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Research Article

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Genetic diversity of Omani barley (*Hordeum vulgare* L.) germplasm

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Abstract: Oman has enormous diversity in important crops of global significance like wheat and barley considered as strategic crops. The country has an ancient cultivation history of barley because of its location on the eastern edge of the Arabian Peninsula and is known to have several landraces spread across all the agro-ecological regions. The present study was undertaken to comprehend genetic diversity in 16 indigenous Omani USDA accessions repatriated recently to select parents for hybridization in national crop improvement programs. The trial was conducted consecutively for two cropping seasons (2017–2018 and 2018–2019) from November to March on the layouts of loamy soil sites under sprinkler irrigation system in augmented design under spacing and crop husbandry practices as per national recommendations. The data on eight quantitative characters and presence (score 1) or absence (score 0) of anthocyanin pigmentation on two plant parts were subjected to both hierarchical cluster analysis (HCA) and principal component analysis (PCA) to know the contribution of characters toward diversity and form prime diverse clusters. The results indicated not only significant differences between accessions ($p < 0.05$) with respect to the most of quantitative characters but also two significant correlations involving four characters associated with maturity and inflorescence ($p < 0.05$). The results of two multivariate analyses led to the formation of four diverse clusters with similar constituents of accessions to the most extent, thus supporting each other in discerning diversity. The parents were selected for hybridization for improving characters of growth for higher yield or productivity with anthocyanin-related characters.

Keywords: anthocyanin, barley, landraces, multivariate analysis, variability

1 Introduction

Barley (*Hordeum vulgare* L.) is grown in about 47.4 million hectares in the world with production of about 140 million metric tons [1,2]. Developing countries account for about 18% (26 million tons) of total barley production and 25% (18.5 million hectares) of the total harvested area in the world [3]. Barley grain is mostly used as feed for animals, malt, and food for human consumption [3]. Due to the fact that barley crop is utilized for animal feed and human nutrition, poor production and any kind of loss after harvest adversely affect farmers' livestock production and consequently socio-economic conditions [4,5].

Barley landraces form the major genetic resource in several countries of the Arabian Peninsula because of their inherent tolerance to biotic (insect pests and diseases) and abiotic (salinity, drought, and high temperature) stresses prevailing in the region [6,7]. These landraces form potential parents for hybridization in crop improvement not only for yield productivity but also for resistance to diseases and pests. However, these landraces have not been fully utilized in modern breeding [8,9].

In Oman, barley is traditionally grown for fodder by planting as a mixture with local alfalfa perennial multicut (*Medicago sativa* L.) across all governorates in plains and mountains of the country. Currently, the cultivation of barley is limited to only 613 ha with a meager production of 1,901 tons [10]. The country is experiencing loss of biodiversity not only because of replacement of landraces with modern cultivars, increasing salinity, and decreasing freshwater resources for irrigation [11] but also because of the shift of lands of field crops cultivation including barley to vegetable cultivation in either open field or plastic

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houses [12]. The first germplasm collection activities were begun with the collection of landraces of field crops during the late 1980s and early 1990s in Oman jointly by the officials of the Ministry of Agriculture and Fisheries (MAF) and international collectors under the FAO program, which ended up with a collection of 510 accessions of 58 crop species, which included 51 barley landrace accessions [13,14]. Most of these accessions were deposited in international gene banks, of which the National Plant Germplasm System (NPGS) of United States Department of Agriculture (USDA) [15] lists 16 accessions of Omani barley used in the present study. These collection activities were continued subsequently either independently or jointly with other international institutions like International Center of Agriculture Research at Dry Areas (ICARDA) and International Center for Biosaline Agriculture (ICBA) by the national collectors from MAF and SQU [16–19], and the collected accessions were deposited in their respective conservation facilities. Despite the farmers being encouraged by MAF through some socio-economic incentives to replace landraces with modern high yielding introduced varieties [19,20], the dual-purpose landraces are still cultivated for both feed and forage by subsistence farmers in Oman. This is because of their high adaptability and tolerance to salinity [21–23].

The existence of genetic diversity and variability among the landraces of any crop species including barley provides prospective competence and plays a vital role in formulating a tangible and successful breeding program for increased food/feed yield, wider adaptation, desired quality, and tolerance to biotic and abiotic stresses [24]. In this respect, the information on genetic diversity within the available germplasm will have an impact on outputs of crop improvement to be resilient to climate change and diverse environments [7]. Hybridization and subsequent selection are one of the most successful approaches utilized for barley breeding [25,26]. There are several multivariate analyses such as hierarchical cluster analysis (HCA), principal component analysis (PCA), and factor analysis (FA), which are used to classify the genotypes/collections into genetically divergent groups in several crops including barley [27–31]. In view of the above, 16 USDA landrace accessions of Omani barley, referred earlier, were subjected to estimate genetic diversity using agro-morphological and qualitative characters like anthocyanin pigmentation and identify effective factors for genetic improvement.

2 Materials and methods

The experiment was conducted at Agriculture Research Station, Jimah (22.93945 N, 57.27220 E, 532 m), of the MAF, which has a long-term mean temperature of 21.89°C and receives an annual rainfall of 12.34 mm during cropping season (November to March) during winter. The trials were undertaken consecutively for two cropping seasons (2017–2018 and 2018–2019) on the layouts of a loamy soil site under a sprinkler irrigation system. Sixteen 6-row indigenous barley (*Hordeum vulgare*) landraces, the USDA-NPGS accessions [15], repatriated by Oman Animal and Plant Genetic Resources Center (OAPGRC) of the Research Council from USDA gene bank were examined (Table 1; Figure 1).

The barley accessions were planted in the plots of 3 m three rows at a spacing of 0.2 m between rows and 0.15 m between plants under augmented design with five check varieties (Jimah 51, Jimah 53, Jimah 58, Jimah 98, and Jimah 136) replicated five times. All the agronomic and cultural practices were applied according to national recommendations of the MAF, Oman [32], to raise a successful crop. The days to flowering and maturity were recorded as when each plot attained about 50% flowering and 90% maturity of grains, respectively. The characters, namely, spike density, spikelets/spike, grains/spike, grain length (mm), grain width (mm), and 1,000-grain weight (g), were measured based on the guidelines in Descriptors of Barley [33,34]. The qualitative traits of pigmentation were recorded as the presence (score 1) or absence (score 0) at respective growth stages of the plants of each plot when the pigmentation on the plant parts was observed intense and clear. Such pigmentation traits have the potential for use as marker characters during distinctness, uniformity and stability (DUS) tests [35].

