Drought adaptations in wild barley (*Hordeum spontaneum*) grown in Iran

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Abstract
Wild barley contains a wide genetic diversity and therefore is adaptable to all kinds of harsh environments. The aim of this research was to determine the extent of drought stress adaptation within *Hordeum spontaneum* L. genotypes from different climates of Iran. From the primary population of 193 genotypes, a core set consisting of 18 genotypes, were selected based on the highest squared Euclidean distance to represent the genetic diversity among wild barley genotypes. The selected genotypes were evaluated for drought stress adaptation. At the beginning of flowering time, two different water treatments; well-watered (90-100% field capacity) and drought stress (20-30% field capacity) were imposed to the plants. A negative correlation of stress tolerance index with phenological traits and relative water loss was observed. Genotypes with the highest relative water loss under drought stress condition were mainly from Mediterranean and Cool steppe climates and genotypes from desert climates seemed to have better adaptability to drought stress shown by less relative water loss. It seems that genotypes from unpredictable climatic conditions are more adapted to harsh environments.

Key words: *Hordeum spontaneum* L., Diversity, Adaptation.

INTRODUCTION

Genetic diversity in barley cultivars has significantly reduced as a result of genetic erosion by which many of the ancient landraces have vanished (Ellis *et al.,* 2000). Domesticated barley cultivars represent only a small fraction of genetic variation presented in wild populations (Brown, 1992; Nevo, 1992). Due to the loss of genetic variation, modern cultivars have become more sensitive to biotic and abiotic stresses (Zhao *et al.,* 2010). Unpredictable drought stress is one of the most serious problems which have restricted agricultural production in about one-third of the world's arable lands (Chaves and Oliveira, 2004). Developing drought tolerant genotypes is a cost-effective and efficient approach to stabilize grain production and ensure agricultural production, in arid and semi arid regions of the world.

Wild barley contains a wide genetic diversity and therefore can have wide adaptability to the most kinds of harsh environments (Baum *et al.,* 1997). Wild barley, *Hordeum spontaneum* L. the progenitor of cultivated barley *Hordeum vulgare*, is a selfing annual grass predominated in Mediterranean and Irano-Turanian regions which has penetrated into desert environments where it maintains stable populations (Harlan and Zohary, 1966). The wide ecological range of wild barley differs in water availability, temperature, soil type and altitude which generats vegetation populations with high potential of adaptive diversity to abiotic stresses (Eglinton *et al.,* 1999). Therefore, it can be used as the primary gene pool in barley breeding programs (Ceccarelli *et al.,* 1995). Several researchers

Table 1. Geographic and climatic information of collecting sites for core set of *H. spontaneum* genotypes based on Gousan climatic zones.

No.	Collection Code	Group in Cluster	Climate	Province
1	309	4	Mediterranean (M)	Ghazvin
2	324	2	Cool Desert (CD)	Markazi
3	554	1	Desert (D)	Fars
4	556/1	3	Desert (D)	Fars
5	951	4	Desert (D)	Khorasan
6	1037	1	Mediterranean (M)	Kermanshah
7	1073	1	Mediterranean (M)	Kermanshah
8	1233	4	Mediterranean (M)	Khorasan
9	1263	6	Cool Steppe (CS)	Azarbaijan garbi
10	1286	3	Mediterranean (M)	Kermanshah
11	1350	1	Cool Desert (CD)	Markazi
12	1363	1	Desert (D)	Illam
13	1375	6	Desert (D)	Illam
14	1377	4	Desert (D)	Illam
15	1389	5	Desert (D)	Fars
16	1674	8	Desert (D)	Khorasan
17	1693	1	Desert (D)	Khorasan
18	1801	1	Cool Steppe (CS)	Azarbaijan garbi
19	Nosrat	-	-	-

have investigated the potential of exploiting the wild relatives of cultivated barley as a source of genetic material (Nevo, 1992; Chen *et al.,* 2010; Zhao *et al.,* 2010). Baum *et al.* (1997) reported an extensive genetic diversity in natural stand of wild barley throughout the Fertile Crescent.

