

Qualitative traits variation in barley landraces (*Hordeum vulgare* L.) from Algeria using Shannon-Weaver diversity index

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Abstract

Variations in useful barley botanical traits are very important among others for improvement and food security. This study was done on 29 Algerian barley landraces from Sahara in presence of four controls and aimed to evaluate the variability among these barley genotypes through nine descriptive traits using Shannon-Weaver diversity index (H').

Results showed a great variation existing within the landraces for the majority of the traits studied. Indeed, high values of Shannon-Weaver diversity index were obtained for the curvature of first rachis segment (0.99), the pigmentation of awn tips (0.95), length of rachilla hair in grain (0.88), the disposition of lodicules in the fertile grain (0.85), lemma awn barbs (0.76) and spike density (0.61). H' was intermediate for lemma type in grain (0.55) and was low for the glume length compared to grain and for the spike shape (0.33 and 0.44 respectively).

The high diversity found for some important botanical traits related to seeds and spikes among barley cultivars open large perspectives for breeding programs on this germplasm and is beneficial for conservation, resiliency and for adapting to environmental variations especially those related to climate change.

Key words: barley; diversity; resilience; botanical traits

INTRODUCTION

Barley (*Hordeum vulgare* subsp. *vulgare*) is one of the major cereals worldwide and is among the oldest domesticated crops (Jakob et al., 2014) playing a significant role in the development of agriculture (Ullrich, 2011). It is grown in a wide eco-geographic range around the world and is thus one of the best-adapted crops to diverse cultivation conditions (Usabaliev et al., 2013).

The primary gene pool of barley includes elite breeding materials, cultivars, landraces and the wild ancestor of cultivated barley, *H. vulgare* ssp. *spontaneum* (Von Bothmer et al., 2003). Barley, *Hordeum vulgare* L., comprises the two subspecies, *vulgare*

and *spontaneum* (C. Koch) Thell. (Von Bothmer et al., 1995).

Genetic diversity is one of the fundamental requirements for plant breeding (Ramanujam et al., 1974) and is strategic for mitigating production risk and protecting food security in resource farming systems (Abay et al., 2009). Summary measures of genetic diversity in cultivated plants and their wild relatives are need to guide managerial decisions, to monitor progress and to warn of emerging problems in agricultural production (Brown, 2008).

The bulk of genetic diversity in domesticated species is located in traditional varieties maintained by traditional farming systems. These traditional varieties, commonly referred to as landraces are

severely threatened by genetic extinction primarily due to their replacement by modern genetically uniform varieties (Villa et al., 2005). The genetic uniformity of current cultivars, due to decades of breeding with elite materials, may lead to greater vulnerability to the negative effects of climate change and it will limit future genetic gains (Geps, 2006). Being one of the most widely adapted crops the barley germplasm pool has the potential to contain enough genetic diversity to breed for adaptation to different environmental conditions (Muñoz-Amatriaín et al., 2014).

Mengistu et al. (2015) reported that crop landraces are described as geographically or ecologically distinct populations that show conspicuous diversity in their genetic composition and display genetic variation for useful quantitative and qualitative characters.

Evaluating genetic diversity in cultivated plants for plant breeding programs and heritable resources protection has a vital usage (Khajavi et al., 2014). Use of crop diversity is one of several approaches to improving agricultural productivity and is a key to achieving global food security (Tilman et al., 2001). In addition and according to Assefa et al. (2010), knowledge of genetic diversity in the crop gene pool is central to the development of effective *ex situ* and *in situ* germplasm conservation strategies.

The Shannon-Weaver Diversity Index (H') has been commonly used in measuring the diversity of germplasm collections and diversity in ecological communities (Jain et al., 1975). Many indices of diversity have been proposed, but the one most commonly used is the Shannon-Weaver diversity index H' (Sarma & Das, 2015).

In Algeria, works relating to the evaluation in particular of the diversity of qualitative traits in local barley resources is greatly limited at few research works like those of (Rahal-Bouziiane, 2006; Rahal-Bouziiane et al., 2015; Taibi et al., 2019) and must therefore to be expanded by new investigations for a better knowledge and protection of the existent germplasm.

This study aimed to evaluate the diversity of qualitative traits related to spikes and grains among barley landraces from arid and semi-arid regions of Algeria using the Shannon-Weaver Diversity Index (H') for contribution of enrichment of the database existing on this strategic species at local and global levels.

