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Evaluation of yield and morphological traits in some Iranian Annual Wild Barley (*Hordeum* spp.)

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Original Research

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Abstract:

The Barley genus (*Hordeum* spp.) has low water requirements and resistance to both cold and salinity. Due to climatic limitations such as drought stress in Iran, the evaluation and identification of high-yielding genotypes used in breeding programs seem necessary. In this study, 27 annual wild barley genotypes belonging to *H. distichon* L., *H. geniculatum* All., *H. glaucum* Steud., *H. Leporinum* Link, *H. marinum* Hudson, *H. spontaneum* C. Koch and *H. vulgare* L. species were collected from seven localities in Iran. Genotypes were cultivated on the farm of the Research Institute of Forests and Rangelands, Karaj, Iran in 2018. The experimental layout was a randomized complete block design with three replications. The cultivation of genotypes was repeated for two consecutive years. The data were collected and analyzed for yield and morphological traits. There were significant variations for all traits between species and between genotypes within species ($p < 0.01$). The genotypes 40293 (*H. glaucum*), 38480 (*H. spontaneum*), and 27939 (*H. leporinum*) with average values of 67.67, 61.67 and 56.33 cm had the highest plant height, respectively. Also, genotypes 27939 (*H. leporinum*) and 32849 (*H. spontaneum*) with values of 1.17 and 1.15 g/plant had higher production than the other genotypes. Using Principal Component Analysis (PCA), the first three independent components with Eigenvalues higher than 1.0 were accounted for 0.76% of the total variation. For PC1; plant height, leaf width, fresh weight, and dry weight, for PC2, tiller number, and spike length, and for PC3, leaf length, leaf number and internode length were the most important traits. Using a cluster analysis (Ward method), the genotypes were classified within the relevant species and there was a good agreement between cluster analysis and PCA. The presence of high genetic diversity for morphology, phenology, and agronomy traits in Iranian wild barley genetic resources indicates a good potential for breeding the improved varieties for cultivating in the degraded rangelands of Iran.

Keywords: Annual barley; Biomass yield; Phenology; Plant height; Vegetative traits

Introduction

Poaceae is the biggest family of flowering plants that includes 600 genera and 10000 species. *Hordeum* ssp. is one of the most important genera of Poaceae with 45 wild grass species, as annual and perennial plants, and some of them are divided into several subspecies (Blattner, 2009; Sahebi et al., 2004). *Hordeum* belongs to the Triticeae tribe of grasses and is characterized by their inflorescence which is a spike instead of the panicle, the open leaf sheath with membranous ligules, and the hairy top of the developing grain (Barkworth and Von Bothmer, 2009). *Hordeum* originated in an area approximately 14 – 10 million years ago that became spread in today's Southwestern Asia and the Mediterranean, afterward spreading to Asia, the Americas, and South Africa (Brassac and Blattner, 2015). They are distributed in temperate and arid regions of the northern and southern hemispheres, the subtropics region of central South America, and the polar regions of North America and Central Asia. A large number of barley species are found in four regions: Southwestern Asia, Central Asia, West North America, and South America (Blattner, 2009). This genus has 11 species in Iran with the common name "wild barley" that grows in different regions of Iran (Mozaffarian, 2006). The most important species of barley are *H. murinum*, *H. distichon*, and *H. spontaneum*, which are naturally grown in most parts of Iran. *H. spontaneum* grows in Iran and Mediterranean areas considered as one of the primary genetic reserves of cultivated barley and crop species improvement, due to its high adaptability and diversity (Nevo, 1992, 2004).

Geographical separation causes genetic and phenotypic variations in the plant species populations (Thorpe, 2002). In particular, habitats, environmental conditions, historical processes, and phylogenetics are the main causes of phenotypic variation among individuals (Russell et al., 20). The response of populations of the same species in different environmental conditions produces genetic and phenotypic divergence between populations (Albarrán-Lara et al., 2019). Thus, morphological characters are used to evaluate distinctness, uniformity, stability (DUS) and to make a description of a genotype. Assessment of the extent of genetic variability within cultivated crops has important consequences in plant breeding and the conservation of genetic resources (Petersen et al., 1994; Rauf et al., 2010).