Researches on plant evolution, physiological adaptation and population genetics indicated that there is a significant positive correlation between genetic variability and adaptation to environmental stress factors in *H. spontaneum* genotypes from different habitats (Maestri *et al.,* 2002; Suprunova *et al.,* 2004). Wild populations, from the highly stressed environments contain the highest genetic diversity (Nevo *et al.,* 1998). Zhao *et al.* (2010) reported a high diversity in drought stress tolerance among Tibet wild barley genotypes. Evaluation of *H. spontaneum* genotypes from Turkey, Iran and Iraq (Bakhteyev and Darevskaya, 2003), showed a high genetic diversity in morphological traits. Volis *et al.* (2002) reported higher adaptation to water limited conditions in desert genotypes compared to Mediterranean genotypes of *H. spontaneum*. Chen *et al.* (2010) suggested that the xeric ecotypes adopted survival strategies while the mesic ecotypes adopted growth-sustain strategies to cope with drought stress.

The knowledge of quality and quantity of genetic diversity and adaptation in plant genetic resources is the essential step toward development of effective applicable strategies (Hodgkin, 1997). Multivariate statistical procedures using agro-morphological traits and characterizing genetic divergence can be used for grouping of the genetic resources (Mead *et al.,* 2002). There is little information about the variation of adaptabilities to different environmental stress factors in wild barley (*H. spontaneum*) ecotypes originated from Iran. This research aimed at determining the extent of drought stress adaptation in wild barley (*H. spontaneum*) genotypes from different climates of Iran.

MATERIALS AND METHODS

The study was carried out in a greenhouse using eighteen Iranian genotypes of *Hordeum spontaneum* L. (Table 1) provided by National Plant GenBank of Iran (NPGBI) and Nosrat cultivar as a check line. The genotypes were selected based on highest squared euclidean distance to represent the diversity of the genetic materials consisting of 193 *H. spontaneum* genotypes from barley germplasm collection in NPGBI (Shahmoradi *et al.,* 2013), (Figure 1). Nosrat cultivar is released from Karoon×Kavir progenies which contain a high yield potential, stability and adaptation. Seeds

were germinated in Petri dishes and seedlings were established in a germinator under controlled conditions (15˚C and no light) for 7 days and then they were transplanted into 3-L pots containing a mixture of soil: sand: peat in a volume ratio of 2:1:1. At first three seedlings were placed in each pot and after establishment, it was reduced to two seedlings. The field capacity of the pots soil was determined before planting through saturating the soil with water, covering the pots with plastic sheets and leaving to drain for three days (Samarah, 2000). The weight of soil moisture at field capacity was calculated as the difference between the soil weight after primary drainage (after saturation) and the soil weight after oven drying in 100˚C for 48 h. The seedlings were thinned to two seedlings per pot after four weeks. The experimental design consisted of three replicates in a factorial design with two different water treatments and each experimental unit consisted of three pots. The pots were maintained at field capacity (well-watered) based on the weight of soil at field capacity (moisture level 19.5% w/w). The moisture level of all filled pots was estimated as subtracting their weight from FC recorded weight. Therefore, all planted pots were watered with necessary amount of water to bring soil water content close to 90-100% FC (moisture level 19% w/w) until the plants reached the Z_{49} time at which 1 cm of awn had emerged from the flag leaf sheath of the main stem (Zadoks *et al.*, 1974). At the beginning of flowering period, two different water treatments; well-watered treatment (90-100% field capacity) and drought stress treatment (20-30% field capacity) were imposed on the plants. Desirable soil moisture content was maintained by weighing the pots daily. Both drought stressed and well-watered (control) plants were weighed daily and water loss was carefully replenished with tap water to maintain soil water content close to the desired FC until the end of the experiment.

Morphological traits including number of fertile tillers per plant, leaf dry weight and stem dry weight were determined in the milky stage. Agronomic traits such as grain yield, hundred grain weight, biological yield and harvest index were scored after physiological maturity and recording the phenological traits were based on Zadoks growth stages including first awns visible(Z_{49}) flowering (Z_{59}) and maturity (Z_{94}) (Zadoks *et al.*, 1974).

Chlorophyll meter (SPAD-502, Japan) was used to determine the relative chlorophyll content (RCC) in the flag leaf of the genotypes. Four flag leaves of each genotype were measured after anthesis stage. Average of three random measurements in the middle of the flag leaf was used for analysis.

