



ABSTRACT

Barley (*Hordeum vulgare* L.) is an important winter cereal crop in Albania. A total of 20 accessions of barley part of base collection of Albanian Gene Bank, were object of the study for agro/morphological characteristics in Experimental field of Agriculture University in Tirana. Data on 16 traits (five quantitative and 11 qualitative) were recorded to assess diversity among the accessions. A range of variability was observed among the barley varieties for plant height trait (with an average of 102.2 cm), AGB 2326 resulted with the lowest value for spike length (± 6.1 cm), AGB 2328 was the accession with the higher number of spikelet per spike recorded (± 34.1). Morphological variation was observed for spike density, rachilla hair length, kernel covering, lemma colour, 1000-grain weight trait, etc.

INTRODUCTION

Albania is an area rich in crop biodiversity, it is characterized by a high diversity of climatic and agronomic conditions. Barley (*Hordeum vulgare* L.) is one of the old winter cereals crop in our country, utilized for various purposes such as food, beverages and livestock feed. Based on the ability to tolerate cold climate the crop serves as an indicator of well-being on the community of remote area. Barley is considered as one of the cereals with the most diversified genetic basis [4]. Morphological characterization is the foundation of genetic diversity research at any taxonomic level [6]. Genetic variability evaluation based on morphological characters of economic interest might be used to choose suitable materials in breeding programs for crop improvement. Also, in comparison to biochemical traits, morphological traits had crucial role in genetic study due to the ease of their identification, and their simple mode of inheritance in comparison to quantitative traits. For that reason, markers to describe genetic diversity are morphological and agronomic traits celebrated as descriptors and presented by the International Plant Genetic Resources Institute (IPGRI). Agro-morphological characterization is still an important tool for the management of crop germplasm collections [3], [2] having been used to identify duplicates, to establish core collections, to investigate relationships between landraces and their wild, and to prioritize material for use in breeding programs. The characterization of accessions allows quantification and structuring of the genetic variability in the germplasm which is highly important for improvement programs and for the conservation and preservation of genetic diversity. To characterize a germplasm basically means to identify and describe differences between the accessions. Besides the information on the origin of the material (passport data) differences related to the agricultural performance of the accessions are normally also considered as well as botanical differences related to normally taxon-specific descriptors. Therefore a total of 20 barley accessions were planted under field condition and their agro morphological characters (5 quantitative traits) such as, plant height, spike length, 1000 kernel weight, days to maturity were recorded to evaluate morphological diversity.

MATERIAL AND METHODS

Plant Materials: Our study is based on the characterization of the diversity of 20 barley accession (*Hordeum vulgare* L.) part of the base collection of Albanian Gene Bank (Agriculture University of Tirana, Table 1).
Experimental site: The study was conducted in the Experimental Station of Institute of Plant Genetic Resources, Valias, Agriculture University of Tirana. It lies at an altitude of 40 m above sea level and at Latitude $41^{\circ}24'6.14''N$ and Longitude $19^{\circ}44'9.93''E$.
Methods (Experimental Design): The plant material is characterized by a survey on land and laboratory, during the year 2016-2017 in the experimental field, Valias of the Agricultural University of Tirana. Each accession was planted in 1 m long plot with a between-row spacing of 25 cm. Fertilizer was broadcast on the plots at the rate of 400 kg ha⁻¹, N.P.K. 8:16:20. At physiological maturity, seeds were harvested and after they were cleaned for analysis. During the crop year, the accessions were evaluated using 5 characters of quantitative type. These characters were: plant height (PH), Tillers per Plant (TP), Spike Length (SL), Number of Spikelet per Spike (NSpSp) and Weight of 1000 Seeds (WS). Part of the field survey were phenotypic traits as: number of days from sowing to germination (SG), number of days from germination to spikelet (GSpk), days from germination to flowering (GF), number of days from germination to maturity (GM). Morphological characterization of the accessions was conducted according to international standards, particularly those of the IPGRI [7].
Statistical analyses: Statistical tests were carried out by the Statistical Package for Social Sciences (version 21) and JPM. Analysis of variance (ANOVA) was used to calculate variation among accessions, using the JPM software. Hierarchical Ascendancy Classification (HAC) or cluster analysis, was used to calculate the mean data of accessions using the SPSS software to better classify the 20 accessions of barley. Principal components analysis (PCA) was carried out on the correlation matrix calculating the mean data of the accessions.

