



OPEN Genetic structure and marker-trait association analysis for agro-morphological and physiological characteristics in germplasm of wild barley (*Hordeum vulgare* subsp. *spontaneum*)

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Wild barley (*Hordeum vulgare* subsp. *spontaneum*) germplasm is a valuable genetic resource for improving cultivated barley. The western regions of Iran, natural habitats for diverse wild barley populations, offer rich genetic diversity for enhancing economically important traits. This study examined 114 genotypes from western Iran, assessing their agro-morphological and physiological traits under both irrigated and rainfed conditions. The goal was also to identify informative SSR markers associated with these traits. Field trials were conducted over two agricultural years (2020–2021 and 2021–2022) using an augmented design with nine control genotypes. Significant variations in agronomic and physiological traits were observed, highlighting the interactive effects of genotype and environmental conditions. Genotype by environment interaction revealed significant differences at the 1% and 5% probability levels for traits other than spike length, number of seeds per spike, and flag leaf length. Population structure analysis classified these genotypes into 7 subpopulations. Marker-trait associations identified SSR markers linked with stress tolerance and yield-related traits. Notably, markers EBMAG0781, BMAG0323, and SCSSR04163 exhibited significant associations with various morphological and physiological traits under both conditions. These findings emphasize the extensive genetic diversity present in wild barley and its potential for breeding programs aimed at enhancing barley's adaptation to diverse environmental.

Keywords *Hordeum spontaneum*, Germplasm, Genetic structure, Marker-trait association

Wild relatives of crop plants have a high potential for tolerance to biotic and abiotic stresses. Studies on drought tolerance in wild and cultivated barley indicate that certain tolerance strategies are present in wild parents, which have been weakened in the domestication and cultivation of barley, focusing on yield and agronomic traits¹. Currently, significant attention is given to wild species and primitive barley landraces, which can serve as rich sources of genetic diversity for improving cultivated varieties. Wild barley, such as *H. spontaneum*, has been used as a source of resistance genes for diseases like powdery mildew, rust, barley leaf scorch, and leaf blotch. Additionally, this species is crucial for providing genetic variations in economic traits².

Genetic diversity in wild barley, particularly *H. spontaneum*, plays a crucial role in breeding stress-resistant cultivars. Studies have shown that wild barley accessions exhibit significant genetic variability in their resistance to phytotoxic aluminum ions, making them valuable genetic resources for developing high-yielding cultivars

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adapted to specific environmental conditions³. Additionally, crop wild gene flow in barley populations, such as *H. agriocrithon*, has led to the emergence of hybrid forms with characteristics of both wild and domesticated barley, contributing to the genetic diversity of the species⁴. The genetic erosion of traditional barley varieties in regions like Ethiopia highlights the importance of conserving genetic resources to meet future food needs and enhance agricultural sustainability⁵.

Furthermore, genomic studies on wild barley populations have revealed insights into the genomic basis of local adaptation, highlighting the role of structural variants and gene expression patterns in response to abiotic stress, such as drought tolerance and flowering time adaptation, which are essential for genetic improvement in cultivated barley⁶. Wild barley varieties and landraces show promise in providing novel opportunities for enhancing abiotic stress tolerance in crops, particularly under changing climatic conditions, emphasizing the potential of utilizing wild relatives in breeding programs for improved resilience in barley cultivation⁷.

In plant breeding, understanding the extent of genetic diversity and the distance between individuals is extremely important because genetic diversity is a cornerstone of sustainable agriculture^{8,9}. Today, molecular markers are widely used to study genetic diversity. Markers based on polymerase chain reaction (PCR), such as AFLP and SSR, are more effective in studying genetic diversity¹⁰.

One of the most important applications of molecular markers in breeding programs is their use in identifying superior individuals in segregating populations, identifying trait-controlling regions, and determining gene loci. One of the most important methods of quantitative genetics that allows for the precise dissection of quantitative traits and understanding of the relationship between gene loci and phenotypic traits is linkage mapping and association mapping or linkage disequilibrium mapping¹¹.

Studying the relationships between molecular markers and agronomic traits has multiple applications, such as the potential to evaluate the genetic potential of specific genotypes before phenotypic evaluations, identifying desirable trait alleles in germplasm collections, facilitating the precise localization of QTLs, and validating candidate genes responsible for quantitative traits like stability and drought resistance¹².

Identifying molecular markers associated with major genes controlling target traits has been achieved in recent years through the development of segregating populations such as F1 in heterozygous plants, F2, RIL, and DH in homozygous plants. Some molecular markers have been used for breeding purposes; however, limitations such as the unavailability of segregating populations for mapping, insufficient time, and lack of sufficient correlation between morphological traits and molecular markers have hindered the identification of markers associated with morphological traits. However, regression correlation analysis does not have these limitations¹³.

The goal of linkage mapping is to identify markers linked to a quantitative trait in a related population. This localization is based on establishing a statistical relationship between alleles controlling a quantitative trait and is widely used in plant populations. In contrast, association mapping uses a large collection of randomly collected individuals and maps based on linkage disequilibrium. Given that linkage mapping has high statistical power and repeatability^{14,15}, association analysis is an alternative method to overcome the limitations of using quantitative trait mapping. This method examines the correlation between genotype and phenotype traits in unrelated individuals. Moreover, this method uses a broad source, unlike quantitative trait mapping^{16–18}.

Given the above, this study aims to investigate and analyze the relationship between the germplasm of wild barley (*H. spontaneum*) in terms of agro-morphological and physiological traits using SSR and EST-SSR molecular markers. This research seeks to identify and understand the genetic and phenotypic patterns of this species under different environmental conditions, to utilize this information for the improvement and development of cultivated barley varieties with desirable traits, such as drought resistance and high productivity.

Results

Analysis of variance

Based on the results of Table 1, the trait's spike length (SL) and number of seeds per spike (NSPS) were not significant across the years. Additionally, the interaction effects of the year by environment and genotype by year for flag leaf length (FLL) showed no significant differences. Spike length (SL) was also non-significant for the interaction effects of year by genotype, environment by genotype, and year by environment by genotype. Similarly, the interaction effects of the year by genotype and environment by genotype for the trait number of seeds per spike (NSPS) did not show significant differences. Other studied traits showed significant differences at the 1% and 5% probability levels. This indicates a varying response pattern of genotypes under different environmental conditions.

Comparison of mean and descriptive statistics for agro-morphological traits

The results of Table 2 highlight high coefficients of variation (CV) under both rainfed and irrigated conditions for traits such as Xteragen Length (XL), flag leaf length (FLL), straw yield (SY), and grain yield (GY) only in rainfed conditions. This indicates significant variability among the wild barley genotypes for these traits. The highest CVs (30.9% and 28.2%) were observed for straw yield (SY) under both rainfed and irrigated conditions, respectively. In contrast, Plant Height (PH) exhibited the lowest CV under both conditions. Due to the extensive amount of information, a supplementary table has been included in the Supplementary Table S4 and S5.

The mean plant height (PH) in rainfed and irrigated conditions was 80.67 and 90.88, with a standard deviation of 7.57 and 8.24, respectively. The highest plant height (PH) was observed in genotypes 88, 64, 32, 33, 31, 107, 35, 74, 75, and 84, while the lowest plant height (PH) was observed in genotypes 17, 30, 106, 114, 34, 56, 4, 19, 26, and 78 in the rainfed conditions. Additionally, genotypes 88, 35, 33, 44, 49, 107, 70, 42, 84, and 87 exhibited the highest plant height (PH) in irrigated conditions, while genotypes 56, 106, 17, 19, 23, 114, 30, 26, 67, and 78 had the lowest plant height (PH).

S.O.V	df	MS							
		PH	XL	SL	AL	FLL	GY	TSW	NSPS
Year	1	1579.733**	275.877**	0.258 ^{ns}	509.197**	1047.348**	14.646**	211.082**	0.283 ^{ns}
Environment	1	9863.242**	1051.109**	503.752**	514.450**	577.041**	19.247**	91.947**	1947.478**
Environment × Year	1	104.512**	5.061*	13.062**	5.259**	0.087 ^{ns}	0.124**	5.940**	115.989**
Error 1	16	3.591	0.934	2.352	0.997	4.674	0.560	0.991	5.187
Genotype	113	193.705**	31.7475**	8.4159**	10.120**	13.454**	0.274**	2.569**	43.799**
Year × Genotype	113	27.488**	10.067**	0.857 ^{ns}	0.890**	1.921**	0.038**	0.469**	3.317 ^{ns}
Environment × Genotype	113	12.630*	6.308**	0.253 ^{ns}	0.802**	0.848 ^{ns}	0.026**	0.342**	1.582 ^{ns}
Environment × Genotype × Year	113	17.7162**	4.674**	1.302 ^{ns}	1.007**	1.057*	0.018**	0.301**	5.797**
Error 2	128	8.562	0.998	1.077	0.492	0.775	0.009	0.171	2.808
S.O.V	df	MS							
		SY	RWC	RWL	CHL a	CHL b	CAR	CHL T	
Year	1	23.918**	595.469**	14327.656**	194.839**	25.396**	1178.680**	9.914**	
Environment	1	20.754**	12648.243**	50.7343**	854.207**	499.807**	2689.220**	2773.585**	
Environment × Year	1	28.755**	2558.989**	2340.888**	34.647**	3.092*	11.898**	43.073**	
Error 1	16	0.321	3.871	3.953	3.587	0.615	9.579	1.610	
Genotype	113	0.870**	159.576**	77.813**	1.886**	1.262**	6.292**	3.447**	
Year × Genotype	113	0.395**	72.319**	13.505**	0.794**	0.632**	1.847**	1.507**	
Environment × Genotype	113	0.177*	27.259**	11.604**	0.322**	0.701**	2.0599**	1.1444**	
Environment × Genotype × Year	113	0.349**	30.966**	12.395**	0.347**	0.777**	1.285**	1.1267**	
Error 2	128	0.132	5.718	3.732	0.199	0.169	0.817	0.469	

Table 1. Results of the combined variance analysis for adjusted treatments in agro-morphological and physiological traits of wild barley. Sources of Variation (S.O.V), Mean of Squares (MS), Degree of freedom (df). * and ** are significant at the 5% and 1% probability level respectively, and ns are not significant. Grain Yield (GY), Number of Seed Per Spike (NSPS), 100-Kernel weight) TSW), Plant Height (PH), Spike Length (SL), Xteragen Length (XL), Straw Yield (SY), Flag Leaf Length (FLL), Awn Length (AL), Chlorophyll a (CHL a), Chlorophyll b (CHL b), Total Chlorophyll (CHL T) and Carotenoid (CAR).