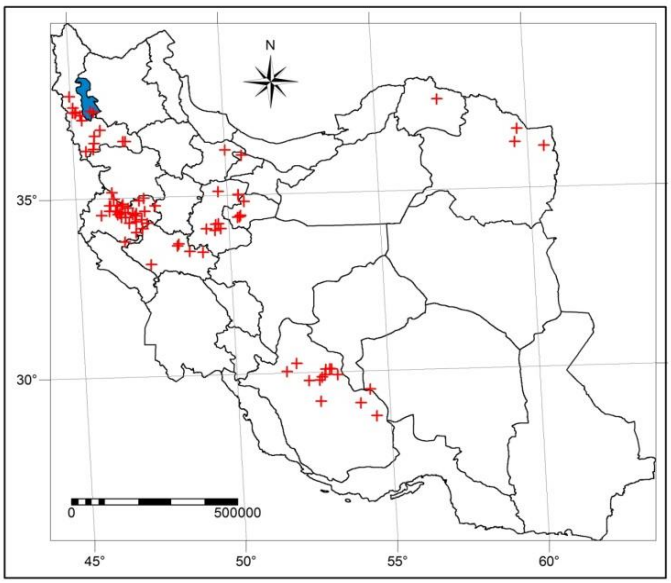

Figure1. Distribution of collection sampling regions for *Hordeum spontaneum* L. genotypes of Iran.

Relative water content (RWC) was determined according to Turner (1986., Fresh leaves were taken each genotype and each replication after anthesis stage and weighed immediately to record fresh weight (FW). Then the samples were placed in distilled water for 4 h and weighed again to record turgid weight (TW). Afterwards they were subjected to oven drying at 70°C for 24 h to record dry weight (DW). The RWC was calculated based on following equation:

(1) $RWC = ((FW - DW)/(TW - DW)) \times 100$

To determine the Relative water loss (RWL), young fully expanded leaves were sampled from each of three replications at anthesis stage. The leaf samples were weighed (FW), wilted for 4 hour at 35°C, reweighed (W4h), and placed in oven for 24 h at 72°C to obtain dry weight (DW). The RWL was calculated using the following formula (Gavuzzi *et al.*, 1997):

(2) $RWL (\%) = [(FM - W4h)/(FW - DW)] \times 100$

Excised leaf water retention was determined based on Farshadfar *et al.* (2002) where the young leaves were collected before anthesis stage and weighed (FW), left for 4 h, then wilted at 20°C and reweighed (W4h). ELWR was calculated using the following formula:

(3) $ELWR (\%) = [1 - ((FW - W4h)/FW))] \times 100$

Variance Analysis of traits under drought and normal

Table 2. Variance analysis of traits for 19 genotypes of *H. spontaneum* and Nosrat cultivar under normal and drought stress condition.

		Mean Square							
Source	df	Relative Chlorophyll Content	Relative Water Content	Relative Water Loss	Excised Leaf Water Retention	Fertile Tillers	Spike Length	Leaf Dry Weight	Spike Dry Weight
Replication	2	21.05	195.7	105.53	0.002	1.66	0.927	0.047	6.77
Drought	1	28.40*	830.03**	735.46**	0.069**	19.37**	1.48	1.56**	132.08**
Genotype	18	75.74**	91.60**	557.88**	0.02**	2.06**	2.53**	0.13**	7.72**
Drought × Genotype	18	16.26*	56.45*	161.10	0.005	0.65	0.44	0.07*	3.72**
Error	74	8.36	34.19	133.12	0.005	0.60	0.63	0.03	1.35

**and* significant at the 1% and 5% probability levels, respectively.

Continue of Table 2.

