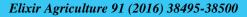
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Phenotypic Diversity for Qualitative Characters of Some Barley (Hordeum vulgare L.) Germplasm

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ABSTRACT

Barley is believed to have originated in Abyssinia (Ethiopia) and Southeast Asia .Sixty four barley genotypes were tested in 8x8 simple lattice design at Atsbi, Ofla and Quiha environments in Tigray region, in 2009/10. The overall objective was to determine the nature and degree of variability in morpho- agronomic traits of barley germplasm. Three types of seed/kernel colors, as quality criteria observed were white, tan/red and black in the percentage of 96.87%, except the genotypes Eritrea07 1, and ISEBON 14 with a seed color of tan red and black respectively added to the variability of 1.56% each. From this study, 60.69 % found as two-row type, 31.26% six-row types and 7.81% irregular type across locations. It was observed that from these barley genotypes had a spike density of which 6.25% were lax, 64.06% intermediate and 29.69% dense. All the testing entries were awnletted and the caryopsis or kernel covering with a percentage of the genotypes were, 21.88%, 10.94% and 65.64% stands for naked, semi-covered and covered types respectively across locations. The phenotypic diversity index values for qualitative traits ranged from 0.0 (monomorphic) for lemma/ hood to 0.86 high polymorphic for row number, for awn color (H'= 0.71), kernel covering (H'=0.84) and spike density (H'=0.82) revealed the highest diversity. Glume color (H'=0.34) and gain color (H'=0.16), relatively showed the lowest diversity.

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Introduction

The center of origin of cultivated barley has been reported to be the Fertile Crescent of the Middle East (Zohary and Hopf, 2000). Even though barley was indicated to have been brought to Ethiopia at least 5000 years ago (Harlan, 1969 and Frost, 1974), new studies supporting the polyphyletic origin of the crop have indicated Ethiopia as one of the centers of origin of barley Molina-Cano et al. (2005). Furthermore, barley is believed to have originated in Abyssinia (Ethiopia) and Southeast Asia (Reddy, 2009). According to Vavilov (1951), he declared that nowhere else in nature he has observed such a diversity of forms and genes. Therefore, he proposed Abyssinia (the former Ethiopian Empire) as a center of origin of cultivated barley. The genus Hordeum has centers of diversity in central and southwestern Asia, western North America, southern South America, and in the Mediterranian (Bothmer, 1992).

Cultivated barley is adapted to and produced over a wider range of environmental conditions than other cereals. It can grow at latitude of 70°North in Norway, on the fringe of the Sahara desert in Algeria and below the equator in Ecuador and Kenya. In addition, it was observed at elevations up to 4200 meter on the Altiplano and slopes of the Andes in Bolivia and at 330 meter below sea level near the Dead Sea (Nilan and Ullrich, 1993; Harlan, 1968). Barley is relatively cold resistant and is considered as the most drought, alkali and salt tolerant among the small grains (Smith, 1995). In contrast, to this, it is

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not well adapted to acid and wet soil conditions (Poehlman, 1985). The relatively early maturity and low water use of barley are the major factors for adaptation to drought and temperature extremes in North Africa with less than 250 mm annual rainfall. It is cultivated in every region of Ethiopia and demonstrates wide ecological plasticity and physiological adaptation throughout the country (Zemede, 1988, 1989 and Berhane et al., 1996). Barley is also reported to tolerate annual temperature of 4.3 to 27.5°C, and soil pH of 4.5 to 8.3 (Duke, 1983).

Despite barley's long history of cultivation, traditional practices and its valuable uses, the improvements made to boost the productivity of the crop have been low. In Ethiopia, research efforts to improve the production and productivity of the crop started in the early 1950s by the former Alemaya College of Agriculture and Mechanical Arts at its branch experimental station in Debre Zeit with the evaluation of landraces and introduced nurseries. Currently, barley research is coordinated from Kulumsa Agricultural Research Center but the breeding work is led by Holetta Agricultural Research Center (HARC). Introduced germplasms have been studied and evaluated at HARC, which serves as a quarantine site (Hailu et al., 1996). Every year, exotic germplasms is evaluated for desirable agronomic characters such as grain yield, lodging resistance, maturity, grain colour and plumpness and resistance to diseases (scald and net blotch) and insect pests (shoot fly and aphids). Between 1966 and

1993 over 22,000 and between 1994 and 2001, about 6,400 entries of introduced germplasms were evaluated. However, most of them were highly susceptible to scald, net and spot blotches, barley shoot fly, and had poor plant vigor and small grains. About 6% were selected for further study (Birhanu et al., 2005).

