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Diversity Study of Some Ethiopian Barley (*Hordeum Vulgare* (L.)) Accessions for Their Agronomical Important Traits

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Abstract – **An experiment was conducted at Wechamo University Main Campus experimental station in 2018 main cropping season and ninety six barley accessions and three standard checks were evaluated using augmented design. Eight quantitative characters were recorded and analysis of variance showed significance difference ($p<0.01$) between the tested genotypes for days to 50% flowering, days to 75% maturity, plant height, thousand seed weight and grain yield. Cluster analysis grouped 99 barley genotypes in to three distinct classes with maximum number of accession 85 in cluster I and minimum 1 in cluster III. Principal component analysis indicated that the first three principal components having eigenvalues > 1 accounts for 82.25 % of the total variation. Generally, the study revealed the existence of wide range of diversity among barley accessions which has paramount importance for further exploitation of the important traits.**

Keywords – **Farmers Varieties, Gene Pool, Genetic Diversity, Hordeum Vulgare.**

I. INTRODUCTION

Ethiopia is the center of genetic diversity for barley along with other crop plant species such as Durum wheat, Sorghum, Field pea, Cowpea, Chickpea and Lentil [1]. The large diversity in the Ethiopian barley farmers' varieties could be due to the various in soils, climate, altitude, and topography together with geographical isolation for long periods [2]. The country also has vast cultural diversity, which has also contributed to the existing crop genetic resource diversity and associated with community indigenous knowledge. The long history of barley cultivation and the diverse agro-ecological zones and the diverse cultural practices have resulted in a country renowned for its large number of farmers' varieties and traditional agricultural practices [3]. In Ethiopia, barley is the third most important cereal crop next to Teff and Maize. Ethiopia has a different type of barley varieties, which highly resist virus diseases (powdery mildew) and also they are rich in protein content. It is used in many traditional foods such as injera, genfo (porridge), dabo (bread), kitta, kinche, atmit/muk, eshet, kollo, beso, chicko, zurbegone and making local beverages (tella, bequre, borde, areki). The straw is used for animal feed during the dry season and it is also a useful material for thatching roofs of houses and for use as bedding [4] [3]. Farmers' varieties are still the backbone of agricultural systems in many developing countries, characterized by high genetic heterogeneity, good adaptation to local environmental conditions and by low productivity[5] and important in marginal areas or seasons where the production of other cereal is limited. These farmers' varieties have developed abundant patterns of variation and would represent a largely untapped reservoir of useful genes for adaptation to biotic and abiotic stresses [6]. Despite barley’s long history of cultivation, diverse farmers’ varieties, traditional practices and its valuable uses, the improvements made to boost the productivity of the crop have been low [7].

Therefore, characterization of farmers' varieties and knowledge on the pattern of variation for important morpho-agronomic traits are needed for proper management and better exploitation of this gene pool [8]. The existence of genetic diversity has special significance for the maintenance and enhancement of productivity in agricultural crops in a country like Ethiopia, which is characterized by highly varied agro-climates and diverse growing conditions[9] [1].

Ethiopian Biodiversity Institute undertook exploration and collection operations in all regions of the country, covering a wide range of agro-ecological conditions and 16,685 barley accessions collected and conserved in a gene bank, of which 5569 accessions were characterized by researchers and further 11116 barley accessions are yet to be screened for their potentially useful characters. Thus, the main objective of this research was to determine the range of variation among barley accessions and to classify them into clusters based on their similarity features regarding the traits understudy and also to generate data on their performance for plant breeders for further evaluation of the crop in particular.

II. MATERIALS AND METHODS

2.1. *Description of the Study Area*

The experiment was conducted at Wachemo University main campus research station in Hadiya Zone of Southern Nation Nationalities Peoples Region (Fig. 1). Geographically, the experimental station is located at $7^0$32'44"N latitude and $37^0$52'50"E longitude with an altitude of 2270 meters above sea level.

