harvest index, grain yield, biological yield, and days to heading were traits associated with PC1 with high loading effect.

Table 4. Mean, range, and variability components for 21 agronomic and quality traits of 100 durum wheat genotypes tested at Debre Zeit and Chefe Donsa (2018)

Traits	Mean	Range	σ2gl	σ2g	σ2p	σ2e	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
Days to heading	68.65	61.25 - 78.5	10.30	34.9	41.33	6.43	8.43	8.58	84.44	11.2	16.31
Days to maturity	107.1	104.00 – 115	8.09	10.74	16.2	5.46	3.29	3.46	66.31	5.51	5.14
Grain filling period	38.45	32.25 - 44.25	15.00	23.06	32.48	9.42	12.5	12.99	71	8.35	21.71
Plant height (cm)	76.75	69.5 - 88.00	7.29	64	69.2	5.2	8.88	9.03	92.48	15.87	20.68
Number of effective tillers	126.97	81.5 - 166.5	248.35	534.02	695.6	161.58	18.12	18.74	76.77	41.77	32.9
Spike length (cm)	6.71	5.18 - 8.43	0.87	1.25	1.85	0.6	16.59	17.62	67.5	1.9	28.26
Number of spikelet per spike	21.03	18.05 -24.00	3.24	4.72	7	2.28	10.29	10.99	67.5	3.68	17.51
Harvest index (%)	23.8	18.04 - 28.67	12.96	22.66	32.36	9.7	20.45	21.77	70.02	8.22	34.53
Grain Yield kg/ha	5789	3515.25 - 7539.25	1727243	3062198	4278385	1216187	30.95	32.56	71.57	3054.17	52.76
Number of kernels per spike	56.06	34.48 - 74.25	106.76	196.12	256.61	60.49	25.39	25.82	76.43	25.26	45.05
Thousands kernels weight (g)	34.04	25.45 - 56.95	77.15	89.81	131.74	41.93	28.17	28.69	68.17	16.14	47.43
Biological yield per hectare (g)	23802	16800.00 - 27100	10958458	14278769	21610129	7331360	15.91	16.94	66.07	6336.67	26.62
Ash Content	0.75	0.61 - 0.86	0.01	0.01	0.01	0	12.28	12.89	72.83	0.18	24.02
Grain starch percentage	66.35	64.53 - 68.13	2.36	2.58	4.17	1.59	2.15	2.35	61.82	2.6	3.92
Grain protein Content (%)	13.39	11.43 - 15.38	1.44	1.88	2.71	0.83	9.89	10.2	69.4	2.36	17.61
Grain gluten Content (%)	33.71	28.41 - 42.61	13.80	27.06	36.48	9.42	15.88	16.46	74.18	9.24	27.42
Wet gluten Content (g)	29.49	23.48 - 35.15	13.90	18.92	28.25	9.33	14.96	15.79	66.99	7.35	24.91
Dry gluten Content (%)	11.58	8.5 - 14.63	2.02	4.23	5.51	1.28	16.95	17.53	76.73	3.72	32.09
Gluten index	59.27	22.15 - 83.33	274.28	623.4	767.17	143.77	38.67	38.91	81.26	46.43	78.35
Sedimentation Volume	38.74	28.00 - 57	26.78	86.13	102.35	16.22	22.63	23.02	84.15	17.56	45.33
Vitreousness	90.72	75.4 - 96.9	65.40	69.12	104.86	35.74	9.27	9.46	65.91	13.92	15.35

σ^2p =Phenotypic variation, σ^2g =Genotypic variation, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H^2= Broad sense heritability, GA=genetic advance, and GAM=Genetic advance as percent of mean

Table 5 The first seven principal components that explain the variation of 21 traits of 100 durum wheat genotypes