		Mean Square							
Source	df	Stem Dry Weight	Grain Yield	Kernel Weight	Biological Yield	Harvest Index	Days to Flowering	Seed Filling Duration	Days to Maturity
Replication	2	21.21	4.42**	0.63	39.33	113.71**	10.5	8.67	22.53
Drought	1	909.79**	37.54**	2.67**	1735.18**	2.21	7.89	452.01**	340.43**
Genotype	18	9.74	6.23**	1.79**	27.55*	131.37**	52.45**	23.02	38.56**
Drought × Genotype	18	11.25	1.97**	0.19	21.27	36.53**	7.65	14.38	13.69*
Error	74	9.74	0.64	0.17	16.06	14.88	8.26	15.16	7.68

**and* significant at the 1% and 5% probability levels, respectively.

conditions were made using SAS 9.1 and mean comparison was based on Duncan multiple test. Reaction of genotypes to drought stress was evaluated based on stress tolerance Index (Fernandez, 1992). Principle component analysis and bi-plot graph drawing were made through Stat Graphics plus 2.1, in order to evaluate the relations between climates and stress tolerance index.

RESULTS

Combined variance analysis of the traits (Table 2) indicated that drought stress had significantly affected most of the evaluated traits excluding spike length, harvest index and days to flowering. Also the genotypes responded differently to drought stress in all traits excluding stem weight and seed filling duration. Interaction between drought stress and genotype was significant in relative chlorophyll content, relative water content, leaf dry weight, spike dry weight, grain weight, harvest index and days to maturity. These results showed that genotypes reacted differently to drought stress through these traits.

Based on mean comparison of traits in different water conditions (Table 3), drought stress resulted in a significant decrease in biological yield, seed filling duration, kernel weight, stem dry weight, fertile tillers, relative water loss and relative water content, and excised leaf water retention was the only trait which increased under drought stress.

Mean comparison of traits in different genotypes (Table 4) indicated that genotypes 4, 12, 11 and 16 had the highest excised leaf water retention and lowest amount of relative water loss, respectively.In contrast, genotypes 1, 3 and 6 exhibited the highest water loss among genotypes. Genotypes 3, 13 and 14 were the earliest maturing genotypes. The biological yield was highest in genotypes 4 and 13, respectively (19 and 18.36 g/pot). Whereas genotypes 8 and 19 had the lowest amount of biological yield (10.78 and 12.11

Table 3. Mean comparison for traits in *H. spontaneum* genotypes under normal and drought stress condition.

Condition	Relative Water Loss	Excised Leaf Water Retention	Fertile Tillers	Stem Dry Weight (g)	Kernel Weight (g)	Seed Filling Duration	Biological Yield (g)
Normal	76.33 a	0.48 b	3.33 a	10.97 a	2.92 a	22.93 a	19.45 a
Drought	71.25 b	0.53 a	2.50 b	5.32 b	2.64 b	18.95 b	11.64 b

Table 4. Mean comparison of traits in *H. spontaneum* genotypes and Nosrat cultivar based on Duncan multiple test.

No.	TN-KC	Excised Leaf Water Retention	Relative Water Loss	Days to Flowering	Spike Length (cm)	Fertile Tillers	Kernel Weight (g)	Biological Yield (g/pot)
1	309	0.43 e	85.89 ab	172.33 ab	6.95 ab	3.00	2.05 gh	13.60 abcd
2	324	0.42 e	80.60 abcd	165.17 efg	6.49 abc	3.33	2.70 def	15.90 abcd
3	554	0.42 e	92.69 a	165.00 fg	5.69 c	3.00	3.46 b	16.42 abc
4	556/1	0.57 ab	63.09 f	168.33	6.53 abc	2.33 cd	3.46 b	18.36 a
5	951	0.54 abc	64.36 de	170.17 bc	7.00 ab	2.67	2.31 fgh	13.60 abcd
6	1037	0.45 cde	83.24 abc	168.00 cdefg	6.62 abc	3.17	2.82 cdef	14.78 abcd
7	1073	0.54 abc	66.58 def	167.33 cdefg	6.92 ab	3.00	4.08 a	17.73 ab
8	1233	0.44 de	78.80 abcde	170.67 bc	6.62 abc	2.33 cd	1.80 h	10.78 d
9	1263	0.54 abc	70.00 cdef	170.50 bc	6.91 ab	3.00	2.76 def	16.14 abc
10	1286	0.49 bcde	78.85 abcde	169.33 bcd	5.72 c	2.67	2.55 defg	12.85 bcd
11	1350	0.59 a	62.14 f	172.50 ab	6.72 abc	2.33 cd	2.63 def	16.74 abc
12	1363	0.56 ab	62.47 f	166.17 defg	6.08 bc	3.50 ab	2.67 def	17.08 abc
13	1375	0.56 ab	64.07 de	165.00 fg	6.33 abc	4.00 a	2.95 bcde	19.00 a
14	1377	0.46 bcde	81.72 abcd	164.83 g	6.58 abc	3.67 ab	2.42 efg	15.36 abcd
15	1389	0.46 bcde	82.88 abc	165.17 efg	6.25 bc	4.00 a	2.35 fg	15.92 abcd
16	1674	0.56 ab	61.51 f	169.00 bcde	6.10 bc	2.83	2.97 bcde	16.34 abc
17	1693	0.46 bcde	80.12 abcd	165.83 defg	7.42 a	2.33 cd	3.00 bcd	17.03 abc
18	1801	0.53 abcd	74.23 bcdef	168.83 bcdef	6.25 bc	2.00 d	3.33 bc	12.11 cd
19	Nosrat	0.53 abcd	69.06 cdef	174.83 a	4.42 d	2.33 cd	2.32 fgh	15.64 abcd
	MAX	0.59	92.69	174.83	7.42	4.00	4.08	19.00
	MIN	0.42	61.51	165.00	4.42	2.00	1.80	10.78