In the early 1970s, the major germplasm contributors to these nurseries were the FAO Near East Regional Program, the USDA, and the Arid Land Agriculture Development. Since the mid-1970s, ICARDA has also been a principal contributor of germplasm. In earlier days, some germplasms were also received from Brazil, Columbia, the former Czechslovakia, Egypt, India, Kenya, Peru, Sweden, and the former Republic of Yugoslavia (Hailu et al., 1996). From these efforts, one hulled-barley variety, AHOR 880/61 was released and some other elite lines are being used as sources of genes for desirable agronomic traits such as grain quality and stiff straw and for disease and insect pest resistance in the national crossing program. According to IBCR (2001), the total number of barley germplasm holdings in the Institute of Biodiversity Conservation (IBC) in 2001 was 14,592 and their characterization is under way (Birhanu et al., 2005).

Assessment of the genetic diversity in a crop species is fundamental to its improvement. Genetic diversity among and within plant species is in danger of being reduced. In wild species genetic diversity maybe lost because of severe reduction in population size, whereas in domesticated crops genetic diversity maybe lost because of the narrow genetic base in many breeding programs (Cao et al., 1998).

Characterization of landraces and knowledge on the pattern of variation for important morpho-agronomic traits is needed for a proper management and a better exploitation of this gene pool (Jain et al., 1975; Gebrekidane, 1982; Assefa 2003).Introduced Barley germplasm from ICARDA have not been broadly studied and characterized and hence the diversity within this germplasm is not known. Therefore, this work was completed with the objectives to conduct the morphological characterization and to determine the extent and nature of variability in morpho- agronomic traits of the barley germplasm.

Material and Methods Description of the Study Sites

The experiment was conducted at three locations of Tigray region, namely Atsbi, Ofla and Quiha where barley grows most with an erratic rainfall where heavy rain alternate with dry periods resulting in alternating floods and dry periods. The region receives the least rainfall compared to other parts of Ethiopia. The average annual rainfall for the period from 1961 to 1987 was 571 mm, which was 38% less than the national average (921mm) for the same period (Webb and Braun, 1994). The mean annual rainfall ranges from 980 mm on the Central plateau to 450 mm on the Northeastern escarpments of the region (Solomon, 1999). The annual rainfall shows a high degree of variation ranging from 20% in the Western to 49% in the Eastern parts of Tigray (CoSAERT, 1994). The map of experimental sites is given in Fig.1 and the different characteristics of each location are presented in Table 1.

Experimental Materials

A total of 64 barley genotypes from ICARDA and one local check (Saesea) were considered in this study. List of barley genotypes, code, pedigree and origin are given in Table 1.

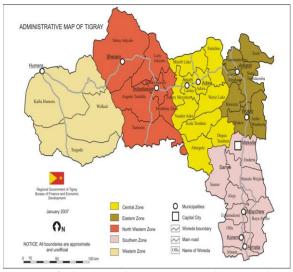


Fig 1. Map of Tigray regional state showing experimental environments.

Source: Regional Government of Tigray Bureau of Finance and Economic development (2007).

Experimental Design, Management and Season

The experiments were conducted in 2009/10 main cropping season. The trials were laid out IN 8x8 Lattice design with two replications at three locations. Each plot was 2m long and 0.8m wide, which consisted of four rows with a spacing of 20 cm between rows. The middle two rows were used for data collection. Planting was done by hand drilling using a seed rate of 80kg/ha for each treatment. All other management practices such as weeding and fertilization (urea 50kg/ha and DAP 100kg/ha) were uniformly applied to all plots.