	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated
	PH (cm)	PH (cm)	XL (cm)	XL (cm)	SL (cm)	SL (cm)	AL (cm)	AL (cm)	FLL (cm)	FLL (cm)
LSD 5%	5.875	5.889	1.233	1.253	1.298	1.083	1.100	1.158	1.200	1.070
LSD 1%	7.847	7.866	1.647	1.674	1.734	1.447	1.470	1.547	1.603	1.429
Minimum	62.000	71.000	4.500	7.500	6.500	8.000	11.000	12.000	3.000	5.000
Maximum	101.000	109.000	21.000	27.000	14.000	16.000	20.000	22.000	12.000	14.000
Average	80.671	90.882	13.886	17.039	9.355	11.202	14.303	16.158	7.070	9.219
Variation Range	39.000	38.000	16.500	19.500	7.500	8.000	9.000	10.000	9.000	9.000
Standard Deviation	7.571	8.243	3.213	3.961	1.599	1.589	1.733	1.932	2.067	1.995
Standard Error	0.066	0.072	0.028	0.035	0.014	0.014	0.015	0.017	0.018	0.017
Coefficient of Variation	9.4	9.1	23.1	23.2	17.1	14.2	12.1	12.0	29.2	21.6
	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated
	TSW (gr)	TSW (gr)	NSPS (Nu)	NSPS (Nu)	SY (gr)	SY (gr)	GY (gr)	GY (gr)		
LSD 5%	0.569	0.265	1.940	2.487	0.225	0.265	0.138	0.167		
LSD 1%	0.760	0.354	2.591	3.321	0.301	0.354	0.184	0.223		
Minimum	3.068	3.241	15.600	18.000	0.910	1.348	0.614	1.155		
Maximum	8.988	10.850	33.600	38.400	4.005	4.815	2.058	2.738		
Average	4.674	5.780	25.507	28.359	1.976	2.783	1.204	1.800		
Variation Range	5.919	7.609	18.000	20.400	3.095	3.467	1.444	1.583		
Standard Deviation	0.848	1.130	3.634	3.210	0.611	0.786	0.280	0.324		
Standard Error	0.007	0.010	0.032	0.028	0.005	0.007	0.002	0.003		
Coefficient of Variation	18.1	19.5	14.2	11.3	30.9	28.2	23.3	18.0		

Table 2. Descriptive statistics in two rainfed and irrigated conditions for morphological traits, yield, and yield components. Grain Yield (GY), Number of Seed Per Spike (NSPS), 100-Kernel weight) TSW), Plant Height (PH), Spike Length (SL), Xteragen Length (XL), Straw Yield (SY), Flag Leaf Length (FLL) and Awn Length (AL).

The mean xteragen length (XL) in rainfed and irrigated conditions was 13.88 and 17.39, with standard deviations of 3.21 and 3.96, respectively. Genotypes 114, 52, 19, 34, 78, 101, 57, 24, 38, and 47 had the lowest xteragen length (XL), while genotype 70, 87, 48, 88, 94, 21, 42, 6, 3, and 7 had the highest xteragen length (XL) in the rainfed conditions. In the irrigated conditions, genotypes 114, 19, 52, 34, 101, 24, 57, 90, 106, and 9 had the lowest xteragen length (XL), while genotypes 42, 48, 89, 51, 32, 70, 88, 21, 87, and 94 had the highest xteragen length (XL).

In rainfed conditions, the mean spike length (SL) was 9.35 with a standard deviation of 7.5. In irrigated conditions, it was 11.20 and 8. Genotypes number 107, 33, 8, 12, 88, 35, 36, 40, 41, and 57 had the highest spike length (SL), while genotypes number 95, 34, 51, 55, 56, 93, 97, 102, 106, and 113 had the lowest spike length (SL) in the rainfed conditions. Similarly, in irrigated conditions, genotypes 93, 4, 2, 5, 48, 55, 56, 59, 66, and 67 had the lowest spike length (SL), while genotypes 107, 33, 71, 8, 12, 34, 36, 41, 62, and 88 had the highest spike length (SL).

The mean awn length (AL) under rainfed and irrigated conditions was 11.20 and 14.30, with standard deviations of 1.73 and 1.93, respectively. Genotypes 5, 9, 15, 10, 51, 65, 91, 100, 103, and 113 exhibited the lowest awn length (AL), while genotypes 12, 78, 88, 70, 38, 89, 13, 34, and 61 had the highest awn length (AL) in the rainfed conditions. Similarly, genotypes 15, 33, 5, 52, 60, 65, 95, 111, 60, 1, and 114 displayed the lowest awn length (AL), whereas genotypes 88, 78, 12, 69, 34, 11, 38, 41, 46, and 76 exhibited the highest awn length (AL) in the irrigated conditions.

In rainfed conditions, the mean flag leaf length (FLL) was 7.07 with a standard deviation of 2.06, while in irrigated conditions it was 9.12 with a standard deviation of 1.21. Genotypes 58, 78, 79, 84, 90, 102, 114, 66, 67, and 77 had the lowest flag leaf length (FLL), whereas genotypes 107, 32, 87, 11, 41, 32, 86, 88, 4, 10, and 98 had the highest flag leaf length (FLL) in the rainfed conditions. Additionally, genotypes 84, 90, 58, 24, 45, 73, 78, 102, 16, and 18 had the lowest flag leaf length (FLL) in the irrigated conditions, while genotypes 107, 86, 87, 88, 44, 41, 47, 70, 32, and 89 had the highest flag leaf length (FLL).

The mean of 100-kernel weight (TSW) in rainfed and irrigated conditions was 4.67 and 5.78, with a standard deviation of 0.848 and 1.130, respectively. Genotypes 103, 51, 14, 25, 39, 107, 47, 9, 56, and 13 have the lowest 100-kernel weight (TSW), while genotype 113, 73, 88, 86, 97, 78, 84, 85, 12, and 77 have the highest 100-kernel weight (TSW) in the rainfed conditions. Additionally, genotypes 103, 96, 51, 25, 39, 107, 47, 9, 56, and 13 exhibit the lowest 100-kernel weight (TSW), while genotypes 72, 73, 113, 6, 114, 86, 88, 66, 69, and 78 display the highest 100-kernel weight (TSW).

The mean number of seeds per spike (NSPS) in rainfed and irrigated conditions was 24.50 and 28.35, with standard deviations of 3.63 and 3.21, respectively. Genotypes 1, 6, 11, 56, 72, 113, 17, 25, 26, and 41 had the lowest number of seeds per spike (NSPS), while Genotypes 8, 42, 48, 62, 74, 86, 97, 31, 32, and 107 had the highest number of seeds per spike (NSPS) in the rainfed conditions. In the irrigated conditions, genotypes 1, 4, 9, 11, 26, 71, 72, 73, 77, and 113 had the lowest number of seeds per spike (NSPS), while genotypes 97, 107, 7, 32, 34, 62, 8, 47, 48, and 42 had the highest number of seeds per spike (NSPS).

The mean straw yield (SY) in rainfed and irrigated conditions was 4.67 and 5.78, with a standard deviation of 0.848 and 1.130, respectively. In rainfed conditions, genotypes 1, 3, 18, 19, 50, 55, 56, 39, 96, and 103 had the lowest straw yield (SY), while genotypes 31, 33, 35, 38, 62, 65, 84, 53, 44, and 88 had the highest straw yield (SY). In irrigated conditions, genotypes 5, 12, 17, 18, 39, 55, 3, 23, 21, and 56 had the lowest straw yield (SY), whereas genotypes 33, 35, 70, 74, 79, 84, 83, 53, 114, and 88 had the highest straw yield (SY).

In rainfed conditions, the mean grain yield (GY) was 1.10 with a standard deviation of 0.786, while in irrigated conditions it was 1.80 with a standard deviation of 0.324. Genotypes 88, 97, 86, 62, 113, 74, 12, 85, and 75 exhibited the highest grain yield (GY), whereas Genotypes 72, 56, 25, 51, 1, 103, 67, 17, 50, and 6 had the lowest grain yield (GY) in the rainfed conditions. Similarly, in irrigated conditions, genotypes 113, 86, 88, 97, 62, 66, 6, 114, 85, and 73 showed the highest grain yield (GY), while genotypes 103, 25, 51, 13, 26, 56, 29, 18, 67, and 17 had the lowest grain yield (GY).

Comparison of mean and descriptive statistics for physiological traits

Table 3 displays the minimum, maximum, mean, range of changes, standard deviation, standard error, coefficient of variation, and the results of the LSD test at the 5% and 1% probability levels for the traits measured in both rainfed and irrigated conditions. The descriptive statistics reveal a significant diversity among wild barley genotypes in terms of physiological characteristics. Based on the coefficient of variation, the RWL trait exhibited the highest amount in both rainfed and irrigated conditions, while the lowest amount was observed in the chlorophyll a trait. Due to the extensive amount of information, a supplementary table has been included in the Supplementary Table S4 and S5.

The mean relative water content (RWC) in rainfed and irrigated conditions was 47.59 and 61.30, with a standard deviation of 8.90 and 8.55, respectively. Genotypes 1, 56, 89, 51, 68, 103, 96, 90, 41, and 55 exhibited the lowest RWC, while genotypes 12, 5, 75, 79, 88, 74, 16, 15, 97, and 86 showed the highest RWC. RWC was measured in rainfed conditions. Additionally, genotypes 51, 18, 17, 1, 13, 89, 56, 9, 11, and 19 had the lowest RWC, while genotypes 6, 79, 5, 62, 74, 12, 94, 81, 15, and 97 had the highest RWC.