RESULTS AND DISCUSSIONS

Simple statistical analysis of the observed data showed a range of variability among the accessions of barley. The differences with high range and diversity indices were observed in Plant Height trait (82.6-117.9 cm), spike characters such as Spike Length (6.1-13.73 cm), and 50% of flowering days (135-153) in quantitative traits. The 20 accession of barley also showed variability in Number of Spikelet per Spike and Weight of 1000 grain (40.5-54.3g) traits (Table 1). Among the accessions AGB 2273 and AGB 2278 resulted with the lowest value for days to maturity (185). We observed the lowest value for days to germination (58) and days to spikelet formation (81) at AGB 2274. Barley genotypes AGB2274, AGB2275, AGB2277, AGB2297, AGB2325, AGB2326, AGB2327 presented all the same number of days to flowering (153 days). In the present study we found that 10% of the plants have green stem pigmentation (Table 2) and 45% of them were purple (basal only), spike density was 5% for dense, 45% intermediate in agreement other authors [6,1].
Hierarchical clustering data: A pair wise association among accessions of barley was measured from the observed agro-morphological traits using Ward and Euclidean distance and revealed a clear clustering into different morphological groups (Table 3). The nearest neighbours clustered together with the lowest dissimilarity level (0.54) between them are AGB 2277 and AGB 2275. These two genotypes are fully similar for trait as TP and WS. Accessions AGB 2280 and AGB 2278 part of 5 accessions grouped in cluster II, are considered as neighbours in trait as NSpS and WS but different in other traits. The dissimilarities with the other genotypes are based in the highest values for quantitative descriptors as TP (± 4), NSpS (± 43.1). Accessions of the last cluster AGB 2325 and AGB 2327 have short distances in similarity basically on TP trait. AGB 2327 accession presented the highest value among the 20 barley genotypes part of the study, with the highest value of WS trait ($\pm 54.3g$).

Table 1. Data of quantitative traits characterization in twenty barley accessions

Accession code AGB	Quantitative traits								
	PH/cm	TP	SL/cm	NSp	WS/g	SG	GSp	GF	GM
2273	97.4	3.3	8.27	31.9	40.76	61	86	142	185
2274	99.9	2.6	8.35	25.9	50.43	58	81	153	188
2275	98.9	2.9	8.15	28	49.3	61	93	153	188
2276	105	2.9	10.52	27.4	50.1	61	86	153	188
2277	107.8	2.8	10.71	32.3	50.4	61	86	153	188
2278	107.4	2.6	11.87	32.6	40.9	61	94	142	185
2279	112	2.5	13.73	31.8	50.4	61	94	142	188
2280	111.8	2.8	10.59	32.6	40.8	61	94	142	193
2281	82.6	2.8	8.56	27.3	40.5	61	86	135	186
2282	98	2.6	9.18	28	44.7	61	94	135	186
2283	116.5	3.7	9	28.1	52	61	94	135	186
2295	106.5	3.5	9.8	29.6	46	61	94	142	188
2296	88.3	3.6	9.4	26.6	50	61	86	142	188
2297	109	3.7	11	28.4	53	61	86	153	188
2298	117.9	3.8	12	31.4	54.1	58	81	142	188
2325	93.5	3.8	7.25	17.1	50	58	81	153	193
2326	89	3.7	6.1	17.2	53.7	61	81	153	193
2327	96.3	3.8	7.65	18.2	54.3	61	86	153	193
2328	114	4	11.9	34.1	53	61	88	135	188
2329	92.2	3.3	7.6	29.4	50	61	86	142	196

Table 3. Composition and characteristics of clusters based on five quantitative ob-

Cluster	Nr. of accessions	Cumulative characteristics of accessions in clusters
I	8	Tillers per Plant and weight of 1000 seeds
II	5	Plant Height, Number of Spikelet per Spike & Weight of 1000 seeds
III	4	Tillers / Plant, Spike Length & Number of Spikelet / Spike
IV	3	Tillers per Plant, Number of Spikelet per Spike



Figure 1. Barley accessions at the experimental site of AUT, Valias, Tiranë.