Data Collected

The Qualitative characters, the barley descriptor by International Plant Genetic Resource Institute (IPGRI, 1994) was adopted and data were recorded on plot basis (Table 2). **Statistical Analysis**

Shannon-Weaver Diversity Index

The Shannon index, sometimes incorrectly referred to as the Shannon-Wiener Index or the Shannon-Weaver Index is one of several diversity indices used to measure diversity in categorical data (Krebs, 1989). It is simply the Information entropy of the distribution, treating species as symbols and their relative population sizes as the probability. This article treats its use in the measurement of biodiversity. The advantage of this index is that it takes into account the number of species and the evenness of the species. The index is increased either by having additional unique species, or by having greater species evenness.

$$H' = -\sum_{i=1}^{s} Pi \ln Pi - \left[\binom{(S-1)}{2N}\right]$$

Where,

ni = The number of individuals in species,

- i= the abundance of species I,
- S = the number of species also known as species richness,
- N = the total number of all individuals and

Pi = the relative abundance of each species, calculated as the proportion of individuals of a given species to the total number of individuals in the community:

	Table 1. List of barley genotypes their code, name, p		•
CODE	NAME	PEDIGREE	ORIGIN
ISEBON 2	Avt/Attiki//M-Att-73-337-1/3/Aths/Lignee686/7/NAKB93-371/6/Hml- 02/5/Cq/Cm//Apm/3/12410/4/Giza134-2L	ICB00-0373-11AP-0AP	ICARDA
ISEBON 7	ArabiAbiad/Arar//H.spont.41-5/Tadmor/3/Sara	ICB00-0725-83AP-0AP	ICARDA
ISEBON 9	Moroc9-75/Hml	ICB92-0809-5AP-0AP-5AP-0AP-4AP-0AP	ICARDA
ISEBON 14	ArabiAswad/WI2269/3/ArabiAbiad/WI2291//Tadmor/4/Akrash//WI2291/WI2269	ICB94-0385-0AP-3A-1AP-0AP-9AP-0AP	ICARDA
ISEBON 16	As46/Aths/3/Giza121/Pue//79An/Mn/4/Khafour/Kasab	ICB98-0173-0AP-24AP-0AP-4AP-0AP	ICARDA
ISEBON 18	Centinela/2*Calicuchima//Kasab	ICB97-0570-0AP-4AP-0AP-1AP-0AP	ICARDA
ISEBON 19	Centinela/2*Calicuchima//Kasab	ICB97-0570-0AP-4AP-0AP-2AP-0AP	ICARDA
ISEBON 29	Alanda/5/Aths/4/Pro/TolI//Cer*2/TolI/3/5106/6/CalMr/CI16155	ICB95-0176-0AP-17AP-0AP-8AP-0AP	ICARDA
ISEBON 36	Baca'S'/3/AC253//CI08887/CI05761/4/Cen/Bglo'S'	ICB95-0516-0AP-1AP-0AP-6AP-0AP	ICARDA
ISEBON 42	Baca'S'/3/AC253//CI08887/CI05761/4/Cen/Bglo'S'	ICB95-0516-0AP-12AP-0AP-8AP-0AP	ICARDA
ISEBON 47	Baca'S'/3/AC253//CI08887/CI05761/4/Cen/Bglo'S'	ICB95-0516-0AP-17AP-0AP-7AP-0AP	ICARDA
