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Traits determining the greatest variability among barley landraces (*Hordeum vulgare* L.) from south Algeria

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Abstract: This study was done on two years of field trials for determining traits explaining the most of diversity among twenty nine barley landraces in presence of three controls and also to confirm the relationships between the different traits studied. Via these two experiments, phenology and agro-morphological traits at maturity were studied. Results of the tests showed a great variability within the germplasm revealed by very highly significant differences ($P<0.001$) between genotypes for all traits considered and statistically analyzed. Principal component analyzes could explain more than 70 % of the total variation and the greatest variability was explained over the two years by the common following traits: days to heading, days to maturity, 1000 grain weight, awn length, spike weight and plant height. Very high correlations existing between the following traits: awn length, 1000 grain weight, spike weight, days to heading and days to maturity, were confirmed through each test. Also, correlations existed between plant height, 1000 grain weight, spike weight, days to heading and days to maturity and between plant height and spike length and also between grain number per spike and spikelet number per spike. Through both seasons, cluster analyzes divided all six-rowed barley into three cluster groups.

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1. INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the most important cereal crops in the world, ranking the forth in terms of planting area only after wheat, rice and maize (FAO, 2005).

Barley is cultivated successfully in wide range of climates (Khajavi et al., 2014). With climate change, Algeria will face increasing scarcity of water and hence the development of resilient crops like barley and pearl millet becomes strategic and necessary (Rahal-Bouziane, 2016).

In Algeria, barley in the past occupied a very important place, more than durum and bread wheat and formed the basis for human food. The local gerpmlasm suffered great genetic erosion following the introduction of new performing varieties (Rahal-Bouziane[1] et al., 2015). For crop breeding, modern varieties of barley need to be improved to obtain high yield and quality. However, the narrow genetic basis and genetic erosion of this crop are barriers against the further improvement of yield and quality, which contrasts with the increasing human population of 9.6 billion by 2050 as predicted by the United Nations (Zeng, 2015).

Diversity in plant genetic resources (PGR) provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (yield potential and large seed, etc.) and breeders preferred traits (pest and disease resistance and photosensitivity, etc.) (Govindaraj et al., 2014). Evaluating genetic diversity in cultivated plants for plant breeding programs and heritable resources protection has a vital usage (Khajavi et al., 2014). According to Ramanujam et al. (1974), genetic diversity is one of the fundamental requirements for plant breeding.

The use of morphological traits remains the most basic method to analyze initial germplasm resources (Zeng, 2015). Determining the genetic basis of agronomic traits has been one of the major scientific challenges in the process of crop improvement (Pasam et al., 2012).

Few works exist on the local resources of cultivated barley in Algeria. On the species *Hordeum vulgare*, studies concerned generally the local approved varieties "Saïda" and "Tichedrett" and hence the diversity within the local materiel is not known (Rahal-Bouziane[2] et al., 2015). These studies done in two years have focused as objectives:

- To evaluate and quantify the diversity among barley landraces
- to determine the traits explaining the greatest variability among the genotypes
- to confirm the relationships between traits studied

2. MATERIAL AND METHODS

28 six-rowed barley landraces and 1 with 2 rows (genotype 14) considered in the studies comes from Saharan regions of Algeria (Table 1). All these

regions are characterized by arid or hyper-arid climate except El-Bayadh which is a semi-arid region.

These studies were conducted at the Institute of Algerian Agricultural Research (INRAA) of Baraki (Algiers) situated in the plain of Mitidja (sub-humid region). The climate data for periods of the trials are presented in figures 1 and 2. Planting occurred during the 2011-2012 and 2014-2015 campaigns for tests concerning phenology and agro-morphological traits at maturity. Al the experiment designs were randomized because the plots were homogenous. Three controls were present: Pane or genotype 6 (Spain) and two approved Algerian varieties Saïda (23) and Tichedrett (33).

The agro-morphological traits evaluated at maturity were: plant height (HPL) (cm), spike length (HEP) (cm), awn length (LBA) (cm), tiller spike number per plant (NTE), grain number per spike (NGE), spikelet number per spike (NEE), 1000 grain weight (PMG) (g), spike weight (PEP) (g) and days to maturity (DC). Also, days to heading (DEP) were studied. In the first test (2011/2012), with three plots, thirty replications were considered for each trait except for PMG, DEP and DC. In the second one (2014/2015) and via two plots, ten measurements were taken per trait. So, to compare the two years with the same number of measurements, ten values were randomly chosen on the total sample for each character studied on the first test.

