



Genetic Diversity and Relatedness among Barley (*Hordium vulgare* L.) Landraces from Diverse Ecological Zones of Pakistan

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Abstract: Barley landraces are the major genetic resources of cultivated barley in Ethiopia. Lack of adequate information on extent of landraces diversity hinders conservation efforts and proper utilization of genetic resource. A field experiment was conducted in order to assess the extent of genetic diversity of barley landraces collection from Southern Ethiopia. A total of 76 genotypes were evaluated during 2019 main cropping season using augmented design at NARC Islamabad. Data were recorded for quantitative and qualitative characters. Analysis of variance indicated highly significant variation among 76 accessions except awn length. Genotypic Coefficient of Variations (GCV) varied from 4.36% for biological yield to 13.22% for number of fertile tillers per plant and phenotypic coefficient of variations varied from 6.40% for plant height to 16.27% for spike length. Estimate of broad sense heritability varied from 38.75% for spike length to 78.13 for grain yield. Estimates of genetic advance as percent of mean ranged from 7.61% for plant height to 23.01% for number of fertile tillers per plant. Phenotypic and genotypic correlation analysis indicated that grain yield had positive and significant phenotypic and genotypic correlation with days to maturity, grain filling period and plant height, number of fertile tillers per plant, thousand seed weight, harvest index and biological yield. Path analysis revealed that plant height, thousand seed weight and number of fertile tillers per plant showed positive and highest direct effect on grain yield. Cluster analysis grouped 105 genotypes into five groups and one genotype remains ungrouped. Principal component analysis revealed that the variance of 31, 15, 12, 10 and 9% were extracted for first five PCs, respectively which contributed 78% of total variation among genotypes. Estimate of Shannon -Weaver diversity index H' varied from 0.09 for hoodedness to 0.97 for

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kernel row number. Pooled over all traits within each zone, H' value ranged from 0.48 for Sidama to 0.69 for South Omo and individual trait showed different levels of diversity across different zones. In general, the result indicated the existence of wider diversity among the barley collection, showing opportunity to improve

important traits of the crop and need to conserve the diversity. As future line work further investigation with inclusion of informative molecular markers and covering different producing area of the region will allow to provide the complete picture of existing diversity.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is a major cereal crop belongs to family Poaceae and of genus *Hordeum* which grow in different ecologies world widely^[1]. Barley is oldest domesticated crops which was originated about ten thousand years ago in the fertile Crescent of Middle east from two rowed wild progenitor (*H. vulgare* L.)^[2]. Barley is 4th most important cultivated crop in the world and its total production is 149 million tons^[3]. According to Mohtashami^[4] barley is second most cultivated cereal crop after wheat in Iran. Barley is a drought and salt tolerated crop. It can grow better in adverse agro climatic conditions, as well as rain fed areas^[5]. Barley can adjust itself to various circumstances and tolerated to numerous abiotic features, like high and low temperature, salty environment and aquatic pressure^[6]. The domesticated barley and their wild ancestor are involved in the prime gene pool (Ferreira *et al.*^[1] and Wild kind have high allelic variations as compare to cultivated one^[7]. It is the fourth important world cereal crop and fifth by cultivation among cereals throughout the world which is mainly used as animal feed, beer and human food^[8].

According to Din *et al.*^[5] barley is used in bread making and other human food and beverages soup lather etc. Barley bread is of in numerable cultures. Gluten is the main ingredient of barley, distilled and base malt beer. Barley with hundreds of landraces and cultivars is common in those areas where adaptation of other crops is difficult, yet it is weakened genetically, especially because of pure breeding and needs genetic reinforcement. *H. spontaneum*, the greatest courage for barley advancement, is a strong environmental generalist, adapted to various kinds of extreme latitudes, altitudes, climates and soils. Its adaptations occur at all levels like genomically, proteomically and phenomically both regionally and locally. Barley has significant nutritional characterizations and it is a best container of various nutrients which includes dietetic stuff mainly beta glucan, mineral deposits and unsaturated fats. The concentration of Protein are different in barley which range from 10-15% but on the basis of end use the range is broader from 7-25% in better varieties^[9]. Dietary fibers in barley ranged from 11-34% DM and soluble dietary fiber from 3-20% DM^[10]. It also comprises a good amount of phenolics and has anti-oxidant stuffs^[11]. Important nutritional macro-element minerals for example phosphorus, calcium, magnesium, potassium and sodium

and micro-elements minerals like iron, manganese, zinc, selenium and cobalt are present in seed of barley^[12]. Wild type barley consists of many genes that enable it to adapt to numerous abiotic and biotic factors^[13]. Genetic diversity inside and amongst crop plant species is necessity for plant survival in nature and crop improvement. Variation in genetic resources permits selection of superior genotypes and emerging advance and developed cultivars with wanted traits for breeders^[14]. Various studies showed about the genetic diversity among Barely varieties are given, i.e., Wenzl *et al.*^[15] conducted that the value of the DArT charts were comparable, if not higher, as compare to framework map. These outcomes climax the prospective of DArT as a generic procedure for genome wherever, according to International Barley Genome Sequencing Consortium^[16] established a data which make available a display place for both genome assisted research and permitting current crop development. Allard and Jain^[17] studied the functions of population variability in both short term success and long term survival among population. Jaradat *et al.*^[18] found the variety for salt acceptance in barley landraces which will enable their usage in genetic development while according to Amezrou *et al.*^[19] plant breeders take interest in the usage of varied genotypes in hybridization that can separate for traits of significance with opportunity of assortment and genetic gain. Genetic markers can be classified into morphological markers, protein markers and DNA markers. Assessment of genetic variability based on morphological traits is time-consuming^[20]. It shows archipelago genetic assembly which is genetically rich and harbors immense adaptive abiotic and biotic resistances precious to barley and cereal improvement. Sequencing the *H. spontaneum* genome will reveal huge, mostly untapped, genetic resources. Nowadays the stresses and global warming are responsible for the big loss of *H. spontaneum* and so it is vital to conserve this cereal crop in *in situ* and in *ex situ* condition to maintain it for future^[21]. Therefore, study on arrangement of landraces variation is the main attention for effective preservation and application of genetic means.

MATERIALS AND METHODS

Description of study site and collection of data: Current experiment was conducted in the field of NARC (National agriculture research centre) Islamabad during the growing

Table 1: Table of Genetic material

Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc
35860	35861	35862	35863	35864	35865	36725	36728
36743	37247	37248	37249	37250	37251	37252	37253
37254	37255	37256	37257	37258	37259	37260	37261
37262	37263	37264	37265	37266	37267	37268	37269
37270	7999	8000(1)	8000(2)	8001	8003(2)	8003(7)	8004(4)
8005	8006	8007	8008(1)	8009	8010	8011(3)	8011(4)
8015(3)	1264	8024(2)	1400	1629	1631	1639	1644
1659	1797	1798	1799	1801	1802	1803	1806
1822	1825	1828	Local Bajuar	Khumasay	Malana	Zeran	Malana
Yousaf Khail	ICBA barley	Jau-83	Snober 96	4044	4063	4113	4119
4157	4159	4165	4166	4168	4191	4271	4290
4298	4319	4322	4323	4324	4325	4328	4329
4331	4332	4333	4334	4335	4336	4342	4343
4344	4345	4346	4347	4357	4359	4369	4382
4399	4400	4410	4418	4419	4420	4450	4451
4452	4455	4456	4457	4476	4494	4498	4503
4507	4531	4532	4554	4557	4558	4569	4599
4600	4601	4615	4635				

Table 2: List of control varieties

Control	Control
Jau-2017	Sultan-2017

season of 2019. Total 76 accessions were planted showed in Table 1 and 2 and in experiment Randomized Complete Block Design (RCBD) were followed.

Parameters evaluated: Data were recorded for following parameters.

Days to 50% flowering: Days to flowering was noted from date of sowing to when 50% plants start flowering in each accession. Days to flowering was counted in days.