In barley, extensive and genetically diverse collections of landraces and wild barley accessions are available that could be used to improve the adaptation potential of cultivated barley and to counteract the reduction of genetic diversity in modern varieties that have been selected for favorable agronomic traits (Russell et al., 20).

In some studies, *H. spontaneum* has been subjected to comprehensive analysis to assess its genetic diversity and agronomical performance using quantitative and qualitative traits. Evaluation of phenotypic diversity for quantitative and qualitative characters of barley accessions native to different climates of Iran (Shahmoradi et al., 2012), west of Iran (Ebrahim et al., 2018), and barley collection of the National Plant Gene-bank of Iran (Zahravi et al., 2011) have been performed.

In the natural resources gene bank of Iran, there is a valuable collection of various genotypes of wild barely with different origins, but their diversity and genetic potential are not fully known. The genetic resources must be evaluated regarding morphological and forage yield traits, to determine the high-yielding genotypes for conservation and propagation. Therefore, the objective of this study was to assess the extent of major morphological traits and forage yield of wild barley genotypes to select the superior genotypes with high performance for breeding improved varieties.

Material and methods

Plant material

The 27 annual genotypes belonging to seven species of *Hordeum* spp. (*H. distichon*, *H. geniculatum*, *H. glaucum*, *H. leporinum*, *H. marinum*, *H. spontaneum*, *H. vulgare*) were investigated for yield and morphological traits to select high-yielding genotypes. The 27 wild barley genotypes included: *H. glaucum* (14 genotypes), *H. spontaneum* (7 genotypes), *H. leporinum* (2 genotypes), *H. distichom*, *H. geniculatum*, *H. marinum* and *H. vulgare* (one genotype for each species) that were provided from the Natural Resources Gene bank of Iran (Table 1).

Field experiments

Seeds of all 27 genotypes of *Hordeum* spp. were sown in jiffy pots at a glasshouse in March 2018. Then, seedlings were planted in the field as spaced plants at the research farm of the Research Institute of Forests and Rangelands, Alborz, Karaj, Iran. A week before planting, the seedbed was prepared for successful seedling establishment. The field experimental layout was a Randomized Complete block design with 3 replications. The plot length was 6 m with a spacing of 100 cm between rows, and each row had 15 plants with 40 cm spacing. The trial was managed according to advice agriculture practice.

The weed removal was done by hand weeding 40 days after planting and then repeated every 40 days until the end of the growing season. Irrigation was applied weekly during the trial. The seed sowing of annual genotypes was repeated for two consecutive years.

Traits measurements

Nine quantitative traits were evaluated at harvest time. Ten plants (normal growth, uniform performance, disease- and pest-free) of each genotype in each plot were randomly selected for data recording. The phenological traits of days to flowering and days to maturity were estimated by days' number from the emergence of the seedlings up to 50% flowering and 90% maturity dates, respectively. Tiller number, plant height (cm), internode number, internode length (in the second internode cm), leaf length (cm), and leaf width (cm) of the second leaf, biomass yield (plant fresh weight and plant dry weight (g) were recorded.

Data analysis

The recorded traits were repeated in the second year and averaged over two years. Analysis of variance was performed using nested ANOVA (between species and genotypes within species). Significant differences among means of genotypes were compared using the DMRT test. Pearson correlation was made between nine traits. Mean values of genotypes were used for cluster analysis (ward method) and principal component analysis (PCA). The statistical analysis was carried out using Minitab software (version 15).

Results

Analysis of variance and comparison of means

The results of the analysis of variance for yield and morphological traits indicated significant differences ($P < 0.01$) between species and between genotypes within species of wild *Hordeum*. That indicates a strong genetic variability within the germplasm (Table 2). The means comparison of yield and morphological traits in seven species of *Hordeum* spp. (*H. distichon*, *H. geniculatum*, *H. glaucum*, *H. leporinum*, *H. marinum*, *H. spontaneum* and *H. vulgare*) is presented in Table 3. The ranges of plant height ($26.67-47.76$ cm), internode length ($5.33-9.5$ cm), and internode number ($4.33-5.33$ cm) were obtained between species. The values of plant height (47.76, 47.67, and 42.83 cm), internode length (8.83, 8.17, and 9.50 cm), and internode numbers (5.33, 5.17 and 5.00) were obtained in *H. spontaneum*, *H. leporinum* and *H. marinum*, respectively (Table 3).