The analysis of variance (ANOVA One-way) was performed by Fisher's least significant difference (LSD) method to test the significance difference between means. The data was statistically analyzed by the Gen Stat Discovery (Edition 3, Stat Soft Inc.) and concerned only characters with 10 repeated measurements (HPL, NTE, HEP, LBA, NEE, NGE and PEP). Correlations, principal Component Analyses and cluster analyses were obtained by STATISTICA (Data analysis Software System, version 6, Stat Soft Inc.). Correlations (Pearson's correlation coefficient), principal component analyses and dendrograms were performed based on ten quantitative characters (HPL, NTE, HEP, LBA, NEE, NGE, PMG, PEP, DEP and DC). Cluster analyses were adopted with the Ward's method (Ward, 1963).

Table 1. Data of barley genotypes studied

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

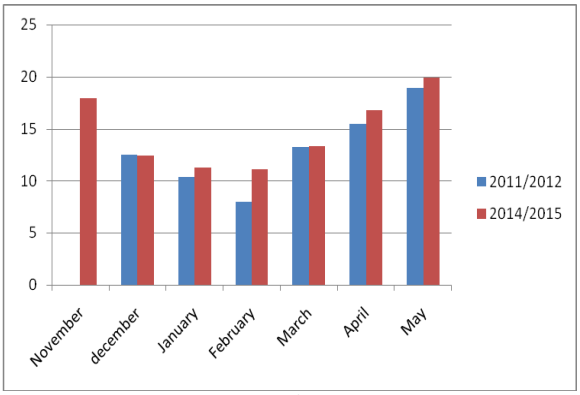

Figure 1. Average temperatures for 2011-2012 and 2014-2015 seasons

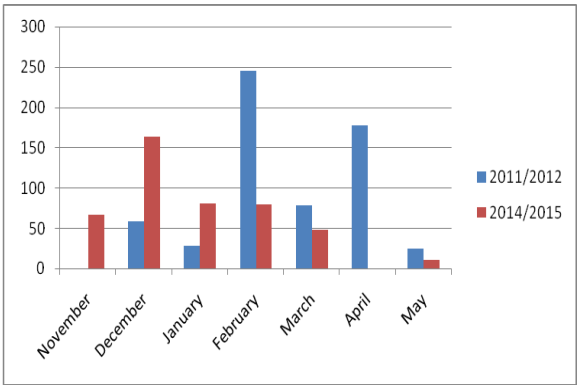

Figure 2. Cumulative precipitations for 2011-2012 and 2014-2015 seasons

3. RESULTS

Concerning these trials studying agro-morphological traits, analyses of variance showed very highly differences among the genotypes for all the characters studied which confirmed existence of a great variability within the germplasm (table 2 and table 3).

To quantify this variability and to determine the principal traits explaining it, multivariate analyses were done by principal component analyses (PC) (table 4, figures 3 and 5) and cluster analyses (figures 4 and 6). For the first experiment, three components explained 76.08 % of total variation (table 4). The PC for the second trial could explain 71.79 % of variation through only two components. Respectively for the trials, first components accounted 43.73 % and 54.78 %. The traits associated to them were: DC, PMG, LBA, DEP, PEP and HPL for the first test (2011/2012) and PEP, DC, LBA, PMG, DEP, HPL and HEP for the second one (2014/2015).

The cluster analyses divided all the six-rowed genotypes studied into three cluster groups (figures 4 and 6). For the first test (2011/2012), the first cluster included the following genotypes: 1, 20, 6, 33, 5, 7, 12, 19, 10, 25, 26, 27, 30 and 32 characterized by high mean values of NEE, NGE and NTE. The second cluster grouped: 2, 4, 21, 24, 22, 29 and 31 presenting the shortest cycle (DEP and DC), high values of NGE and generally the lowest mean values of awns and plant height. The third cluster consisted of: 8, 16, 9, 13, 15, 23, 11, 17, 18 and 28 which had the longest cycle and the highest mean values of LBA, PMG, HPL and PEP (figure 4). The two rowed genotype (14) was distinguished by the highest mean values of NTE, HEP and NEE and by the lowest mean value of NGE.