Days to 80% maturity: The total number of days from sowing till it reaches to maturity was recorded.

Plant height (cm): Plant height was measure from soil surface to tip of the plant.

Number of tillers per plant: Number of tillers was counted by the number of shoots in addition to the main stem of five plants in each accession.

Spikes density: Spikes density was measure through a subjective observation of barley spikes when 100% of plant spikes were comes out in a growing accession. Either spike was lax, intermediate or dense.

Number of spikes per plant: Total number of spikes was counted from 5 selected plants in each accession.

Number of seeds per plant: Total number of seeds from each 5 typical selected plants in each accession was taken.

Number of spikelet's group (triplets) per spike: An average of 5 typical spikes was select from a growing accession.

Awn type: An awn or (bristle-like appendage) was check for either it's smooth or rough. This data was recorded from 5 plants in each accession.

Spike length without awn: Total length of spike was measure from base to the tip excluding awns. Data of 5 plants were recorded.

Spike length with awn: Total length of spike was measure including awn (cm) using measuring scale. Data were recorded from 5 selected plants in each accession.

Length of rechilla hair: Length of rechilla was categorized into 2 categories (short or long) on the basis of length of hairs on rechilla. It was observe by using magnifying glass. Data were taken from 5 selected plants in each accession.

Row number/lateral florets: The total number of rows in spike of 5 plants in each line was checked to see if it is either two or six rowed.

Spikes color: Spikes color was recorded from 5 plant of each accession before maturity of spikes.

The 100 seed weight: Seed weight was counted after thrashing of barley spikes of each accession.

Protein analysis: Cluster analysis of data for seed storage proteins on the basis of SDS-PAGE electrophoresis results was conducted using unweight Pair Group Matrix Average (UPGMA) Method. Statistica 7.0 was used for cluster analysis and construction of dendrogram.

Statistical analysis: The Data of the above parameters were analyzed by statistical package statistic 8.1, to calculate the Genetic variability and correlation coefficients for different parameters of genotypes. Least significant differences (LSD) was also applied.

RESULTS AND DISCUSSION

Time to 50% flowers formation: ANOVA (Analysis of variance) indicated non significant differences of accessions for days to 50% flowering. The coefficient of variation was 8.13% of accessions for days to 50% flowering (Table 3).

Average value of accessions for days to 50% flowers formation ranged from 114 to 164 days, while maximum days of all studied accessions was found for accessions 37252 (164 days) which is followed by accessions 37251, 37268 and 37249. Least days to 50% flowering were found for accessions 1629, 1801, 1802, 1803, 1806, 1822 and 1825 (114 days) (Table 4). Days to 50% flowering didn't show high variation in statistical analysis. Days towards 50% flowers formation revealed positive and significant and association with days to when plant

mature, height of plant, seeds in each plant and kernel yield of each plant while time to when 50% flowers formed showed non-significant association with spike length with awn, spike length without awn, hundred seed weight. Days to 50% flowering showed negative association with tillers per plant, spikelets per plant (Table 4).

Caccarelli *et al.*^[22] and Parzier *et al.*^[23] found non-significant differences of accessions for days to 50% flowers formation.

Days to 80% maturity: ANOVA (Analysis of variance) indicated significant difference of accessions for days 80% maturity. The coefficient of variation was 4.39% of accessions for days to 80% maturity (Table 5). Average value of accessions for days to 80% maturity ranged from 153-186 days while maximum days of all studied

Table 3: ANOVA table of Days to when 50% flowers formed

SOV	DF	SS	MS	F-value	p-value
Rep	3	2770.4	923.46		
Accessions	18	958.1	53.23	0.427927	0.09751
Error	54	6716.8	124.38		
Total	75	10445.2			

CV = 8.13

Table 4: Mean table of days to 50% flowering

Accession	DTF	Accession	DTF	Accession	DTF
35860	135 ^a	37264	142 ^a	1639	133 ^a
35861	135 ^a	37265	141 ^a	1644	140 ^a
35862	119 ^a	37266	135 ^a	1659	131 ^a
35863	135 ^a	37267	135 ^a	1797	119 ^a
35864	149 ^a	37268	156 ^a	1798	119 ^a
35865	141 ^a	37269	140 ^a	1799	119 ^a
36725	149 ^a	7999	139 ^a	1801	114 ^a
36728	149 ^a	8000 (1)	135 ^a	1802	114 ^a
36743	151 ^a	8000 (2)	135 ^a	1803	114 ^a
37247	141 ^a	8001	140 ^a	1806	114 ^a
37248	151 ^a	8003 (2)	140 ^a	1822	114 ^a
37249	154 ^a	8003 (7)	135 ^a	1825	114 ^a
37250	151 ^a	8004 (4)	138 ^a	1828	119 ^a
37251	161 ^a	8005	139 ^a	Local Bajaur	138 ^a
37252	164 ^a	8006	140 ^a	Khumasay	142 ^a
37253	149 ^a	8008 (1)	141 ^a	Malana	141 ^a
37254	133 ^a	8009	141 ^a	Zeran	141 ^a
37255	151 ^a	8010	141 ^a	Malana	141 ^a
37256	128 ^a	8011 (3)	141 ^a	Yousaf Khail	140 ^a
37257	152 ^a	8011 (4)	140 ^a	ICBA Barley	138 ^a
37258	149 ^a	8015 (3)	140 ^a	Jau-83	140 ^a
37259	152 ^a	1264	136 ^a	Snober-96	140 ^a
37260	141 ^a	8024 (2)	136 ^a	Jau-2017	138 ^a
37261	140 ^a	1400	119 ^a	Sultan-2017	142 ^a
37262	139 ^a	1629	114 ^a		
37263	141 ^a	1631	119 ^a		

LSD^{0.05} of Genotypes = 15.81

Table 5: ANOVA table of days to maturity

SOV	DF	SS	MS	F value	p-value
Rep	3	3042.8	1014.267		
Accessions	75	122.05	1.627333	0.126472	0.03751
Error	225	2895.1	12.86711		
Total	303	6059.9			

CV = 4.39

Table 6: Mean value of days to maturity

Accession	DTM	Accession	DTM	Accession	DTM
35860	162 ^a	37264	170 ^a	1639	153 ^a
35861	163 ^a	37265	166 ^a	1644	164 ^a
35862	155 ^a	37266	167 ^a	1659	166 ^a
35863	163 ^a	37267	172 ^a	1797	159 ^a
35864	178 ^a	37268	176 ^a	1798	159 ^a
35865	174 ^a	37269	173 ^a	1799	158 ^a
36725	177 ^a	7999	172 ^a	1801	153 ^a
36728	178 ^a	8000 (1)	177 ^a	1802	153 ^a
36743	179 ^a	8000 (2)	171 ^a	1803	153 ^a
37247	174 ^a	8001	171 ^a	1806	153 ^a
37248	179 ^a	8003 (2)	172 ^a	1822	153 ^a
37249	178 ^a	8003 (7)	171 ^a	1825	153 ^a
37250	182 ^a	8004 (4)	169 ^a	1828	157 ^a
37251	186 ^a	8005	172 ^a	Local Bajaur	161 ^a
37252	174 ^a	8006	169 ^a	Khumasay	159 ^a
37253	179 ^a	8008 (1)	170 ^a	Malana	160 ^a
37254	169 ^a	8009	171 ^a	Zeran	158 ^a
37255	178 ^a	8010	168 ^a	Malana	157 ^a
37256	170 ^a	8011 (3)	168 ^a	Yousaf Khail	156 ^a
37257	178 ^a	8011 (4)	166 ^a	ICBA Barley	160 ^a
37258	179 ^a	8015 (3)	165 ^a	Jau-83	156 ^a
37259	178 ^a	1264	163 ^a	Snober-96	166 ^a
37260	179 ^a	8024 (2)	153 ^a	Jau-2017	170 ^a
37261	165 ^a	1400	153 ^a	Sultan-2017	172 ^a
37262	166 ^a	1629	153 ^a		
37263	165 ^a	1631	153 ^a		