g/pot, respectively).

Principle component analysis was conducted to study relations between traits and stress tolerance index, under normal and drought stress conditions (data not shown). In normal condition five principle components contributed in coefficient matrix and cumulative variance of these five components was 83.72%. The first component contributed maximum toward the variability (36.81%), explained by variation in biological yield, harvest index, spike dry weight, kernel weight and stress tolerance index. Second principle component explained 20.39% of variation due to variation among genotypes in excised leaf water retention (ELWR) and relative water loss (RWL). High coefficient of stress tolerance index in first component indicates that genotypes with higher values in the first component are more tolerant genotypes.

The bi-plot analysis of the two first components (Figure 2) exhibited the relation between traits in normal condition and stress tolerance index. There was a close relationship between stress tolerance index (STI) and biological yield (BY), harvest index (HI), spike dry weight (SPW) and kernel weight (KW) under normal condition. Also the negative correlation between stress tolerance index and phenological traits (DF and DM) identifies the late maturity as a susceptibility characteristic to drought stress. Therefore, based on the first component, genotypes were divided into two main

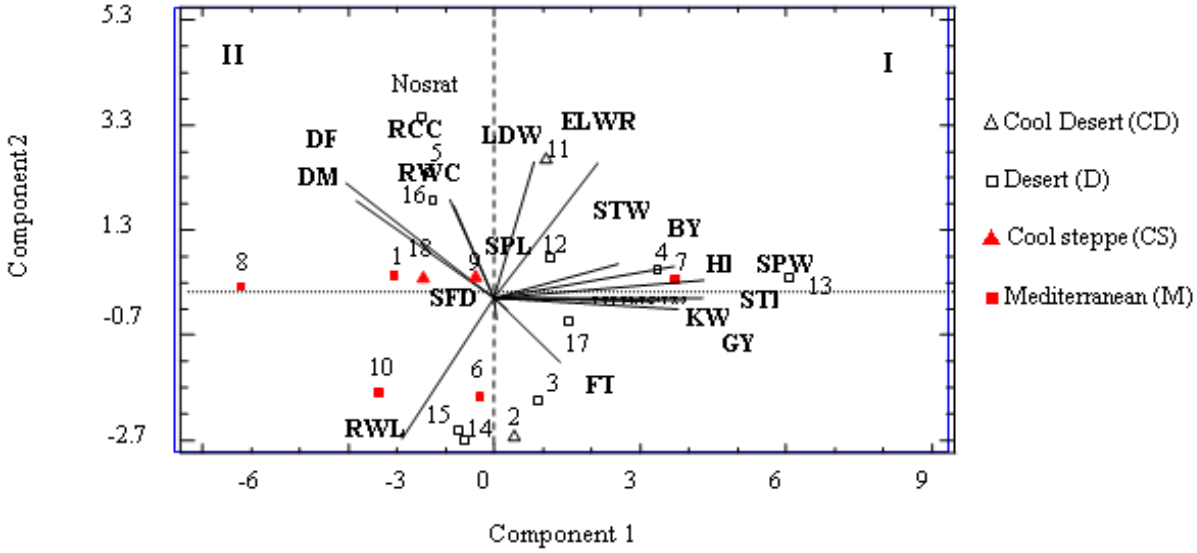

Figure 2. Bi-plot of first two principal components for traits and stress indices in *H. spontaneum* genotypes under normal condition (STI :stress tolerance index, BY: biological yield, RCC: relative chlorophyll content, ELWR: excised leaf water retention, RWL: relative water loss, DF: days to flowering, DM: days to maturity, RWC: relative water content, NSG: number of spikelet groups, SPL: spike length, FT: fertile tillers, SFD: seed filling duration, KW: kernel weight, STW: stem dry weight, LDW: leaf dry weight and HI: harvest index).

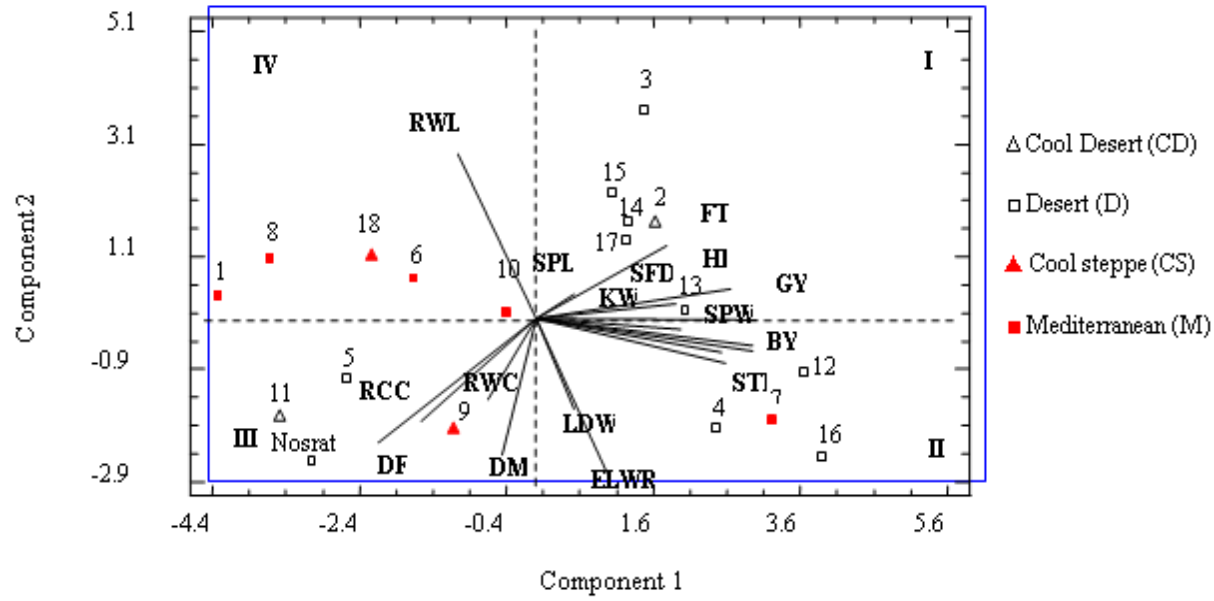

Figure 3. Bi-plot of first two principal components for traits and stress indices in *H. spontaneum* genotypes under drought stress condition (STI :stress tolerance index, BY: biological yield, RCC: relative chlorophyll content, ELWR: excised leaf water retention, RWL: relative water loss, DF: days to flowering, DM: days to maturity, RWC: relative water content, NSG: number of spikelet groups, SPL: spike length, FT: fertile tillers, SFD: seed filling duration, KW: kernel weight, STW: stem dry weight, LDW: leaf dry weight and HI: harvest index).

groups, group I (the right side of plot), the tolerant genotypes and group II, susceptible genotypes.