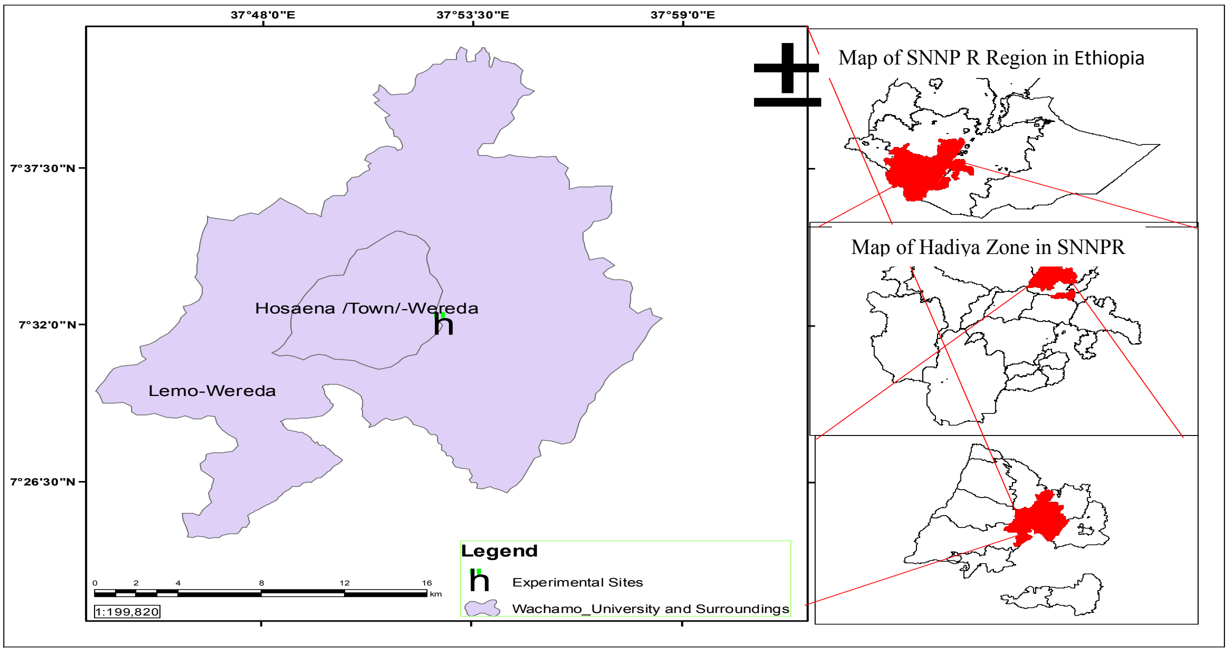

Fig. 1. Location Map of experimental site, Wechamo University main Campus experimental Station and Hadiya Zone, Southern Nation Nationalities Peoples Region (SNNPR), Ethiopia obtained from Arc GIs version 10.2.2.

2.2. *Experimental Details*

The experiment was laid out in augmented design with no replication among the barley accessions due to insufficient seed availability and three standard checks replicated in every block. Ninety six barley accessions from Ethiopian Biodiversity Institute gene bank and three standard checks (Chefo, Awedo and Bira) which were locally growing barley verities (Table 1). The accessions were sowed on 9 August 2018 in Main cropping season with diammonium phosphate (DAP) at the rate of 100 kg ha^{-1} and UREA at the rate of 80 kg ha^{-1} (complete application at sowing) and other management practices were applied as per recommended for the site. The gross plot size was 2 m x 0.6 m (1.2 m^2). Each plot accommodated four rows of 2 m length with 20 cm distance. The outer most rows at both ends of plots were considered as borders. The second and third rows at one side of each plot were designated as sampling area. The distance between plots and blocks was 0.5 m and 1 m apart, respectively.

Table 1. List of barley accessions and standard checks used for the research.