In rainfed conditions, the mean relative water loss (RWL) was 23.67, with a standard deviation of 5.68, and in irrigated conditions, it was 29.50 and 5.57, respectively. Genotypes 62, 12, 15, 20, 77, 88, 16, 8, 35, and 4 had the lowest RWL, while genotypes number 103, 96, 72, 74, 69, 56, 51, 64, 114, and 102 had the highest RWL in the rainfed conditions. Similarly, in irrigated conditions, genotypes 5, 12, 15, 16, 8, 7, 62, 10, 61, and 20 exhibited the lowest RWL, while genotypes 92, 70, 68, 69, 96, 102, 66, 64, 51, and 79 had the highest RWL.

The mean chlorophyll a content in rainfed and irrigated conditions was 4.15 and 7.29, with standard deviations of 0.51 and 0.77, respectively. In rainfed conditions, genotypes 65, 108, 109, 56, 1, 22, 51, 50, 17, and 112 exhibited the lowest levels of chlorophyll a, while genotypes 88, 77, 73, 64, 97, 78, 86, 12, 85, and 15 had

	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated	Rainfed	Irrigated
	RWC (%)	RWC (%)	RWL (%)	RWL (%)	CHL a (mg g ⁻¹ fw)	CHL a (mg g ⁻¹ fw)	CHL b (mg g ⁻¹ fw)	CHL b (mg g ⁻¹ fw)	CAR (mg g ⁻¹ fw)	CAR (mg g ⁻¹ fw)	CHL T (mg g ⁻¹ fw)	CHL T (mg g ⁻¹ fw)
LSD 5%	0.408	2.178	2.062	2.178	0.408	0.709	0.349	0.513	0.816	1.279	0.571	0.878
LSD 1%	0.546	2.909	2.755	2.909	0.546	0.947	0.466	0.685	1.090	1.708	0.762	1.172
Minimum	32.234	42.048	11.818	17.364	2.970	5.043	1.224	2.789	6.575	9.509	4.468	8.893
Maximum	68.085	87.333	35.291	39.862	5.687	9.546	3.534	5.961	13.954	20.621	8.842	15.252
Average	47.596	61.304	23.672	29.502	4.159	7.291	2.455	4.626	10.654	15.593	6.614	11.918
Variation Range	35.851	45.285	23.473	22.498	2.716	4.503	2.311	3.173	7.379	11.112	4.374	6.359
Standard Deviation	8.902	8.554	5.687	5.578	0.517	0.773	0.478	0.715	1.475	1.600	0.913	1.321
Standard Error	0.078	0.075	0.050	0.049	0.005	0.007	0.004	0.006	0.013	0.014	0.008	0.012
Coefficient of Variation	18.7	14.0	24.0	18.9	12.4	10.6	19.5	15.4	13.8	10.3	13.8	13.8

Table 3. Descriptive statistics of physiological trait components under rainfed and irrigated conditions. Chlorophyll a (CHL a), Chlorophyll b (CHL b), Total Chlorophyll (CHL T) and Carotenoid (CAR).

the highest levels. Similarly, genotypes 1, 13, 26, 51, 18, 17, 103, 29, 11, and 112 showed the lowest chlorophyll a levels, while genotypes 62, 61, 66, 6, 5, 73, 12, 15, 86, and 88 exhibited the highest levels in the irrigated conditions.

In rainfed conditions, the mean chlorophyll b content was 2.45, with a standard deviation of 0.47, while in irrigated conditions, it was 4.62 and 0.71. Genotypes 1, 56, 51, 17, 50, 41, 6, 55, 60, and 9 had the lowest chlorophyll b levels in the rainfed conditions, while genotypes 62, 35, 12, 61, 32, 15, 88, 33, 77, and 108 exhibited the highest levels. Additionally, genotypes 110, 103, 71, 106, 30, 112, 102, 51, 78, and 98 showed the lowest chlorophyll b levels, while genotypes 86, 88, 62, 61, 97, 44, 34, 35, 32, and 85 had the highest levels in the irrigated conditions.

The mean total chlorophyll in rainfed and irrigated conditions was 6.61 and 11.91, with a standard deviation of 0.91 and 1.32, respectively. Genotypes 1, 56, 51, 17, 50, 41, 6, 55, 60, and 103 had the lowest total chlorophyll, while genotypes 88, 77, 73, 12, 62, 35, 78, 97, 15, and 86 had the highest total chlorophyll in the rainfed conditions. Similarly, genotypes 1, 56, 51, 17, 50, 41, 6, 55, 60, and 103 had the lowest total chlorophyll, and genotypes 88, 77, 73, 12, 62, 35, 78, 97, 15, and 86 had the highest total chlorophyll in the irrigated conditions.

In the rainfed condition, the mean carotenoid level was 10.65, with a standard deviation of 1.60, while in the irrigated condition, it was 15.59, with a standard deviation of 1.47. In rainfed conditions, genotypes 114, 12, 62, 35, 15, 88, 61, 32, 20, and 33 exhibited the highest carotenoid levels, whereas genotypes 1, 56, 51, 50, 17, 41, 25, 55, 73, and 6 showed the lowest carotenoid levels. Additionally, in irrigated conditions, genotypes 62, 110, 61, 78, 27, 86, 88, 71, 97, and 85 had the highest carotenoid levels, while genotypes 1, 103, 106, 51, 102, 98, 56, 95, 3, and 37 had the lowest carotenoid levels.

Genotypic grouping of genotypes under rainfed and irrigated conditions based on cluster analysis

Cluster analysis using the Ward method was employed to group the studied genotypes under stress and non-stress conditions into eight clusters. In rainfed conditions (Fig. 1), the first group consisted of 21 genotypes, the second group of 9 genotypes, the third group of 8 genotypes, the fourth group of 21 genotypes, the fifth group of 26 genotypes, the sixth group of 17 genotypes, the seventh group of 9 genotypes, and the eighth group of 3 genotypes.

Based on the results, the first group exhibited the lowest values for grain yield (GY), RWC, chlorophyll a, chlorophyll b, total chlorophyll, and carotenoids. Additionally, the second group had the lowest straw weight. The third group had the highest RWC and the lowest awn length (AL) and relative water loss (RWL). The fourth group showed the lowest values for plant height (PH), peduncle length, spike length (SL), flag leaf length (FLL), 100-kernel weight (TSW), number of seeds per spike (NSPS), and straw yield (SY). The seventh group had the highest 100-kernel weight (TSW), number of seeds per spike (NSPS), straw yield (SY), grain yield (GY), chlorophyll a, chlorophyll b, total chlorophyll, and carotenoids. The eighth group exhibited the highest values for plant height (PH), peduncle length, spike length (SL), awn length (AL), flag leaf length (FLL), and RWL.

In irrigated conditions (Fig. 2), the first group comprised 23 genotypes, the second group 12 genotypes, the third group 10 genotypes, the fourth group 7 genotypes, the fifth group 11 genotypes, the sixth group 12 genotypes, the seventh group 26 genotypes, and the eighth group 13 genotypes.

According to this grouping, the first group had the lowest number of seeds per spike (NSPS), and the second group had the lowest peduncle length, awn length (AL), straw weight, grain yield (GY), RWC, chlorophyll a, and carotenoids. The third group had the highest 100-kernel weight (TSW), grain yield (GY), RWC, chlorophyll a, and the lowest RWL. The fourth group exhibited the highest awn length (AL) and number of seeds per spike (NSPS). The sixth group had the lowest plant height (PH), spike length (SL), flag leaf length (FLL), number of seeds per spike (NSPS), chlorophyll b, and total chlorophyll. The seventh group had the highest RWL, and the eighth group had the highest plant height (PH), peduncle length, spike length (SL), flag leaf length (FLL), straw yield (SY), chlorophyll b, carotenoids, and total chlorophyll.

Molecular marker analysis

Genetic diversity among the studied genotypes was assessed using a set of 50 molecular markers, comprising both SSR and EST-SSR types. Of these, 35 markers (21 SSR and 14 EST-SSR) produced clear, polymorphic, and scorable bands (Supplementary Figure S2). The total number of alleles detected per locus ranged from two to four for both marker types. SSR markers amplified a total of 57 alleles, while EST-SSR markers generated 40 alleles, reflecting substantial allelic variation. The overall polymorphism rate was high, exceeding 96% for both SSR and EST-SSR markers, indicating considerable genetic variability. Among SSR markers, loci such as BMAC0154, BMAG0508A, BMAG0323, and EBMAC0775 demonstrated the highest polymorphic information content (PIC) values. Similarly, EST-SSR markers including GBM1221, GBM1461, and SCSSR04163 exhibited superior informativeness. Discriminatory power metrics, such as Marker Index (MI), Effective Multiplex Ratio (EMR), and Resolving Power (RP), identified EBMAC0775, BMAG0131, HVLTPPB, and SCSSR04163 as highly effective in detecting genetic diversity. Furthermore, the mean number of effective alleles and Shannon's Information Index supported the presence of substantial allelic diversity, especially for EBMAC0775, HVLTPPB, and SCSSR04163¹⁹.

Population structure analysis

Results showed that based on the LnP(D) and ΔK indices, $K = 7$ was identified as the optimal number (Fig. 3; Table 4) for characterizing population structure and calculating the Q-matrix, which estimates the membership proportions of individuals in each cluster²⁰.