2.1 Statistical analyses

The required statistical analyses were performed using XLStat software [36]. The 2-year data on five check varieties were subjected to combined analysis of variance (ANOVA) to know the effects of blocks, varieties, years, and their interactions in respect of eight agro-morphological characters studied. The accessions were compared for their significant differences for each character using the corresponding least significant difference (LSD). The results indicated insignificant effects blocks and GxE interaction ($p > 0.05$).

HCA [37,38] was performed to group genotypes and construct a dendrogram by Ward's method. The measure of dissimilarity was Euclidean distance. Six agronomical traits/plant descriptor characters, namely, plant height,

Table 1: Indigenous barley (*Hordeum vulgare* L.) accessions with their USDA-NPGS accession numbers and wilayats, governorates, latitude (N), longitude (E), and altitude of each location of collection during 1990s by MAF-FAO joint collecting missions

S. No.	USDA Accession No.	Village	Wilayat	Governorate	Latitude (N)	Longitude (E)	Altitude (m)
1	PI 564646	12 km northwest of Sohar, North Batinah	Sohar	Batinah North	24.366667	56.75	0
2	PI 564647	Majis, North Batinah	Sohar	Batinah North	24.456389	56.65361	6
3	PI 564648	25 km west of Rustag, Western Hajar	Rustaq	Batinah South	23.50001	57.16667	450
4	PI 564649	2 km northeast of Al Hamra, Interior province	Al Hamra	Al Dakhiliya	23.166667	57.33333	500
5	PI 564661	12 km from Al Hamra, Interior province	Al Hamra	Al Dakhiliya	23.166667	57.33333	500
6	PI 564662	8 km north of al Ayshi, Interior province	Al Hamra	Al Dakhiliya	23.166667	57.16667	500
7	PI 564663	10 km northeast of Al Ayshi, Interior province	Al Hamra	Al Dakhiliya	23.166667	57.16667	500
8	PI 564664	15 km northeast of Ibri, Dhahirah	Ibri	Al Dhahirah	23.333333	56.66667	300
9	PI 564665	30 km northeast of Ibri, Dhahirah	Ibri	Al Dhahirah	23.50001	56.66667	400
10	PI 564666	Yankul, Dhahirah	Yankul	Al Dhahirah	23.585556	56.54083	500
11	PI 564667	25 km west of Rustag, Western Hajar	Rustaq	Batinah South	23.333333	57.33333	650
12	PI 564668	35 km south of Jabrin, Interior province	Bahla	Al Dakhiliya	22.666667	57.33333	400
13	PI 564669	3 km southwest of Bahla, Interior province	Bahla	Al Dakhiliya	23.0001	57.33333	500
14	PI 564670	20 km north of Birkat al Mauz, Jebel Akhdar	Nizwa	Al Dakhiliya	23.166667	57.66667	1,800
15	PI 564671	20 km north of Birkat al Mauz, Jebel Akhdar	Nizwa	Al Dakhiliya	23.166667	57.66667	1,800
16	PI 564672	50 km southwest of Sohar, Western Hajar	Sohar	Batinah North	24.00001	56.50001	400

no. of tillers, row number/lateral florets, lemma awn/hood, lemma awn barbs, glume color, and lemma type, were not included in the analysis as landraces/accessions were found similar (Table 2). PCA was performed on the correlation matrix between 2-year means of eight agro-morphological characters and scores of growth habit and presence (1) and absence (0) of anthocyanin pigmentation on two plant parts such as stem and auricle, in indigenous barley accessions, to determine principal components, proportions of eigenvalues, and the scores of the principal components.

3 Results

3.1 Analysis of variability among the accessions

The accessions were assessed for their variability in terms of range and compared for their significant differences based on LSD (at $p = 0.5$) obtained from the ANOVA of check varieties (Tables 2 and 3).

The higher degrees of variability among the accessions was observed in respect of five characters, namely, days to maturity (95–123), flowering (63–90 days), grains/spike (47–80), spikelets/spike (49–83), and 1,000-grain weight (30–48.1 g; Table 3). There were three distinct groups in terms of flowering and maturity. Five accessions were early in days to flowering and maturity (PI 564648 and PI 564672 [63 and 95 days], PI 564646 [65 and 95 days], PI 564647 [66 and 97 days], and PI 564661 [68 and 99 days]), whereas three accessions were late (PI 564667 [85 and 123 days], PI 564649 [86 and 120 days], and PI 564665 [90 and 120 days]). The accession PI 564666 was found to flower (78 days) but mature along with late varieties (120 days; Table 2). The remaining seven accessions were intermediate in flowering (70–82 days) and maturity (112–116 days).

In respect of spikelets/spike and grains/spike, the accessions showed greater range of variation from 49 to 83 and 47 to 80, respectively. Two accessions PI 564646 (49 and 47) and PI 564671 (52 and 50) had the least, whereas two accessions PI 564466 (83 and 80) and PI 564464 (76 and 73) had the highest number of spikelets/spike and grains/spike, respectively. The remaining 12 accessions had spikelets/spike and grains/spike ranging from 55 to 71 and 53 to 69, respectively. In respect of 1,000-grain weight, PI 564667 had the highest 1,000-grain weight of 48.1 g followed by PI 564661 (43.8 g),

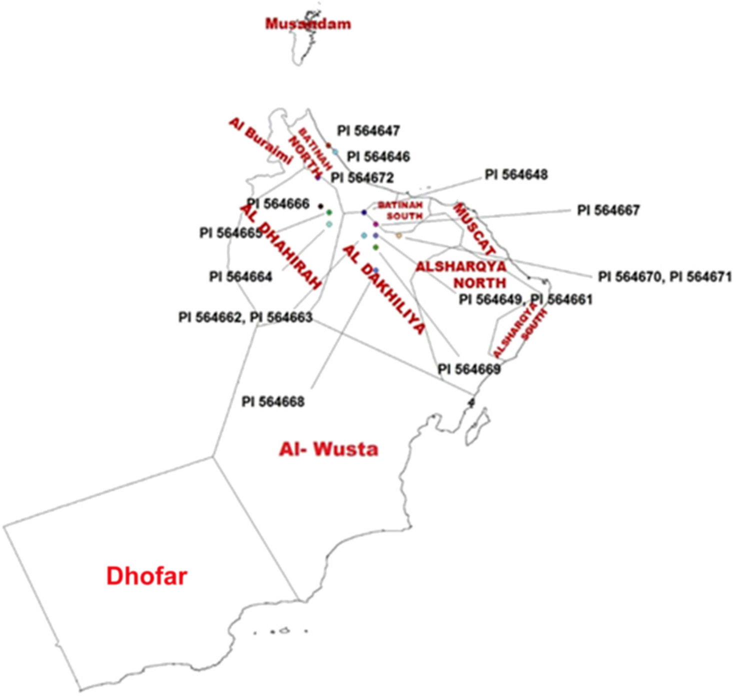

Figure 1: Locations of 16 indigenous barley (*Hordeum vulgare* L.) USDA accessions in five different governorates of Oman.