MATERIAL AND METHODS

Plant materials and experiment design

Twenty nine barley landraces from Saharan regions and four controls (Table 1) were considered in this study conducted at the Algerian National Institute of Agricultural Research (INRAA) of Baraki (Algiers) situated in the plain of Mitidja which is a rainy sub-humid region with an average rainfall exceeding 500 mm (Latitude: 36, 68; Longitude: 3, 11; altitude: 18m).

Cultivation trial was carried out during 2011/2012 season and sowing date occurred on December 8, 2011. Taken without irrigation and fertilization, the experiment design with three homogenous plots was completely randomized. Rows were 4.80 m each with spacing of 40 cm between themselves. With 25 seeds by row, the distance between plants was 20 cm. The texture of the soil was a sandy clay loam texture with an alkaline pH around 7.5 and a low electrical conductivity of 0.17 dS / m.

Nine qualitative traits were recorded and are reported on table 2. A great random sampling was done for each qualitative character and consisted of 30 observations per trait and per cultivar. Characters studied were determined basing on descriptors of Della (1985) and IPGRI (1994). Some characters were observed visually and others under a binocular magnifier or stereomicroscope.

Statistical analysis

To estimate the diversity among the genotypes via qualitative traits, the Shannon diversity index (H') was calculated using the Shannon-Weaver equation reported in Hennink & Zeven (1991):

$$H' = - \sum_{i=1}^n pi \ln pi$$

Where n is the number of phenotypic classes for a character and pi is the proportion of the total number of entries consisting of the i^{th} class.

To express the values of H' in the range of 0-1, each value of H' was divided by $\ln n$ (where $\ln n$ represents the natural logarithm of (n)).

$$H' = \frac{H}{H_{max}}$$

$$\text{And } H_{max} = \ln(N)$$

The nine qualitative traits were designed in classes by using the descriptors for barley by Della (1985) and by IPGRI (1994).

Table 1. List of 33 barley genotypes evaluated, local appellation and geographical origin

Genotypes	Local appellation	Geographical origin
1	-	Biskra: Southeast of Algeria. Low Sahara.
2	Azrii	Adrar (Tsabit Ksar Oudjlane): South-West of Algeria.
3 (Barberousse*)	Hamra	France
4	Bourabaa	Adrar (Tsabit Ksar Hammad) South: West of Algeria.
5	Chair de Sebseb	Ghardaïa (SebsebM'Zab): Low Sahara.
6 (Pané*)	-	Spain
7	-	Biskra: Southeast of Algeria. Low Sahara.
8	-	El Bayadh(High steppe plains) : South-West of Algeria
9	-	Biskra: Southeast of Algeria. Low Sahara.
10	-	Biskra: Southeast of Algeria. Low Sahara.
11	-	Ouargla: Southeast of Algeria. Low Sahara
12	-	Ouargla: South-East of Algeria. Low Sahara
13	-	El Bayadh(High steppe plains) : South-West of Algeria
14 (2 row)	-	Béchar: South-Western of Algerian Sahara
15	-	Béchar: South-Western of Algerian Sahara
16	-	Biskra: South-East of Algeria (Low Sahara)
17	Chair de Meggarine	Touggourt (Haut Oued Righ – Ksar Meggarine): Southeast of Algeria. Low Sahara.
18	Chair de Blidet Ammour	Touggourt (Haut Oued Righ – Blidet Ammour): Southeast of Algeria. Low Sahara.
19	-	Touggourt (Haut Oued Righ – Temacine): Southeast of Algeria. Low Sahara.
20	Ras El Mouch	Adrar (Tsabit): South-West of Algeria.
21	Safira Hammad	Adrar (Ksar Hammad): South-West of Algeria.
22	Safira Oudjlane	Adrar (Tsabit Ksar Oudjlane): South-West of Algeria.
23 (Saïda*)	Saïda	Algiers. ITGC
24	Selt	Adrar (Ksar Ouled ALI): South-West of Algeria.
25	-	Touggourt (Haut Oued Righ – Temacine): Southeast of Algeria. Low Sahara.
26	Chair Beldi	Touggourt (Haut Oued Righ – Zone Goug): Southeast of Algeria. Low Sahara.
27	Chair El Arbi	Touggourt Haut Oued Righ – Zone Nezla): South-East of Algeria. Low Sahara
28	-	Tamanrasset (Izernenne): Central Sahara of Algeria
29	-	Tamanrasset (In Dalegue): Central Sahara of Algeria
30	-	Tamanrasset(In Amguel): Central Sahara of Algeria
31	-	Tamanrasset (In Dalegue): Central Sahara of Algeria
32	-	Tamanrasset (Tahifet): Central Sahara of Algeria
33 (Tichedrett*)	Tichedrett	Algiers. ITGC