LSD^{0.05} of Genotypes = 10.38

Table 7: Table of ANOVA for height (cm) of plant

SOV	DF	SS	MS	F-value	p-value
Rep	3	598.8	199.6		
Accessions	75	1672.3	22.29733	0.888718	0.04935
Error	225	5645.1	25.08933		
Total	303	7916.1			

CV = 8.41%

accessions was found for accessions 37251 (186 days) which is followed by accessions 37250, 37248 and 37243. Least days to 80% maturity were found for accessions 1629, 1801, 1802, 1803, 1806, 1822, 1825, 1400, 1631, 1639 and 8024(2) (153 days) (Table 6). Days to 80% maturity showed high variation in statistical analysis. Days to maturity of 80% plants revealed significant and positive and associated with days to 50% flowers formation and kernel yield of each plant while days to when 80% plants mature showed non-significant relation to plant height, spike length with awn, seeds per plant and hundred seed weight. Days to when 50% flowers formed showed negative association with tillers in each plant, length of spike without awn, spikelets in each plant.

Kebebew *et al.*^[24] and Hamza *et al.*^[25] found similarly significant variances of accessions for days to when 80% plants mature.

Plant height (cm): ANOVA (Analysis of variance) showed significant variance of accessions for height of plant. Coefficient of variation was 8.41% of accessions for plant height (Table 7).

Average value of accessions for plant height ranged from 99.6-145.4 cm while maximum plant height of all

studied accessions was found for accessions 8000 (1) (145.4 cm) which is followed by accessions 37267, ICBA Barley 37252 and 37260. Least plant height were found for accessions 8024 (2) (99.6 cm), followed by 37254, 1801, 1639 (Table 8). Plant height showed high variation in statistical analysis. Height of Plant revealed significant and positive and link with seed per plant, yield of seed of each plant and days to when 50% flowers formed while plant height indicated non-significant association with spike length with awn, spikelet per spike, maturity days and hundred seed weight.

ANOVA (Analysis of variance) showed significant variance of accessions for height of plant. Manjunatha *et al.*^[26] and Malysheva-Otto *et al.*^[27] also found significant variances of accessions for plant height.

Number of tillers in each plant: ANOVA (Analysis of variance) revealed significant variation of accessions for tillers quantity in each plant. The coefficient of variation was 29.44% of accessions for number of tillers per plant (Table 9).

Average value of accessions for numbers of tiller in each plant ranged from 9.2-32.0 while maximum numbers of tillers in each plant of all studied accessions was found

Table 8: Mean table of plant height (cm)

Accession	PH	Accession	PH	Accession	PH
35860	115.2 ^b	37264	130.8 ^a	1639	105.2 ^b
35861	121.8 ^{ab}	37265	131.0 ^a	1644	112.2 ^b
35862	109.0 ^b	37266	130.8 ^a	1659	123.6 ^{ab}
35863	115.4 ^b	37267	137.8 ^a	1797	121.4 ^{ab}
35864	115.8 ^b	37268	106.6 ^b	1798	113.6 ^b
35865	115.8 ^b	37269	124.4 ^{ab}	1799	109.8 ^b
36725	124.4 ^{ab}	7999	125.6 ^{ab}	1801	102.2 ^b
36728	113.4 ^b	8000 (1)	145.4 ^a	1802	111.2 ^b
36743	112.0 ^b	8000 (2)	124.8 ^{ab}	1803	110.8 ^b
37247	129.2 ^{ab}	8001	121.4 ^{ab}	1806	110.0 ^b
37248	126.4 ^{ab}	8003 (2)	129.8 ^a	1822	115.2 ^b
37249	129.8 ^a	8003 (7)	110.0 ^b	1825	106.0 ^b
37250	136.2 ^a	8004 (4)	119.4 ^{ab}	1828	115.2 ^b
37251	115.2 ^b	8005	116.2 ^b	Local Bajaur	134.6 ^a
37252	137.2 ^a	8006	136.2 ^a	Khumasay	134.4 ^a
37253	116.2 ^b	8008 (1)	131.2 ^a	Malana	134.0 ^a
37254	101.6 ^b	8009	116.0 ^b	Zeran	131.8 ^a
37255	109.8 ^b	8010	133.0 ^a	Malana	135.4 ^a
37256	117.8 ^b	8011 (3)	118.6 ^{ab}	Yousafkhail	134.8 ^a
37257	116.4 ^b	8011 (4)	124.2 ^{ab}	ICBA Barley	137.4 ^a
37258	117.8 ^b	8015 (3)	133.8 ^a	Jau-83	121.0 ^{ab}
37259	118.2 ^{ab}	1264	115.6 ^b	Snober-96	119.0 ^{ab}
37260	136.6 ^a	8024 (2)	99.6 ^b	Jau-2017	127.8 ^{ab}
37261	124.4 ^{ab}	1400	118.8 ^{ab}	Sultan-2017	121.4 ^{ab}
37262	130.6 ^a	1629	113.8 ^b		
37263	133.0 ^a	1631	115.2 ^b		

LSD^{0.05} of Genotypes = 14.50

Table 9: ANOVA table of number of tiller per plant

SOV	DF	SS	MS	F value	p-value
Rep	3	513.76	171.2533		
Accessions	75	391.4	5.218667	1.023357	0.045
Error	225	1147.4	5.099556		
Total	303	2052.57			

CV = 29.44

Table 10: Mean table of number of tillers per plant

Accession	TP	Accession	TP	Accession	TP
35860	12.2 ^c	37264	11.6 ^c	1639	15.2 ^{abc}
35861	14.4 ^{abc}	37265	14.8 ^{abc}	1644	17.2 ^{abc}
35862	12.8 ^{bc}	37266	11.4 ^c	1659	12.2 ^c
35863	11.2 ^c	37267	12.4 ^{bc}	1797	12.4 ^{bc}
35864	11.8 ^c	37268	13.8 ^{bc}	1798	12.6 ^{bc}
35865	12.6 ^{bc}	37269	11.4 ^c	1799	14.2 ^{abc}
36725	13.6 ^{bc}	7999	14.6 ^{abc}	1801	15.4 ^{abc}
36728	10.2 ^c	8000 (1)	9.2 ^c	1802	17.2 ^{abc}
36743	14.0 ^{abc}	8000 (2)	15.4 ^{abc}	1803	26.4 ^a
37247	16.2 ^{abc}	8001	12.0 ^c	1806	12.8 ^{bc}
37248	9.4 ^c	8003 (2)	25.0 ^a	1822	16.2 ^{abc}
37249	9.4 ^c	8003 (7)	30.8 ^a	1825	19.2 ^a
37250	13.4 ^{bc}	8004 (4)	19.8 ^a	1828	16.4 ^{abc}
37251	10.4 ^c	8005	27.2 ^a	Local Bajaur	15.4 ^{abc}
37252	11.0 ^c	8006	25.2 ^a	Khumasay	13.8 ^{bc}
37253	12.2 ^{bc}	8008 (1)	29.6 ^a	Malana	15.8 ^{abc}
37254	11.6 ^c	8009	32.0 ^a	Zeran	12.2 ^c
37255	13.4 ^{bc}	8010	27.0 ^a	Malana	13.8 ^{bc}
37256	13.2 ^{bc}	8011 (3)	19.2 ^a	Yousaf Khail	14.2 ^{abc}
37257	14.0 ^{abc}	8011 (4)	21.0 ^a	ICBA Barley	15.4 ^{abc}
37258	13.6 ^{bc}	8015 (3)	13.4 ^{bc}	Jau-83	26.0 ^a
37259	13.2 ^{bc}	1264	15.4 ^{abc}	Snober-96	13.4 ^{bc}
37260	14.8 ^{abc}	8024 (2)	13.2 ^{bc}	Jau-2017	17.45 ^{abc}
37261	12.6 ^{bc}	1400	17.0 ^{abc}	Sultan-2017	18.75 ^a
37262	11.0 ^c	1629	13.2 ^{bc}		
37263	14.2 ^{abc}	1631	24.4 ^a		