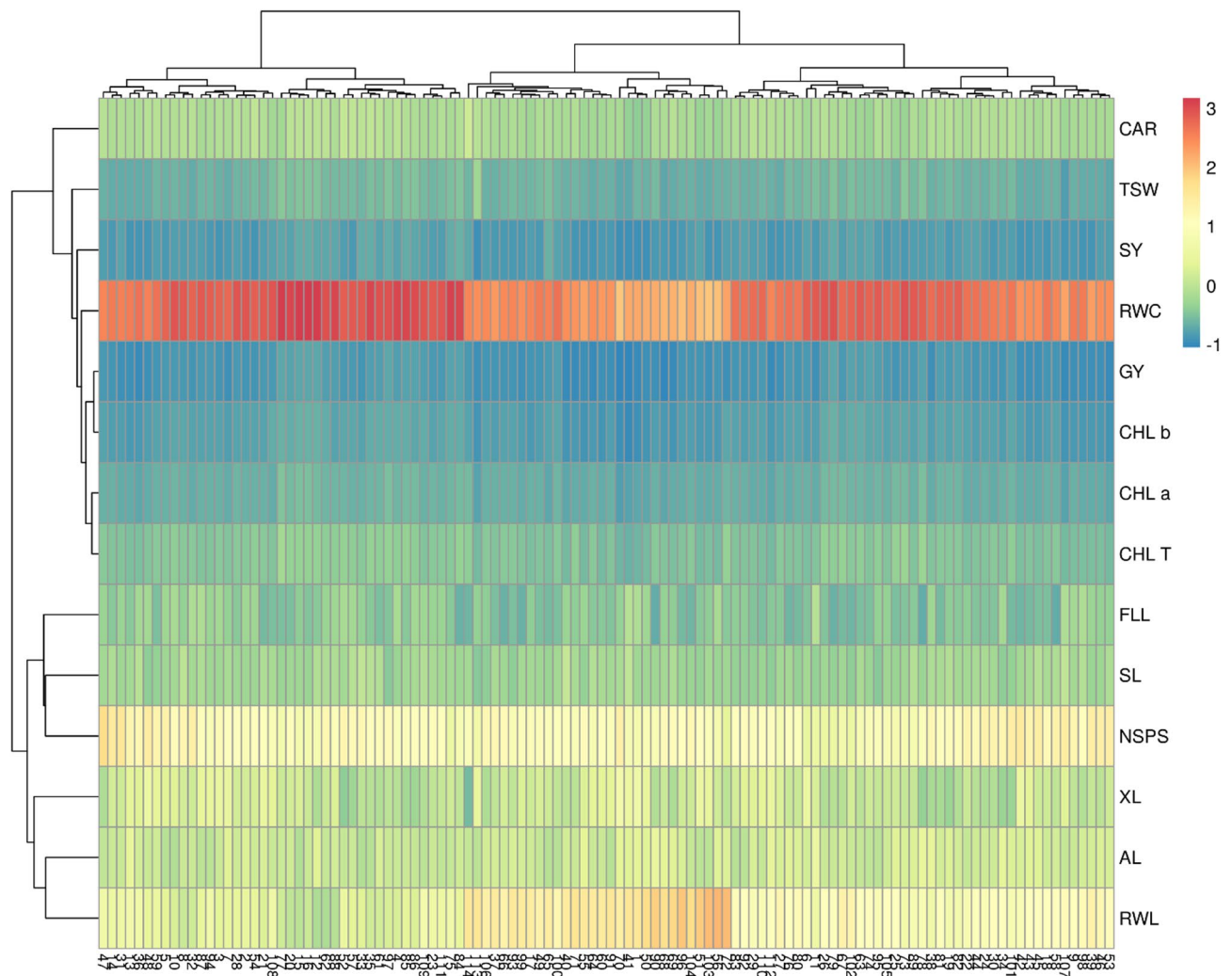


Fig.1. Dendrogram resulting from cluster analysis by Ward's method in rainfed conditions for *H. spontaneum* wild barley genotypes. Grain Yield (GY), Number of Seed Per Spike (NSPS), 100-Kernel weight (TSW), Plant Height (PH), Spike Length (SL), Xteragen Length (XL), Straw Yield (SY), Flag Leaf Length (FLL) and Awn Length (AL), Chlorophyll a (CHL a), Chlorophyll b (CHL b), Total Chlorophyll (CHL T) and Carotenoid (CAR).

Based on the observed results in the barplot (Fig. 4), the 114 barley genotypes studied were classified into seven families. Specifically, 17 genotypes belonged to the first structure, 31 genotypes to the second structure, 12 genotypes to the third structure, 15 genotypes to the fourth structure, 11 genotypes to the fifth structure, 14 genotypes to the sixth structure, and 14 genotypes to the seventh structure. The second and fifth groups accounted for the highest (31) and lowest (11) number of individuals, respectively²¹.

Association analysis

Association analysis of the genome was conducted using the Mixed Linear Model (MLM), and markers associated with morphological and physiological traits under rainfed and irrigated conditions are listed in Table 5. The significance level of marker-trait associations (P-Marker) at the 0.05 level is indicated.

Results from the analysis of relationships between morphological and physiological traits and 97 amplified alleles under rainfed conditions showed that the markers EBMAC0781, BMAG0323, and SCSSR04163 are associated with grain yield (GY). Spike length (SL) is associated with markers WMC1E8, SCSSR15864, GBM1461, and SCSSR18076. Awn length (AL) is associated with markers EBMAC0521, BMAG0323, GBM1126, WMC1E8), and BMAG0131. Flag leaf length (FLL) is associated with markers SCSSR25691, EBMAC0775, HVLTPPB, BMAG0692, and EBMAC0781. Xteragen Length (XL) is associated with markers EBMAC0521, BMAG0323, GBM1110, and SCSSR05599. Number of seeds per spike (NSPS) is associated with markers BMAG0131, EBMAC0775, EBMAC0521, SCSSR15864, SCSSR25691, and GBM1126. Straw yield (SY) is associated with markers BMAC0273 and EBMAC0775. Plant height (PH) is associated with markers HVLTPPB, SCSSR04163 and EBMAC0775. (TSW) 100-Kernel weight is associated with markers SCSSR15864, SCSSR15864, BMAC0154, BMAC0154, WMC1E8, GBM1110, and EBMAC0775. Relative water loss (RWL) is

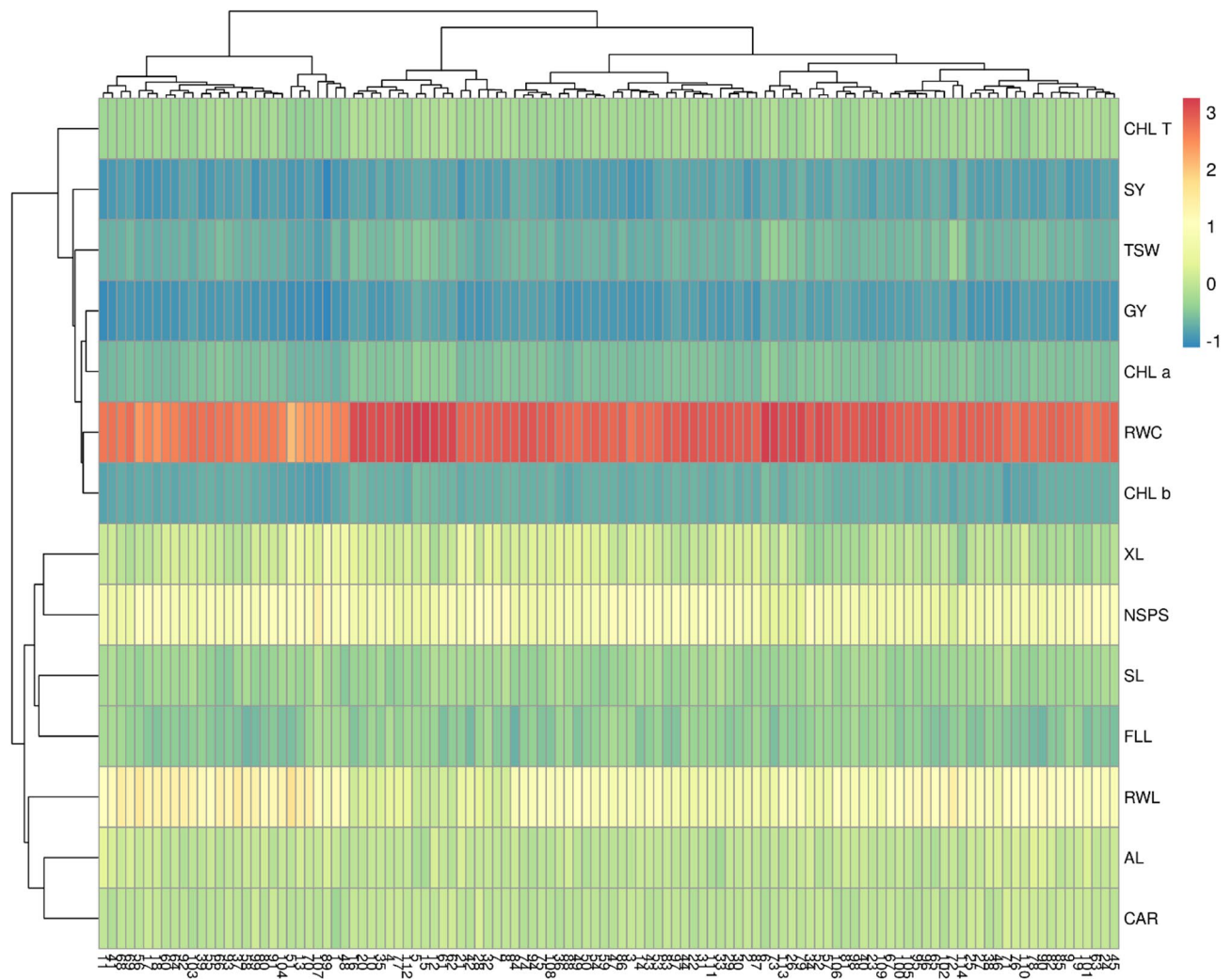


Fig.2. Dendrogram resulting from cluster analysis by Ward's method in irrigated conditions for *H. spontaneum* wild barley genotypes. Grain Yield (GY), Number of Seed Per Spike (NSPS), 100-Kernel weight (TSW), Plant Height (PH), Spike Length (SL), Xteragen Length (XL), Straw Yield (SY), Flag Leaf Length (FLL) and Awn Length (AL), Chlorophyll a (CHL a), Chlorophyll b (CHL b), Total Chlorophyll (CHL T) and Carotenoid (CAR).

associated with markers SCSSR04163, BMAG0131, and GBM1176. Relative water content (RWC) is associated with markers BMAG0323, GBM1176, and BMAG0341. Total chlorophyll (Chl T) is associated with markers GBM1461, EBMAC0415, BMAC0189, WMC1E8, BMAG0341, and BMAG0323. Chlorophyll b is associated with markers BMAG0692 and GBM1176. Chlorophyll a is associated with markers BMAG0323, GBM1126, and EBMAC0521. Carotenoid is associated with markers EBMAC0775, BMAC0273, GBM1212, and SCSSR05599.