PI 564649 (43.3 g), and PI 564662 (40.0 g). However, the barley accessions did not show greater variation for spike density, grain length, and grain width owing to their lower level of standard deviation (Table 3).

3.2 Correlation analysis

Of 28 possible correlation coefficients estimated from eight yield-related characters (Table 4), only two were highly significant ($p < 0.01$). These two were among either maturity or spike associated traits, for example, the correlation coefficient (r) between days to flower and days to maturity was 0.900**, whereas it was to the extent of 0.992** between spikelets/spike and grains/spike. However, the remaining coefficients were nonsignificant ($p > 0.05$).

3.3 Cluster analyses

Cluster analysis was performed to assess the quantum of genetic diversity within and between the clusters of the barley accessions studied based on the dissimilarity index as indicated by the genetic distance between them to generate a dendrogram that classified them into four clusters with distinct features (Figure 2). The distance between the centroids of barley accessions is presented in Table 5. The critical examination of dendrogram features indicated four clusters with 41.96% dissimilarity in a clustering pattern. Each of the first three clusters, cluster 1, cluster 2, and cluster 3, consisted of five accessions each. Clusters 1 and 3 were composed of accessions of wilayats of different governorates, whereas cluster 2 consisted of all its five accessions from one governorate, Al-Dakhiliya.

The accessions of cluster 1 were from three governorates – one from Al-Hamra Al-Dakhiliya governorate (PI 564661), one from Al-Rustaq represented by mountains of South Batinah (PI 564648) and three accessions from Sohar of North Al-Batinah (PI 564646, PI 564647 and PI 564672) (Figures 1 and 2). Five accessions of cluster 3 were from three governorates – three from Al-Dhahirah governorate (one from Yankul – PI 564666 and two from Ibri – PI 564664 and PI 564665) and one each from Al-Dakhiliya (PI 564662 of wilayat Al-Hamra) and South Batinah (PI 564667 of wilayat Rustaq) governorates (Figures 1 and 2). However, five Al-Dakhiliya accessions of cluster 2 included one accession, PI 564649, from wilayat Al-Hamra and two accessions each from wilayat Bahla (PI 564668 and PI 564669) and wilayat Nizwa (PI 564670 and PI 564671; Figures 1 and 2). Cluster 4 was represented by a solitary accession, PI 564663 from Al-Hamra of Al-Dakhiliya governorate. Interestingly, this accession was found farthest to cluster 1 to the extent of

Table 2: Aggregate means of the agro-morphological quantitative characters of two cropping seasons and of 16 indigenous Oman accessions repatriated from USDA gene bank

Accession No.	Days to flower	Days to mature	Spike density	Spikelets/ spike	Grains/ spike	Grain length (mm)	Grain width (mm)	1,000 grain weight (g)	Growth habit	Stem color	Auricle pigmentation
PI 564646	65	95	7	49	47	9.5	3.7	38.2	7	1	1
PI 564647	66	97	7	63	57	7.2	2.4	31.6	5	3	2
PI 564648	63	95	6	56	53	9.3	2.5	36.1	5	3	3
PI 564649	86	120	7	55	53	9.9	3.6	43.3	7	1	1
PI 564661	68	99	5	71	67	9.3	3.7	43.8	5	1	1
PI 564662	82	115	6	69	65	8.2	2.8	40.0	5	1	1
PI 564663	84	115	7	71	69	9.1	3.4	39.0	5	1	1
PI 564664	82	116	7	76	73	10.0	2.9	37.4	7	1	1
PI 564665	90	120	6	72	68	9.0	3.1	38.9	7	1	1
PI 564666	78	120	7	83	80	9.3	3.5	38.9	5	3	3
PI 564667	85	123	9	70	68	10.9	3.7	48.1	7	1	1
PI 564668	70	116	8	53	49	10.0	2.8	36.6	7	1	1
PI 564669	81	116	9	62	58	9.0	3.1	37.4	7	1	1
PI 564670	81	112	7	58	53	7.7	1.9	30.0	7	1	1
PI 564671	79	116	8	52	50	9.3	2.4	36.6	7	1	1
PI 564672	63	95	7	59	54	8.1	2.6	33.4	5	3	3
									3-Prostrate	1-Green	1-Purple
									5-Intermediate	2-Purple (base only)	2-Pale purple
									7-Erect	3-Purple (half or more)	3-Purple
											4-Dark purple

The accessions showed similarity in respect of the following descriptor traits and hence not included in statistical analysis:

Plant height: Tall (visual) >120 cm.

Number of tillers: 4–6.

Row no./lateral florets: Score 5 (1 – two-rowed, large or small sterile spikelets; 2 – two-rowed, deficient; 3 – irregular, variable lateral florets; 4 – six-rowed-awnless or awnleted; 5 – six-rowed, long awned).

Lemma awn/hood: Score-3 (1 – awnless; 2 – awnleted; 3 – awned; 4 – sessile hoods; 5 – elevated hoods).

Lemma awn barbs: Score-5 (3 – smooth; 5 – intermediate [small barbs on upper half]; 7 – rough).

Glume color: Score-3 (1 – white; 2 – yellow; 3 – brown; 4 – black).

Lemma type: Score-3 (1 – no lemma teeth; 2 – lemma teeth; 3 – lemma hair).

Table 3: Statistical parameters for the mean values of agro-morphological characters of 16 indigenous Omani barley USDA accessions over two years along with standard error (SE) and coefficient of variation (CV%) for the analyses of five check varieties ($r = 5$)

Character	Minimum	Maximum	Mean	Std. Dev. (accessions)	*F*-test	LSD of checks (df 16; $p = 0.05$)	CV (%)
Days to flower	63.0	90.0	76.43	9.063	*	22.41	11.86
Days to maturity	95.0	123.0	110.62	10.411	*	25.74	9.41
Spike density	5.0	9.0	7.06	1.063	*	2.63	15.05
Spikelets/spike	49.0	83.0	63.69	9.755	*	24.12	15.31
Grains/spike	47.0	80.0	60.25	9.788	*	24.20	16.24
Grain length (mm)	7.2	10.9	9.11	1.010	*	2.50	11.22
Grain width (mm)	1.9	3.7	3.00	0.543	*	1.34	18.95
1,000 grain weight (g)	30.0	48.1	38.08	9.644	ns	23.85	25.33

*Significant ($p < 0.05$); ns, nonsignificant ($p > 0.05$).

45.811 Euclidean distance in comparison with cluster 2 (40.036) and cluster 3 (37.152; Figures 1 and 2). However, distances between clusters 1 and 2 (25.117) and that between clusters 2 and 3 (26.396) were at about mid-distance to the highest (Table 5). The average features of the clusters in terms of quantitative characters are presented in Table 6.