LSD^{0.05} of Genotypes = 6.53

for accessions 8009 (32.0) which is followed by accessions 8003 (7), 8008 (1) and 8005. Least number of

tillers per plant were found for accessions 8000 (1) (9.2), followed by 37248, 37249, 36728 (Table 10). Number of

Table 11: Table of spike density

Code	Description	No. of Acc.	Age (%)
1	Lax	20	26.7
3	Intermediate	42	56.0
5	Dense	13	17.3

Table 12: Mean table of spikes per plant

Accession	SP	Accession	SP	Accession	SP
35860	11.6	37264	16.8	1639	6.0
35861	11.0	37265	13.2	1644	8.8
35862	9.6	37266	18.4	1659	9.0
35863	14.6	37267	10.8	1797	7.2
35864	8.4	37268	9.2	1798	11.2
35865	9.6	37269	14.8	1799	9.2
36725	12.8	7999	11.6	1801	7.0
36728	9.6	8000 (1)	9.2	1802	8.6
36743	9.6	8000 (2)	12.8	1803	7.0
37247	13.6	8001	9.4	1806	10.4
37248	8.6	8003 (2)	18.2	1822	10.0
37249	18.0	8003 (7)	12.2	1825	7.4
37250	13.2	8004 (4)	10.0	1828	8.2
37251	7.6	8005	14.8	Local Bajaur	11.6
37252	12.0	8006	5.8	Khumasay	19.0
37253	8.0	8008 (1)	13.8	Malana	11.8
37254	11.4	8009	12.4	Zeran	10.0
37255	10.2	8010	17.6	Malana	16.2
37256	12.6	8011 (3)	22.0	Yousaf Khail	10.0
37257	12.6	8011 (4)	20.6	ICBA Barley	9.0
37258	7.6	8015 (3)	11.6	Jau-83	19.4
37259	13.4	1264	7.8	Snober-96	15.2
37260	13.2	8024 (2)	6.8	Jau-2017	20.45
37261	13.6	1400	8.0	Sultan-2017	17.8
37262	26.0	1629	6.8		
37263	23.0	1631	7.0		

tillers per plant showed high variation in statistical analysis. Numbers of tiller in each plant did not show significant and positive and association to any parameter while number of tillers per plant showed non significant link to seed in each plant, yield of seed in plant and spikelets in each spike.

ANOVA (Analysis of variance) revealed significant variation of accessions for tillers quantity in each plant. Brantestam *et al.*^[28] and Ahmad *et al.*^[29] also found significant variances of accession for number of tillers per plant in barley.

Spikes density: Spike density also showed high variation among different accessions and control variety of barley (Table 11). The spike density was classified into three classes, i.e., Lax, intermediate and dense. Around 42 genotypes showed intermediate spike density, 20 genotypes showed lax spike density, while only 13 genotypes showed dense spikes density. So as the resultant, maximum genotypes tend to intermediate spikes density. Brantestam *et al.*^[28] and Manjunatha *et al.*^[26] found alike results for spike density.

Number of spikes in each plant: ANOVA (Analysis of variance) revealed significant variance of accessions for the number of spikes per plant. The coefficient of variation was 35.21% of accessions for total spikes in

each plant (Table 11). Average value of accessions for total spikes in each plant ranged from 5.8-26.0 while maximum number of spikes per plant of all studied accessions was found for accessions 37262 (26.0) which is followed by accessions 37263, 8011 (3) and 8011 (4). Least number of spikes per plant were found for accessions 8006 (5.8), followed by 1639, 8024 (2), 1629 and 1801 (Table 12). Total number of spikes in each plant showed great variation in statistical analysis.

Spikes number in each plant revealed significant and positive and relation to yield of every plant seed, days to form 50% flowers, height of plant and hundred seed weight while total number of spikes in each plant showed non significant association with maturity days and total spikelets in a spike. Total number of spikes in a plant showed negative association with spike length with awn and length of spike without awn.

Hamza *et al.*^[25] and Manjunatha *et al.*^[26] also found significant variations of accessions for number of spikes in plant.

Number of spikelet's group (triplets) per spike: ANOVA (Analysis of variance) indicated significant variation of accessions for number of spikelet's per spike. Coefficient of variation was 14.91% of accessions for number of spikelet's per plant (Table 13). Average value of accessions for number of spikelet's per spike ranged

Table 13: ANOVA table of Number of spikelets group (triplets) per spike

SOV	DF	SS	MS	F-value	p-value
Rep	3	114.58	38.19333		
Accessions	75	114.74	1.529867	0.415519	0.09786
Error	225	828.41	3.681822		
Total	303	1057.73			

CV = 14.91%

Table 14: Mean table of number of spikelets group (triplets) per spike

Accession	SS	Accession	SS	Accession	SS
35860	28.0	37264	22.0	1639	23.2
35861	27.2	37265	30.8	1644	23.4
35862	29.0	37266	24.0	1659	24.0
35863	27.6	37267	30.0	1797	32.0
35864	24.0	37268	24.4	1798	17.4
35865	22.8	37269	27.4	1799	27.6
36725	27.6	7999	25.6	1801	28.0
36728	32.0	8000 (1)	31.6	1802	26.4
36743	19.2	8000 (2)	24.4	1803	27.2
37247	25.6	8001	25.2	1806	27.2
37248	17.6	8003 (2)	27.4	1822	28.8
37249	25.2	8003 (7)	29.2	1825	18.8
37250	27.6	8004 (4)	17.2	1828	33.2
37251	22.8	8005	22.0	Local Bajaur	29.6
37252	22.2	8006	26.8	Khumasay	31.2
37253	26.8	8008 (1)	28.4	Malana	22.8
37254	29.6	8009	23.2	Zeran	28.4
37255	20.0	8010	28.8	Malana	28.8
37256	29.6	8011 (3)	25.2	Yousaf Khail	27.2
37257	27.6	8011 (4)	27.2	ICBA Barley	26.8
37258	27.6	8015 (3)	19.2	Jau-83	26.8
37259	20.8	1264	23.2	Snober-96	25.2
37260	30.0	8024 (2)	29.2	Jau-2017	32.25
37261	25.6	1400	27.6	Sultan-2017	33.8
37262	30.8	1629	25.2		
37263	27.2	1631	26.8		

from 17.2-33.8 while maximum number of spikelet's per spike of all studied accessions was found for genotype Sultan-2017 (33.8) which is followed by accessions 1828, Jau-2017 and 36728. Least number of spikelet's per spike was found for accessions 8004 (4) (17.2), followed by 1798, 37248, 1825 and 36743 (Table 14). Number of spikelet's per spike showed high variation in statistical analysis.

Spikelets group present in a spike did not show significant and positive and link with any parameter while spikelets group in a spike showed non significant association with tillers group in a plant, plant height, length of spike with awn and without awn. Total group of spikelets in a spike showed negatively associated with days to formation of 50% flowers, days to when plant mature and hundred seed weight.

Kebebew *et al.*^[24] and Hamza *et al.*^[25] also found significant differences of accessions of barley for total number of spikelets group per spike.

Awn type: Awn type did not show high variation among different accessions and control variety of barley. The awn type was classified into two classes, i.e., Rough and smooth. There was all genotypes showed rough awn type, not single genotype showed smooth awn type (Table 15).

Table 15: Table for Awn type

Code	Description	No. of Acc.	Age (%)
1	Rough	75	100.0
3	Smooth	0	0.0

This results show, there is no variability among all studied genotypes for awn type. The awn type was classified into two classes, i.e., Rough and smooth. Kebebew *et al.*^[24] and Manjunatha *et al.*^[26] and found similarly the results of accessions of barley for awn type. There was all genotypes showed rough awn type, not single genotype showed smooth awn type. This results show, there is no variability among all studied genotypes for awn type.