ISEBON 48	Baca'S'/3/AC253//CI08887/CI05761/4/Cen/Bglo'S'	ICB95-0516-0AP-19AP-0AP-7AP-0AP	ICARDA
ISEBON 53	Aths/Lignee686/3/DeirAlla106//SvAsa/Attiki/4/Cen/Bglo'S'	ICB95-0522-0AP-8AP-0AP-8AP-0AP	ICARDA
ISEBON 56	Aths/Lignee686//Alanda/CI16155	ICB95-0394-0AP-12AP-0AP-10AP-0AP	ICARDA
ISEBON 59	Arta/KEEL	ICB09-0842-167AP-0AP	ICARDA
ISEBON 66	Alanda/Hamra/5/U.Sask.1766/Api//Cel/3/Weeah/4/Arar	ICB00-0842-107AI-0AI ICB01-1057-12TR-0AP	ICARDA
ISEBON 69	Soufara-02/3/RM1508/Por//WI2269/4/Hml-02/ArabiAbiad//ER/Apm	ICB01-1037-121R-0AP ICB92-0926-0AP-7AP-0AP-5TR-7TR-0AP	ICARDA
ISEBON 09	Soufara-02/3/RM1508/Pot//WI2269/4/Hml-02/ArabiAbiad//ER/Apm	ICB92-0926-0AP-7AP-0AP-51K-71K-0AP ICB92-0926-0AP-7AP-0AP-12TR-9TR-	ICARDA
		0AP	
ISEBON 85	Arizona5908/Aths//Lignee640/3/Lignee527/Ssn//Bc/4/Gloria'S'/Copal'S'	ICB94-0105-0AP-0AP-4AP-0AP-7TR-7TR- 0AP	ICARDA
ISEBON 88	Arizona5908/Aths//Lignee640/3/Lignee527/Ssn//Bc/4/Gloria'S'/Copal'S'	ICB94-0105-0AP-0AP-4AP-0AP-12TR- 2TR-0AP	ICARDA
ISEBON 90	Local check (Saese'a)		ETHIOPIA
ISEBON 90 ISEBON 92	Arizona5908/Aths//Lignee640/3/Lignee527/Ssn//Bc/4/Gloria'S'/Copal'S'	ICB94-0105-0AP-0AP-4AP-0AP-17TR-	ICARDA
		2TR-0AP	
ISEBON 93	Arizona5908/Aths//Lignee640/3/Lignee527/Ssn//Bc/4/Gloria'S'/Copal'S'	ICB94-0105-0AP-0AP-4AP-0AP-17TR- 6TR-0AP	ICARDA
ISEBON 94	Arizona5908/Aths//Lignee640/3/Lignee527/Ssn//Bc/4/Gloria'S'/Copal'S'	ICB94-0105-0AP-0AP-4AP-0AP-17TR- 8TR-0AP	ICARDA
ISEBON 96	Cr115/Por//Bc/3/Api/CM67/4/Giza120/5/H272/Bgs/3/Mzq/Gva//PI002917/6/BF891M-612	ICB95-0332-0AP-7AP-0AP-12TR-3TR- 0AP	ICARDA
Eritrea07 1	WI3159/6/ANCA/2469//TOJI/3/SHYRI/4/ATACO/5/ALELI	ICB01-1137-15AP-0AP	ICARDA
Eritrea07 3	Atahualpa/DD-21	ICB01-1165-36AP-0AP	ICARDA
Eritrea07 6	Keel/Demhay	ICB01-1105-50/u 0/u ICB02-0450-0AP-5TR-0AP	ICARDA
Eritrea07 7	Keel/Demhay	ICB02-0450-0AP-7TR-0AP	ICARDA
Eritrea07 9	Keel/Demhay	ICB02-0450-0AP-9TR-0AP	ICARDA
Eritrea07 11	Barque/Demhay	ICB02-0451-0AP-3TR-0AP	ICARDA
Eritrea07 23	Rika/Demhay	ICB02-0452-0AP-10TR-0AP	ICARDA
Eritrea07 23	Tilga/Demhay	ICB02-0452-0AI-101R-0AI ICB02-0453-0AP-3TR-0AP	ICARDA
Eritrea07 24	Tilga/Demhay	ICB02-0453-0AP-11TR-0AP	ICARDA
Eritrea07 34	WI3277/Demhay	ICB02-0455-0AP-3TR-0AP	ICARDA
Eritrea07 37	WI3277/Denhay	ICB02-0455-0AP-9TR-0AP	ICARDA
Eritrea07 40	WI3295/Demhay	ICB02-0456-0AP-2TR-0AP	ICARDA
	······································		-
Eritrea07 43	CI07117-9/DeirAlla106//Bda/3/Arar/5/11012- 2/Impele//Dirange/2/Arahi a higd/d/5604/1005/6/Demhey	ICB02-0458-0AP-1TR-0AP	ICARDA