* Barberousse (3), Pane (06), Saïda (23) and Tichedrett (33) are the four controls

RESULTS

For the qualitative traits studied (table 3), the highest Shannon-Weaver diversity index was obtained for the curvature of first rachis segment (0.99) followed by the pigmentation of awn tips (0.95). Also, length of rachilla hair, disposition of lodicules in the fertile grain, lemma awn barbs and spike density presented high values of

H' (0.88, 0.85, 0.76 and 0.61, respectively). The glume length compared to grain and the spike shape presented the lowest H' (0.33 and 0.44, respectively).

In spike, the parallel shape and the very lax density were dominant with proportions of 90.9 % and 72.73 % respectively (table 3). The curvature of first rachis segment showed the greatest proportion for the strong phenotypic class with proportion of 55 %.

Table 2. Qualitative traits scored and their description

Characters	Description
Spike Shape	Is observed in drought stage and can be: tapering, parallel or fusiform
Spike density	Related to the importance of the spaces between the spikelets and can be: lax, intermediate or dense
Lemma awn barbs	Barley awns may be with or without denticulate margins. Awns with denticulate margins are rough, smooth or intermediate
Pigmentation of awn tips	The tip of the barbs is either strongly, moderately or weakly pigmented
Curvature of first rachis segment	The curvature can be weak or medium or strong
Glume length compared to grain	Length of glume and awn can be shorter than kernel; length of glume and awn can be as long as kernel or Glume plus awn longer than kernel
Lemma type in grain	Can be: no lemma teeth ; lemma teeth or lemma hair
Length of rachilla hairs (grain)	The hair is either short or long
Disposition of lodicules in the fertile grain	The lodicules can be frontal or clasping

Table 3. Morphological qualitative traits studied, respective classes, percentage of entries for each phenotypic class and mean diversity index (H') for each trait.

Morphological traits	Phenotypic class observed	Class	Proportion (%)	Diversity index (H')
Spike Shape	Parallel	2	90.91	0.44
	Fusiform		9.09	
	Lax	15.15		
Spike density	Dense	4	9.09	0.61
	Very lax		72.73	
	Very dense		3.03	
Curvature of first rachis segment	Medium	2	45.00	0.99
	Strong		55.00	
Glume length compared to grain	Shorter than kernel	2	93.94	0.33
	As long as kernel		6.06	
Lemma type in grain	No lemma teeth	3	79.00	0.55
	Lemma teeth		18.00	
	Lemma hair		3.00	
Lemma awn barbs	Rough	3	67.00	0.76
	Smooth		24.00	
	Intermediate		9.00	
Pigmentation of awn tips	Moderately pigmented	2	36.00	0.95
	Weakly pigmented		64.00	
Length of rachilla hair	Short	2	30.00	0.88
	Long		70.00	
Disposition of lodicules in the fertile grain	Frontal	2	27.00	0.85
	Clasping		73.00	

Shorter glume length compared to grain had the greatest proportion (93.94 %). No lemma teeth for lemma type in grain dominated with proportion of 79 %. Rough phenotypic class was the highest class for lemma awn barbs with 67 % as proportion. Awn tips were mostly weakly pigmented (64 %). Long length of rachilla hair had the highest percent of presence (70 %). Clasp phenotypic class was the most dominated concerning the disposition of lodicules in the fertile grain (73 %).

DISCUSSION

Diversity in plant genetic resources (PGR) provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics (Govindaraj et al., 2015).

For the nine qualitative traits considered in our study, the average genetic diversity based in Shannon diversity index (H') averaged 0.706 for all traits studied on 33 barley genotypes (29 landraces from arid and semiarid regions of Algeria and four controls) tested in sub-humid conditions of Mitidja (Algeria), thus revealing existence of a high diversity among genotypes for these traits. In their study taken on 34 traditional and exotic accessions of barley tested in some arid and semi-arid regions of Algeria, Taibi et al. (2019) found an average of diversity index of only 0.53 for 18 qualitative traits studied. Studying genetic diversity in the Batini barley landraces from Oman, Jaradat et al. (2004) found an average of 0.533 for genetic diversity of 21 qualitative traits. For 207 barley accessions from Ethiopia, Derbew et al. (2013) found 0.63 as average diversity index of eight qualitative traits.