Cluster 1 was characterized by early maturing accessions, whereas accessions of clusters 3 and 4 were late maturing and having a higher number of spikes and grains per spike. However, the accessions of cluster 2 were characterized by higher grain length, whereas that of cluster 3 had a highest 1,000-grain weight (Table 6).

3.4 Principal component analysis (PCA)

The PCA was performed to comprehend which combination type of eight quantitative characters such as days to flowering and maturity, spike density, spikelets/spike, grains/spike, grain length, grain width, and 1,000-grain weight. In addition, three qualitative characters, namely, growth habit, stem, and auricle pigmentation, were included for higher productivity of the indigenous barley germplasm with identification markers for DUS tests [39–42]. Of total 11 characters, only the first four principal components (PCs) exhibited more than 1.0 eigenvalue (Table 7) and showed maximum variability of 81.946% among the traits investigated. The PC1 had the highest variability (36.500%) followed by PC2 (24.918%), PC3 (10.351%), PC4 (10.178%), PC5 (7.984%), and PC6 (6.111%) (Table 7). The PC1 had higher magnitudes of positive loading in respect of characters of pigmentation on stem (0.420) and auricle (0.395) and that of negative loading for days to flowering (−0.411), days to maturity (−0.414), and growth habit (−0.401). PC2 had only higher magnitudes of positive loadings for spikelets/spike (0.586) and grains/spike (0.588), whereas PC3 had a higher magnitude of positive loading for 1,000-grain weight (0.574) and negative loading for grain length (−0.512). PC4 had only higher magnitudes positive loading for spike density (0.442) and 1,000-grain weight (0.685). PC5 had a higher magnitude of positive loading for grain width (0.818) and negative loading for spike density (−0.402). Similarly, PC6

Table 4: Simple correlation coefficients among yield associated characters in indigenous Omani barley germplasm

Variables	Days to flower	Days to maturity	Spike density	Spikelets/ spike	Grains/spike	Grain length (mm)	Grain width (mm)	1,000 grain weight (g)
Days to flower	1	**0.900****	0.232	0.416	0.458	0.295	0.307	−0.023
Days to maturity		1	0.430	0.385	0.431	0.363	0.328	0.091
Spike density			1	−0.217	−0.187	0.230	0.086	0.037
Spikelets/spike				1	**0.992****	−0.283	0.188	−0.032
Grains/spike					1	−0.244	0.275	−0.030
Grain length (mm)						1	0.193	−0.143
Grain width (mm)							1	0.043
1,000 grain weight (g)								1

*Significant at $p < 0.05$; **Significant at $p < 0.01$; ns, $p > 0.05$.

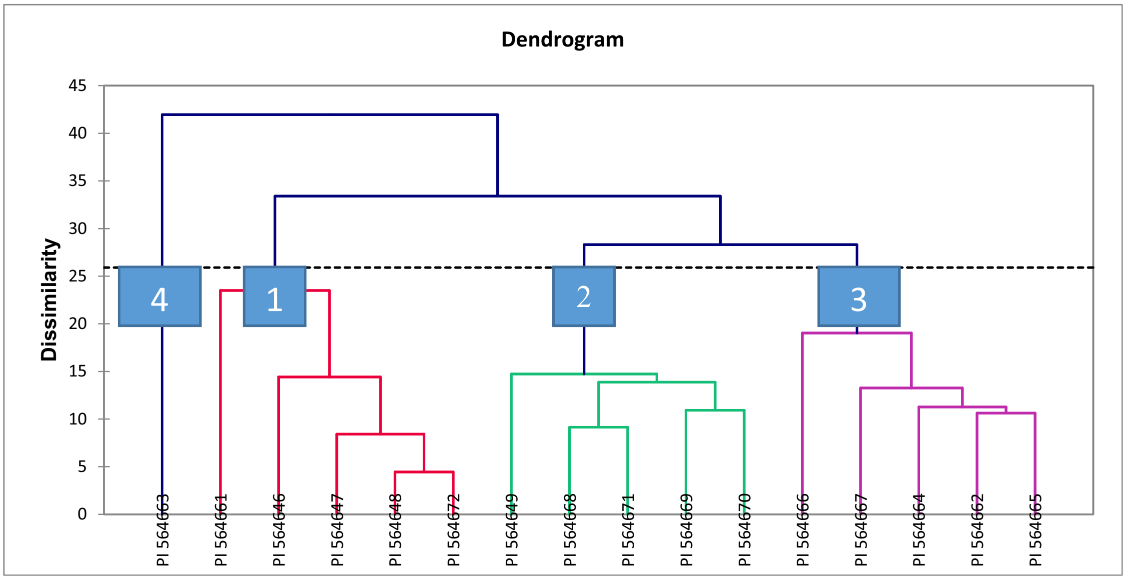

Figure 2: Dendrogram showing clustering pattern of 16 indigenous barley accessions using Ward's method.

Table 5: Distance between centroids of four clusters of 16 indigenous barley accessions

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	0	25.117	36.146	45.811
Cluster 2	25.117	0	26.396	40.036
Cluster 3	36.146	26.396	0	37.152
Cluster 4	45.811	40.036	37.152	0

had positive loading for grain length (0.580) and negative loadings for spike density (–0.539) and grain width (–0.461).

The distribution of 16 indigenous barley accessions in the biplot graph of the first two principal components as *X* and *Y*-axes that contributed together to 61.418% of variation (Figure 3). This is a major proportion of total variation, which reflected clustering in all the four quadrants of the graph and separated correspondingly into four clusters. The closely positioned accessions formed clusters in whichever quadrants of the graph they belonged due to their similarities (Figure 3). The number of barley accessions in clusters ranged from two (cluster I) to the highest of five (cluster II and cluster III) with cluster IV containing four accessions. Cluster I was formed of two accessions from two different governorates, Al-Dakhiliya (PI 564661 from wilayat Al-Hamra) and Al-Dhahirah (PI 564666 from wilayat Yankul). The clusters II and III were composed of five accessions each, which belonged to three different governorates – two from wilayat Al-Hamra of Al-Dakhiliya (PI 564662 and PI 564663), two from wilayat Ibri of Al-Dhahirah

Table 6: Mean values of morpho-agronomic characters and anthocyanin pigmentation in two plant parts of four clusters of 16 indigenous barley accessions

S. No.	Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Grand centroid
1	Days to flowering	65.00	79.40	83.40	84.00	77.95
2	Days to maturity	96.20	116.00	118.80	115.00	111.50
3	Spike density	6.40	7.80	7.00	7.00	7.05
4	Spikelets/spike	59.60	56.00	74.00	71.00	65.15
5	Grains/spike	55.60	52.60	70.80	69.00	62.00
6	Grain length (mm)	8.27	9.85	8.88	9.06	9.01
7	Grain width (mm)	2.68	2.76	3.05	3.39	2.97
8	1,000 grain weight (g)	36.62	36.78	40.66	39.00	38.26
9	Growth habit	5.40	7.00	6.20	5.00	
10	Stem pigmentation	2.20	1.00	1.40	1.00	
11	Auricle pigmentation	2.00	1.00	1.40	1.00	

(PI 564664 and PI 564665), and one from Rustaq of Al-Batinah South (PI 564667; Figures 1 and 3). The composition of accessions in cluster III of PCA was found exactly similar to cluster-2 of HCA (Figure 1). However, cluster IV of PCA was formed of four accessions from two governorates – three from Al-Batinah North (PI 564646, PI 564647, and PI 564672) from wilayat Sohar and one from Al-Batinah South (PI 564648 from wilayat Rustaq; Figures 1 and 3).