Eritrea07 62	2/Impala//Birence/3/ArabiAbiad/4/5604/1025/6/Demhay DD-21/Atsa	ICB02-0469-0AP-9TR-0AP	ICARDA
Eritrea07 62 Eritrea07 64	Burguda_2R/Demhay	ICB02-0409-0AP-91R-0AP ICB02-0476-0AP-2TR-0AP	ICARDA
Eritrea07 64 Eritrea07 72		ICB02-04/6-0AP-21R-0AP ICB99-0729-0AP-4AP-0AP	
	Saesea/Atahualpa		ICARDA
Eritrea07 73	Saesea/Atahualpa DD-21	ICB99-0729-0AP-6AP-0AP	ICARDA
Eritrea07 74		Sel-1AP-0AP-0AP-7AP-0AP ICB00-1222-39AP-0AP	ICARDA
Eritrea07 81	BSH-19/Atahualpa		ICARDA
Eritrea07 82	Saaaaa/Atabualma		ICARDA
EDETIIO7 2	Saesea/Atahualpa	ICB00-1226-16AP-0AP	
ERETH07 2	Mzq/Gva//PI002917/3/WI2291/WI2269/4/BSH-25	ICB00-0415-0AP-2AP-0AP	ICARDA
ERETH07 5	Mzq/Gva//PI002917/3/WI2291/WI2269/4/BSH-25 BSH-25/BSH-15	ICB00-0415-0AP-2AP-0AP ICB00-0439-0AP-8AP-0AP	ICARDA ICARDA
ERETH07 5 ERETH07 11	Mzq/Gva//PI002917/3/WI2291/WI2269/4/BSH-25 BSH-25/BSH-15 BSH-15/Saesea	ICB00-0415-0AP-2AP-0AP ICB00-0439-0AP-8AP-0AP ICB00-0453-0AP-8AP-0AP	ICARDA ICARDA ICARDA
ERETH07 5 ERETH07 11 ERETH07 13	Mzq/Gva//PI002917/3/WI2291/WI2269/4/BSH-25 BSH-25/BSH-15 BSH-15/Saesea BSH-15/Lignee1335	ICB00-0415-0AP-2AP-0AP ICB00-0439-0AP-8AP-0AP ICB00-0453-0AP-8AP-0AP ICB00-0456-0AP-1AP-0AP	ICARDA ICARDA ICARDA ICARDA
ERETH07 5 ERETH07 11 ERETH07 13 ERETH07 25	Mzq/Gva//PI002917/3/WI2291/WI2269/4/BSH-25 BSH-25/BSH-15 BSH-15/Saesea BSH-15/Lignee1335 Shege/Rika	ICB00-0415-0AP-2AP-0AP ICB00-0439-0AP-8AP-0AP ICB00-0453-0AP-8AP-0AP ICB00-0456-0AP-1AP-0AP ICB04-0203-0AP	ICARDA ICARDA ICARDA ICARDA ICARDA
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ERETH07 5 ERETH07 11 ERETH07 13 ERETH07 25 ERETH07 29 ERETH07 31	Mzq/Gva//PI002917/3/WI2291/WI2269/4/BSH-25 BSH-25/BSH-15 BSH-15/Saesea BSH-15/Lignee1335 Shege/Rika Burguda/Birka Misratch/Osiris	ICB00-0415-0AP-2AP-0AP ICB00-0439-0AP-8AP-0AP ICB00-0453-0AP-8AP-0AP ICB00-0456-0AP-1AP-0AP ICB04-0203-0AP ICB04-0208-0AP ICB04-0210-0AP	ICARDA ICARDA ICARDA ICARDA ICARDA ICARDA
ERETH07 5 ERETH07 11 ERETH07 13 ERETH07 25 ERETH07 29 ERETH07 31 ERETH07 39	Mzq/Gva//PI002917/3/WI2291/WI2269/4/BSH-25 BSH-25/BSH-15 BSH-15/Saesea BSH-15/Lignee1335 Shege/Rika Burguda/Birka Misratch/Osiris Bakur/Dumari	ICB00-0415-0AP-2AP-0AP ICB00-0439-0AP-8AP-0AP ICB00-0453-0AP-8AP-0AP ICB00-0456-0AP-1AP-0AP ICB04-0203-0AP ICB04-0208-0AP ICB04-0210-0AP ICB04-1102-0AP	ICARDA ICARDA ICARDA ICARDA ICARDA ICARDA ICARDA ICARDA
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Table 1. List of barley genotypes their code, name, pedigree and Origin