The highest tiller number with a value of 11 tillers per plant was obtained in *H. distichon* while in other species, the tiller number varied from (1.48 in *H. spontaneum*) to (3.07 in *H. glaucum*). Spike length varied from 2.67 cm in *H. geniculatun* to 5 cm in *H. leporinum*. The highest values of fresh and dry weight (2.68 and 1.04 g/plant) were observed in *H. leporinum*, respectively, than the other species, except for *H. spontaneum* (1.77 and 0.76 g/plant). For leaf length, *H. distichon* with a value of 21 cm had the longest leaf, and the leaf width varied from 0.30 to 0.49 mm. *H. spontaneum* had the widest leaf (0.49 mm), and the thinnest one (0.30 mm) was observed in both *H. geniculatum* and *H. vulgare* species.

Twenty-seven genotypes of *Hordeum* spp. were compared for yield and morphological traits (Table 4). The values of plant height varied from 26.67 cm in both *H. geniculatum* (8619) and *H. glaucum* (39132) to 67.67 cm in *H. glaucum* (40293). Also, the highest values of plant heights (61.67 and 56.33 cm) were obtained in *H. spontaneum* (38480) and *H. leporinum* (27939), respectively. The highest and lowest values of internode length (11.33 and 3.93 cm) were observed in two genotypes of *H. glaucum* (40293 and 39132), respectively. The highest values of internode length were observed in *H. spontaneum* (38480 and 32849), *H. leporinum* (27939), *H. marinum* (25915), *H. glaucum* (39131),

Table 1. The list of studied 27 annual barley genotypes collected from different parts of Iran.

Taxa	G.B.C≠	Origin region	Origin province	Longitude	Latitude	Altitude (masl)
H. distichon L.	25219	-	Kohkoleyeh &Boyerahmad	51° 15´ E	30° 50´ N	1865
H. geniculatum All.	8619	Sarband	Merkezi, IR	49° 13´ E	33° 45´ N	2020
H. glaucum Steud.	823	-	Lorestan, IR	47° 50´ E	33° 20´ N	1250
	3229	-	Mazandaran, IR	53° 53´ E	36° 60´ N	54
	30512	Eivan	Ilam, IR	46° 21´ E	33° 42´ N	1319
	32129	Alamut	Qazvin, IR	50° 12´ E	36° 22´ N	2150
	32937	-	Kermanshah, IR	47° 41´ E	34° 33´ N	1774
	36294	Khoramabad	Lorestan, IR	47° 31´ E	33° 43´ N	1290
	39123	Taft	Yazd, IR	54° 09´ E	31° 33´ N	2439
	39124	Mehriz	Yazd, IR	54° 21´ E	31° 32´ N	1926
	39129	Taft	Yazd, IR	53° 49´ E	31° 45´ N	2310
	39130	Taft	Yazd, IR	54° 07´ E	31° 36´ N	2374
	39131	Taft	Yazd, IR	53° 56´ E	31° 42´ N	2101
	39132	Khatam	Yazd, IR	54° 10´ E	29° 48´ N	1969
	39133	Taft	Yazd, IR	53° 39´ E	31° 43´ N	2332
	40293	Salas Babajani	Kermanshah	46° 18´ E	34° 07´ N	1316
H. Leporinum Link	2533	Dashteh Azadeghan	Khozestan, IR	48° 80´ E	31° 72´ N	800
	27939	Khoramabad	Lorestan, IR	48° 17´ E	33° 34´ N	1217
H. marinum Hudson	25915	Mehriz	Yazd, IR	54° 44´ E	31° 57´ N	1480
H. spontaneum C.Koch	4518	Khoramabad	Lorestan, IR	48° 10´ E	33° 30´ N	1250
	6598	Poledokhter	Lorestan, IR	47° 40´ E	33° 12´ N	770
	14933	Arak	Merkezi, IR	49° 70´ E	34° 09´ N	1775
	15012	Shazand	Merkezi, IR	49° 40´ E	33° 93´ N	2050
	32849	Eslamabad	Kermanshah, IR	46° 08´ E	34° 26´ N	1460
	36275	Poledokhter	Lorestan, IR	47° 40´ E	33° 05´ N	898
	38480	-	Kohkoleyeh &Boyerahmad	51° 34´ E	30° 34´ N	1895
H. vulgare L.	20402	-	*external seed			

≠G.B.C.: Gene Bank Code * = The country origin of the genotype is unknown.