It is clear from Figure 3 that the accessions of cluster I were greatly influenced by two pigmentation characters as indicated by the direction and length of arrows (vectors) [28], whereas as many as four of five characters, namely, days to flowering and maturity, spikelets/spike, and grains/spike greatly influenced the accessions of cluster II and two out of remaining four characters, growth habit and grain length influenced the accessions of cluster III. However, the accessions of cluster IV corresponding to the fourth quadrant were not greatly influenced by any of the characters studied (Figure 3).

4 Discussion

Genetic variability and diversity can be both significant and relevant as the sources of novel traits and their combinations for plant breeding to face the unexpected challenges of end-user needs of the products (new varieties) because of climate change throughout the world [43,44]. The diversity *per se* has been of very limited application [45,46], whereas sources of diversity and variation have merits in breeding programs in the integration of ideal sources of diversity within each program to formulate crossing schemes. Within this scope, 16 indigenous barley races repatriated from the USDA gene bank were studied to assess their potential in terms of their variability and genetic diversity. The landraces were characterized by substantial variability in respect of days to flowering and maturity and for the number of spikelets and grains per spike ($p < 0.05$). In the present study, availability of the vast ranges of 63–90 days in flowering and 95–123 days to maturity observed among the accessions, provided wider scope in selection for parents to breed for early, medium, and late varieties. Such a vast range of germplasm differing in maturity was not observed in any previous or other contemporary studies wherein barley germplasm had a very narrow range of variation in heading/flowering in the early group (74–107 days) [47] or middle group (127–134 days) [48] or late group [49]. Furthermore, the germplasm in the present study revealed higher ranges of variation either in spikelets/spike (49–83) or grains/spike (47–80), which were on the same range in the Hungarian barley germplasm (spikelets/spike 61 to 87; grains/spike 45 to 83) [50]. On the contrary, a lower range of variation in grains/spike in their Iranian germplasm (29–49) was also observed [49], whereas large ranges of variation from 23 to 96 and 22 to 63 were found in the Indian and exotic germplasm [47] and in both Iranian and European germplasm [49]. In respect of 1,000-grain weight, our germplasm had a moderate range of variation from 30 to 48.1 g, which could provide scope in selecting parents

Table 7: Eigenvectors and eigenvalues associated with each character with respect to nine agro-morphological characters and presence/absence of pigmentation in two plant parts as explained by the first eight principal components (PC) in 16 indigenous *Hordeum vulgare* accessions

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to flowering	−0.411	0.257	−0.056	−0.055	−0.150	0.132	0.513	0.455
Days to maturity	−0.414	0.228	−0.154	0.172	−0.172	0.094	0.413	−0.405
Spike density	−0.233	−0.170	−0.336	0.442	−0.402	−0.539	−0.223	−0.146
Spikelets/spike	−0.023	0.586	0.022	0.042	−0.089	0.087	−0.390	0.025
Grains/spike	−0.053	0.588	0.003	0.047	−0.024	0.047	−0.368	−0.005
Grain length (mm)	−0.260	−0.206	−0.512	−0.053	0.256	0.580	−0.245	−0.271
Grain width (mm)	−0.194	0.167	−0.160	0.098	0.818	−0.461	0.081	0.065
1,000 grain weight (g)	−0.055	−0.049	0.574	0.685	0.183	0.259	0.054	−0.187
Growth habit	−0.401	−0.275	0.040	0.210	0.006	0.143	−0.340	0.621
Stem pigmentation	0.420	0.081	−0.318	0.331	−0.056	0.094	0.144	0.319
Auricle pigmentation	0.395	0.095	−0.375	0.364	0.079	0.167	0.151	0.083
Eigenvalue	4.015	2.741	1.139	1.120	0.878	0.672	0.261	0.116
Variability (%)	36.500	24.918	10.351	10.178	7.984	6.111	2.375	1.052
Cumulative (%)	36.500	61.418	71.769	81.946	89.931	96.042	98.417	99.469

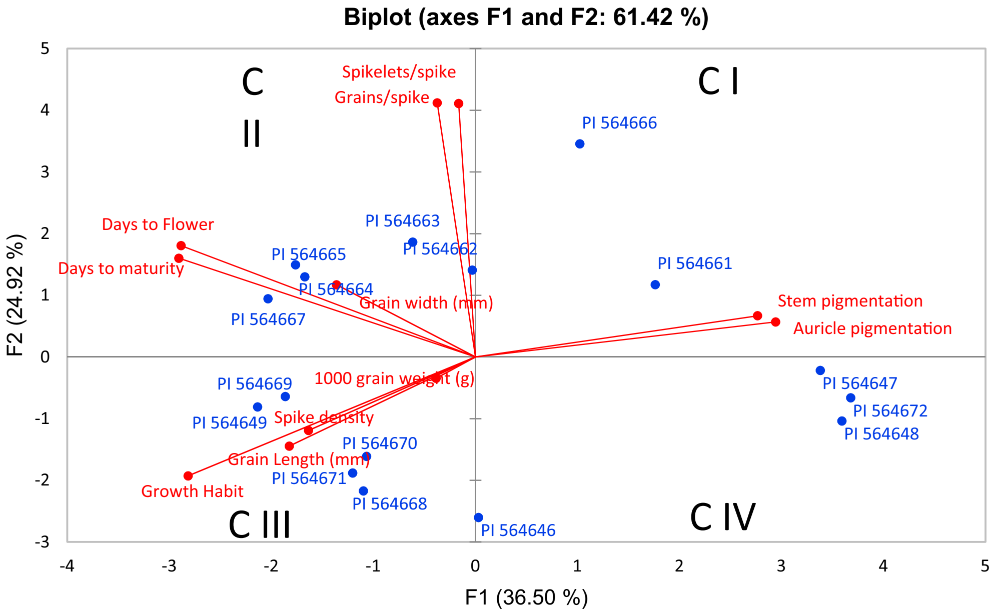

Figure 3: Biplot graph of PC 1 (Factor 1) and PC 2 (Factor 2) showing distribution of 16 *Hordeum vulgare* accessions into its four quadrants as clusters (I–IV) along with eigenvectors of the characters that most influence on corresponding axis.

for grain size (large or small). These results are similar to the findings with other germplasm, for example, 30.00–45.83 g [48] or 34.5–48.48 g [50], and 31.32–40.76 g [49]. On the contrary, in both Indian and exotic germplasm, a wider range of variation in 1,000-grain weight (12–63 g) was also reported [47]. The results of variability among the accessions in our study are in line and comparable to the reports of NPGS of USDA gene bank from their studies of barley core collections. Sixteen Omani landrace USDA accessions studied by us were part of these core collections [15].