Table 2. ANOVAs of agro-morphological traits in 32 barley genotypes via two experiments

	Minimum value	Maximum value	Grand mean	SE	LSD	CV (%)	Prob.
	2011/2012 experiment						
HPL	82.6	111.7	99.31	3.81	7.5	8.6	<0.001
NTE	9.9	30.6	15.77	3.21	6.32	45.5	<0.001
HEP	3.9	10.2	6.9	0.43	0.84	13.9	<0.001
LBA	7.24	14.08	10.32	0.45	0.88	9.8	<0.001
NEE	8.2	11.8	9.98	0.77	1.51	17.2	<0.001
NGE	29.6	61.7	46.86	4.2	8.29	20.1	<0.001
PEP	1.44	3.79	2.39	0.27	0.53	25.4	<0.001
PMG	26	60.9	44.91	-	-	-	-
DEP	102	132	117.69	-	-	-	-
DC	144	173	164.06	-	-	-	-
	2014/2015 experiment						
HPL	74.8	128.9	110.08	3.4	6.69	6.9	<0.001
NTE	5.8	16.4	9.96	1.89	3.72	42.4	<0.001
HEP	3.94	10.07	7.76	0.36	0.7	10.8	<0.001
LBA	7.92	15.18	11.24	0.38	0.76	7.7	<0.001
NEE	7.9	14.8	10.71	0.56	1.11	11.8	<0.001
NGE	28.8	65.2	52.86	4.11	8.1	16.9	<0.001
PEP	1.7	5.16	3.33	0.32	0.63	21.6	<0.001
PMG	30.5	73	52.36	-	-	-	-
DEP	122	166	123.77	-	-	-	-
DC	166	188	175.63	-	-	-	-

In the second test (2014/2015), the first cluster comported: 1, 2, 4, 20, 21, 22, 24, 25, 32, 26, 30 and 31 distinguished by the shortest cycle (DEP and DC) and the lowest mean values of NGE, NEE, HPL and HEP. The two rowed genotype (14) was also distinguished by the highest mean values of NEE and NTE (after genotype 10) and by the lowest mean value of NGE. The second cluster included: 5, 7, 10, 27 and 29 with high values of NTE and HPL especially for genotype 10 having the highest mean value of NTE and genotype 7 with the highest value of HPL. The Third cluster composed with: 6, 9, 18, 8, 23, 13, 12, 33, 11, 16, 28, 17, 15 and 19 having the longest cycle and the highest mean values of LBA, PMG, PEP, HPL and HEP (figure 6).

Through the first test, very high positive correlations existed between the following traits: awn length, 1000 grain weight, spike weight, days to heading and days to maturity (table 5). These results were confirmed by the second trial (2014/2015) for all these traits (table 6). Also, positive correlations existed between plant height, 1000 grain weight, spike weight, days to heading and days to maturity via two trials. 1000 grain weight and spike weight were positively and very highly correlated via two tests. Plant height and spike length were positively and strongly correlated via two trials. Grain number and spikelet number per spike were also positively correlated via two seasons.