No.	Accession number	No.	Accession number	No.	Accession number	No.	Accession number
1	236102	26	236808	51	237360	76	238729
2	236104	27	236815	52	237361	77	238771
3	236105	28	237002	53	237365	78	238773
4	236106	29	237003	54	237366	79	238776
5	236107	30	237020	55	237367	80	238800
6	236113	31	237328	56	237368	81	238807
7	236115	32	237329	57	237530	82	238810
8	236116	33	237330	58	237532	83	238814
9	236118	34	237332	59	237533	84	238819
10	236119	35	237333	60	237534	85	238829
11	236120	36	237334	61	237536	86	238835
12	236138	37	237335	62	237542	87	238837
13	236145	38	237338	63	237543	88	238839
14	236146	39	237339	64	237544	89	238841
15	236147	40	237340	65	237807	90	238843
16	236148	41	237341	66	237808	91	238844
17	236149	42	237342	67	237809	92	238846
18	236150	43	237343	68	237850	93	238847
19	236151	44	237344	69	237852	94	239516
20	236152	45	237345	70	238352	95	240795
21	236153	46	237346	71	238353	96	242065
22	236154	47	237347	72	238354	97	Chefo (Check 1)
23	236253	48	237352	73	238369	98	Awedo (Check 2)
24	236254	49	237354	74	238374	99	Bira (Check 3)
25	236402	50	237359	75	238654		

Morphological data was recorded using the International Plant Genetic Resources Institute's descriptor list [10] nowadays known as "Bioversity International" descriptor list for barley (Table 2). All data of eight quantitative characters were recorded on randomly selected and tagged 20 individual plants for the research from each plot of accession, except days to 50% flowering, days to 75% maturity, thousand seed weight and gr-

-ain yield which were recorded on plot basis. Grain yield was adjusted to 12% moisture content.

Table 2. List of quantitative characters recorded along with their code and definition.

Characters	Code	Character definition
Days to 50% flowering (count)	DF	Number of days from planting to the day when 50% of the heads fully flower (heading) emerge from the boot of the flag leaf in each plot
Days to 75% maturity (count)	DM	Number of days starting from planting to the day when 75% of the plots plants peduncles of the spikes become complete yellow and mature.
Plant height (cm)	PH	Length of selected plants measured from the ground to the tip of the spike excluding awns at maturity.
Spikelet per spike (count)	SPS	Number of spikelet per spike on selected plants counted at maturity.
Number of kernels per spike (count)	KPS	Number of seed per spike on selected plants counted at maturity.
Spike length (cm)	SL	Length measured from base of spike to top of spikelets excluding the awns at maturity.
Thousand seed weight(g)	TSW	The weight of 1000 seeds taken from each plots of accession.
Grain yield	GY	The weight of all harvested seeds from each plots of accession converted to quintal/ha.

2.3. *Statistical Analysis*

The collected data were calculated with statistical analysis of variance, principal component analysis, descriptive statistics and clustering with the help of SAS (9.4) software.

III. RESULTS AND DISCUSSION

3.1. *Analysis of Variance*

The ANOVA of the 8 quantitative traits of the Barley genotypes is given below in Table 3. The mean square value of all the eight morphological characters under study suggested a significant difference ($P < 0.05$ and <0.01) between the tested genotypes, except for spike length, number of kernels per ear and spikelet per spike among the accessions and the rest of the traits studied elucidated the presence of genetic variability for the character considered, which can be exploited through further selection. Based on yield potential 236815, 237020, 237328, 237330, 237359, 237365, 237533, 237850, 238374, 238800 and 238844 accessions were selected for further evaluation for 2019 main cropping season.

Table 3. Analysis of variance of the eight quantitative characters barley accessions along with the three standard checks.