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Days to heading	**-0.33**	-0.10	**-0.48**	0.07	0.01	-0.12	-0.22
Days to maturity	-015	-0.02	-0.24	**0.39**	**-0.30**	0.01	0.17
Grain filling period	0.28	0.10	**0.34**	0.19	-0.22	0.15	**0.38**
Plant height (cm)	0.14	-0.03	0.14	**0.42**	0.25	0.16	**-0.35**
Number of effective tillers	0.17	0.03	-0.10	-0.26	**0.30**	-0.17	0.24
Spike length (cm)	0.04	**0.41**	-0.05	-0.09	-0.17	0.19	-0.22
Number of spikelet per spike	0.11	0.23	-0.06	-0.07	0.21	**0.52**	-0.09
Harvest index (%)	**0.43**	-0.02	**-0.30**	-0.05	-0.07	-0.01	-0.12
Grain Yield kg/ha	**0.48**	-0.09	-0.26	0.01	-0.10	0.00	-0.06
Number of kernels per spike	0.18	-0.18	-0.28	-0.19	**-0.33**	-0.05	0.03
Thousands kernels weight (g)	0.13	-0.10	0.11	**0.47**	-0.09	-0.20	0.12
Biological yield per hectare (g)	**0.43**	-0.08	-0.16	0.10	-0.08	0.02	0.04
Ash Content	-0.10	0.08	-0.25	0.13	0.07	-0.12	0.18
Grain starch percentage	-0.07	-0.19	-0.16	**0.35**	0.25	-0.06	0.13
Grain protein Content (%)	-0.03	**-0.36**	0.13	-0.23	-0.10	-0.13	-0.12
Grain gluten Content (%)	-0.02	-0.46	0.21	-0.10	-0.15	0.06	0.07
Wet gluten Content (g)	0.20	-0.21	0.11	-0.11	0.62	-0.23	-0.26
Dry gluten Content (%)	0.04	-0.31	0.06	0.02	0.42	0.17	0.08
Gluten index	-0.04	-0.33	-0.09	0.16	-0.08	0.48	-0.27
Sedimentation Volume	-0.18	-0.26	-0.05	-0.20	-0.22	0.39	0.19
Vitreousness	0.02	-0.03	-0.27	-0.06	0.31	0.23	0.50
Eigen value	3.46	2.23	1.96	1.85	1.47	1.2	1.13
Individual variation (%)	26.5	20	13.1	8.3	7.7	4.7	3.4
Cumulative (%)	**26.5**	**46.5**	**59.6**	**67.9**	**75.6**	**80.3**	**83.7**

Data presented in boldface point toward significant traits with component loading >± 0.3.

Principal component two (PC2) possesses an eigen value of 2.23 and showed 20% of the variation mainly due spike length, grain protein content, grain gluten content, dry gluten content and gluten index. An eigen value of 1.96 and 13.1% of variation was reflected by principal component three (PC3), mainly due to days to heading, grain filling period and harvest index. The result agrees with the previous finding of Mostafa *et al.* (2011). Principal component four (PC4) and principal component five (PC5) had eigen values of 1.85 and 1.47 and contributed 8.3% and 7.7% of the variation, respectively which were from days to maturity, plant height, number of effective tillers, number of kernels per spike, thousands kernels weight, grain starch percentage, wet gluten content, dry gluten content and vitreousness. Traits like number of spikelets per spike, gluten index and sedimentation volume loaded the highest values on the sixth component which had an eigen value of 1.2 with individual variation of 4.7. However, grain filling period, plant height and vitreousness exerted high loading and great effect in principal component seven which contributed 3.4 for the variation.

There is a wide range of genetic variation among the 100 durum wheat genotypes as shown by the scatter plot presented in Figure 3. In the scatter plot, genotypes closer to each other had similar value of quantitative traits, while those near the origin are similar and the others far from the origin are more distant. However, quadrant I consists of genotypes which had similar days to maturity and ash content, while the genotypes found in quadrant II had comparable spike length, number of kernels per spike, vitreousness, number of effective tillers, grain filling period, plant height and harvest index. Quadrant III contained genotypes which were related in terms of their days to maturity, sedimentation volume, grain starch percentage, gluten index and grain gluten content, while genotypes found in quadrant IV were similar based on thousand grain weight, number of kernels per spike, wet gluten content and dry gluten content.

The loading plot (Figure 1) shows the comparison and variances among the 21 traits and the result revealed that the traits found near the origin like ash content, days to maturity, vitreousness, number of effective tillers, plant height, thousand grain weight, number of kernels per spike, number of spikelets per spike, sedimentation volume, and grain starch percentage have smaller lodging and influence little in this classification (Table 5), while those found far from the origin like wet gluten content, dry gluten content, gluten index, grain protein content, harvest index, biological yield, grain yield and date of heading exerted higher loading and great influence in this classification.