Table 3. Mean values of pheno-agro-morphological traits of two seasons

G	HPL		NTE		HEP		LBA		NEE		NGE		PMG		PEP		DEP		DC	
	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2
1	83.2	74.8	17.1	10.3	5.21	5.54	11.44	11.63	8.7	8.5	46	49.2	48.63	54.5	2.05	2.93	114	125	163	183
2	92.8	94.2	17.6	9	6.8	5.18	8.2	9	10.7	10	55.4	52.4	34.53	36.9	2.26	2.31	102	123	144	171
4	94.5	93.3	12.7	10.5	5.5	5.85	7.9	8.79	9.8	10.8	49.3	60.3	34.7	35.7	1.91	2.12	102	122	144	171
5	99.5	121.1	13.3	10.8	7.5	8.34	8.95	9.83	10.1	11	45.1	56.4	33.6	46.3	1.84	2.66	129	136	163	175
6	94.6	125.9	13.5	12.1	5.91	7.23	11.46	13.13	10.5	12.8	49.9	65.2	52.1	65.7	2.56	5.19	127	136	173	186
7	97.4	128.9	15.4	11.1	6.91	8.74	9.9	9.92	10.3	124	47.3	58.4	36.8	48.3	1.88	2.88	121	132	173	171
8	101.1	119.5	9.9	10.2	7.4	9.03	12.23	12.88	9.2	11.7	40.8	58	54.5	59.5	2.11	4.54	129	138	173	186
9	101.1	118.4	13.8	11.1	7.2	9.88	12.12	13.38	9.2	12.1	40.5	63.1	60.9	59	3.3	5.11	127	139	173	175
10	103.3	124.9	24.5	16.4	7.4	9.23	11.53	11.14	10.5	13.7	55.2	63.3	43.2	50.3	3.79	3.37	114	130	168	175
11	108.4	123.3	11.9	10.4	7.22	7.91	11.53	13.48	9.5	9.78	47	51.67	48.63	60.1	2.4	3.55	132	143	173	183
12	99.8	113	13.2	7.8	7.4	9.05	11.7	14.44	9.2	10.4	43.7	57.7	39.53	55.4	2.05	4.21	129	141	173	186
13	107.8	126.3	20.1	9.2	7.2	9.88	12.06	12.66	8.2	12.1	37.5	53.7	60	59	2.72	4.28	121	138	173	186
14	101	101.5	30.6	15.2	10.2	9.81	8.24	7.92	11.8	14.6	29.6	28.8	57.23	61.7	1.82	2.23	114	125	168	175
15	111	115	16.1	7.3	7.63	8.39	12.21	13.49	9.9	10.5	39.2	53.1	56.83	68	3.23	4.53	129	136	173	188
16	99.5	124.7	12.8	11.5	7.63	8.49	11.99	13.25	9.7	10.6	39.8	52.5	56.2	68.34	2.76	4.63	127	141	173	183
17	107.1	123.8	11.2	8.8	8.2	7.9	12.43	12.95	11	10.5	49.6	48.3	59.53	73	3.23	4.03	127	139	173	186
18	110.4	118.6	13.7	10.7	7.8	10.07	12.25	12.84	10.6	12.7	48.3	64.8	59.03	63	3.44	5.04	129	140	173	182
19	106.6	118.5	12.5	9	7.1	9.24	12.41	12.12	8.8	11.5	38.8	58.2	42.23	67.8	2.94	4.84	114	138	173	186
20	82.8	85	14.2	5.8	3.9	9.94	8.6	9.56	11.8	10.9	56.1	50.7	35.9	44.6	2.65	2.7	114	137	163	175
21	92.3	81.5	14.8	6.8	5.12	4.54	8.06	8.79	9.7	8.4	48.1	43.5	34.13	37.2	1.85	2.14	102	123	144	171
22	89.9	86.3	14.8	6.7	6.2	6.72	7.6	9.54	8.6	8.7	43.2	45.9	35.8	43.1	1.92	2.25	102	123	150	171
23	107.6	124	17.5	8.7	7.21	9	12.2	12.68	9.4	11.5	39.3	58	58.73	58	2.71	4.96	127	138	173	188
24	97.8	89	15.1	8.1	5	5.39	8.4	8.94	9.3	9.2	50.4	51.8	37.7	45.9	1.96	2.25	102	123	144	166
25	102.5	111.9	15.8	7.9	7.7	9.38	12.08	11.75	11.5	9.2	61.7	48.2	46.63	50.1	3.16	2.67	114	130	162	175
26	102	100.8	19	7.4	7.02	5.31	7.7	8.67	11.1	9.8	53.7	45.3	30	39.3	1.55	2.06	118	129	163	171
27	94.2	110.9	19.7	11	7.81	8.04	8.6	9.83	11.4	12	53.6	61.44	31	30.5	1.44	2.15	118	136	163	177
28	111.7	123	14	6.4	7.4	8.14	11.63	13.34	9.8	10.7	49	53.6	58.87	65	2.82	4.92	121	138	173	183
29	87	117.5	15	14.1	6.7	6.77	7.8	8.68	9.5	10.2	49.9	53.2	35.4	34.3	2.13	1.7	102	129	150	175
30	108.27	100.9	18.09	12.3	7.14	6.84	7.24	9.15	11.5	8.1	54.5	42.1	34.2	43.9	1.84	1.96	109	123	161	175
31	96	101.3	16.5	11.2	7.33	7.56	9.33	11.78	8.9	9	45.1	47.7	37.63	46.2	1.83	2.75	114	126	145	182
32	104.1	111.6	16.4	11	6.2	5.85	8.33	8.9	8.6	7.9	44.3	43	37.7	44.7	1.83	2.1	109	126	160	171
33	82.6	113.3	13.9	10	4.8	5.05	14.08	15.18	10.8	11.5	47.7	52.1	45.3	61	2.56	3.71	127	141	173	188