In respect of relationships between quantitative characters studied, only two correlation coefficients (*r*), for example, between days to flower and days to maturity (0.900**) and that between spikelets/spike and grains/spike (0.992**), were found to be very highly significant. These correlations can be useful in selecting varieties for particular maturity group like early, medium early, intermediate, late, and very late with higher productivity. In the earlier studies also, significant correlations were reported between days to flowering and days to maturity in exotic and Indian barley germplasm (0.4811**) [51] and in Ethiopian landraces (0.74*) [52]. However, there were no reports of the correlation between the number of spikelets/spike and the number of grains/spike in any barley germplasm, so far, although their strong relation would be an indicator of sustenance of germplasm in converting spikelets into grains. This fact has been reported in several earlier studies in wheat germplasm [53–55].

In respect of clustering of genotypes, the present study adopted HCA and PCA for classifying barley landraces into clusters under the influence of characters/variables considered in terms of their contribution to the four clusters. The results clearly indicated differential patterns of classification of the two multivariate analyses used in terms of the composition of four clusters, formulated in each case. However, critical examination of landraces in the four clusters formulated by HCA dendrogram (clusters 1–4) and PCA biplot graph (clusters I–IV) clearly indicated a more or less similar pattern of clustering in terms of inclusions of accessions either in the same or different clusters. Regarding similarities of clustering between the two methods, C2 of HCA and CIII of PCA had the same composition of five accessions: PI 564649, PI 564668, PI 564669, PI 564670, and PI 564671. Furthermore, all the four accessions (PI 564646, PI 564647, PI 564648, and PI 564672) of cluster IV in PCA were included in cluster 1 of HCA (dendrogram) and four accessions (PI 564662, PI 564664, PI 564665, and PI 564667) were included together in cluster 3 of HCA and cluster II of PCA (Figures 2 and 3). However, in terms of dissimilarities between two methods, PI 564663 was alone isolated as cluster 4 in HCA (dendrogram), whereas PI 564661 and PI 564662 were isolated as cluster IV in the biplot graph of PCA (Figures 2 and 3). In general, in the present study, both the multivariate analyses were found to support each other in the dispersion or clustering of the accessions. However, recently conducted study to compare different graphical dispersion analysis techniques like HCA dendrogram and PCA biplot graphs indicated that the principal coordinate analysis was superior in the dispersion of the genotypes [56].

In the present study, the pattern of distribution of landrace accessions of barley indicated that few clusters contained the accessions of the same region or governorate, and the most contain the accessions of two or more governorates together, indicating the existence of widespread exchange of landraces of barley between wilayats of neighboring governorates. This has happened since the beginning of barley cultivation in Oman, and our collected landraces/accessions could be the products of centuries of selection by the farmers in their location (governorates) for adaptation to local climatic, edaphic, and cultural factors. Such accessions formed unique gene complexes reflecting similarities and differences in agroclimatic conditions through evolution [12,57]. The landraces are known not only for their dual-purpose utility by the local farmers' community (green fodder and grains) but also for unique adaptive traits to survive under harsh conditions of drought, heat, and salinity [1,19,23,58]. Hence, appropriate accessions from these landraces can be chosen as parents for hybridization in crop breeding.

The results of two multivariate cluster analyses had revealed the existence of considerable diversity among the Omani landrace USDA accessions, which could be used for the selection of appropriate accessions as parents based on characters to be improved, for producing transgressive segregants in F2 in the crop improvement program [5,7,29] Accordingly, the accession PI 564666 of Yankul of Al-Dhahirah governorate could be chosen from the cluster-I of PCA and cluster 3 of HCA (dendrogram) as one of the parents for higher yield through higher test weight, stem, or auricle pigmentation as identification markers (Figures 1–3). Similarly, PI 564663 of Al-Hamra of Al-Dakhiliya governorate can be chosen from cluster-II of PCA and cluster 4 of HCA for higher yield with different maturity groups and spikelet features with glume color as marker trait (Figures 1–3). PI 564668 of Al-Bahla of Al-Dakhiliya from cluster-III of PCA and cluster 2 of HCA can be selected for improving high yield required through growth habit and spike features with glume color as a marker trait. PI 564646 of Sohar, North Al-Batinah governorate from cluster-IV of PCA and cluster 1 of HCA can be preferred for improving productivity with glume color as marker trait (Figures 1–3). In view of their merits of having specific quantitative characters studied and inherent adaptability to local conditions, it is required to conserve and use these USDA Omani landrace accessions for developing dual-purpose high yielding barley varieties through hybridization in Oman.

5 Conclusion

Sixteen Oman landrace USDA accessions were found significantly different ($p < 0.05$) with respect to days to flowering and maturity, spikelets and grains/spike, and 1,000-grain weight. Only two correlations involving four characters such as between days to flowering and maturity and between spikelets/spike and grains/spike were significant ($p < 0.05$). Two multivariate analyses applied in the present study supported each other to the most extent in discerning diversity with each forming four diverse clusters with different contents of accessions. PI 564646, PI 564663, PI 564666, and PI 564668 were recommended for use as parents for hybridization for higher productivity with at least one identifying marker character of pigmentation on certain plant parts, which act as reference traits in the future released varieties to protect the genetic resources through Intellectual Property Rights.

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References

[1] USDA World Agriculture Production. Circular series 2020. WAP 4-20; 2020 April. Available from: https://apps.fas.usda.gov/psdonline/circulars/production.pdf

[2] Statista. Barley production worldwide 2008/2009–2018/2019; 2020. Available from: https://www.statista.com/statistics/271973/world-barley-production-since-2008/.