No.	Characters	Code/scores	Description
1	Lemma awn/hood	1	Awn less
	(LAH) :	2	Awnleted
		3	Awned
		4	Sessile hoods and
		5	Elevated hoods
2	Glume color (GC) :	1	White
		2	Yellow
		3	Brown and
		4	Black
3	Awn color (AC) :	1	Amber/ white
		2	Yellow
		3	Brown
		4	Reddish
		5	Black
4	Kernel covering (KC) :	1	Naked grain
		2	Semi-covered
			grain
		3	Covered grain
5	Grain (pericarp) color	1	White
	(PC):	2	Tan/red
		3	Purple
		4	Black/gray
6	Row number/ lateral	1	Two rowed
	florets (RN):	2	six rowed
		3	Irregular
7	Spike density (SD) :	3	Lax
		5	Intermediate
		7	Dense

 Table 2. Qualitative characters studied and their

 descriptions as per IPGRI descriptor list of 1994.

Cluster analysis (CA)

The qualitative variables were quantified by using appropriate scale (IPGRI, 1994). The associations among the accessions for qualitative traits were examined by hierarchical agglomerative cluster analysis of observations using proc cluster of observations using proc cluster of SAS with average linkage method of clustering strategy (SAS Institute, 2008).

Result and Discussion

Phenotypic frequency and diversity index

The frequency of distribution and amount of traits was found to be similar across locations. Caryopsis type is one character that is used for barley classification both under the traditional and the modern systems that is easier for routine application. Formal taxonomy (Orlov and Åberg 1941; Grillot 1959) begins with spike row number, but also uses caryopsis type as one of the essential criteria since it is a distinct character on the spike. Two rowed types were more common (60.94%) than six rowed (31.25%) and irregular (7.81%). Similarly, Fetien et al. (2009) reported that, two rowed types were more common (40.2%) than irregular-deficient (37.7%)and six rowed (22.2%). Spike density is another important qualitative trait, that dense spike length had relatively higher yield as compared to the lax one. On the other hand, lax spike density had better resistance to fusarium head blight (Thin, 2006). It was observed that from these barley genotypes had a spike density of which 6.25% were lax, 64.06% intermediate and 29.69% dense.

Three types of seed/kernel colors, as quality criteria observed were white, tan/red and black in the percentage of 96.87%, except the genotypes Eritrea 07 1, and ISEBON 14 with a seed color of tan red and black respectively added to the variability of 1.56% each. Similarly, Fetien et al. (2009) reported that, most of the populations were white (71.5%) than black (15.5%) purple (0.4%) and red (12.6%).

There was a similar trend for the trait Lemma/awnhood across locations that is all the testing entries were awnletted. Efforts to improve barley have demonstrated a preference for a limited number of modern, genetically uniform cultivars. Caryopsis type was used as a morphological character, where barley types can be easily categorized into three major groups as hulled (covered), hull-less (naked), and partially hulled (semi-covered) types. From this study it had been observed that the percentage of the genotypes were, 21.88%, 10.94% and 65.64% stands for naked, semi-covered and covered types respectively across locations. The farmers claimed that their frequency has diminished, and they are being replaced by covered types, which they regarded as hardier and higher yielding. Some hull-less and some partially hulled types owe their existence to women who cultivate them in small plots around living quarters with loving care. While men generally considered the hull-less type more demanding in the field, low yielding, and short lasting, women value them highly as they are less labor intensive to prepare (Zemede, 2000). Therefore, identifying this trait from the introduced ICARDA barley materials was so far important to address a gender sensitive issue (criteria) through agriculture.

Estimates of diversity for individual qualitative characters were indicated in Table 3. Polymorphism was common in varying degrees for most characters, thus implying the existence of wide range of variation in the materials. The H' values ranged from 0.00 (monomorphic) for lemma/ hood to 0.86 which is with the highest polymorphic for row number. In addition, character wise phenotypic diversity was obtained for awn color (H'= 0.71), kernel covering (H'=0.84) and spike density (H'=0.82) revealed the high diversity. Glume color (H'=0.34) and gain color (H'=0.16), relatively showed the lower diversity. That is, majority of the population tends to fall within the same state, so that these barley genotypes are not highly diversified for these two traits. Similarly, Fasil et al. (2001) reported that high variation was observed for kernel row number (H' = 0.95), spike density (H' = 0.95), rachilla length (H' = 0.94), glume awn length (H' = 0.91).