Under irrigated conditions, results from the analysis of relationships between morphological and physiological traits and 97 amplified alleles showed that grain yield (GY) is associated with marker EBMAC0775. Spike length (SL) is associated with marker WMC1E8. Awn length (AL) is associated with markers BMAC0189 and EBMAC0415. Flag leaf length (FLL) is associated with markers BMAG0603, GBM1110, BMAC0189, and EBMAC0775. Xteragen Length (XL) is associated with markers BMAG0603, EBMAC0674, and BMAG0603. Number of seeds per spike (NSPS) is associated with marker BMAC0189. Straw yield (SY) is associated with markers BMAC0273, BMAC0273, and EBMAC0775. Plant height (PH) is associated with markers BMAG0508A, WMC1E8, BMAC0273, and HVLTPPB. (TSW) 100-Kernel weight is associated with markers EBMAG0781, GBM1110, and EBMAG0781. Relative water content (RWC) is associated with markers BMAG0323 and SCSSR25691. Relative water loss (RWL) is associated with marker SCSSR04163. Total chlorophyll (CHL T) is associated with markers BMAC0189 and SCSSR15864. Chlorophyll b is associated with markers BMAG0341, GBM1110, GBM1126, EBMAG0781, BMAC0189, SCSSR04163, and SCSSR15864. Chlorophyll a is associated with marker SCSSR25691. Carotenoid is associated with markers EBMAC0775, BMAG0692, BMAG0603, EBMAC0054, EBMAC0775, and BMAG0603.

The results demonstrate that marker WMC1E8 is significantly associated with spike length (SL), marker EBMAC0775 with flag leaf length (FLL), markers BMAC0273 and EBMAC0775 with straw yield (SY), marker

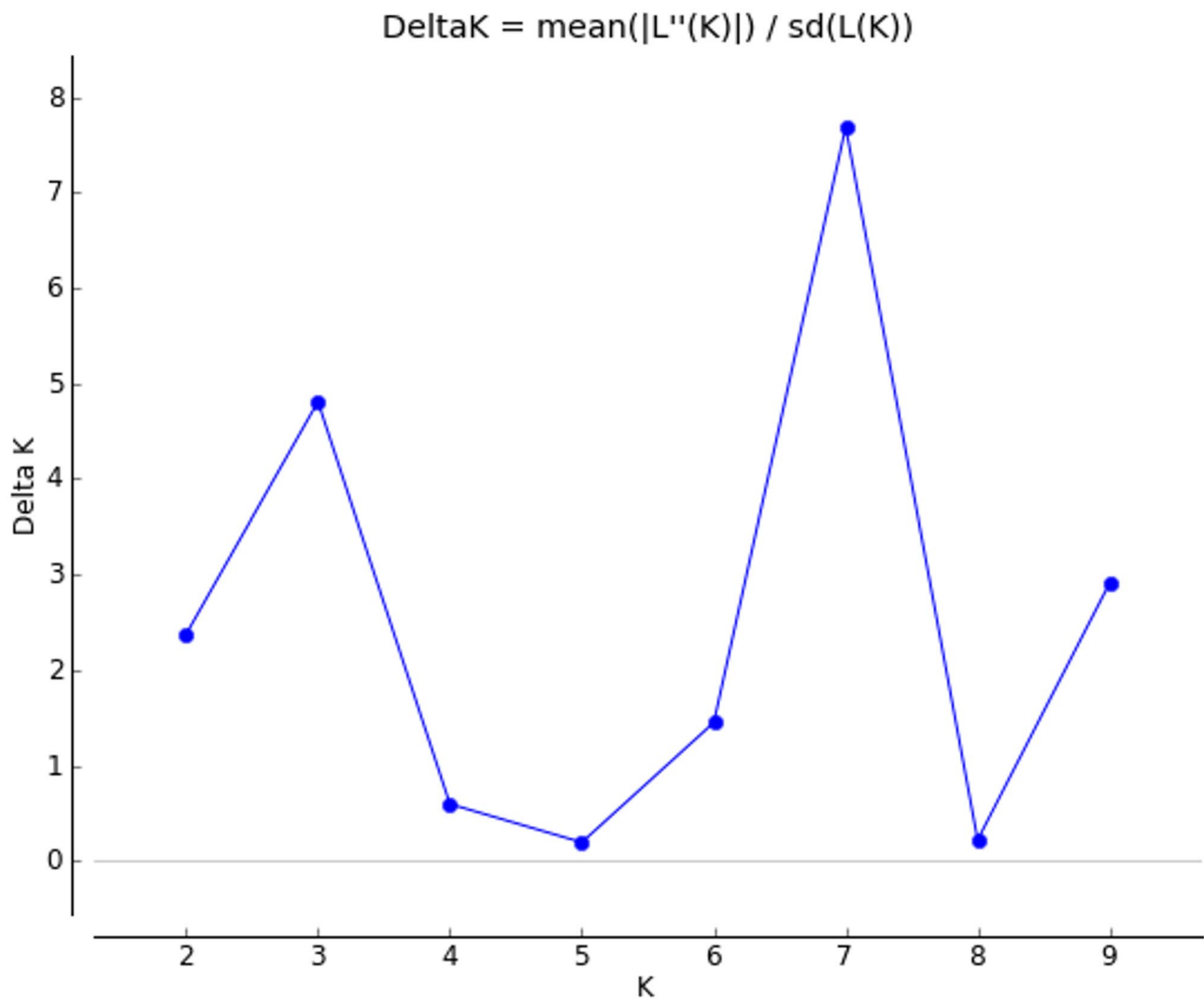


Fig.3. Determination of the optimal number of subpopulations ($K=7$) in wild barley using the ΔK method via STRUCTURE 2.3.4.

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	5	-4903.12	0.294958	—	—	—
2	5	-4834.86	13.52601	68.26	32.12	2.374684
3	5	-4734.48	19.48902	100.38	93.72	4.808861
4	5	-4727.82	26.60521	6.66	15.9	0.597627
5	5	-4737.06	62.23715	-9.24	12.2	0.196024
6	5	-4734.1	91.13471	2.96	132.18	1.45038
7	5	-4598.96	20.54137	135.14	157.88	7.685952
8	5	-4621.7	135.9594	-22.74	30.26	0.222566
9	5	-4614.18	106.0401	7.52	308.66	2.910786
10	5	-4915.32	588.1693	-301.14	—	—

Table 4. Results of Evanno method in selecting optimal K to investigate the structure of wild barley genotypes.

HVLTTPB with plant height (PH), marker GBM1110 with 100-kernel weight (TSW), marker SCSSR04163 with relative water loss (RWL), marker BMAG0323 with relative water content (RWC), marker BMAC0189 with total chlorophyll content, and marker EBMAC0775 with carotenoid content. Notably, these associations were consistent across both rainfed and irrigated conditions.

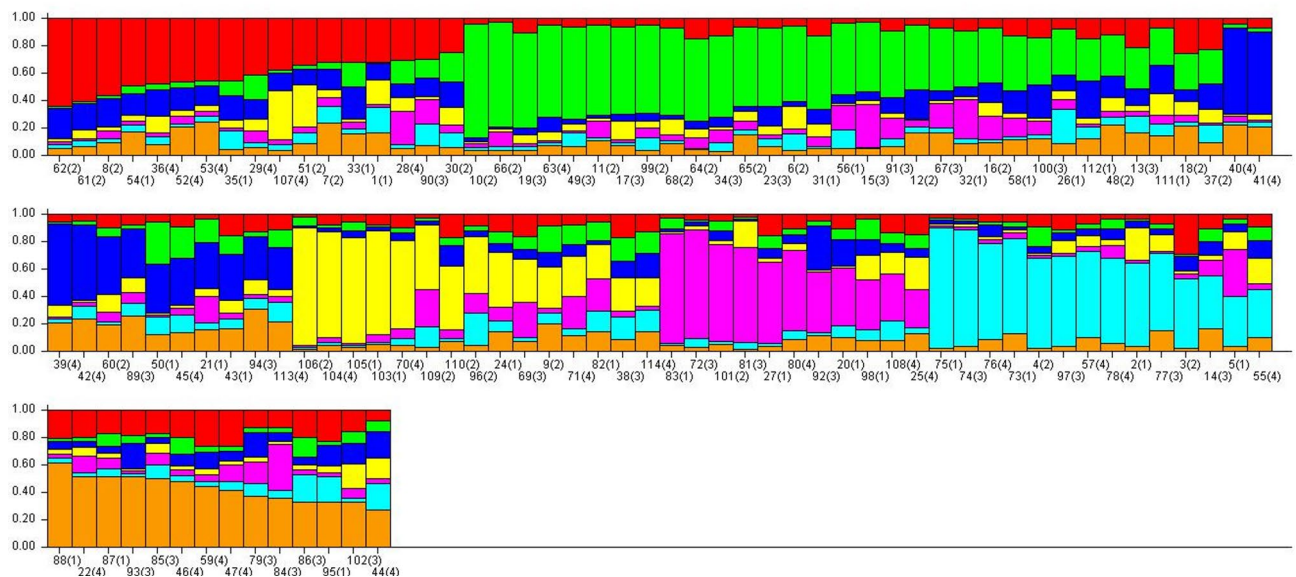


Fig.4. Population structure of 114 wild barley genotypes based on 35 microsatellite markers ($K=7$) using the bayesian model (Evanno Method). The vertical axis shows the coefficient of each person's belonging to each sub-population.

- Grain Yield (GY), Number of Seed Per Spike (NSPS), 100-Kernel weight (TSW), Plant Height (PH), Spike Length (SL), Xteragen Length (XL), Straw Yield (SY), Flag Leaf Length (FLL) and Awn Length (AL), Chlorophyll a (CHL a), Chlorophyll b (CHL b), Total Chlorophyll (CHL T) and Carotenoid (CAR).