[3] FAO. Barley: post-harvest operations. Edited by AGST/FAO: Danilo Mejía, PhD, FAO (Technical) Rome, Italy: Food and Agriculture Organization of United Nations; 2004, p. 64. Available from: http://www.fao.org/fileadmin/user_upload/inpho/docs/Post_Harvest_Compendium_-_BARLEY.pdf

[4] Zhou M. Barley production and consumption. Adv Top Sci Technol China. 2010;7:1–17. doi: 10.1007/978-3-642-01279-2_1.

[5] Vaezi BP, Aboughadareh PA, Mohammadi R, Armion M, Mehraban A, Hossein PT, et al. GGE biplot and AMMI analysis of barley yield performance in Iran. Cereal Res Commun. 2017;45(3):500–11. doi: 10.1556/0806.45.2017.019.

[6] Dawson I, Russell J, Powell W, Steffenson B, Thomas W, Waugh R. Barley: a translational model for adaptation to climate change. N Phytologist. 2015;206(3):913–31. doi: 10.1111/nph.13266.

[7] Monteagudo A, Casas AM, Cantalapiedra CP, Contreras-Moreira B, Gracia MP, Igartua E. Harnessing novel diversity from landraces to improve an elite barley variety. Front Plant Sci. 2019;10:434. doi: 10.3389/fpls.2019.00434.

[8] Fischbeck D. Diversification through breeding. In: von Bothmer R, van Hintum T, Knupffer H, Sato K, editors. Diversity in barley (Hordeum vulgare). Amsterdam: Elsevier Science BV; 2003. p. 29–52.

[9] Langridge P, Waugh R. Harnessing the potential of germplasm collections. Nat Genet. 2019;51:200–1. doi: 10.1038/s41588-018-0340-4.

[10] MAF. Annual report. Department of Statistics. Ministry of Agriculture and Fisheries. Sultanate of Oman; 2019.

[11] Naifer A, Al-Rawahy SA, Zekri S. Economic impact of salinity: the case of Al-Batinah in Oman. Int J Agric Res. 2011;6:134–42. doi: 10.3923/ijar.2011.134.142.

[12] Al-Saady NA, Nadaf SK, Al-Subhi AS, Al-Hinai SA, Al-Farsi SM, Al-Habsi KM, et al. Multicrop legume germplasm collection in Oman. Int J Agric Biol. 2014;16:231–41.

[13] Guarino L. Barley collecting in southern Arabia. FAO/IBPGR. Plant Genet Resour Newsl. 1989;73:34–6.

[14] Guarino L. Crop collecting in the Sultanate of Oman in the context of the Arabian Peninsula. FAO/IBPGR. Plant Genet Resour Newsl. 1990;77:27–33.

[15] NGPS (National plant germplasm system). Germplasm resources information network (GRIN). Database management unit (DBMU) NPGS, USDA, Beltsville, MD; 2020. Available from: https://npgsweb.ars-grin.gov/gringlobal/search.aspx?q=

[16] MAF. Annual report. 2012. Directorate general agriculture and livestock research. Ministry of Agriculture and Fisheries. Sultanate of Oman; 2012.

[17] MAF. Annual report. Directorate general agriculture & livestock research. Ministry of Agriculture & Fisheries. Sultanate of Oman; 2013.

[18] MAF. Annual report. Directorate general agriculture and livestock research. Ministry of Agriculture & Fisheries. Sultanate of Oman; 2014.

[19] Jaradat AA, Shahid M, Al-Maskri AY. Genetic diversity in the Batini barley landrace from Oman: I. Spike and seed quantitative and qualitative traits. Crop Sci. 2004;44:304–15. doi: 10.2135/cropsci2004.3040.

[20] Kebebew F, Tsehaye Y, McNeilly T. Morphological and farmers cognitive diversity of barley (*Hordeum vulgare* L. [Poaceae]), at Bale and North Shewa of Ethiopia. Genet Res Crop Evol. 2001;48:1–10. doi: 10.1023/A:1012082812073.

[21] International Center for Biosaline Agriculture (ICBA). Annual report. ICBA, Dubai, UAE; 2000. Available from: https://www.biosaline.org/sites/default/files/Annualreportpdf/2000-_annual_report_english_version.pdf

[22] MAF. Oman salinity strategy, agricultural status and salinity impact, Ministry of agriculture and fisheries (Oman) and international center for biosaline agriculture (ICBA). Dubai: UAE; 2012.

[23] Maniruzzaman, Islam MZ, Begum F, Khan MAA, Amiruzzaman M, Hossain A. Evaluation of yield stability of seven barley (*Hordeum vulgare* L.) genotypes in multiple environments using GGE biplot and AMMI model. Open Agriculture. 2019;4:284–93. doi: 10.1515/opag-2019-0027.

[24] Grausgruber H, Bointner H, Tumpold R, Ruckenbaucer P. Genetic improvement of agronomic and qualitative traits of spring barley. Plant Breed. 2002;121:411–6. doi: 10.1046/j.1439-0523.2002.756385.

[25] Abeledo LG, Calderini DF, Slafer GA. Nitrogen economy in old and modern malting barleys. Field Crop Res. 2008;106:171–8. doi: 10.1016/j.fcr.2007.11.006

[26] Lillemo M, Reitan L, Bjørnstad C. Increasing impact of plant breeding on barley yields in central Norway from 1946 to 2008. Plant Breed. 2010;129:484–90. doi: 10.1111/j.1439-0523.2009.01710.x.

[27] Nielsen JP, Munck L. Evaluation of malting barley quality using exploratory data analysis. I. Extraction of information from micromalting data of spring and winter barley. J Cereal Sci. 2003;38:173–80.

[28] Yan W, Tinker NA. An integrated biplot analysis system for displaying, interpreting, and exploring genotype × environment interaction. Crop Sci. 2005;45(3):1004–16. doi: 10.2135/cropsci2004.0076.

[29] Žáková M, Benková M. Characterization of spring barley accessions based on multivariate analysis. Commun Biom Crop Sci. 2006;1:124–34.

[30] Abdullah AM, Subhani MG, Ahmad J, Anwar J. Multivariate analysis of some yield and yield related traits of barley (*Hordeum vulgare* L.) genotypes. Acad J Agric Res. 2018;6(7):189–97. doi: 10.15413/ajar.2018.0137.

[31] Enyew M, Dejene T, Lakew B, Worede F. Clustering and principal component analysis of Barley (*Hordeum volugare* L.) Landraces for major morphological traits from North Western Ethiopia. Int J Agric Sci Food Technol. 2019;5:58–63. doi: 10.17352/2455-815X.000043.

[32] Akhtar M, Nadaf SK. Scientific production of field crops in Oman. Sultanate of Oman: Ministry of Agriculture & Fisheries; 2001. p. 87.