In principle component analysis of traits under drought stress condition, considering eigen values greater

than or equal to 1.0, five principle components were identified which accounted for 85.85% of the variability (Table not shown). The highest variation was explained by the first component (40.67% of total variance) in which kernel weight, spike dry weight, biological yield, harvest index, and stress tolerance index, had the largest values. Second principle component explained 19.01% of variation due to the variation in excised leaf water retention (ELWR) and relative water loss (RWL). Third component (11.11% of total variance) was elucidated by diversity in days to flowering (DF) and days to maturity (DM). The same as normal condition, high coefficient of stress tolerance index in the first component, indicates that genotypes with higher values in the first component are more tolerant ones.

The first two components under drought stress, together accounted for 59.68 % of the total variability. The relation between traits and stress tolerance index in drought stress condition are displayed in bi-plot (Figure 3). Close relation between stress tolerance index (STI) and biological yield (BY), harvest index (HI), spike dry weight (SPW), kernel weight (KW) is clearly demonstrated. Also the negative correlation between stress tolerance index and relative water loss (RWL) identifies the leaf water loss as a susceptibility index to drought stress. Therefore higher values in the first component and lower values in the second component could easily distinguish tolerant genotypes from susceptible ones. Genotypes 16, 12, 7 and 4 seem to be more tolerant to drought stress rather than other genotypes, Nosrat cultivar was among susceptible genotypes. The important point shown in this plot is that genotypes with the highest values in the second component, (highest amount of relative water loss) are mainly from Mediterranean and Cool Steppe climates and genotypes from desert climates had lower amounts of relative water loss.

Cluster analysis based on traits and five principle component in genotypes (Figure 4), divided them into three groups upon cutting line 10. Mean traits, stress indices and principle components in each cluster under stress condition is shown in Table 5. First group included four genotypes (4, 7, 12 and 16) which exhibited highest values in component one and the lowest values in component two, therefore, it is predicted that these genotypes are tolerant and mean STI (0.77) in this group confirms it. Another character of this group is the low value of relative water loss (59.0). The second group showed the highest amount of relative water loss. Most susceptible genotypes including 7 *H. spontaneum* genotypes and Nosrat cultivar, are in third group which are characterized with high relative water content (71.48), late flowering (171 days to flowering) and the least seed filling duration (17 days). Also almost all agronomic traits had the least scores in this group.

Table 5. Mean traits, stress indices and principle components of *H. spontaneum* genotypes in each cluster under stress condition.

Parameter	Cluster		
	1	2	3
Component 1	3.20	-4.32	-3.18
Component 2	-1.81	.37	-1.75
Component 3	-1.22	-1.91	2.54
Component 4	1.41	-.39	1.33
Component 5	1.34	2.28	-1.81
Days to Flowering	168	166	171.25
Seed Filling Duration	21.5	19.33	17.33
Relative Water loss	59.0	76.74	72.56
Excised Leaf Water	0.59	0.50	0.53
Relative Water Content	69.52	66.20	71.48
Spike Length (cm)	6.44	6.29	6.19
Fertile Tillers	2.58	2.90	2.12
Leaf Dry Weight (g)	0.38	0.29	0.28
Days to Maturity	189.5	185.33	188.58
Relative Chlorophyll	39.1	35.44	43.5
Stem dry Weight (g)	6.65	5.50	4.49
Spike Dry Weight (g)	7.97	6.63	5.23
Grain Yield (g/pot)	2.90	2.31	1.16
Kernel Weight (g)	3.19	2.64	2.36
Biological Yield (g/pot)	14.63	12.14	9.73
Harvest Index	19.66	18.88	11.52
Mean Productivity	17.38	16.07	14.17
Tolerance	5.51	7.86	8.89
Stress Susceptibility Index	0.65	0.93	1.14
Geometric Mean	17.12	15.52	13.39
Stress Tolerance Index	0.77	0.64	0.48

DISCUSSION

Utilizing the rich genetic diversity in wild species with high potential of adaptation to harsh environments is the basis of cereal breeding programs. Desirable traits including the resistance to abiotic stresses can be transferred from wild barley to cultivated ones (Nevo *et al.*, 2004). Identification of traits related to drought stress adaptations in wild barley can improve the efficiency of screening for drought tolerance.