Table 2. Analysis of Nested (ANOVA), between species and genotypes within *Hordeum* species for yield and morphological traits.

Sources	DF	MS								
		Plan height	Internode length	Internode number	Tiller number	Spike length	Fresh weight	Dry weight	Leaf length	Leaf width
Replication	2	16.36	0.05	0.23	0.20	0.34	0.38	0.19	2.23	0.26
Species	6	593.95^{**}	10.56^{**}	1.37^{**}	24.37^{**}	2.40^{**}	2.35^{**}	0.39^{**}	202.93^{**}	2.81^{**}
Gen (spec)	20	258.18^{**}	8.71^{**}	1.14^{**}	2.25^{**}	1.88^{**}	0.97^{*}	0.15^{*}	26.60^{**}	1.07
Error	52	30.31	1.69	0.25	0.68	0.34	0.47	0.08	6.72	0.78
Total	80									

**, * Significant at 0.01 and 0.05 levels.

and *H. glaucum* (39129) with values of 11.33, 10.50, 9.50, 9.50, 9.50, and 9.33 cm, respectively. The lowest internode number of 3.67 in *H. glaucum* (3229), and the highest numbers of 6.33 and 6.00 were obtained in *H. spontaneum* (14933) and (32849), respectively. Spike length ranged from 2.03 to 6 cm. The highest values spike lengths given as 6.0, 5.17, and 5.0 cm were obtained in *H. leporinum* (27939), *H. glaucum* (39132), and *H. spontaneum* (38480), respectively (Table 3).

For fresh and dry weight, genotypes of *H. leporinum* (27939) and *H. spontaneum* (32849) with average values of 2.80 and 2.77g/plant fresh weight, and 1.17 and 1.15 g/plant dry weight had the highest production, respectively. The leaf length ranged from 4 cm in *H. glaucum* (36294) to 21 cm in *H. distichon* (25219). Also, the longest leaves with values of 18.5 and 17 cm were obtained in *H. spontaneum* (15012), and *H. leporinum* (27939), respectively. While the range of leaf width between genotypes was 0.30 – 0.67 cm (Table 3).

Correlation between traits

The result of correlation analysis among the mentioned traits in the tested wild barley genotypes revealed the existence of several significant positive coefficients ($P < 0.05$) (Table 5). Plant height was positively correlated with internode length ($r = 0.77^{**}$), internode number ($r = 0.61^{**}$), and leaf width ($r = 0.37^{*}$) and negatively correlated with tiller number ($r = -0.52^{*}$). Internode length was positively correlated with internode number ($r = 0.30^{*}$), and leaf width ($r = 0.42^{*}$), and negatively correlated with tiller number ($r= -0.52^{*}$). Internode number was positively correlated with leaf length ($r = 0.36^{*}$) and fresh and dry weight ($r = 0.33^{*}$ and 0.30^{*}), respectively.

The tiller number was positively correlated with spike length ($r = 0.30^{*}$). Similarly, spike length was positively correlated with leaf length ($r = 0.31^{*}$) and forage weight ($r = 0.38^{*}$). There was a strong correlation between fresh and dry weight ($r = 0.89^{**}$). Dry weight was positively correlated with leaf length ($r = 0.35^{*}$) and leaf width ($r = 0.26^{*}$). For other traits, there were no significant correlations ($p > 0.05$) (Table 5).

Principal component analysis (PCA)

The variation studied through PCA revealed that three principal components had eigenvalues higher than 1.00, which explained 46%, 17% and 13% variations for PC1, PC2, and PC3, respectively, with a sum of 76% of the total variation (Table 2). Those traits that contributed to PC1 positively were plant height (0.452), leaf width (0.372), fresh weight (0.395), and dry weight (0.379). For PC2, tillers number (−0.615), and spike length (−0.382) and for PC3, leaf length (0.571), internodes number (0.443), and intern-

Table 3. Means comparison of nine traits in seven species of *Hordeum* spp.