The chromosomal positions of the SSR and EST-SSR markers analyzed in this study are illustrated in Fig. 5, with the corresponding agronomic and physiological traits indicated adjacent to each marker. Across both rainfed and irrigated environments, significant marker–trait associations were detected and distributed across all seven barley chromosomes (1–7 H). Under rainfed conditions, chromosome 2 H harbored WMC1E8, which was associated with spike length (SL), and BMAG0323, linked to relative water content (RWC). Chromosome 4 H contained EBMAC0273, associated with flag leaf length (FLL), while chromosome 5 H included BMAC0275 and EBMAC0775, both linked to straw yield (SY). Under irrigated conditions, chromosome 1 H carried GBM1110, associated with thousand-seed weight (TSW), whereas chromosome 3 H hosted BMAC0189, and chromosome 6 H contained EBMAC0415, both consistently linked to grain yield (GY). Notably, BMAG0323 (2 H) and BMAG0223 (7 H) were associated with RWC under both moisture regimes, indicating positional stability. Among all chromosomes, 2 H and 5 H showed the highest frequency of significant associations, suggesting their central role in controlling both yield components and physiological traits under contrasting water availabilities.

Discussion

The presence of various biological and non-biological stresses in cultivated areas in Iran underscores the importance of conservation and utilization programs for genetic diversity. Genetic diversity is essential for successful breeding, as the selection of superior genotypes within breeding populations depends on its presence²². This diversity has been developed over thousands of years and has remained stable, giving it superiority over artificial diversity. Based on significant differences in the mentioned traits, it can be concluded that the genotypes under study possess sufficient genetic diversity. This diversity enables the selection of superior genotypes based on these traits under drought stress conditions²³.

Genotype differences under favorable moisture conditions indicate the production potential in different genotypes, which can yield different performances depending on genotype capacity if suitable conditions are provided. Analyses of genetic diversity in wild barley defense genes have indicated greater variation in biotic stress-related genes compared to abiotic stress-related genes²⁴. This diversity is valuable for barley improvement, as it provides a rich source of genetic variations for breeding programs²⁵. A study conducted to evaluate agromorphological and physiological traits in wild barley (*H. spontaneum*) germplasm revealed a wide range of phenotypic expression for various traits, including days to spike emergence, plant height, spike length, spikelet triplet groups, 100-grain weight, total root length, and root dry weight²⁶.

According to the results of the analysis of variance, the studied traits are significantly influenced by moisture conditions, as both spatial and genotypic effects, as well as their interaction, have shown significant differences. Therefore, these traits can serve as criteria for selecting wild barley genotypes under rainfed conditions. Additionally, most of these traits have shown significant differences among genotypes under both rainfed and irrigated conditions. The composite variance analysis showed a significant effect of rainfed and irrigated conditions on the measured traits, and genotype responses in these two experimental environments were significantly different. These results indicate extensive diversity among wild barley genotypes in different moisture conditions, which can be utilized for selecting genotypes tolerant to drought stress and with higher

Rainfed					Irrigated				
Traits	R ²	p	F	Locus	Traits	R ²	p	F	Locus
GY	0.172	0.005	8.108	EBMAG0781	GY				
	0.146	0.025	5.170	BMAG0323		0.142	0.030	4.841	EBMAC0775
	0.146	0.025	5.154	SCSSR04163					
SL	0.169	0.006	7.737	WMC1E8*	SL				
	0.147	0.023	5.323	SCSSR15864		0.141	0.034	4.589	WMC1E8*
	0.141	0.035	4.550	GBM1461					
	0.135	0.049	3.980	SCSSR18076					
AL	0.160	0.011	6.775	EBMAC0521	AL				
	0.151	0.017	5.837	BMAG0323		0.153	0.016	5.978	BMAC0189
	0.144	0.028	4.975	GBM1126		0.143	0.029	4.866	EBMAC0415
	0.138	0.039	4.377	WMC1E8					
	0.137	0.043	4.190	BMAG0131					
FLL	0.159	0.012	6.546	SCSSR25691	FLL	0.157	0.013	6.450	BMAG0603
	0.148	0.023	5.341	EBMAC0775*		0.141	0.034	4.610	GBM1110
	0.141	0.035	4.548	HVLTTPPB		0.136	0.046	4.072	BMAC0189
	0.138	0.043	4.187	BMAG0692		0.136	0.047	4.021	EBMAC0775*
	0.137	0.044	4.161	EBMAG0781					
XL	0.145	0.015	6.065	EBMAC0521	XL	0.146	0.018	5.807	BMAG0603
	0.136	0.031	4.763	BMAG0323		0.136	0.034	4.586	EBMAC0674
	0.134	0.034	4.610	GBM1110		0.131	0.050	3.932	BMAG0603
	0.134	0.036	4.507	SCSSR05599					
NSPS	0.162	0.007	7.615	BMAG0131	NSPS				
	0.151	0.014	6.273	EBMAC0775					
	0.147	0.017	5.826	EBMAC0521					
	0.144	0.022	5.408	SCSSR15864		0.160	0.011	6.746	BMAC0189
	0.139	0.031	4.800	SCSSR25691					
	0.135	0.039	4.386	SCSSR25691					
	0.133	0.047	4.034	GBM1126					
SY	0.143	0.045	4.105	BMAC0273*	SY	0.141	0.035	4.540	BMAC0273*
	0.142	0.048	3.996	EBMAC0775*		0.140	0.036	4.494	BMAC0273
						0.139	0.040	4.318	EBMAC0775*
PH	0.171	0.006	7.912	HVLTTPPB*	PH	0.151	0.019	5.658	BMAG0508A
	0.148	0.023	5.347	SCSSR04163		0.149	0.021	5.504	WMC1E8
	0.144	0.028	4.976	EBMAC0775		0.139	0.039	4.349	BMAC0273
						0.139	0.040	4.341	HVLTTPPB*
TSW	0.193	0.002	10.289	SCSSR15864	TSW				
	0.189	0.002	9.778	SCSSR15864					
	0.174	0.005	8.159	BMAC0154		0.164	0.009	7.114	EBMAG0781
	0.152	0.019	5.685	BMAC0154		0.154	0.015	6.101	GBM1110*
	0.150	0.020	5.543	WMC1E8		0.144	0.028	4.943	EBMAG0781
	0.142	0.034	4.636	GBM1110*					
	0.137	0.047	4.045	EBMAC0775					
RWL	0.161	0.010	6.818	SCSSR04163*	RWL				
	0.151	0.019	5.663	BMAG0131		0.155	0.015	6.113	SCSSR04163*
	0.135	0.050	3.930	GBM1176					
RWC	0.150	0.017	5.909	BMAG0323*	RWC	0.189	0.002	10.066	BMAG0323*
	0.144	0.024	5.221	GBM1176		0.154	0.015	6.110	SCSSR25691
	0.135	0.044	4.143	BMAG0341					
CHL T	0.164	0.009	7.131	GBM1461	CHL T				
	0.152	0.019	5.718	EBMAC0415					
	0.148	0.023	5.341	BMAC0189*		0.151	0.018	5.801	BMAC0189*
	0.145	0.027	5.002	WMC1E8		0.144	0.027	5.054	SCSSR15864
	0.141	0.035	4.569	BMAG0341					
	0.139	0.040	4.309	BMAG0323					
Continued									

Rainfed					Irrigated				
Traits	R ²	p	F	Locus	Traits	R ²	p	F	Locus
CHL b					CHL b	0.160	0.010	6.803	BMAG0341
						0.160	0.011	6.736	GBM1110
	0.135	0.047	4.044	BMAG0692		0.159	0.011	6.706	GBM1126
	0.135	0.047	4.026	GBM1176		0.140	0.036	4.503	EBMAG0781
						0.139	0.037	4.441	BMAC0189
						0.135	0.048	3.988	SCSSR04163
						0.135	0.050	3.937	SCSSR15864
CHL a	0.152	0.008	7.278	BMAG0323	CHL a				
	0.142	0.018	5.790	GBM1126		0.134	0.048	4.015	SCSSR25691
	0.134	0.033	4.647	EBMAC0521					
CAR					CAR	0.148	0.021	5.522	EBMAC0775*
	0.161	0.011	6.732	EBMAC0775*		0.147	0.021	5.475	BMAG0692
	0.140	0.037	4.467	BMAC0273		0.142	0.030	4.846	BMAG0603
	0.140	0.037	4.463	GBM1212		0.142	0.030	4.832	EBMAC0054
	0.137	0.046	4.068	SCSSR05599		0.139	0.035	4.543	EBMAC0775
						0.135	0.047	4.029	BMAG0603

Table 5. Analysis of the relationship between SSR and EST-SSR markers and agro-morphological and physiological traits in rainfed and irrigated conditions using a mixed linear model (MLM). *: Common markers for the examined traits in both rainfed and irrigated conditions.

yields. As observed, the range of variations in all traits had a relatively high spectrum, indicating high diversity in terms of the studied traits among the studied genotypes. Given the high coefficients of variation for the studied traits and their importance in selecting superior genotypes, these traits can be considered valuable breeding resources. The evaluation of morphological diversity in wild barley (*H. spontaneum*) germplasm revealed significant variation in quantitative characters, including plant height, spike length, root length, grain width, number of grains per spike, grain length, number of leaves, and days for flowering²⁷.

The results showed significant differences in the performance of the best genotypes under rainfed and irrigated conditions. However, what was significant was the different grouping of genotypes for different traits under stress and non-stress conditions, indicating a different trend in genotype responses to different moisture conditions. The selection and separation of genotypes tolerant to stress are performed directly (performance measurement) and indirectly (based on morphological and physiological traits correlated with stress tolerance). Drought tolerance in a plant genotype is owed to a number of its physiological and morphological characteristics, and efforts are ongoing to identify effective criteria for selecting resistant genotypes. Hamza et al.²⁸ in examining the diversity among 26 winter barley genotypes in Tunisia, used 12 agronomic traits and conducted cluster analysis on traits and samples. Cluster analysis showed genetic similarity of *H. spontaneum* barley samples with their geographic success to some extent. In the study of Shakhaterh et al.²⁹ cluster analysis of wild barley samples also corresponded to their ecological and geographic patterns.

Relative leaf water content (RWC) has been introduced as an index to demonstrate damage caused by drought stress. Higher relative leaf water content increases photosynthesis and consequently enhances performance under stress conditions. Water deficiency reduces relative leaf water content and leaf water potential, leading to cellular dehydration, stomatal conductance, and photosynthesis reduction, thereby affecting growth and crop production. Therefore, this trait can be considered one of the best indicators of plant water status in selecting varieties under stress conditions³⁰. The results of the present study showed that the loss of plant water content under rainfed conditions is greater than under irrigated conditions, but the minimum amount of lost water under rainfed and irrigated conditions differs slightly, indicating resistance to water scarcity in genotypes. It can be said that the results obtained from the study of water loss depend on environmental conditions and genetic materials under study, and accordingly, the results of different studies have been different. Therefore, the maintenance and availability of water in these genotypes under moisture stress conditions are highly significant and directly affect performance.