Spike length without awn: Analysis of variance (ANOVA) showed significant difference of accessions for spike length without awn. The coefficient of variation was 16.13% of accessions for spike length without awn (Table 16).

Average value of accessions for spike length without awn ranged from 7.7-20.2 cm while maximum spike length without awn of all studied accessions was found for genotype 37252 (20.2 cm) which is followed by accessions 8000 (1), 37260, local Bajaur and 1801. Least spike length without awn was found for accessions 8004

Table 16: Table of ANOVA of Spikes length without awn

SOV	DF	SS	MS	F value	p-value
Rep	3	11.36	3.786667		
Accessions	75	57.75	0.77	1.270441	0.0244
Error	225	136.37	0.606089		
Total	303	205.5			

CV = 16.13%

Table 17: Mean table of spike length without awn

Accession	SLwA	Accession	SLwA	Accession	SLwA
35860	9.4 ^b	37264	9.5 ^b	1639	9.3 ^b
35861	8.9 ^b	37265	9.1 ^b	1644	9.1 ^b
35862	9.7 ^b	37266	9.8 ^b	1659	9.4 ^b
35863	7.8 ^b	37267	8.7 ^b	1797	8.7 ^b
35864	9.0 ^b	37268	11.4 ^b	1798	8.8 ^b
35865	9.2 ^b	37269	8.7 ^b	1799	9.5 ^b
36725	10.1 ^b	7999	9.3 ^b	1801	11.4 ^b
36728	8.9 ^b	8000 (1)	15.8 ^a	1802	9.7 ^b
36743	9.9 ^b	8000 (2)	10.3 ^b	1803	9.9 ^b
37247	11.0 ^b	8001	9.4 ^b	1806	11.0 ^b
37248	9.2 ^b	8003 (2)	9.8 ^b	1822	10.6 ^b
37249	8.9 ^b	8003 (7)	9.4 ^b	1825	10.0 ^b
37250	9.0 ^b	8004 (4)	7.7 ^b	1828	9.9 ^b
37251	8.8 ^b	8005	9.9 ^b	Local bajaur	12.0 ^b
37252	20.2 ^b	8006	8.9 ^b	Khumasay	10.0 ^b
37253	10.1 ^b	8008 (1)	8.7 ^b	Malana	10.1 ^b
37254	10.9 ^b	8009	8.9 ^b	Zeran	9.9 ^b
37255	10.9 ^b	8010	9.7 ^b	Malana	10.8 ^b
37256	10.2 ^b	8011 (3)	9.7 ^b	Yousaf Khail	9.9 ^b
37257	10.3 ^b	8011 (4)	7.9 ^b	ICbA barley	8.1 ^b
37258	9.7 ^b	8015 (3)	9.0 ^b	Jau-83	8.8 ^b
37259	8.4 ^b	1264	9.9 ^b	Snober-96	9.6 ^b
37260	12.5 ^b	8024 (2)	10.4 ^b	Jau-2017	10.1 ^b
37261	9.2 ^b	1400	9.1 ^b	Sultan-2017	10.5 ^b
37262	9.3 ^b	1629	9.4 ^b		
37263	9.5 ^b	1631	10.0 ^b		

LSD ^{0.05} of Genotypes = 2.25

Table 18: Table of ANOVA for Spikes length with awn

SOV	DF	SS	MS	F-value	p-value
Rep	3	9.46	3.153333		
Accessions	75	58.45	0.779333	1.450492	0.01466
Error	225	120.89	0.537289		
Total	303	188.82			

CV = 7.83%

(4) (7.7 cm), followed by 35863, 8011 (4), ICBA Barley and 37259 (Table 17). Spike length without awn showed high variation in statistical analysis.

Spike length without awn showed significant and positive and association with spike length with awn while spike length without awn showed non significant association to days of formation of 50% flowers, number of spikelets in a spike, seeds yield in a plant and hundred seed weight.

Manjunatha *et al.*^[26] and Ahmad *et al.*^[29] also found significant differences of accessions of barley for spike length without awn.

Spike length with awn: Analysis of variance (ANOVA) showed significant variations of accessions for spike length with awn. The coefficient of variation was 7.83% of accessions for spike length with awn (Table 18).

Average value of accessions for spike length with awn ranged from 14.4-22.1 cm while maximum spike length with awn of all studied accessions was found for genotype 8000 (1) (20.2 cm) which is followed by genotype Malana, accession 37251, 37248 and 1806. Least spike length with awn was found for accessions 35865 (14.4 cm), followed by 37247, 8004 (4), 35861 and 7999 (Table 19). Spike length with awn showed high variation in statistical analysis.

Spike length with awn revealed significant and positive and relations with spike length without awn while spike length with awn showed non significant association with days to 50% flowering, days to maturity, plant height, number of spikelets per spike, seed yield per plant and hundred seed weight.

Brantestam *et al.*^[28] and Malysheva-Otto *et al.*^[27] also found significant variances of accessions for spike length with awn.

Table 19: Mean table of spike length with awn

Accession	SLwoA	Accession	SLwoA	Accession	SLwoA
35860	18.0 ^c	37264	20.2 ^a	1639	18.6 ^{abc}
35861	16.6 ^c	37265	19.2 ^{abc}	1644	19.7 ^{bc}
35862	20.0 ^{ab}	37266	19.2 ^{abc}	1659	20.9 ^a
35863	17.0 ^c	37267	17.9 ^c	1797	18.5 ^{abc}
35864	17.3 ^c	37268	21.1 ^a	1798	19.4 ^{bc}
35865	14.4 ^c	37269	18.6 ^{abc}	1799	19.3 ^{bc}
36725	20.8 ^a	7999	17.1 ^c	1801	19.0 ^{bc}
36728	18.7 ^{abc}	8000 (1)	22.1 ^a	1802	19.3 ^{bc}
36743	19.1 ^{abc}	8000 (2)	18.9 ^{abc}	1803	18.3 ^{abc}
37247	15.5 ^c	8001	18.6 ^{abc}	1806	21.3 ^a
37248	21.6 ^a	8003 (2)	18.9 ^{abc}	1822	17.3 ^c
37249	18.6 ^{abc}	8003 (7)	20.3 ^a	1825	19.7 ^{bc}
37250	17.9 ^c	8004 (4)	15.9 ^c	1828	20.2 ^a
37251	21.8 ^a	8005	17.9 ^c	Local Bajaur	20.6 ^a
37252	21.1 ^a	8006	18.1 ^{bc}	Khumasay	21.2 ^a
37253	20.0 ^a	8008 (1)	16.3 ^c	Malana	20.4 ^a
37254	20.2 ^a	8009	16.9 ^c	Zeran	20.7 ^a
37255	18.0 ^c	8010	19.6 ^{bc}	Malana	21.9 ^a
37256	21.1 ^a	8011 (3)	19.8 ^{bc}	Yousaf Khail	20.0 ^a
37257	20.5 ^a	8011 (4)	17.8 ^c	ICBA Barley	18.0 ^c
37258	19.1 ^{abc}	8015 (3)	20.0 ^a	Jau-83	17.5 ^c
37259	17.5 ^c	1264	20.3 ^a	Snober-96	18.3 ^{bc}
37260	17.4 ^c	8024 (2)	20.4 ^a	Jau-2017	20.01 ^a
37261	18.4 ^{abc}	1400	20.0 ^a	Sultan-2017	20.91 ^a
37262	17.9 ^c	1629	17.8 ^c		
37263	19.6 ^{ab}	1631	19.4 ^{bc}		

LSD^{0.05} of Genotypes = 2.12

Table 20: Table of length of rechilla hair

Code	Description	No. of Acc.	Age (%)
1	Long	41	54.7
3	Short	34	45.3

Length of rechilla hair: Length of rechilla hair also showed high variation among different accessions and control variety of barley. The length of rechilla hair was classified into two classes, i.e., long and short length of rechilla hair (Table 20).