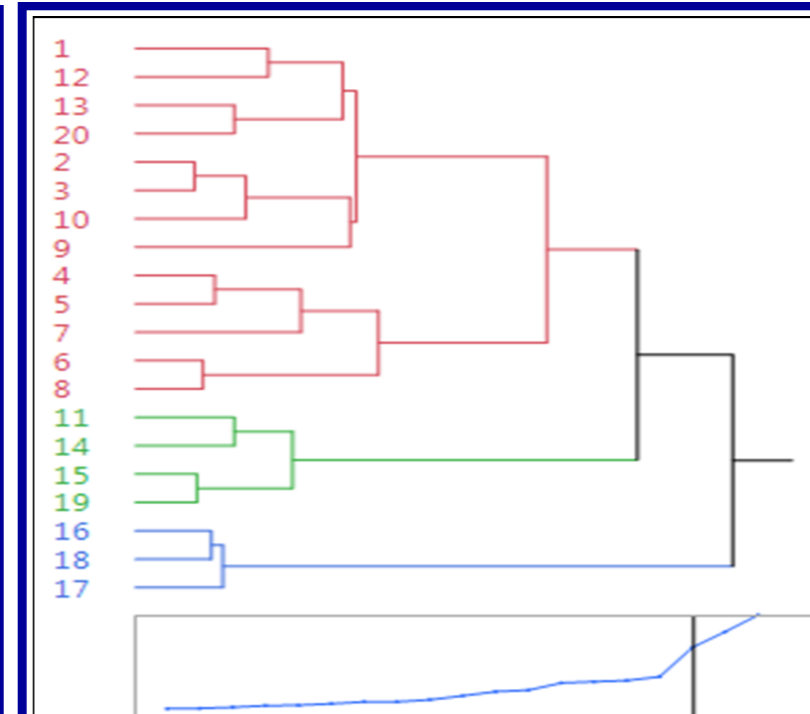
Table 2. Percentage of Phenotypic classes of the qualitative characters

Characters	No. Class	Code	Classes	Frequency distribution
Growth habit	3	3	Prostrate	0
	5	5	Intermediate	0
Stem pigmentation	7	7	Erect	100%
	1	1	Green	10%
	2	2	Purple (basal only)	45%
Spike density	3	3	Purple (half or more)	45%
	1	1	Lax	50%
	2	2	Intermediate	45%
Hoodedness/awnedness	3	3	Dense	5%
	1	1	Awn less	0
	2	2	Awnleted	10%
	3	3	Awned	90%
	4	4	Sessile hoods	0
Lemma awn bar	5	5	Elevated hoods	0
	3	3	Smooth	10%
	5	5	Intermediate	30%
	7	7	Rough	60%
	Glume and glume awn	5	1	Length of glume &awn shorter
2		2	Length of glume &awn as long	55%
3		3	Glume plus awn longer than	0
4		4	Glume plus awn nearly twice as	0
Glume color	5	5	Lemma like	0
	4	1	White	0
	2	2	Yellow	90%
	3	3	Brown	10%
	4	4	Black	0
Length of rachilla hairs	2	1	Short	70%
	2	2	Length	30%
Kernel covering	3	1	Naked grains	0
	2	2	Semi-covered grain	0
	3	3	Covered grains	100%
Grain color	3	1	white	0
	2	2	Tan/red	80%
	3	3	Purple	20%
Aleurone color	2	1	White	95%
	2	2	Blue	5

PCA on correlations of quantitative morphological and agronomical traits identified the variances of the principal components (PC) and the proportion of the total variance accounted for by each factor (Table 4). All quantitative variables contribute to 100% of total variation. The first two PCs explain 82.8% > 65.0% and about equal to 70% of the total variation, acceptable for evaluation and characterization of ex situ collections in gene bank. The traits with more significant weighting on respective PC variance can be utilized successfully as quantitative markers for evaluation, characterization and classification of the germplasm & plant breeding programs.