G: genotypes; S1: 2011/2012 season; S2: 2014/2015 season SE: Standard error; LSD: Least significant differences of means at 5% level; CV: coefficient of variation

Table 4. Comparison of principal component analyses (PC) for two trials based on ten traits

First trial (2011/2012)				Second trial (2014/2015)	
Parameter	**PC 1**	**PC 2**	**PC 3**	**PC 1**	**PC 2**
Eigen values	4.37	1.75	1.48	5.48	1.7
% of variance	43.73	17.53	14.82	54.78	17.01
Cumulative %	43.73	61.27	76.08	54.78	71.79
Characters		**Eigen Vector**			
HPL	-0.638	0.361	0.062	-0.781	0.322
NTE	0.113	-0.825	0.039	-0.064	0.819
HEP	-0.529	0.727	0.101	-0.672	0.347
LBA	-0.854	0.368	-0.136	-0.868	-0.368
NEE	0.104	-0.462	-0.799	-0.583	0.658
NGE	0.471	0.138	-0.785	-0.556	0.201
PMG	-0.879	0.004	0.071	-0.820	-0.217
PEP	-0.683	0.177	-0.378	-0.929	-0.183
DC	-0.879	-0.001	-0.154	-0.896	-0.114
DEP	-0.836	0.119	-0.130	-0.819	-0.322

Table 5. Correlation matrix on ten traits of 32 barley genotypes (test of 2011/2012)

	HPL	**NTE**	**HEP**	**LBA**	**NEE**	**NGE**	**PMG**	**PEP**	**DEP**
NTE	0.04**NS**								
HEP	0.64***	0.39*							
LBA	0.31**NS**	-0.3**NS**	0.17**NS**						
NEE	-0.06**NS**	0.31**NS**	0.18**NS**	-0.17**NS**					
NGE	-0.24**NS**	-0.13**NS**	-0.37*	-0.25**NS**	0.5**				
PMG	0.48**	-0.03**NS**	0.41*	0.74***	-0.14**NS**	-0.50**			
PEP	0.39*	-0.12**NS**	0.16**NS**	0.72***	0.04**NS**	0.02**NS**	0.66***		
DEP	0.41*	-0.27**NS**	0.37*	0.74***	0.04**NS**	-0.31**NS**	0.61***	0.39*	
DC	0.46**	-0.07**NS**	0.39*	0.76***	0.08**NS**	-0.34**NS**	0.67***	0.51**	0.86***

*NS: Non-significant – non significant ; * P ‹ 0.05 ; ** P ‹ 0.01 ; *** P ‹ 0.001*

Table 6. Correlation matrix on ten traits of 32 barley genotypes (test of 2014/2015)

	HPL	**NTE**	**HEP**	**LBA**	**NEE**	**NGE**	**PMG**	**PEP**	**DEP**
NTE	0.32**NS**								
HEP	0.55**	0.15NS							
LBA	0.55**	-0.14**NS**	0.37*						
NEE	0.53**	0.46**	0.62***	0.22**NS**					
NGE	0.47**	0.07**NS**	0.29NS	0.45**	0.41*				
PMG	0.53**	-0.01**NS**	0.48**	0.77***	0.37*	0.13**NS**			
PEP	0.62***	-0.10**NS**	0.54**	0.86***	0.46**	0.55**	0.84***		
DEP	0.71***	-0.11**NS**	0.58***	0.8***	0.44*	0.5**	0.65**	0.77***	
DC	0.5**	-0.06**NS**	0.37*	0.85***	0.27**NS**	0.28**NS**	0.75***	0.77***	0.73***

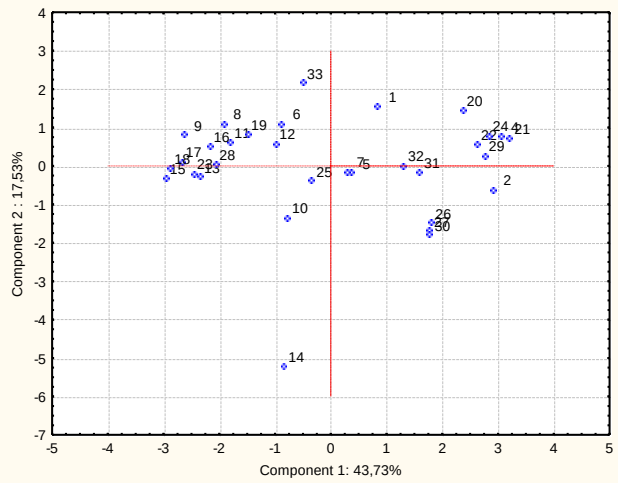

Figure 3. Distribution of genotypes (2011/2012 season)