Differences in the degree of curvature for the first rachis segment are useful for grouping barley varieties during the stages of maturity and glume length compared to grain is useful for varieties grouping between anthesis and full maturity (FAO, 2015). In our case, the curvature of first segment had the highest diversity index (0.99) and the lowest value concerned the glume length compared to grain (0.33). Taibi et al. (2019) found only 0.64 as index of diversity for the curvature of first segment for traditional cultivars tested in some arid and semiarid regions of Algeria.

On 21 qualitative traits studied by Jaradat et al. (2004), the highest phenotypic diversity index concerned the spike density (0.805), the lowest one was

for dorsal view of grain (0.149) and the shape of spike had a high phenotypic diversity index (0.783). Using eight qualitative characters, Kemelew & Alemayehu (2011) found a diversity ranging from 0.32 for kernel covering to 0.90 for spike density. Studying 11 qualitative traits for 36 barley landraces, Fekadu et al. (2018) found 0.52 as index of diversity for spike density. In our case, spike density showed a high diversity index (0.61) but the spike shape had a low H' (0.44). According to Negassa (1985), spike density, spike length and spike attitude are among the phenotypic markers used by farmers to distinguish the barley varieties.

Rachilla length is considered as one of the best taxonomic characteristics in barley (Nilan, 1964). This trait presented a high diversity index (0.88) in our study with the highest proportion for long length of rachilla hair (70 %). In the contrary, for this trait, the short phenotype maintained a high frequency (about 70 %) in the Batini barley landraces studied by Jaradat et al. (2004). In the study of Taibi et al. (2019) on traditional barley accessions of Algeria, the diversity for rachilla hair was lower than we found (0.59). At barley landraces of Ethiopia, H' for rachilla hair was 0.49 in the study of Fekadu et al. (2018).

The paired lodicules are situated next to the embryo near the base on the dorsal side of the grain (Sparks & Malcolm, 1978). The size and number of hairs on the lodicules are useful in the identification of varieties (McMullan, 1968). Heslop-Harrison & Heslop-Harrison (1996) reported that critical role of lodicules in opening the floret at the time of anthesis was fully appreciated and thus lodicules had a critical role in cleistogamy of barley. Remind that cleistogamy in barley provides more resiliency to Fusarium heat blight (Honda et al., 2005) and to *Ustilago nuda* (Neergaard, 1977). In our case, the disposition of lodicules in the fertile grain presented a high diversity index (0.85) with 73 % of clasp phenotypic class which promotes cleistogamy, thus better resilience to the cultivars concerned by this class. Taibi et al. (2019) found 0.63 as index of diversity for this trait therefore lower than we obtained.

The glumes and awns may represent significant (and sometimes the only) photosynthetic tissue with the potential to fix atmospheric carbon through grain-filling (Rebetzke et al., 2016). Direct vascular linkage between the awns and the lemma should permit direct carbon movement to the developing

grain (Evans et al., 1972; Li et al., 2010). In our case, values of index diversity were 0.33 (low) for glume length compared to grain, 0.55 (intermediate) for lemma type in grain. A same intermediate index of diversity for lemma type (0.55) was found by Fekadu et al. (2018) concerning Ethiopian barley landraces. For lemma awn barbs, we registered a high diversity index (0.76). For this trait, Fekadu et al. (2018) found an intermediate value of H' (0.51) concerning Ethiopian barley landraces. In our study, rough phenotypic class for lemma awn barbs was the highest class with 67 % as proportion and 24 % was noted for smooth awn. These results agree strongly with those of Derbiew et al. (2013) who found that proportions of genotypes in awn roughness were 67.2% for rough and 32.3% for smooth awn.

CONCLUSION

The diversity in crops is an advantage for food security but also for breeding programs. It is obvious that the greater the diversity, the more favorable opportunities are open for the creation of new varieties adapted, among other things, to the difficult conditions especially in the face of the harmful consequences of climate change. Beside quantitative traits related to grain size, grain weight and grain quality of barley landraces, some useful qualitative traits are determinant for their value and choice by farmers and breeders. Our study focused in the study of diversity in qualitative traits revealed existence of a great variability among the landraces for the majority of the traits studied. This study also made it possible to confront the results found in terms of values of the Shannon-weaver diversity index with those registered for the same species by some researchers around the world but also in Algeria. This allows, among other things, to give an idea of the highest limits existing in the variability of qualitative traits in this strategic species, knowing that variation is caused either by genotypic variation or by the effect of environmental factors in the expression of genetic potentials as phenotypic variation.

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