Species	Plant height (cm)	Internode length (cm)	Internode number	Tiller number	Spike length (cm)	Fresh weight (g)	Dry weight (g)	Leaf length (cm)	Leaf width (cm)
H. distichon	29.00 b	5.33 c	5.33 a	11.00 a	4.67 ab	1.25 b	0.50 b	21.00 a	0.40 ab
H. geniculatum	26.67 b	5.83 c	4.33 b	2.67 bc	2.67 d	0.79 b	0.37 b	8.17 c	0.30 b
H. glaucum	37.86 ab	7.83 ab	4.67 ab	3.07 b	3.87 bc	1.41 b	0.52 b	7.07 c	0.44 a
H. leporinum	47.67 a	8.17 ab	5.17 a	2.17 bc	5.00 a	2.68 a	1.04 a	12.17 b	0.43 a
H. marinum	42.83 a	9.50 a	5.00 ab	2.33 bc	4.17 bc	0.91 b	0.44 b	7.33 c	0.47 a
H. spontaneum	47.76 a	8.83 a	5.33 a	1.48 c	3.76 c	1.77 ab	0.76 ab	14.45 b	0.49 a
H. vulgare	36.17 ab	6.67 bc	5.00 ab	2.00 bc	3.67 c	0.85 b	0.38 b	7.50 c	0.30 b

Different letters indicate significant differences among species. $P < 0.01$.

Table 4. Means comparison of nine traits in 27 *Hordeum* spp. genotypes.

Taxa	Gene bank code	Plant height (cm)	Internode length (cm)	Internode number	Tiller no	Spike length (cm)	Fresh weight (g)	Dry weight (g)	Leaf length (cm)	Leaf width (cm)
H. distichon	25219	29.00gh	5.33hi	5.33b-d	11.00a	4.67b-d	1.25c-f	0.50c-g	21.00a	0.40a-c
H. geniculatum	8619	26.67h	5.83g-i	4.33e-g	2.67c-g	2.67f-h	0.79f	0.37e-g	8.17e-g	0.30c
	823	37.33d-h	8.50b-f	4.67d-f	3.67b-d	4.50b-e	1.43c-f	0.53c-g	5.67fg	0.40a-c
	3229	34.00e-h	7.52c-h	3.67g	2.00d-g	4.00c-e	0.92f	0.44c-g	11.5c-e	0.67bc
	30512	31.67f-h	8.33b-g	4.00fg	3.33c-e	4.67b-d	1.38c-f	0.63b-g	7.33e-g	0.47a-c
	32129	35.33e-h	7.67c-h	4.33e-g	2.00d-g	3.50e-f	0.83f	0.28g	6.67e-g	0.43a-c
	32937	33.17e-h	6.83d-h	4.67d-f	3.00c-f	3.67d-f	1.22d-f	0.39d-g	6.50e-g	0.43a-c
H. glaucum	36294	33.67e-h	7.67c-h	4.67d-f	2.67c-g	3.83de	0.97ef	0.35fg	4.00g	0.40e-h
	39123	34.67e-h	6.00f-i	4.67d-f	2.67c-g	3.33e-g	1.81a-f	0.74a-g	6.17fg	0.43a-c
	39124	35.33e-h	6.50e-h	5.00c-e	3.33c-e	3.67d-f	1.40c-f	0.47c-g	8.17e-g	0.37bc
	39129	42.33c-h	9.33a-d	5.00c-e	2.33d-g	3.83de	1.65a-f	0.61c-g	6.17fg	0.47a-c
	39130	36.00d-h	8.67b-e	4.33e-g	4.33bc	4.00c-e	1.75a-f	0.76a-g	7.33e-g	0.53ab
	39131	41.67c-h	9.50a-c	5.00c-e	3.33c-e	3.67d-f	1.59a-f	0.64a-g	8.33e-g	0.40a-c
	39132	26.67h	3.93i	5.00c-e	5.33b	5.17ab	2.58a-c	0.55c-g	9.83d-f	0.47a-c
	39133	40.50d-h	7.83c-h	4.33e-g	3.67b-d	4.33b-e	1.46b-f	0.66a-g	6.67e-g	0.50ab
	40293	67.67a	11.33a	6.00ab	1.33fg	2.03h	0.81f	0.21g	4.67g	0.50bc
H. leporinum	2533	39.00d-h	6.83d-h	4.67d-f	3.00c-f	4.00c-e	2.55a-d	0.9a-f	7.33e-g	0.37f-h
	27939	56.33ab	9.50a-c	5.67a-c	1.33fg	6.00a	2.80a	1.17a	17.00ab	0.50ab
H. marinum	25915	42.83c-h	9.50a-c	5.00c-e	2.33d-g	4.17b-e	0.91f	0.44c-g	7.30e-g	0.47c-h
H. spontaneum	4518	38.67d-h	8.67b-e	4.33e-g	2.33d-g	3.83de	1.89a-f	0.92a-e	6.83e-g	0.40a-c
	6598	48.67b-e	8.67b-e	5.33b-d	2.33d-g	3.67d-f	2.29a-e	0.93a-d	16.00bc	0.43a-c
	14933	52.00b-d	8.00b-g	6.33a	1.67e-g	4.00c-e	2.33a-d	0.98a-c	16.00bc	0.57a
	15012	44.00c-g	7.17c-h	4.67d-f	1.00g	2.33gh	1.41c-f	0.47c-g	18.50ab	0.47a-c
	32849	42.33c-h	10.50ab	6.00ab	1.00g	3.67d-f	2.77ab	1.15ab	13.67b-d	0.57a
	36275	47.00b-f	7.50c-h	5.67a-c	1.00g	3.83de	0.73f	0.42d-g	15.50bc	0.43a-c
	38480	61.67ab	11.33a	5.00c-e	1.00g	5.00a-c	0.93f	0.42d-g	14.67bc	0.53ab
H. vulgare	20402	36.17d-h	6.67e-h	5.00c-e	2.00d-g	3.67d-f	0.85f	0.38d-g	7.50e-g	0.30c