Source of variation		Mean square							
	Df	DF	DM	PH	SPS	KPS	SL	TSW	GY
Block	5	4.99	7.8	26.45	25.497	28.222	0.688	1.16	1.95
Genotypes	98	36.11**	14.08**	176.20**	91.487	96.1844	0.6595	26.263**	70.524**
Accessions	95	30.122**	53.693**	140.68**	66.57	68.951	0.6384	22.94**	64.912**
Checks	2	147.1**	657.93**	700.72**	1195.31**	1332.55**	1.9332*	153.86**	254.13**
Checks vs accessions	1	382.641**	14.29**	2501.83**	251.042*	210.62	0.1079	86.77**	236.41**
Error	10	2.722	4.662	20.855	48.97	61.524	0.3296	0.7998	1.28
Total	113	38.392	73.6	197.84	154.74	172.23	1.129	32.23	70.24

Source of variation		Mean square							
	Df	DF	DM	PH	SPS	KPS	SL	TSW	GY
CV		2.494	2.68	4.285	21.1	24.24	7.143	2.1	3.014

*, ** Significant at ($p< 0.05$ and ($p < 0.01$), respectively. Df, Degree of freedom; CV, coefficient of variation (%), DF, days to 50% flowering; DM, days to 75% maturity; PH, plant height; SPS, number of spikelet per spike; KPS, number of kernels per spike; SL, spike length; TSW, thousand seed weight in gram; GY, grain yield in kg/ha; Genotypes, accessions + checks (control).

3.2. *Mean and Range Values*

For each of the traits considered for this study, the descriptive statistics, including the maximum and minimum quantitative traits' as well as mean values, were derived from the average data value for each of the accessions (Fig. 2). The overall barley genotypes revealed a wide range of diversity for all of the traits under study, resulting in extreme values for the maximum and the minimum genotype mean values. For instance, days to 50% flowering ranged from 56 to 93 days with a mean of 66.16, while days to 75% maturity was ranging from 89 to 140 days with a mean of 106.57. Similarly, plant height ranged from 62.05 cm to 99.30 cm with a mean height of 80.72 cm. whereas the number of spikelet per spike ranged from 20 to 57.70 cm. The number of kernels per spike ranged from 18.85 to 57.30 with a mean of 32.35, and the spike length of the tested genotypes ranged from 5.08 to 10.10 cm with a mean of 8.03 cm. Thousand seed weight ranged from 28.28 gm to 55.78 gm with a mean of 42.92 gm, and grain yield in quintals per hectare ranged from 20.42 to 60.5 with a mean value of 37.49. Eventually, it is possible to select the best-performing accessions for further improvement programs by their grain yield capacity through direct selection.

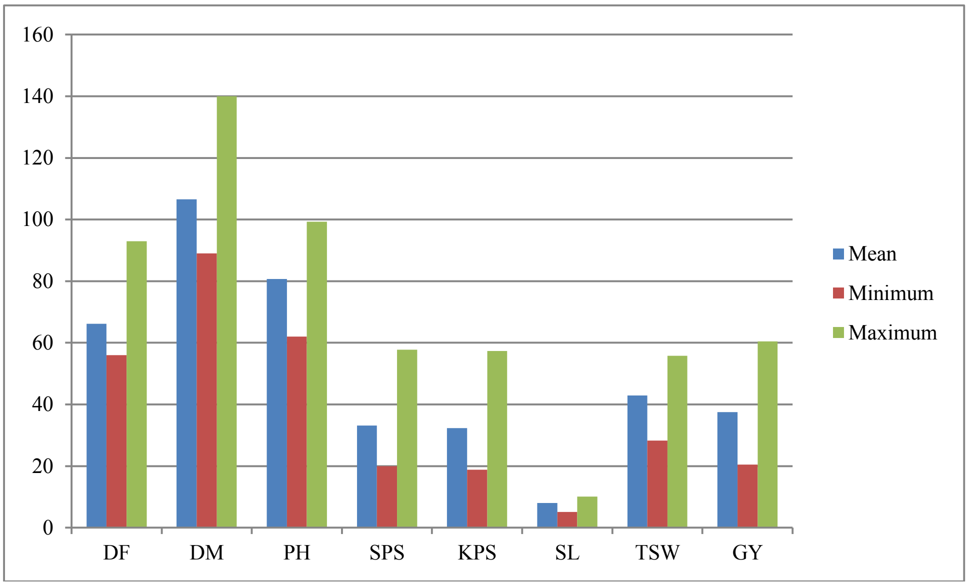

Fig. 2. The minimum, maximum and mean values for the 8 quantitative characters of 99 barley genotypes.