Table 4. Eigen values matrix of principal components analyzed

Nr.	Eigenvalue	Percent	Cum Percent	Chi Square	DF	Prob>ChiSq
1	2.5029	50.057	50.057	45.841	9.250	<.0001*
2	1.6405	32.810	82.867	27.814	8.108	0.0006*
3	0.4630	9.261	92.128	4.396	5.489	<.0001*
4	0.2173	4.346	96.474	0.169	1.961	<.0001*
5	0.1763	3.526	100.000	0.000	0.008	<.0001*



Plant height and Tiller per Plant were the most important traits contributing to the first principal components. Spike Length and grain weight were the important traits contributing to the second and third principal component. Scattered plot (Fig. 2) of these genotypes clearly indicated that there is presence of variability.

Figure 2. Dendrogram and Scattered plot 3D of 20 barley genotypes.

CONCLUSIONS

Among *Hordeum vulgare* L. genotypes object of this study, differences exist in phenotype and this suggest differences in genetic makeup. The differences with high range and diversity indices were observed in trait as Plant Height (82.6-117.9 cm), Spike Length (6.1-13.73cm), and 50% of flowering days (135-153) in quantitative traits. The 20 accession of barley also showed variability in number of spikelet per spike and weight of 1000 seeds (40.5-54.3g) traits. Among the accessions AGB 2273 and AGB 2278 resulted with the lowest value for days to maturity (185). We observed the lowest value for days to germination (58) and days to spike formation (81) at AGB 2274. The study identified the agronomical traits with more significant weighting on PC variance (PH & SL significant at the probability $F < P(0.01)$). The significant differences found in the present study show the existence of a genetic variability among the barley genotypes and quantitative traits analysed, sufficient for selection of desirable traits, and creation of new favourable gene combinations. This work has been a contribution to increase the knowledge about the barley germplasm conservation in Albanian Gene Bank (AUT). This better understanding should allow a better conservation and use of the collection in breeding programs. The research will also assist in the conservation of valuable germplasm, as is the case of local varieties.

LITERATURE

- Asfaw Z: The barleys of Ethiopia. In Stephen B.Brush (eds.) Genes in the field: on farm conservation of crop diversity 2000, 77- 108.
- Annicchiarico P, Pecetti L: Morpho-physiological traits as descriptors for discrimination of durum wheat germplasm. Genet. Resour. Crop Evol. 1994, 41:47-54.
- Ariyo OJ: Genetic diversity in West African okra (*Abelmoschus esculentus* L. (Chev.) Stevels): Multivariate analysis of morphological and agronomic characteristics. Genet. Resour. Crop Evol. 1993, 40:25-32.
- Baik BK, Ullrich SE: Barley for food: characteristics, improvement, and renewed interest. J. Cereal Science 2008, 48(2): 233-242.
- Bode D, Elezi F, Gixhari B: Morphological characterization and relationship among descriptors in *Phaseolus vulgaris* L. accessions. Agriculture and Forestry 2013 (59): 175-185.
- Chandran K, Pandya SM: Morphological characterization of *Arachis* species of section *Arachis*. Plant Genet. Resour. Newsl. 2000, 121:38-41.
- Chiorato AF, Carbonell SAM, Colombo CA, Dias LAS, Moura R, Chiavogato MB, and Colombo CA: Identification of common bean (*Phaseolus vulgaris*) duplicates using agronomical and molecular data. Journal of Genetics and Molecular Biology 2006, 29 (1): 105-111.
- Derbey Sh, Mohammed H, Urge E: Phenotypic diversity of qualitative traits of barley (*Hordeum vulgare*) landraces collections from south Ethiopia. International Journal of Science and Research 2003: 34-40.
- IPGRI: Descriptors for barley (*Hordeum vulgare* L.). International Plant Genetic Resources Institute - Rome, Italy 1994.