There was 41 genotypes showed long length of rechilla hair, 34 genotypes showed short length of rechilla hair. This results show the variation among the studied genotypes for length of rechilla hair (Table 20).

The length of rechilla hair was classified into two classes, i.e., long and short length of rechilla hair. Malysheva-Otto *et al.*^[27] and Manjunatha *et al.*^[26] also found high variation among different accessions of barley for length of rechilla hair.

Row number/lateral florets: Row number/lateral floret also showed high variation among different accessions and control variety of barley. The Row number/lateral floret was classified into three classes i.e. six rowed, four rowed and two rowed (Table 21).

There were 68 genotypes showed six rowed, 2 genotypes showed four rowed while 5 genotypes showed 5 two rowed. This results show the variation among the studied genotypes for row number/lateral florets (Table 21).

Table 21: Table of Row number/lateral florets

Code	Description	No. of Acc.	Age (%)
1	Six rowed	68	90.7
3	Four rowed	2	2.7
5	Two rowed	5	6.7

Table 22: Table of spikes color

Code	Description	No. of Acc.	Age (%)
1	Green	21	28.0
3	Purple	12	16.0
5	Brown	42	56.0

Hamza *et al.*^[25] also found high variation among different accessions of barley for row number/lateral floret.

Spikes color: Spikes color also showed high variation among different accessions and control variety of barley. The spikes color was classified into three classes, i.e., green, purple and brown (Table 22).

There were 21 genotypes showed green spike color with the average of 28%, 12 genotypes showed purple spike color with the average of 16 while 42 genotypes showed brown spikes with the average of 56%. This results show the variation among the studied genotypes for spikes color and maximum genotypes showed tendency towards brown spikes.

The spikes color was classified into three classes i.e. green, purple and brown. Brantestam *et al.*^[28] and Malysheva-Otto *et al.*^[27] also found high variation among different accessions of barley for spike color.

Table 23: Table of hundred seed weight (g)

SOV	DF	SS	MS	F-value	p-value
Rep	3	2.424	0.808		
Accessions	75	16.04	0.213867	1.382361	0.00785
Error	225	34.81	0.154711		
Total	303	53.28			

CV = 28.67%

Table 24: Mean table of hundred seed weight (g)

Accession	HSW	Accession	HSW	Accession	HSL
35860	2.5 ^{bcd}	37264	3.4 ^{ab}	1639	3.1 ^{abcd}
35861	1.7 ^d	37265	1.9 ^d	1644	3.3 ^{abc}
35862	2.9 ^{abcd}	37266	7.1 ^a	1659	3.0 ^{abcd}
35863	2.5 ^{bcd}	37267	2.0 ^d	1797	2.8 ^{abcd}
35864	1.9 ^d	37268	2.3 ^{cd}	1798	3.0 ^{abcd}
35865	2.4 ^{cd}	37269	2.7 ^{abcd}	1799	2.2 ^{cd}
36725	2.9 ^{abcd}	7999	2.9 ^{abcd}	1801	2.7 ^{abcd}
36728	3.2 ^{abcd}	8000 (1)	3.2 ^{abc}	1802	2.4 ^{cd}
36743	3.4 ^{ab}	8000 (2)	3.3 ^{abc}	1803	2.7 ^{abcd}
37247	2.5 ^{bcd}	8001	2.2 ^{cd}	1806	2.8 ^{abcd}
37248	2.8 ^{abcd}	8003 (2)	3.4 ^{abc}	1822	2.7 ^{abcd}
37249	2.4 ^{bcd}	8003 (7)	3.4 ^{abc}	1825	2.4 ^{cd}
37250	3.9 ^a	8004 (4)	3.1 ^{abcd}	1828	2.1 ^d
37251	2.5 ^{bcd}	8005	1.9 ^d	Local Bajaur	2.8 ^{abcd}
37252	3.1 ^{abcd}	8006	1.7 ^d	Khumasay	2.5 ^{bcd}
37253	3.3 ^{abc}	8008 (1)	2.4 ^{cd}	Malana	2.5 ^{bcd}
37254	2.8 ^{abcd}	8009	1.7 ^d	Zeran	1.7 ^d
37255	2.0 ^d	8010	1.8 ^d	Malana	3.1 ^{abcd}
37256	3.2 ^{abc}	8011 (3)	1.5 ^d	Yousaf Khail	2.3 ^{cd}
37257	3.5 ^{ab}	8011 (4)	1.7 ^d	ICBA Barley	3.3 ^{abc}
37258	2.0 ^d	8015 (3)	4.2 ^a	Jau-83	4.5 ^a
37259	2.6 ^{abcd}	1264	2.8 ^{abcd}	Snober-96	4.6 ^a
37260	2.2 ^{cd}	8024 (2)	2.9 ^{abcd}	Jau-2017	3.77 ^a
37261	3.6 ^{ab}	1400	2.5 ^{bcd}	Sultan-2017	3.8 ^a
37262	4.0 ^a	1629	2.5 ^{bcd}		
37263	1.9 ^d	1631	2.6 ^{bcd}		

LSD ^{0.05} of Genotypes = 1.14

The 100 seed weight: ANOVA (Analysis of variance) indicated high significant difference of accessions for hundred seed weight. The coefficient of variation was 28.67% of accessions for hundred seed weight (Table 23). Average value of accessions for hundred seed weight ranged from 1.5-7.1 g while maximum hundred seed weight of all studied accessions was found for genotype 37266 (7.1 g) which is followed by genotype Snober-96, Jau-83, accession 8015 (3) and 37262. Least hundred seed weight was found for accessions 8011 (3) (1.5 g), followed by 8009, 35861 and 8006 (Table 24). Hundred seed weight showed high variation in statistical analysis. Hundred seed weight showed significant and positive and link to total spikes in a plant and seed yield in a plant while hundred seed yield showed non significant relation with days to when 50% flowers form, maturity days of a plant, height of plant, length of spike with awn without awn. Hundred seed weight indicated negative relationship with total group of tillers in a plant and number of spikelets in spike.

Koebner *et al.*^[30] and Ahmad *et al.*^[29] and too found significant variances of accessions of barley for hundred seed weight.

Seed yield per plant: ANOVA (Analysis of variance) revealed high significant difference of accessions for seed yield in each plant. Coefficient of variance was 13.70% of accessions for seed yield of a plant (Table 25).

Average value of accessions for seed yield of each plant extended from 3.3-43.3 g, per plant whereas maximum seed yield of all calculated accessions were found for genotype 37266 (43.3 g) which is followed by genotype 37269, 8003 (7) and 37260. Minimum seed yield of a plant were examined for accessions 8006 (3.3 g), followed by 1806, 8011 (3) and 1828 (Table 26). Hundred seed weight showed high variation in statistical analysis.

Seed yield of a plant indicated significant and positive and association with days to 50% flowers formation, days of plant maturity, plant height, total spikes of spike while seed yield per plant revealed non significant relation with tillers group in a plant, length of spike with awn, length of spike without awn and total group of spikelets per spike (Table 26).

ANOVA (Analysis of variance) revealed high significant difference of accessions for seed yield in each plant. Brantestam *et al.*^[28] and Ahmad *et al.*^[29] also found highly significant differences of accessions of barley genotypes for seed yield of a plant.