[33] IPGRI. Descriptors for barley (Hordeum vulgare L.). International Plant Genetic Resources Instit., (IPGRI), Rome (Italy); 1994. p. 46. Available from: https://www.bioversityinternational.org/fileadmin/user_upload/online_library/publications/pdfs/333.pdf

[34] Bioversity International (BI). Key access and utilization descriptors for barley genetic resources. Bioversity International; 2009. p. 3. Available from: https://www.bioversityinternational.org/e-library/publications/detail/key-access-and-utilization-descriptors-for-barley-genetic-resources/

[35] Selvan RT, Parthiban KT, Palanikumaran B. Distinctness, uniformity and stability (DUS) characterization of Neolamarckia cadamba genetic resources. Curr Agri Res. 2019;7(2):268–75. doi: 10.12944/CARJ.7.2.15.

[36] XLStat. The leading data analysis and statistical solution for Microsoft Excel. Addinsoft, Paris, France; 2021. Available from: https://www.xlstat.com

[37] Ward Jr JH. Hierarchical grouping to optimize an objective function. J Am Stat Assoc. 1963;58:236–44. doi: 10.1080/01621459.1963.10500845.

[38] Murtagh F, Legendre P. Ward's hierarchical agglomerative clustering method: which algorithms implement ward's criterion? J Classif. 2014;31:274–95. doi: 10.1007/s00357-014-9161-z.

[39] Basnet KM, Adhikari NR, Pandey MP. Multivariate analysis among the Nepalese and exotic mungbean (Vigna radiata (L.) Wilczek) genotypes based on the qualitative parameters. Univers J Agric Res. 2014;2(5):147–55. doi: 10.13189/ujar.2014.020502.

[40] Kumar R, Prasad BK, Singh MK, Singh G, Verma A. Genetic divergence analysis for morpho-physiological traits, under timely and late sown condition in bread wheat (Triticum estivum L.). J Wheat Res. 2015;7(1):27–30.

[41] Wang LX, Qiu J, Chang F, Liu LH, Li H, Pang BS, et al. Assessment of wheat variety distinctness using SSR markers. J Integr Agriculture. 2015;14(10):1923–35. doi: 10.1016/S2095-3119(15)61057-7.

[42] CPVO. Protocol for distinctness, uniformity and stability tests Triticum aestivum L. emend. Fiori et Paol. Wheat. UPOV. UPOV Species Code: TRITI_AES. CPVO-TP/003/5; 2019. Available from: https://cpvo.europa.eu/sites/default/files/documents/triticum_aestivum_5.pdf

[43] Tester M, Langridge P. Breeding technologies to increase crop production in a changing world. Science. 2010;327:818–22. doi: 10.1126/science.1183700.

[44] Kabbaj H, Sall AT, Al-Abdallat A, Geleta M, Amri A, Filali-Maltouf A, et al. Genetic diversity within a global panel of durum wheat (*Triticum durum*) landraces and modern germplasm reveals the history of alleles exchange. Front Plant Sci. 2017;18(8):1277. doi: 10.3389/fpls.2017.01277.

[45] Royo C, Voltas J, Romagosa I. Remobilization of pre-anthesis assimilates to the grain for grain only and dual-purpose (forage and grain) triticale. Agronony J. 1999;91:312–6. doi: 10.2134/agronj1999.00021962009100020021x.

[46] Novoselović D, Bentley A, Šimek R, Dvojkovic K, Sorrells K, Gosman M, et al. Characterizing croatian wheat germplasm diversity and structure in a european context by DArT markers. Front Plant Sci. 2016;7:184. doi: 10.3389/fpls.2016.00184.

[47] Sarkar B, Sarkar A, Sharma RC, Verma RPS, Sharma I. Genetic diversity in barley (*Hordeum vulgare*) for traits associated with feed and forage purposes. Indian J Agric Sci. 2014;84:650–5.

[48] Khajavi A, Aharizad S, Ahmadizadeh M. Genetic diversity of promising lines of barley based on pheno-morphological traits in Ardabil area. Int J Adv Biol Biomed Res. 2014;2(2):456–62.

[49] Saroei E, Cheghamirza K, Zarei L. Genetic diversity of characteristics in barley cultivars. Genetika. 2017;49:495–510. doi: 10.2298/GENSR1702495S.

[50] Dyulgerova B, Dimova D, Valcheva D. Genetic diversity in six-rowed winter barley (Hordeum sativum jess., ssp. Vulgare L.) genotypes. Bulg J Agric Sci. 2016;22:114–8.

[51] Vinesh B, Prasad LC, Prasad R. Variability and diversity studies in exotic and indigenous barley (Hordeum vulgare L.). Int J Curr Microbiology Appl Sci. 2018;7:2007–19. doi: 10.20546/ijcmas.2018.707.237.

[52] Negash G, Lule D, Jalata Z. Correlations and path Analysis of some quantitative characters in barley (Hordeum vulgareum L.) landraces in western Oromia, Ethiopia. Afr J Plant Sci. 2019;13:34–46. doi: 10.5897/AJPS2018.1744.

[53] Ali Y, Atta BM, Akhter J, Monneveux P, Lateef Z. Genetic variability, association and diversity studies in wheat (*Trititicum aestivum* L.) germplasm. Pak J Bot. 2008;40:2087–97.

[54] Zarei L, Chegamirza K, Farshadfar E. Evaluation of grain yield and some agronomic characters in durum wheat (*Triticum turgidum* L.) under rainfed conditions. Australian J Agric Res. 2013;7:609–17.

[55] Ayed-Slama O, Bouhaouel I, Chameskh Z, Trifa Y, Sahli A, Aissa NB, et al. Genetic variation of salt-stressed durum wheat (Triticum durum subsp. Durm Desf.) genotypes under field conditions and gynogenetic capacity. J Genet Eng Biotechnol. 2018;16:161–7. doi: 10.1016/j.jgeb.2017.11.004.

[56] Sant'Anna IDC, Silva GN, Carneiro VQ, Pontes DS, Nascimento M, Cruz CM. Comparison of projection of distance techniques for genetic diversity studies. Acta Sci Agron. 2020;42:e42483. doi: 10.4025/actasciagron.v42i1.42483.

[57] Al-Saady NA, Nadaf SK, Al-Lawati AH, Al-Hinai SA. Germplasm collection and seed diversity of cowpea (Vigna unguiculata (L.) Walp.). Asian J Agric Food Sci. 2018;6:129–39. doi: 10.24203/ajafs.v6i4.5349.

[58] Jilal A, Grando S, Henry RJ, Rice N, Ceccarelli S. Agronomic and quality attributes of worldwide primitive barley subspecies. In: Zhang G, et al., editors. Advance in Barley Sciences: Proceedings of 11th International Barley Genetic Symposium. Dordrecht: Zhejiang University Press and Spriger Science, Business Media Dordrechi; 2013. doi: 10.1007/978-94-007-4682-4_9.