Considering the obtained results, it is evident that drought stress causes a reduction in greenness in all genotypes, but the reduction in sensitive cultivars was greater than in tolerant varieties. Wild barley accessions have shown improved RWC percentages and reduced relative water loss (RWL) under drought conditions compared to cultivated barley, indicating their superior drought tolerance mechanisms³¹. Additionally, the application of biochar has been found to enhance RWC by up to 33% and reduce RWL by 54% in stressed barley plants, highlighting the potential of soil amendments in improving water retention and stress tolerance in crops³². These findings underscore the importance of monitoring RWC and RWL as indicators of drought stress responses and the potential for utilizing wild barley genetic resources to enhance drought tolerance in cultivated barley.

Chlorophyll maintenance is crucial under drought stress conditions in cereals, and drought-tolerant genotypes show less chlorophyll reduction compared to drought-sensitive genotypes. Moreover, under drought

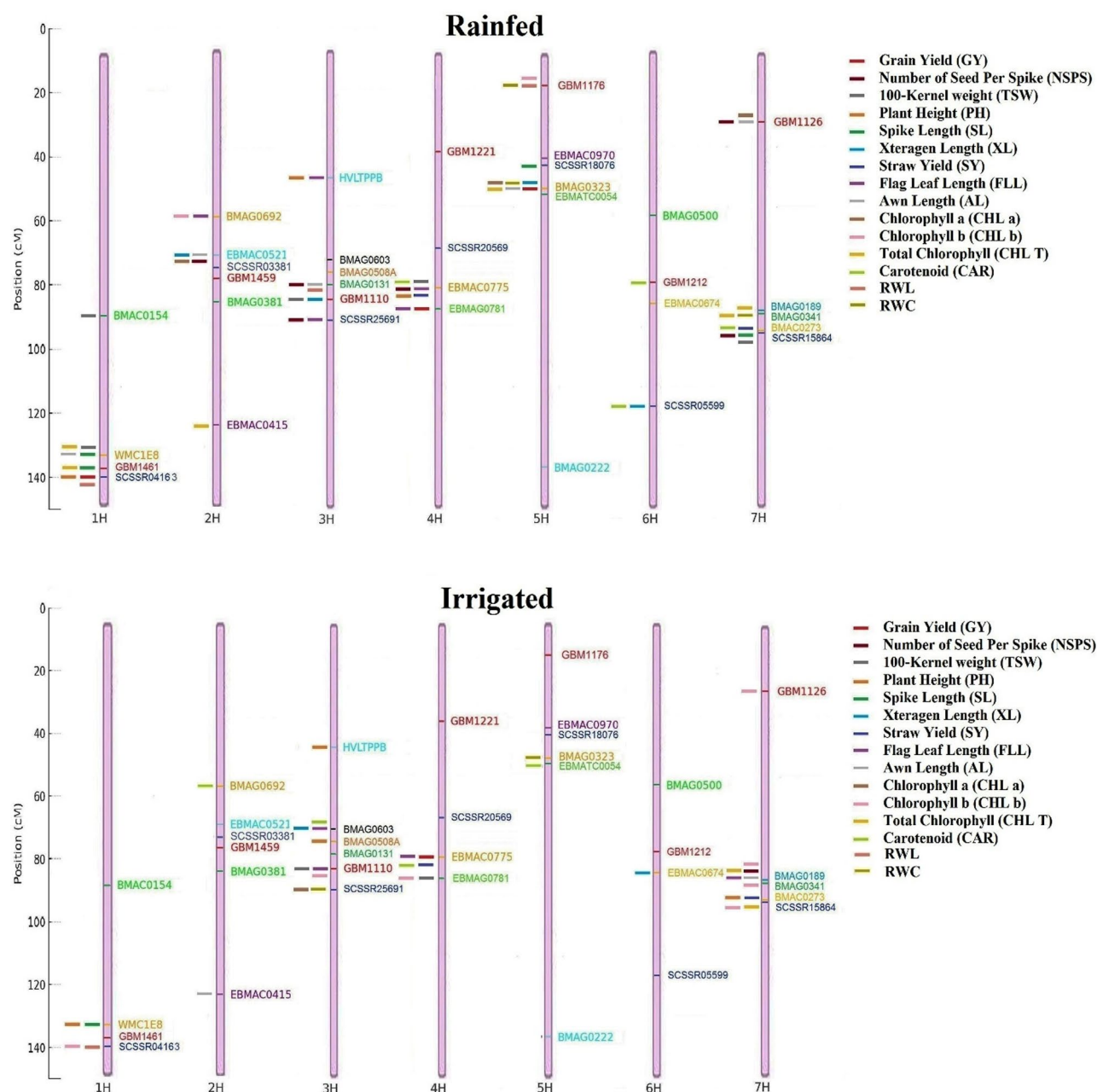


Fig.5. The chromosomal locations of the markers utilized and their associations with the evaluated traits under both rainfed and irrigated conditions are illustrated. This figure was generated using the ggplot2 package within the R programming environment, with marker position information obtained from the GrainGenes database (<https://wheat.pw.usda.gov/GG3/>).

conditions, a decrease in chlorophyll and carotenoids content has been observed, suggesting an adaptive response to minimize the formation of reactive oxygen species in photosynthetic membranes³³.

Association analysis of wild barley has been a topic of interest in recent literature. Wild barley has been identified as a valuable source of genetic variation for abiotic stress tolerance in crop improvement. Studies have shown that wild barley collections from various regions, particularly the Mediterranean, harbor genetic diversity that could be beneficial for developing stress-tolerant cultivars. Research has highlighted the importance of exploring the differences between wild barley and cultivated varieties to harness untapped genetic reserves³⁴. Furthermore, genetic strategies involving wild barley germplasm have been successful in identifying positive alleles for stress tolerance traits, such as drought tolerance, in barley³⁵. The use of wild barley in breeding programs has shown promise in introducing new disease-resistance genes and enhancing stress tolerance in cultivated barley³⁴.

Results have shown that based on LnP(D) and ΔK indices, the number 7 was identified as the best K. Based on the observed results, 114 barley genotypes studied were divided into seven families. Ferreira et al.³⁶

examined the genetic diversity of Brazilian barley (6 wild barley samples, 35 cultivars, and 16 breeding lines) using UPGMA clustering on traits and found that genotype grouping classified them into three groups. They also classified genotypes using Structure software and identified two subpopulations using the Evanno method. The first subgroup included wild barley and breeding lines, and the second subgroup included Brazilian barley with very low diversity.

Results of the correlation between morphological and physiological traits and 97 duplicated alleles under irrigated conditions showed that BMAC0189, BMAG0603, and EBMAC0775 had the highest correlation with five traits. Similarly, under rainfed conditions, BMAG0323, EBMAC0775, and GBM1126 markers had significant correlations with six traits. Common markers for some traits are likely due to chromosomal linkage controlling these traits or pleiotropy.

Wojcik-Jagla et al.³⁷ studied the mapping of trait associations related to drought tolerance in 109 spring barley genotypes and examined the associations between sequence-tagged sites (DARtseq) and single nucleotide polymorphisms (SNPs) with various physiological indices related to plant responses to drought stress. It was concluded that mapping associations could increase the density of existing QTL maps without reconstructing mapping populations. The examination of traits such as plant height (PH), yield, flowering time, grain weight, and grain protein content in a population composed of 770 barley lines showed that 91 QTLs controlled these traits³⁸. Abou-Elwafa³⁹ used association mapping to examine correlations between 76 SSR markers and six drought-related traits in a set of 107 barley evaluated under drought and irrigated conditions. Significant differences were measured between irrigated suitable and drought stress conditions for all traits, with a high level of polymorphism observed with SSR markers. A significantly positive correlation was found between several molecular markers and more than one phenotypic trait, indicating the possibility of polytropic effects or indirect effects. Association mapping using SSR markers in barley identified 51 chromosomal regions associated with performance traits, plant height (PH), and yield stability⁴⁰.

The chromosomal distribution pattern of marker–trait associations highlights specific genomic regions with potential importance for barley adaptation to different water regimes. Chromosome 5 H, with multiple loci (BMAC0275 and EBMAC0775) affecting biomass related traits, appears to be a hotspot for QTLs controlling vegetative growth and yield potential, particularly under rainfed conditions. Chromosome 2 H demonstrated dual functionality, carrying loci such as WMC1E8 and BMAG0323 that influence both agro-morphological (Spike Length) and physiological (RWC) traits, which may be linked to drought adaptive processes like improved water use efficiency and spike architecture optimization. The stability of associations for RWC related markers on 2 H and 7 H across environments indicates the presence of conserved drought responsive genes, possibly involved in osmotic adjustment or cell membrane stability. In contrast, loci like GBM1110 on 1 H and BMAC0189 on 3 H exhibited environment specific effects, being significant only under irrigated conditions, which suggests their role in optimizing performance under favorable growth circumstances. The identification of these chromosomal regions provides a targeted genetic framework for integrating stable and environment specific QTLs into breeding programs, enabling the development of barley genotypes with improved performance in both high input and water limited systems.

Conclusion

This study highlights the significant genetic diversity within wild barley (*H. spontaneum*) populations in western Iran and underscores the potential of these genotypes for improving cultivated barley varieties. Through comprehensive analysis of agro-morphological and physiological traits using SSR and EST-SSR molecular markers, several key findings and applications have emerged. Firstly, the identification of significant marker-trait associations provides valuable insights for breeding programs aimed at enhancing barley's resilience to abiotic stresses such as drought and salinity. Markers such as EBMAG0781, BMAG0323, and SCSSR04163, which showed strong associations with various traits, are particularly noteworthy for their potential use in marker-assisted selection (MAS) strategies. The genetic diversity observed in traits such as grain yield, plant height, and relative water content across different environmental conditions further emphasizes the adaptability and robustness of these wild barley genotypes. Additionally, the population structure analysis revealed the existence of seven subpopulations, indicating a rich genetic stratification that can be exploited for breeding purposes. The presence of significant genotype by environment interactions for most traits suggests that future breeding efforts should consider environmental specificity to maximize the expression of desirable traits. In conclusion, the genetic resources found in wild barley populations present a valuable opportunity for the development of high yielding, stress tolerant barley varieties. By leveraging the genetic diversity and marker-trait associations identified in this study, future breeding programs can significantly contribute to global food security and agricultural sustainability.