Table 25: Table of seed yield per plant (g)

SOV	DF	SS	MS	F-value	p-value
Rep	3	1054	351.3333		
Accessions	75	776.76	10.3568	1.028962	0.0045
Error	225	2264.69	10.06529		
Total	303	4095.44			

CV = 13.70%

Table 26: Mean table of seed yield per plant (g)

Accession	SYP	Accession	SYP	Accession	SYP
35860	9.7 ^c	37264	13.1 ^{abc}	1639	7.5 ^c
35861	9.8 ^c	37265	12.5 ^{abc}	1644	7.8 ^c
35862	9.3 ^c	37266	43.3 ^a	1659	7.7 ^c
35863	7.9 ^c	37267	21.6 ^a	1797	10.0 ^c
35864	12.7 ^{abc}	37268	23.5 ^a	1798	11.3 ^{abc}
35865	7.2 ^c	37269	32.0 ^a	1799	10.0 ^c
36725	15.9 ^{abc}	7999	17.5 ^{ab}	1801	10.5 ^{bc}
36728	15.5 ^{abc}	8000 (1)	19.4 ^{ab}	1802	7.3 ^c
36743	10.9 ^{bc}	8000 (2)	15.1 ^{abc}	1803	7.8 ^c
37247	16.2 ^{abc}	8001	15.4 ^{abc}	1806	4.8 ^c
37248	18.2 ^{ab}	8003 (2)	19.2 ^{ab}	1822	21.0 ^a
37249	14.5 ^{abc}	8003 (7)	30.8 ^a	1825	7.0 ^c
37250	14.9 ^{abc}	8004 (4)	12.5 ^{abc}	1828	5.8 ^c
37251	12.1 ^{abc}	8005	12.4 ^{abc}	Local Bajaur	24.5 ^a
37252	22.9 ^a	8006	3.3 ^a	Khumasay	11.9 ^{abc}
37253	16.0 ^{abc}	8008 (1)	14.2 ^{abc}	Malana	26.0 ^a
37254	7.1 ^c	8009	20.7 ^a	Zeran	13.5 ^{abc}
37255	9.4 ^c	8010	9.5 ^c	Malana	19.3 ^{ab}
37256	11.9 ^{abc}	8011 (3)	5.0 ^c	Yousaf Khail	13.5 ^{abc}
37257	14.5 ^{abc}	8011 (4)	22.5 ^a	ICBA Barley	23.8 ^a
37258	11.0 ^{abc}	8015 (3)	16.5 ^{ab}	Jau-83	23.4 ^a
37259	15.4 ^{abc}	1264	9.3 ^c	Snober-96	11.0 ^{abc}
37260	30.5 ^a	8024 (2)	8.6 ^c	Jau-2017	25.705 ^a
37261	24.1 ^a	1400	6.9 ^c	Sultan-2017	23.225 ^a
37262	15.4 ^{abc}	1629	8.0 ^c		
37263	17.4 ^{ab}	1631	8.7 ^c		

LSD^{0.05} of Genotypes = 9.18

Table 27: Correlation coefficients among pairs of traits of barley germplasm

Trait of interest	DF	DM	T/P	PH	SL-WA	SL-WoA	S/P	S/S	SY/P	HSW
DF (50%)	1.00									
DM	0.81**	1.00								
T/P (No.)	-0.18	-0.15	1.00							
PH (cm)	0.38**	0.22	-0.03	1.00						
SL-WA (cm)	0.15	0.04	-0.12	0.08	1.00					
SL-WoA (cm)	0.05	-0.11	-0.22	-0.02	0.34**	1.00				
S/P (No.)	0.28*	0.18	0.10	0.46**	-0.03	-0.04	1.00			
S/S (No.)	-0.19	-0.19	0.06	0.14	0.04	0.11	0.21	1.00		
SY/P (g)	0.32**	0.27*	0.03	0.44**	0.16	0.01	0.39**	0.09	1.00	
HSW (g)	0.04	0.02	-0.16	0.08	0.04	0.12	0.24*	-0.05	0.45**	1.00

Table 28: Descriptive statistics of barley germplasm

Trait of interest	Mean	Minimum	Maximum	SD	Variance
DF (50%)	137.2	114.0	164.0	11.9	141.0
DM	166.5	153.0	186.0	9.0	80.2
T/P (No.)	15.7	9.4	32.0	5.2	27.2
PH (cm)	121.2	99.6	137.8	10.0	99.3
SL-WA (cm)	9.8	7.7	20.2	1.5	2.3
SL-WoA (cm)	19.1	14.4	21.9	1.6	2.4
S/P (No.)	12.1	5.8	26.0	4.4	19.2
S/S (No.)	26.2	17.2	33.7	3.7	13.9
SY/P (g)	14.7	3.3	43.3	7.4	54.7
HSW (g)	2.8	1.5	7.1	0.8	0.7

Protein analysis: Cluster analysis on the basis of seed storage proteins shows there are 13 clusters at linkage distance of 1. A major cluster has 33 accessions while there are 8 accessions in another cluster (Table 27). It

means almost half of accessions have similar banding patterns while half are scattered in 11 clusters. It indicates that there is significant genetic diversity in barley germplasm studied during the experiment (Table 28).

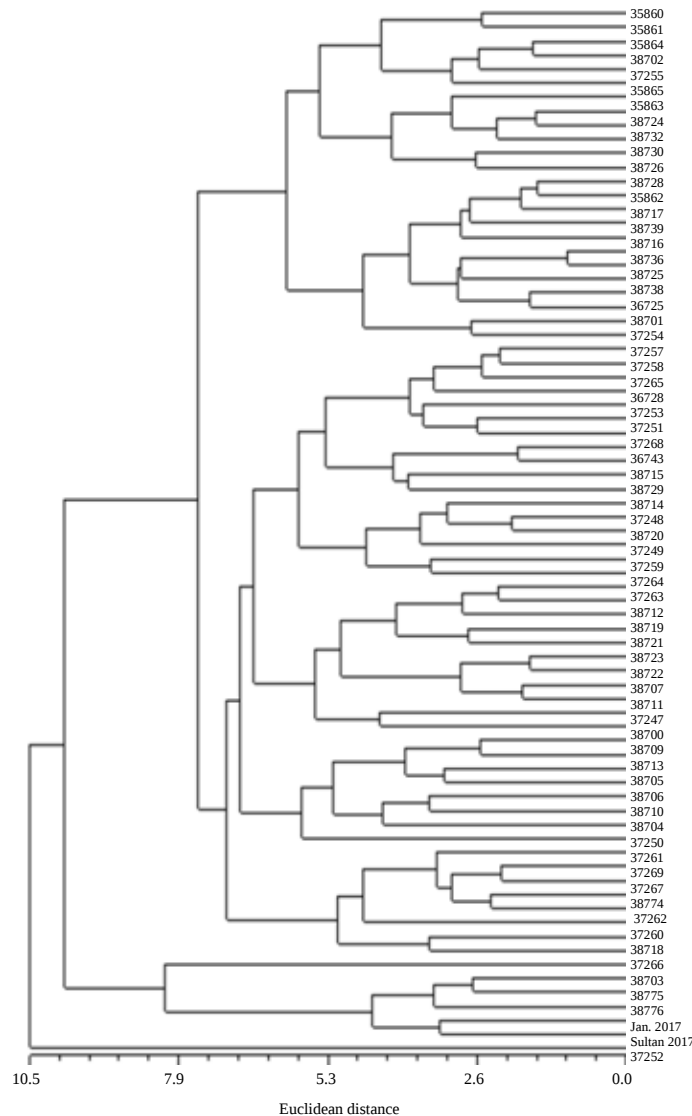


Fig. 1: Principal Component Analysis (PCA)

Principal Component Analysis (PCA): Six constituents were extracted from the 10 examined characters through principal component analysis. First four constituents that illuminated 88% of all difference was used for clustering accessions. With this technique, 10 variants were reduced to 4. Five clusters were shaped (Fig. 1). The most active characters in the firstly constituents were height of plant, spike per plant and spikelets group in a spike. For the second component height of plant and number of tillers group in each plant and for third component days to 50% flowers formation, for fourth component plant maturity days and height of plant. The fifth component mostly affected by distance from spike length without awn.