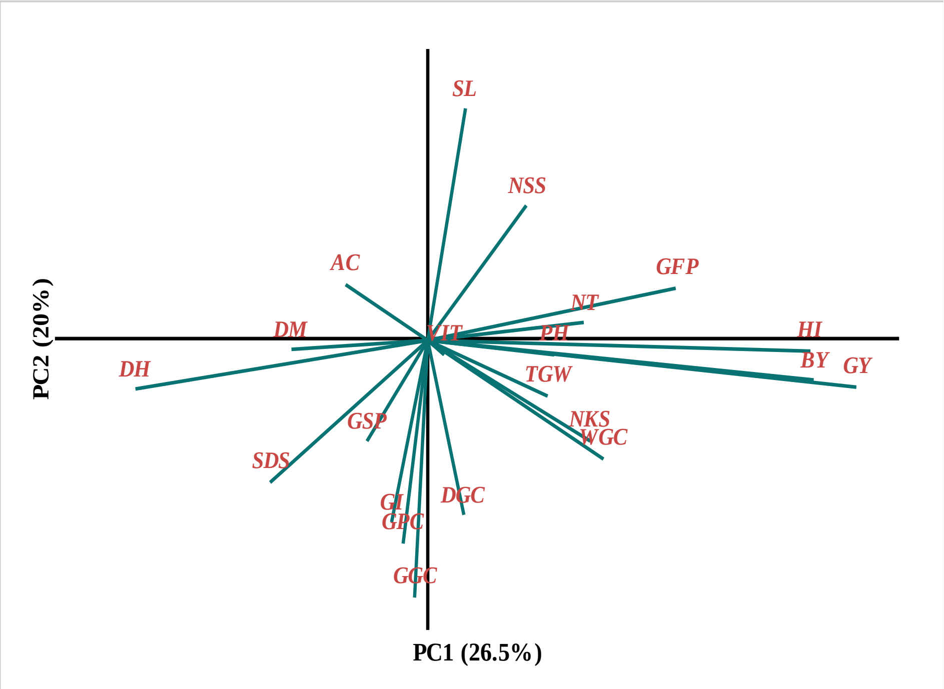

Figure 1. Loading plot of principal component analysis for 21 quantitative traits of 100 durum wheat genotypes DH=days to heading, DM= days to maturity, GFP= Grain filling period, PH= plant height, NT= tiller number, SL= spike length, NSS= number of spikelet per spike, HI= harvest index, NKS= number of kernels per spike, TGW= thousand grain weight, BY= biological yield, AC=, GSP= grain starch percentage, GPC= grain protein content, GGC= grain gluten content, WGC= wet gluten content, DGC= dry gluten content, GI=gluten index, SDS= sedimentation volume, VIT= vitreousness

Conclusions

The experiment was conducted to assess the extent of genetic variability for yield and agronomic traits of durum wheat under waterlogged conditions. In this study, the traits that had high phenotypic and genotypic coefficients of variations were grain yield followed by thousand-grain weight, number of kernels per spike, sedimentation volume and harvest index. The estimated values of broad sense heritability ranged from 61.82 % for grain starch percentage to 92.48% for plant height and genetic advance as percent of mean ranged from 3.92 % for grain starch percentage to 78.35% for gluten index.

Seven significant principal components (PC) which explained cumulatively 83.7% of the total variation were extracted. The first PC had an eigenvalue of 3.46 and accounted for 26.5% of the variation. This variation was revealed by harvest index, grain yield (kg/ha), biomass yield (kg/ha) and days to heading; while PC2 possessed an eigenvalue of 2.23 and showed 20% of the variation mainly due to spike length, grain protein content, grain gluten content, dry gluten content and gluten index.

The result indicated considerable variations among the tested durum wheat genotypes. This provides substantial information for breeders to select potential parents for the traits of interest to develop a variety which is tolerant to water logging. However, the exploitation of this information in breeding programs needs additional studies to identify appropriate genetic backgrounds of the genotypes and the evaluation of the breeding lines in multi-environmen trials. Moreover, molecular studies such as QTL mapping could be initiated using these durum wheat materials to identify chromosomal regions controlling waterlogging tolerance in durum wheat.

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