Different letters indicate significant differences among genotypes within species. P $<$ 0.01.

Table 5. Simple correlation matrix for the eleven traits of *Hordeum* spp. genotypes.

Traits	Plant height	Internode length	Internode number	Tiller number	Spike length	Fresh weight	Dry weight	Leaf length
internode length	0.77**							
internode number	0.61**	0.30*						
tiller number	-0.53*	-0.52*	-0.13					
spike length	-0.05	-0.02	0.00	0.30*				
fresh weight	0.07	-0.00	0.33*	0.02	0.38*			
dry weight	0.16	0.19	0.30*	-0.09	0.38*	0.89**		
leaf length	0.16	-0.10	0.36*	0.15	0.31*	0.28	0.35*	
leaf width	0.37*	0.42*	0.11	-0.23	0.21	0.21	0.26*	0.24

*, ** Significant at 0.05 and 0.01 probability levels.

ode length (−0.498) were the important traits (Table 6). The 27 genotypes were scattered in a biplot of PC1 vs PC2 (figure 1). This diagram completely separated all the genotypes belonging to species from the rest of the genotypes belonging to other genotypes. All *H. spontaneum* genotypes had positive values for the PC1. These genotypes were characterized by higher values of plant height and leaf width and lower values of tiller number. Genotypes 38480 and 32849 were placed on the up and right sides of the X-axis. The 38480 had higher values of plant height and spike length and 32849 had higher values of leaf width, and fresh and dry weight, respectively (figure 1).

Two genotypes of *H. liporinum* (2533 and 27939) had different values in PC1, but their values in PC2 were close to each other. Genotype 27939 had the higher value of all traits, except for the tiller number. In genotype 27939, the values of plant height and leaf width were higher so that it was located on the right side of the X-axis.

H. geniculatum (8619) and *H. vulgare* (20402) were located on the up and left of the X-axis and had lower values in PC1. *H. distichon* (25219) species was located down and the left of the X-axis had low values of PC1 and higher values of PC2.

Most of the genotypes of *H. glaucum* were placed on the left side of the X-axis, for the low values of the plant height. Genotype 39132 of *H. glaucum* was placed at the bottom of the X-axis, and had higher values of the important traits in PC2. Seven genotypes of *H. spontaneum* were placed on the right of the X-axis. The cluster analysis (Ward method) classified the genotypes within the relevant species. There was a good agreement between cluster analysis and PCA (figure 1).