Materials and methods

Plant samples

This study was conducted on 114 genotypes of wild barley (*H. spontaneum*) collected from the western provinces of Iran, including 29 genotypes from Kermanshah, 28 genotypes from Kurdistan, 28 genotypes from Ilam, and 29 genotypes from Lorestan (Dr Ali Ashraf Mehrabi undertook the formal identification, the Ilam University gene bank code (IUGB), genotype numbers, locations/regions, and geographic coordinates can be found in the Supplementary Table S1) Voucher specimens of all 114 genotypes of *H. spontaneum* were deposited in the Ilam University Gene Bank (IUGB), which is a public collection providing access to deposited material. The experiment was carried out during the agricultural years 2020–2021 and 2021–2022 at the research farm of the Agricultural and Natural Resources Research Center of Kermanshah Province, located in the Mahidasht region.

Experimental design and agricultural operations

This research was conducted in an augmented design (augmented RCBD) with five blocks and nine control genotypes {Genotypes 1 (Kermanshah-Mahidasht), 24 (Kermanshah-Sarpol Zahab), 35 (Kermanshah-Harsin), 10 (Ilam-Ilam), 51 (Ilam-Mehran), 74 (Kurdistan-Kambaran), 34 (Kurdistan-Bijar), 104 (Lorestan-Kuhdasht), and 113 (Lorestan-Aligudarz)}. Each plot consisted of two three-meter rows with a row spacing of 50 cm. Sampling for measuring morphological and physiological traits was done considering the climatic conditions of the area, after pollination and ensuring the application of drought stress on the genotypes under study. In both drought-stressed and non-stressed conditions, the first rainfall was considered the planting date, and in drought stressed conditions, no irrigation was provided throughout the growth period. Drought stress intensity (SI) was calculated according to Fischer and Maurer⁴² as $SI = 1 - (YS/YP)$, where YS and YP are the mean yields under stress and non-stress conditions, respectively; the resulting value indicated a 33% yield reduction, corresponding to a moderate drought stress level. For recording observations, 20 plants were randomly selected from each genotype in each replication, considering the edge effect.

Location specifications

The field experiment was carried out at the Mahidasht Research Station, situated 20 km along the Kermanshah–Islamabad-e-Gharb road, at an altitude of 1,380 m above sea level (34°16' N, 46°50' E). According to the USDA Soil Taxonomy, the soil at the experimental site is classified as Fine, Mixed, Thermic, Vertic Calcixerepts, with a silty clay texture, indicating a heavy to very heavy soil class. Irrigation water quality corresponds to the C3–S1 class, and the long-term (10-year) mean annual precipitation is approximately 335 mm. Detailed physico-chemical properties of the soil, including texture, field capacity, and water-holding capacity, are provided in Supplementary Table S2. Climatic data for the 2020–2021 and 2021–2022 growing seasons were obtained from the Mahidasht Meteorological Station. The region is characterized by a semi-arid to sub-humid climate, and environmental variables were continuously monitored during the study period. Monthly patterns of temperature and precipitation, illustrating seasonal climatic fluctuations, are shown in Supplementary Figure S1. Prior to sowing, no basal fertilizer was applied. During the growing season, each plot received 50 g of urea fertilizer, and weeds were removed manually to avoid competition with the crop.

Traits studied in the field

The evaluated agronomic traits included grain yield (GY), number of seeds per spike (NSPS), 100-kernel weight (TSW), plant height (PH), spike length (SL), exaragen length (XL), straw yield (SY), flag leaf length (FLL), and awn length (AL).

Relative water content (RWC)

0.5 gr of the youngest fully developed leaf from each plant (FW) was separated, and then the samples were floated in distilled water for 4 h. After this period, the leaf pieces were gently dried with paper towels and immediately weighed to obtain the turgid weight (TW). The leaf pieces were then dried in an oven at 70 degrees Celsius for 48 h to obtain the dry weight (DW). RWC was calculated using the following formula:

$$RWC\% = \left[\frac{(FW - DW)}{TW - DW} \right] \times 100 \quad (1)$$

Relative water loss (RWL)

For this trait, 5 flag leaves were randomly selected from each genotype in each replication during the flowering stage and immediately weighed. The weighed samples were placed at 35 degrees Celsius for 4 h to obtain the wilting weight. Finally, to obtain the dry weight, the samples were placed in an oven at 72 degrees Celsius for 24 h and then weighed. The water loss was calculated using the following formula:

$$RWL\% = \left[\frac{(FW - F4h)}{FW - DW} \right] \times 100 \quad (2)$$

Determination of chlorophyll a, b, total chlorophyll, and carotenoid concentrations

0.25 gr of dry leaf powder was weighed with a digital scale with an accuracy of 0.0001 gr and placed in capped tubes. Five milliliters of 99.5% methanol were added. The samples were kept in the dark for 2 h, then shaken to homogenize the solution and centrifuged for 10 min at 10,000 rpm. The absorbance of the supernatant was read at 650, 665, and 470 nm using a spectrophotometer, and the concentrations were calculated using the following formulas⁴³:

$$\begin{aligned} \text{Chlorophyll a (mg/mL)} &= 16.5 \times A_{665} - 8.3 \times A_{650} \\ \text{Chlorophyll b (mg/mL)} &= 33.8 \times A_{650} - 12.5 \times A_{665} \\ \text{Total Chlorophyll (mg/mL)} &= 25.8 \times A_{650} + 4.0 \times A_{665} \\ \text{Car} &= (1000 A_{470} - 3.27 [Chl a] - 104 [Chl b]) / 227 \end{aligned}$$

Statistical analysis of morphological and physiological studies

Variance analysis with five replications and nine control genotypes for two years in two environments (rainfed and irrigated) was performed using SPSS.22 software for agro-morphological and physiological traits, and mean

comparisons were made using the LSD method at the 5% and 1% levels. Cluster analysis using the Ward method was also performed for the traits using ClustVis software⁴⁴.

Genotypic evaluation

DNA extraction was performed using the modified CTAB method⁴⁵ for each population. The quality and quantity of the extracted DNA were assessed using 0.8% agarose gel electrophoresis and a spectrophotometer. Polymerase Chain Reaction (PCR) was carried out in a 20 µl volume (50 ng template DNA, 2 mM MgCl₂, 0.05 mM of each dNTP, 0.2 µmol primers, one unit Taq DNA Polymerase enzyme, and 1x reaction buffer). The thermal cycle included an initial denaturation at 95 degrees Celsius for 5 min, followed by 35 cycles of 30 s at 95 degrees Celsius, 30 s at a primer-specific annealing temperature (52 to 60 degrees Celsius), and 60 s at 72 degrees Celsius. A final extension was done for 5 min at 72 degrees Celsius. A 4% agarose gel with 1X TBE reaction buffer was used in this experiment. The Quantum ST4 Gel Document device was used to visualize the DNA bands.

Population structure and association analysis

The genetic structure of the evaluated barley genotypes was characterized using a Bayesian model-based clustering strategy implemented in STRUCTURE software version 2.3.4⁴⁶. Thirty-five polymorphic SSR primers (primer sequences provided in Supplementary Table S3) were employed, with chromosomal positions obtained from the GrainGenes database (<https://wheat.pw.usda.gov/GG3/>) based on established barley linkage maps^{41,47}. The number of possible genetic clusters (K) was explored within a range of 1 to 10. Each K value was analyzed in five independent runs under an admixture model with independent allele frequencies. A burn-in phase of 10,000 iterations was followed by 100,000 Markov Chain Monte Carlo (MCMC) replications to ensure likelihood convergence. The Q-matrix generated by STRUCTURE quantified the proportion of each genotype's genome assigned to each inferred cluster. A genotype was classified into a specific subpopulation if its membership coefficient (Q value) was ≥ 0.70 ; otherwise, it was considered admixed⁴⁸. The most likely number of subpopulations was determined by examining the posterior probability [LnP(D)] across K values, as well as applying the ΔK method of Evanno et al.⁴⁹, which identifies the optimal K through the second-order rate of change in LnP(D).

Marker-trait association (MTA) was evaluated using a Mixed Linear Model (MLM) in TASSEL version 3.0. Quality control procedures included removal of genotypes with excessive missing data, exclusion of alleles showing poor amplification, and elimination of markers with a minor allele frequency (MAF) below 5%. Hardy-Weinberg equilibrium (HWE) testing and linkage disequilibrium (LD) analysis were also conducted in TASSEL. To correct for population structure and relatedness, both the Q-matrix from STRUCTURE and the kinship matrix (K-matrix) from TASSEL were included in the MLM (Q + K) framework. This approach reduced the risk of spurious associations while improving detection power.

Marker positions were expressed in centimorgans (cM) and visualized as chromosome maps generated using the ggplot2 package in R, allowing precise graphical representation of marker distribution for interpretation of MTA results.

Data availability

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

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Author contributions

All authors contributed to the study conception and design. Material preparation, Investigation, Methodology, Data curation, Formal analysis, Visualization, Validation, Software, Writing – original draft [Hoosman Shirvani], Investigation, Methodology, Data curation, Formal analysis, Visualization, Validation, Software, Writing – original draft [Ali Ashraf Mehrabi], Supervision, Funding administration, Writing – review & editing [Mohsen Farshadfar], Supervision, Writing – review & editing [Hooshmand Safari], Supervision, Writing – review & editing [Ali Arminian] and Supervision, Writing – review & editing [Foad Fatehi].

Declarations

Competing interests

The authors declare no competing interests.

Ethics approval

This study focused exclusively on plant research and did not involve any human or animal subjects. As a result, it did not require approval from an ethics committee. The research adhered to all applicable guidelines and regulations for plant studies to ensure ethical and responsible conduct of the research.

Additional information

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1038/s41598-025-22401-8>.

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