Comparing these results shown the traits with the chief effect on the components indicated the maximum level of dissimilarity and can be used for clustering genotypes, efficiently. The degree of resemblance among dendrogram (obtained from cluster analysis) and dendrogram gotten from the cluster analysis created on Principal Component Analysis (PCA) was estimated at 68.5%.

The degree of resemblance among dendrogram (obtained from cluster analysis) and dendrogram gotten from the cluster analysis created on Principal Component Analysis (PCA) was estimated at 68.5%. Amabile *et al.*^[31] also found similar results in principal component analysis.

CONCLUSION

Given results indicated, there is high genetic diversity among studied accessions barley. This Genetic diversity could be use in further breeding methods and barley crop improvement.

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REFERENCES

01. Ferreira, J.R., J.F. Pereira, C. Turchetto, E. Minella and L. Consoli, 2016. Assessment of genetic diversity in Brazilian barley using SSR markers. *Gene. Mol. Bio.*, 39: 86-96.
02. Badr, A., K. Mueller, R. Schaefer-Pregl, H. El-Rabey and S. Effen *et al.*, 2000. On the origin and domestication history of barley (*Hordeum vulgare*). *Mol. Biol. Evol.*, 17: 499-510.
03. FAO, 2018. FAOSTAT: Crops (national production). Food and Agriculture Organization of the United Nations, Rome, Italy.
04. Mohtashami, R., 2015. The correlation study of important barley agronomic traits and grain yield by path analysis. *Biol. Forum*, 7: 1211-1219.
05. Din, S.M.U., A. Abu-Bakar and A. Regupathi, 2017. Does insurance promote economic growth: A comparative study of developed and emerging/developing economies. *Cog. Eco. Finance*, Vol. 5, 10.1080/23322039.2017.1390029
06. Goyal, A. and M. Ahmed, 2012. Barley: Production, improvement and uses. *Crop. Sci.*, 52: 2852-2854.
07. Nandha, P.S. and J. Singh, 2014. Comparative assessment of genetic diversity between wild and cultivated barley using gSSR and EST-SSR markers. *Plant Breeding*, 133: 28-35.
08. Tricase, C., V. Amicarelli, E. Lamonaca and R.L. Rana, 2018. Economic Analysis of the Barley Market and Related Uses. In: *Grasses as Food and Feed*. Tadele, Z. (Ed.). IntechOpen, .
09. Newman C.W. and R.K. Newman, 2005. Hulless Barley for Food and Feed. In: *Specialty Grains for Food and Feed*, Abdelaal, E. And P. Wood (Eds.), AACC International, St Paul, Minnesota, pp: 167-202.
10. Mahdi, G.S., M. Abdal, B.C. Behera, N. Verma and A. Sonone, 2008. Barley is a healthful food: A review. *Elect. J. Environ. Agr. F. Chem.*, 7: 2686-2694.
11. Lahouar, L., A. El Arem, F. Ghrairi, H. Chahdoura, H.B. Salem, M.E. Felah and L. Achour, 2014. Phytochemical content and antioxidant properties of diverse varieties of whole barley (*Hordeum vulgare* L.) grown in Tunisia. *Food Chem.*, 145: 578-583.
12. Marconi, E., M. Graziano and R. Cubadda, 2000. Composition and utilization of barley pearling by products for making functional pastas rich in dietary fiber and β -glucans. *Cer. Chem.*, 77: 133-139.
13. Nevo, E., Y.B. Fu, T. Pavlicek, S. Khalifa, M. Tavasi and A. Beiles, 2012. Evolution of wild cereals during 28 years of global warming in Israel. *Proc. Natl. Acad. Sci. USA.*, 109: 3412-3415.
14. Bhandari, H.R., A.N. Bhanu, K. Srivastava, M.N. Singh and H.A. Shreya, 2017. Assessment of genetic diversity in crop plants-an overview. *Plants Agri. Res.*, 7: 279-286.
15. Wenzl, P., J. Carling, D. Kudrna, D. Jaccoud and A. Kilian *et al.*, 2004. Diversity Arrays Technology (DArT) for whole-genome profiling of barley. *Proc. Natl. Acad. Sci. USA.*, 101: 9915-9920.
16. International Barley Genome Sequencing Consortium, 2012. A physical, genetic and functional sequence assembly of the barley genome. *Nature*, 491: 711-716.
17. Allard, R.W. and S.K. Jain, 1962. Population studies in predominantly self-pollinated species. II. Analysis of quantitative genetic changes in a bulk-hybrid population of barley. *Evolution* 21: 90-101.
18. Jaradat, A.A., M. Shahid and A. Al-Maskri, 2004. Genetic diversity in the Batini barley landrace from Oman: II. Response to salinity stress. *Crop Sci.*, 44: 997-1007.
19. Amezrou, R., S. Gyawali, L. Belqadi, S. Chao and M. Arbaoui *et al.*, 2018. Molecular and phenotypic diversity of ICARDA spring barley (*Hordeum vulgare* L.) collection. *Gene. Res. Crop. Evol.*, 65: 1-15.
20. Fang, J., Z. Zhang, L. Zhou, C. Chen and C. Wang, 2001. The possibility of using RAPD marker for the identification of fruit sport. *J. Afr. Sci.*, 18: 182-185.
21. Hawkes, J.G., N. Maxted and B.W. Ford-Lloyd, 2012. *The Ex Situ Conservation of Plant Genetic Resources*. Springer Berlin, Germany,.
22. Ceccarelli, S., S. Grando and J.A.G. Van Leur, 1987. Genetic diversity in barley landraces from Syria and Jordan. *Euphytica*, 36: 389-405.
23. Parzies, H.K., W. Spoor and R.A. Ennos, 2000. Genetic diversity of barley landrace accessions (*Hordeum vulgare* sp. *vulgare*) conserved for different lengths of time in *ex situ* gene banks. *Heredity*, 84: 476-486.

24. Kebebew, F., Y. Tsehay and T. McNeilly, 2001. Morphological and farmers cognitive diversity of barley (*Hordeum vulgare* L. [Poaceae]) at Bale and North Shewa of Ethiopia. Genet. Res. Crop Evol., 48: 467-481.
25. Hamza, S., W.B. Hamida, A. Rebai and M. Harrabi, 2004. SSR-based genetic diversity assessment among Tunisian winter barley and relationship with morphological traits. Euphytica, 135: 107-118.
26. Manjunatha, T., I.S. Bisht, K.V. Bhat and B.P. Singh, 2007. Genetic diversity in barley (*Hordeum vulgare* L.) landraces from Uttarakhand Himalaya of India. Gene. Resour. Crop. Evol., 54: 55-65.
27. Malysheva-Otto, L., W.M. Ganai, J.R. Law, J.C. Reeves and M.S. Roder, 2007. Temporal trends of genetic diversity in European barley cultivars (*Hordeum vulgare* L.). Mole. Br., 20: 309-322.
28. Brantestam, A.K., B.R. Von, C. Dayteg, I. Rashal, S. Tuveesson and J. Weibull, 2007. Genetic diversity changes and relationships in spring barley (*Hordium vulgare* L.) germplasm of Nordic and Baltic areas as shown by SSR markers. Gen. Res. Crop. Evo., 54: 749-758.
29. Ahmad, Z., S.U. Ajmal, M. Munir, M. Zubair and M.S. Masood, 2008. Genetic diversity for morpho-genetic traits in barley germplasm. Pak. J. Bot., 40: 1217-1224.
30. Koebner, R.M.D., P. Donini, J.C. Reeves, R.J. Cooke and J.R. Law, 2003. Temporal flux in the morphological and molecular diversity of UK barley. Theor. Applied Genet., 106: 550-558.
31. Amabile, R.F., F.G. Faleiro, F. Capettini, J.R. Peixoto and R.M. Sayd, 2017. Genetic variability in elite barley genotypes based on the agro-morphological characteristics evaluated under irrigated system. Ciencia Agrotecnologia, 41: 147-158.