Table 6. Eigenvalues, the proportion of variance, and morphological traits that contributed to the first five PCs plant height.

variable	PC1	PC2	PC3
Plant height	**<u>0.452</u>**	0.271	-0.019
Fresh weight	**<u>0.395</u>**	-0.386	0.045
Dry weight	**<u>0.379</u>**	-0.335	-0.006
Leaf width	**<u>0.372</u>**	-0.028	-0.228
Tiller number	-0.226	**<u>-0.615</u>**	-0.040
Spike length	0.188	**<u>-0.382</u>**	-0.317
Leaf length	0.278	0.034	**<u>0.571</u>**
Internode number	0.349	-0.062	**<u>0.443</u>**
Internode length	0.330	0.322	**<u>-0.498</u>**
Eigenvalue	4.120	1.565	1.126
Proportion	0.458	0.174	0.125
Cumulative	0.458	0.632	0.757

The bold and underlined coefficients have significant correlations with the relevant axes.

Discussion

The present study indicated high genetic variation and a great morphological distinction between different genotypes of seven species (*H. distichon*, *H. geniculatum*, *H. glaucum*, *H. leporinum*, *H. marinum*, *H. spontaneum*, *H. vulgare*) for all studied quantitative traits. In both *H. glacaum* and *H. spontaneum*, variability among genotypes of the same species was greater for certain traits than the variability between species (Tables 2-4). The variation is a potential and inherent resource that could be used to improve and modify crops. A high variation among 25 winter barley genotypes has been reported for traits related to yield and quality of feed barley (Dyulgerova et al., 2016). A study of the genetic and geographical diversity of ecotypes of wild barley (*H. spontaneum*) native to different climates of Iran showed a little variation in some qualitative traits, but most of the investigated traits had a relatively high variation (Shahmoradi et al., 2012). Zahravi et al. (2011) concluded that auricle and stem pigmentation were the most variant of all qualitative traits in agronomical traits in *Hordeum spontaneum* germplasm of Iran. A study of the genetic variation of durum wheat landraces from Iran and Azerbaijan for morphological traits showed significant differences among populations (Ahmadizadeh et al., 2011).

A comparison between species (*H. distichon*, *H. geniculatum*, *H. glaucum*, *H. leporinum*, *H. marinum*, *H. spontaneum*, *H. vulgare*) for vegetative and phenological traits showed that *H. leporinum*, *H. marinum* and *H. spontaneum* had the higher values of plant height, internode length and internode number. Also, *H. leporinum* and *H. spontaneum* had higher values for fresh and dry weight. Kumar et al. (2016) showed a significant variation in plant height, fertile tillers per plant, and length of the main spike in 64 released varieties of barley in the collection of Wheat Research, Karnal, India. Therefore, the barley genotypes and species tested in the current study could be used for cultivation in different areas to select the best genotype with a high yield.

Two genotypes, *H. leporinum* (27939) and *H. spontaneum* (32849) had the highest values of fresh weight (2.80, 2.77 g/plant) and dry weight (1.17, 1.15 g/plant), respectively. They were the best candidate genotypes for forage production. According to Chebouti et al. (2019), this ability can be used in fodder breeding programs to select an adapted plant material for the arid and semi-arid areas.

Life cycle events of plants are influenced by seasonal and annual variations and habitat factors (Wilczek et al., 2010). These traits are controlled by both genetic and environmental factors such as temperature, rainfall, photoperiod (duration and intensity of light), and nutrition. In wild barley, different development stages of growth such as spikelet initiation and duration of grain development can seriously influence yield and quality (Castro et al., 2008).