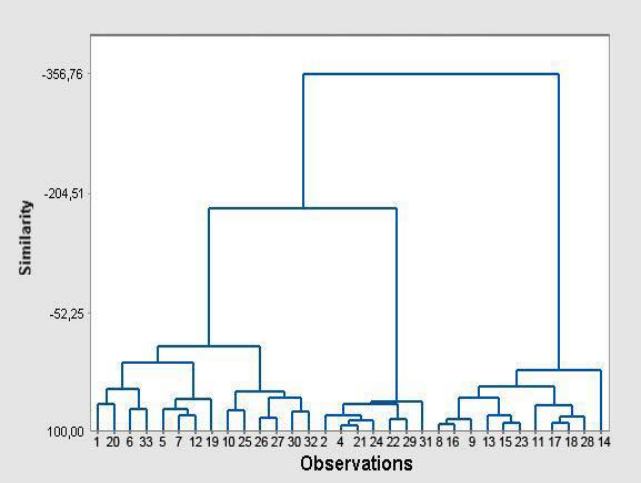

Figure 4. Dendrogram of genotypes (2011/2012 season)

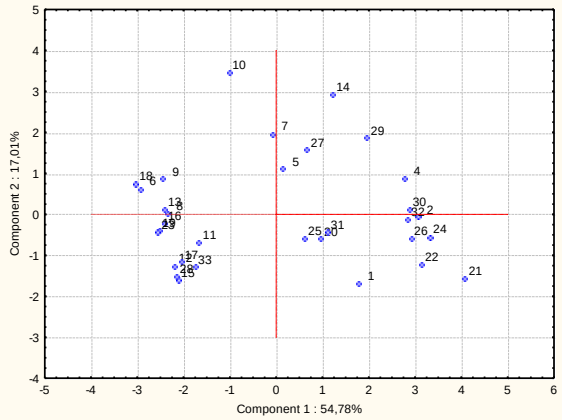

Figure 5. Distribution of genotypes (2014/2015 season)

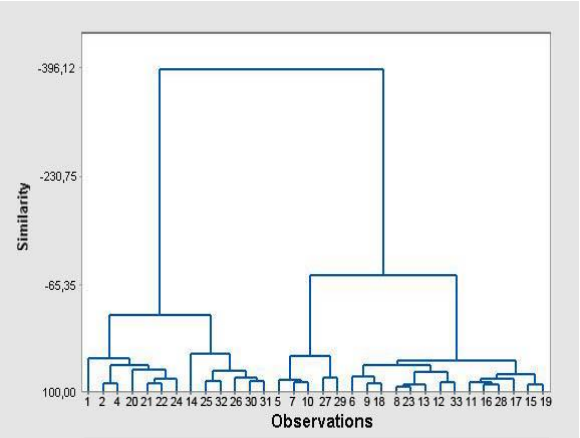

Figure 6. Dendrogram of genotypes (2014/2015 season)

4. **DISCUSSION**

Via two trials, it was showed that differences among genotypes were very high significant for all characters submitted to analyses of variance, testifying to the existence of a high genetic variability within the germplasm. Genetic diversity is the base of plant breeding, which has been caused by natural development and is one of the important components of biological systems stability (Khajavi et al., 1998). For all quantitative traits studied by Derbiew et al. (2013) in barley landraces from Southern Ethiopia, highly significant differences were also found. According to Gegnaw and Hadado (2014), the barley landraces exhibit variation both between and within populations.

Based on the principal component analyses of two tests, it was concluded that the common traits explaining the greatest variability among genotypes were: DC (days to maturity), PMG (1000 grain weight), LBA (awn length), DEP (days to heading), PEP (spike weight) and HPL (plant height). In a study taken by Al-Nashash et al. (2007), plant height, spike weight, 1000 grain weight, biological yield/plant and awn length were the traits presenting the highest diversity index. At Ambo in Ethiopia, Setotaw et al. (2010) found that days to heading, days to maturity, grain filling period, kernel weight per spike and yield per plant have high canonical loading in the first canonical variation.