Table 3. Estimates of frequency and diversity index for

Quantative characters								
Trait	State	Code	Freq.	%	H'			
LAH	Awned	3	64	100.00	0.00			
	Awnless	1	0	0.00				
GC	White	1	54	84.38	0.43			
	Brown	3	10	15.63				
AC	Amber/white	1	42	65.63	0.71			
	Brown	3	21	32.81				
	Reddish	4	1	1.56				
KC	Naked	1	14	21.88	0.84			
	Semi-naked	2	7	10.94				
	Covered	3	43	67.19				
RN	Two-row	1	39	60.94	0.86			
	Six-row	2	20	31.25				
	Irregular	3	5	7.81				
SD	Lax	3	4	6.25	0.82			
	Intermediate	5	41	64.06				
	Dense	7	19	29.69				
GPC	White	1	45	96.88	0.16			
	Tan/red	2	1	1.56				
	Black/gray	4	18	28.13				

Frequency = Frequency of genotypes for a Trait, %= Percentage of the frequency, LAH= Lemma/Awn Hood, GC= Glume Color, AC= Awn Color, KC= Kernel Covering, RN= Row Number and SD= Spike Density, GPC= Grain/ pericarp Color.

Cluster analysis

Clustering was made to group the study barley materials into components based on their qualitative traits (Figure 1). The dendrogram obtained from the cluster analysis grouped the 64 genotypes into six clusters across location, based on the value of Pseduo F and Pseduot-square value. The dendrogram was combined across locations because except for the trait auricle pigmentation, which showed a little differentiation at Atsbi more than 90% of the genotypes, obtained in the same cluster group. Cluster II had the largest member of all clusters, included 26 (40.63%) genotypes, followed by cluster I and III which included 15 (23.44%) genotypes each. Similarly, cluster V constituted 3 (4.69%) genotypes followed by cluster IV which included 2 genotypes (3.13%), and cluster VI consisted of the smallest group 1 (1.56%) genotype. This cluster analysis revealed that qualitative traits were highly heritable ones and less environmentally affected. Similarly, Ahmed et al. (2008) grouped 35 barely accessions. The results showed that, corresponding to the barley row-type, the 32 accessions and three checks clustered into two main clusters; the first cluster consists of accessions, which have two-row type. The second cluster consists of all accessions of six-row type.

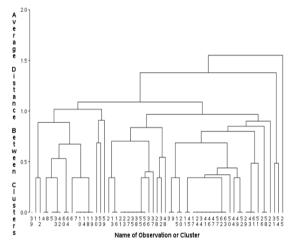


Figure 2. Dendrogram showing the clusters for Qualitative traits of 64 ICARDA's barley genotypes tested in three locations of Tigray, 2009.

Conclusion

Three types of seed/kernel colors, as quality criteria observed were white, tan/red and black in the percentage of 96.87%, except the genotypes Eritrea07 1, and ISEBON 14 with a seed color of tan red and black respectively added to the variability of 1.56% each. From this study, 60.69 % found as two-row type, 31.26% six-row types and 7.81% irregular type across locations. It was observed that from these barley genotypes had a spike density of which 6.25% were lax, 64.06% intermediate and 29.69% dense. All the testing entries were awnletted. It was observed that the caryopsis or kernel covering with a percentage of the genotypes were, 21.88%, 10.94% and 65.64% stands for naked, semi-covered and covered types respectively across locations.

The phenotypic diversity index values for qualitative traits ranged from 0.0 (monomorphic) for lemma/ hood to 0.86 high polymorphic for row number. In addition, character wise phenotypic diversity was obtained for awn color (H'= 0.71), kernel covering (H'=0.84) and spike density (H'=0.82) revealed the highest diversity. Glume color (H'=0.34) and gain color (H'=0.16), relatively showed the lowest diversity. The results showed that there is wide diversity among the

sample germplasm studied for the qualitative traits. This information can be used for the conservation of these germplasm resources and future improvement work of the barley crop.

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