Based on the results of the correlation between analyses, there was a positive and significant correlation between plant height and both internode length and internode number. The existence of positive and significant correlation between plant length with internode length in genotypes of rice (Montazeri et al., 2017), and internode number in sainfoin populations has been proved (Zarabiyan et al., 2014). This indicates that tall plants produce longer and numerous internodes. Also, a positive relationship was observed between spike length with both fresh and dry weight and leaf length. The existence of a positive correlation between dry weight and leaf size was proved. This relationship was proved also in wild wheat relatives (Jabari et al., 2022), which means the plant with long leaves produces long spikes and high fresh and dry weights, or higher production

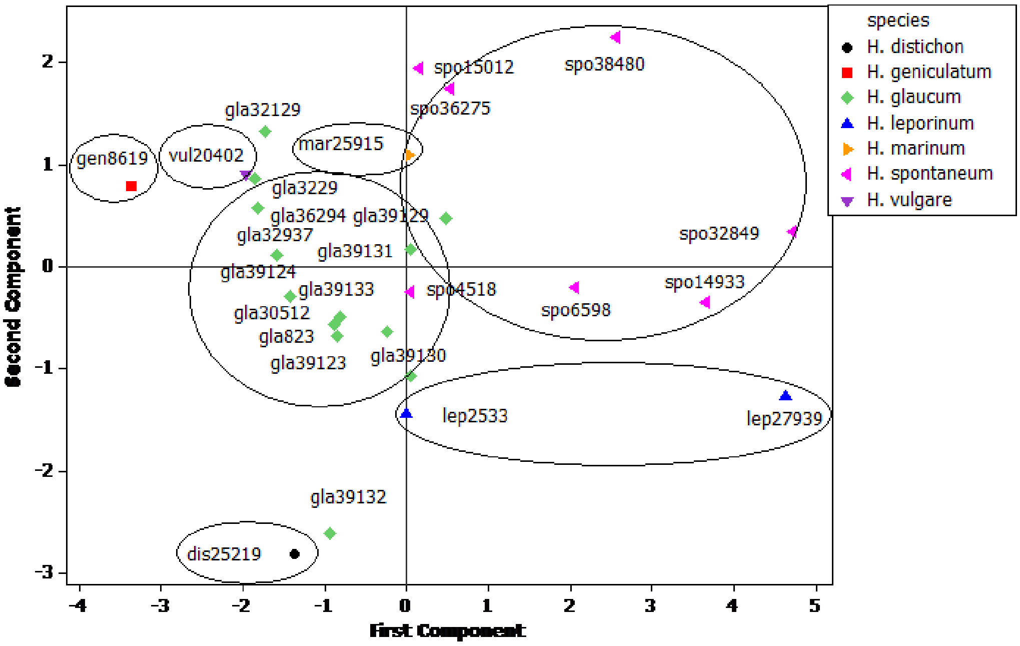

Figure 1. Scatter plots of 27 genotypes belonging to seven wild barley species based on the first two principal component. dis (*Hordeum distichon*), gen (*Hordeum geniculatum*), gla (*Hordeum glaucum*), lep (*Hordeum leporinum*), mar (*Hordeum marinum*), spo (*Hordeum spontaneum*), vul (*Hordeum vulgare*).

weights are produced by long and broad leaves and spikes (Table 5).

The most important characters that created variability were: plant height, leaf width, fresh and dry weight, as the first component, and tiller number and spike length as the second component, which explained 46% and 17% of the total variation, respectively. In the third component, leaf length, length, and number of internodes contributed 13% of all variation. Genotypes 32849 and 38480 of *H. spontaneum* that were located on the right of X-axis of figure 1 had higher values of plant height and leaf width in 32849 and 38480 genotypes, respectively. So, these genotypes recommend producing tall plants coupled and wide leaves. Similar results were obtained for accessions of barley (Rahal-Bouziane et al., 2015).

Conclusion

Our findings showed that different varieties of wild barley can be cultivated as fodder in dryland farming and pastures with reasonable fresh and dry forage yields to meet the livestock requirements. Genotypes 40293 of *H. glaucum* (Babajani, Kermanshah), 38480 of *H. spontaneum* (Kohkoleyeh & Boyerahmad), and 27939 of *H. leporinum* (Khoramabad, Lorestan) were recommended as tall plant. Genotype 279393 of *H. leporinum* (Roudbar, Gilan) was superior in terms of fresh and dry forage yields due to having high plant height, spike length, leaf length, leaf width and internode length.

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Authors Contributions
All authors have contributed equally to prepare the paper.

Availability of Data and Materials
The data that support the findings of this study are available from the corresponding author upon reasonable request.

Conflict of Interests
The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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