Through the two field experiments, cluster analyses divided all the thirty one six-rowed barley genotypes studied into three cluster groups. In a work of Dimitrova-Doneva et al. (2014) and for twenty one advanced lines of barley in presence of three standard varieties, the cluster analysis divided the barley studied into three cluster groups. The cluster analysis with the agronomic data of forty winter barley generated five cluster groups in Ibrahim's et al research of 2011. The study taken in barley by Mekonnon et al. (2015) showed that cluster analysis grouped one hundred two accessions into five distinct groups.

It was showed that genotypes: 8, 9, 23, 15, 16, 13, 11, 28, 17 and 18 were found in the same group in both seasons with their long cycle and high values of LBA, PMG, PEP, HPL and HEP.

Genotypes 2, 4, 21, 22, 24 and 31 were in the same group in both seasons by their shortest cycle and by low values of HPL, LBA, PEP, PMG and HEP.
Genotypes 5, 7, 10 and 27 were regrouped in both seasons with generally their high values of NTE, NEE and NGE.

Over two field trials, the genotypes with long cycle have the greatest weight of 1000 grain and the highest stems. These results agree with finding of Al-Tabbal and Fraihat (2012). Also, late genotypes have longer awns and heavier grains and spikes. Several authors (Hadjichristodoulou 1993; Bort et al., 1994; Merah and Monneveux 2014) have reported the role played by the awns in drought resistance and in grain filling.

Also, comparison of the tests of 2011/2012 and 2014/2015, showed existence of a great gap in cycle (days to maturity and days to heading). These differences could be explained by the different climatic conditions of the two seasons. Indeed, assessment of local barley resources in Ethiopia showed that variation in heading and maturity dates may be associated with agro-climatic variation (Lakew et al., 1995). Tiller spike number per plant (NTE) was stronger in the first test compared to the second one. As for the other characters such as 1000 grain weight, grain number per spike (NGE) and spike length (HEP), the mean values recorded in the second trial were considerably better than those of the first experiment. These differences could be explained by the different sowing dates (December 8/ 2011 for the first test and November 13/2014 for the second one). In the study conducted by Rahimi-Baladezaie et al. (2011), early sowing date was increased unfertile tiller

numbers per plant and result in decrease fertile tiller numbers per plant. Zaman Khan et al. (1990) found that early sown crops gave maximum grain weight which decreased with delay in sowing from November 15 to December 15; it was the same with grains per spike. However, NoworoInik (2012) found that under conditions of late planting, the rate of productive tillers decreased in some cultivars, while in others; late planting increased the number of grains per spike. The second season of our test which was characterized by a lower average rainfall than the first season, had registered a higher mean of 1000 grain weight. Also, in the study by Desheva (2016) on winter bread wheat, the weight of 1000 grain was stronger in the second season recording an average rainfall of 461.4 l / m^2 compared to that of the first with a higher mean annual rainfall (478.4 l / m^2).

Through these tests, very high positive correlations existed between the 1000 grain weight and the spike weight. Similar results were found by Gocheva (2014) and Dimitrova-Doneva et al. (2014). These traits were also highly correlated with the awn length and cycle (days to heading and maturity). Mohtashami (2015) found high positive correlations between awn length and days to heading and days to maturity. Also, positive correlations existed between plant height, 1000 grain weight and spike weight. In the study taken by Dimitrova-Doneva et al. (2014), plant height had positive and significant correlation with grain weight per spike. Babaiy et al. (2011) and Al-Tabbal et al. (2012) found a positive and significant correlation between plant height and 1000 grain weight. Also, 1000 grain weight and spike weight were highly and positively correlated with days to heading and days to maturity via two trials. On the contrary, 1000 grain weight had strong negative correlation with days to heading and days to maturity in a study of Al-Tabbal et al. (2012). Plant height and spike length were positively and strongly correlated via two trials. Muhammad et al. (2012) and Dimitrova-Doneva et al. (2014) found also a significant positive correlation between these two characters. Grain number per spike and spikelet number per spike were also positively correlated via two seasons. These results agree with those of Gocheva (2014).

5. CONCLUSION

Barley is a strategic crop that can cope with the challenges of climate change.

Assessment of genetic variability is strategic both for conservation and valorization of local germplasm and also for breeding programs.

Studies of pheno-agro-morphological traits via two seasons confirmed the existence of a strong variability among barley landraces of south Algeria. This observed variability and existence of association between many traits shows that genetic improvement is very promising for the creation of high-performance varieties.

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