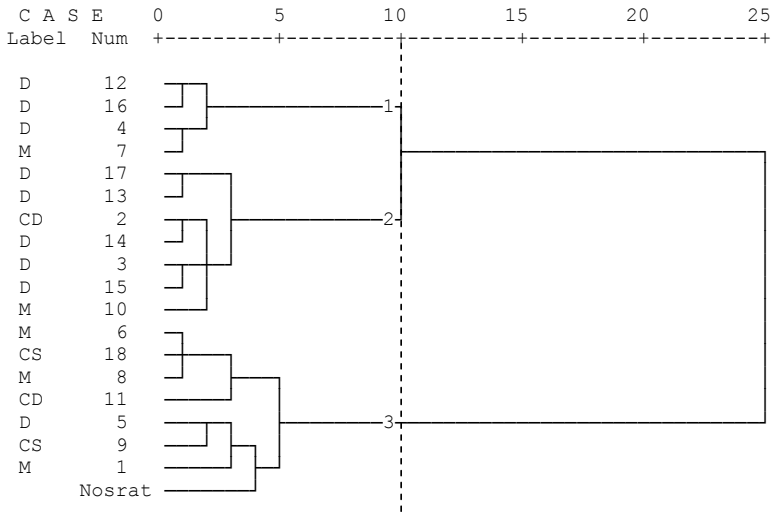

Figure 4. Cluster analysis of *H. spontaneum* genotypes based on five principle components under stress condition (M: Mediterranean, CS: Cool Steppe, CD: Cold Desert, D: Desert).

Results in this study indicated that interaction between drought stress and *H. spontaneum* genotypes was significant in relative chlorophyll content, relative water content leaf dry weight, spike dry weight, kernel weight, harvest index and days to maturity. These results showed that genotypes responded differently to drought stress through these traits. Drought stress significantly decreased the biological yield, seed filling duration, kernel weight, stem dry weight and relative water content. Ivandic *et al.* (2000) also reported reduction in wild barleys yield component as a result of drought stress.

The close relation between stress tolerance index (STI) and biological yield (BY), harvest index (HI), spike dry weight (SPW), kernel weight (KW) was demonstrated through component analysis of traits under normal and stress condition. Also the negative correlation between stress tolerance index and phenological traits (DF and DM) and relative water loss (RWL) identifies these traits as susceptibility characteristic to drought stress.

Genotypes with highest amount of relative water loss (RWL) under drought stress conditions were mainly from Mediterranean and cool steppe climates and genotypes from desert climates seem to have better adaptability to drought stress through decline in the relative water loss, which seems to be a very important trait for drought adaptation (Lonbani and Arzani, 2011).

Genotypes were divided into three groups based on traits and principle components. As it was expected, the first and second group including tolerant and semi tolerant genotypes, were mainly from desert climate with highest stress tolerance index and low value of relative water loss, whereas susceptible genotypes (third group) were mainly from Mediterranean and cool steppe climates which are characterized with high relative water content, late flowering and the least seed filling duration. These results are in line with Ivandic *et al.* (2000) reports concluding that xeric genotypes are less susceptible to drought stress conditions. It seems that genotypes from unpredictable climatic conditions are more adapted to harsh environments. It is also suggested that the xeric genotypes adopted survival strategies while the mesic genotypes adopted growth-sustain strategies to cope with drought stress (Chen *et al.*, 2010). Based on cluster analysis, Nosrat cultivar which is known as a high potential cultivar even in drought stress condition was among susceptible genotypes of *Hordeum spontaneum.* This indicates the susceptibility of breeding materials relative to wide ecological range of adaptations in wild barley. Therefore, this valuable primary gene pool can be used as a source of genetic material in barley breeding programs.

The improvement of a biotic stress tolerance in barley depends mainly on understanding the range of genetic diversity in cultivated and wild barley (Robinson *et al.*, 2000). Wild barley (*H. spontaneum*) harbor rich genetic resources and is the best hope for barley improvement. Desirable traits including the tolerance to a variety of a biotic stresses can be transferred easily from *H. spontaneum* to cultivated barley, (Nevo *et al.*, 2004). Most adaptive traits genes

are untapped in wild barley, while can provide potential sources for cereal improvement.

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