3.3. *Cluster Analysis*

Cluster analysis was performed on the Euclidean distance matrix utilizing Ward's linkage method, and the resulting dendrogram (Fig. 3). Cluster analysis grouped the 99 barley genotypes to three distinct groups and the number of genotypes per cluster varied from 85 in cluster I, 13 in cluster II and 1 in cluster III which comprises 85.9%, 13.1% and 1.0% of the total experimental genotypes respectively. The three standard checks used were grouped into Cluster-1. The clustering pattern indicated the existence of variability among the barley genotypes.

Characterization of the genotypes and clustering them on the basis of their morphological traits and genetic similarity will help in identification and selection of the best parents for hybridization [11]. Therefore, grouping of genotypes by using multivariate methods of analysis based on their similarity in the present study would be valuable for barley breeders in that the most important accessions in the population may be selected from different clusters for barley improvement programmes.

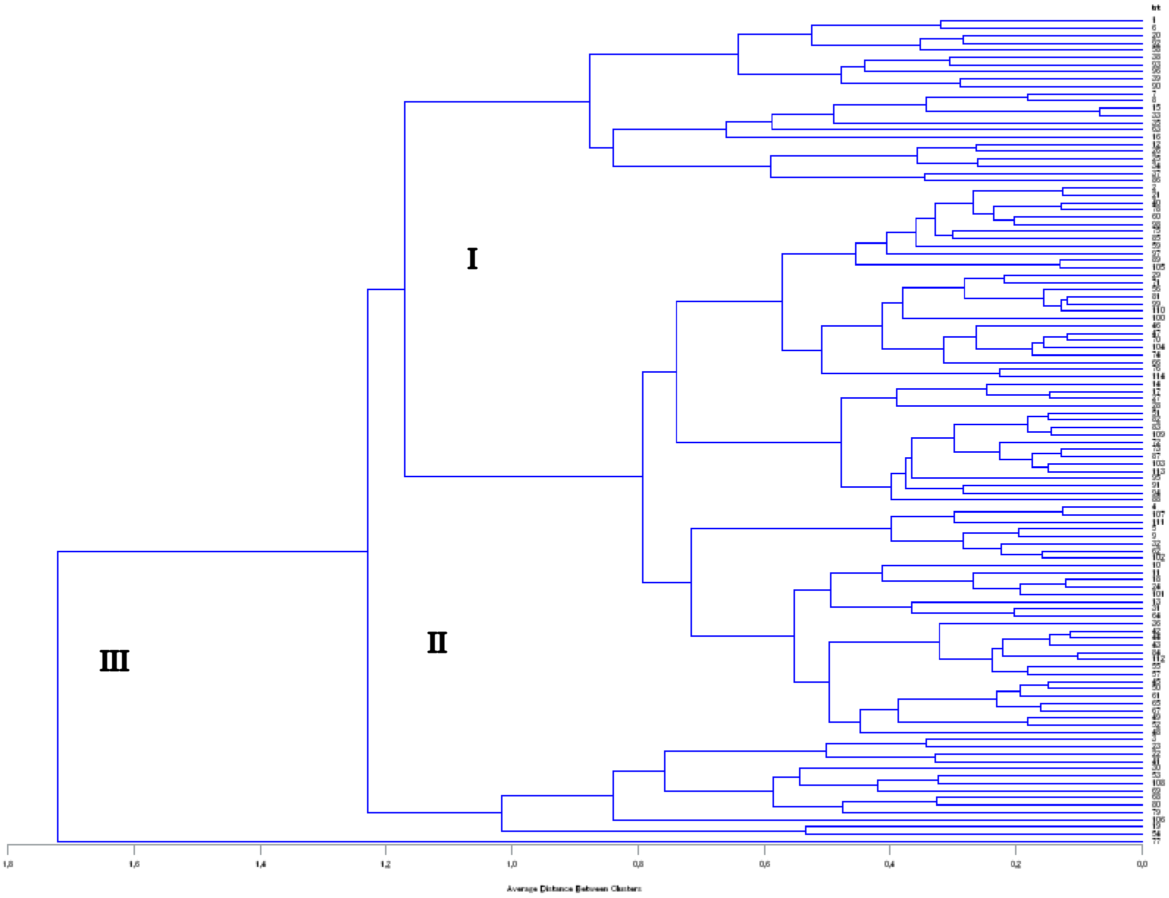

Fig. 3. Dendrogram of barley genotypes based on 8 quantitative characters, depicting genotypic relationships among accessions (average linkage clustering methods).

3.4. *Principal Component Analysis*

The principal component analysis (PCA) was computed to reduce the number of variables into a few correlated components that can explain much of the variability. And also helps to identify characters that load the most in explaining the observed variation [12]. The first three principal components having eigenvalues > 1 account for 82.25 % of the total variation captured among the barley genotypes. The first component accounts for 40.95 % of the total variability, while the second and the third for 24.75 % and 16.59 %, respectively, of the total variability among the genotypes for traits considered for the research (Table 4). Principal component one is more related to traits such as spike length, and number of kernels per spike. While the second principal component was positive for the number of spikelet per spike and days to 75% maturity were more related traits. The third principal component was positive for plant height, days to 50% lowering and grain yield, respectively.

Table 4. Eigenvectors and eigenvalues of the eight principal components of the 99 barley genotypes

Characters	Eigenvectors							
	Prin1	Prin2	Prin3	Prin4	Prin5	Prin6	Prin7	Prin8
DF	-0.168	0.305	0.356	0.831	-0.18	-0.17	0.021	-0.002
DM	0.07	0.631	-0.29	-0.126	-0.14	0.084	0.688	-0.004
PH	0.079	0.305	0.654	-0.465	0.06	-0.50	-0.03	0.003
SPS	0.128	0.628	-0.25	-0.029	0.082	0.149	-0.70	0.006
KPS	0.511	-0.0163	0.279	0.084	0.091	0.368	0.07	0.71
SL	0.509	-0.0114	0.287	0.079	0.101	0.377	0.061	-0.704
TSW	-0.443	0.051	0.332	-0.251	-0.54	0.567	-0.09	0.004
GY	-0.476	0.129	0.169	0.012	0.789	0.298	0.123	0.008
Eigenvalue	3.272	1.979	1.327	0.781	0.265	0.227	0.142	0.003
Proportion	0.409	0.247	0.166	0.098	0.033	0.028	0.017	0.0004
Cumulative	0.409	0.657	0.823	0.92	0.953	0.981	0.999	1.00

DF, days to 50% flowering; DM, days to 75% maturity; PH, plant height; SPS, number of spikelet per spike; KPS, number of kernels per spike; SL, spike length; TSW, thousand seed weight; GY, grain yield.

IV. CONCLUSION

A total of ninety six accessions and three standard checks were characterized for eight quantitative characters and analysis of variance indicated the existence of diversity among barley accessions. Also clustering pattern of the study indicated that the existence of variability between barley accessions that will help in identification and selection of the best parents. The principal component analysis showed the variability of the accessions that the first component accounts for 40.95 %, the second and the third for 24.75 % and 16.59 %, respectively, of the total variability among the genotypes for traits considered for the study. Generally, the accessions used in this study are diversified and offer an opportunity for plant breeders to conduct further breeding activities through selecting the most promising base populations of the crop accession.

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List of Research Publications:

1. A. Delessa, "The Impact of Invasive Alien species on Forage and Pasture Genetic Resource Diversity in Pastoral Area of Afar National Regional State, Northeastern of Ethiopia". *International Journal of Environment, Agriculture and Biotechnology* (ISSN: 2456-1878). 3(5):1929-1934.Doi:10.22161/ijeab/3.5.46.
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List of Research Publications:

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