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Multivariate Analysis of Variability in Ethiopian Barley (*Hordeum Vulgare* L.) Accessions at Lemo Wereda Hadiya Zone, Southern Ethiopia

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***Abstract* – Genetic diversity assessment allows breeders to take advantage of existing genetic resources, which helps to improve agricultural yields and ensure food security. In the 2019 main cropping season, eighty barley accessions and three standard check types were tested for eight quantitative traits in Lemo Wereda Hadiya Zone of southern Ethiopia. The experiment was laid down in an augmented block design with three standard checks that were replicated in every block. Analysis of variance showed very significant differences (P0.01) between tested genotypes for days to 50% flowering and days to 75 % maturity, spike length, spikelets per spike, kernel per spike, and grain yield. Plant height and thousand grain weight also differed significantly (P0.05) between genotypes. The grain yield varies between 10.2 and 44.63 quintals per hectare. The highest grain yield was harvested from Awedo (check variety) and the lowest yield was from the farmers' varieties accession 243590. Even though, the highest grain yield was measured from the one improved variety; 35 farmer's varieties were able to produce higher grain yield than the Chefo improved variety. On the other hand, 65 farmer's varieties were able to produce higher grain yield than the bira improved varieties. The principal component analysis indicated that the two principal components (PC1 to PC2) with eigenvalues ranged from 2.05 to 3.48 containing variability of 43.59% and 25.68% respectively. The genotypes were broadly grouped into four distinct clusters. The first cluster contains 38 (45.78%) genotypes including one improved variety. The second cluster was also constructed by 26 (31.33%) genotypes including two of the improved varieties. The third and fourth clusters comprises 11 (13.25%) and 8 (9.64%) genotypes, respectively. In general, the research revealed the farmers' varieties accessions' hidden potential for increasing yield through the use of conserved germplasm.**

***Keywords* – Cluster Analysis, Genetic Diversity, Principal Component Analysis, Quantitative Traits.**

I. INTRODUCTION

Barley (*Hordeun vulgare* L.) belongs to the genus *Hordeun* in the *Triticaceae* of Gramineae family. It is self-pollinated diploid 2n=14. Barley is one of the main important cereal crops cultivated worldwide in a wide range of environments from temperate to sub-tropical, arid to semi-arid. It ranks fourth in world cereal production after maize, rice, and wheat, it is mainly used for feed (55-60%), brewing malts (30-40%), and the remaining percent for food purposes [1][2]. Cultivated barley (Hordeum vulgare ssp. vulgare) evolved from its wild progenitor H. spontaneum(C. Koch) Thell, in the Fertile Crescent of Middle East about 10,000 years ago [3][4][5].

In Ethiopia, barley is an important cereal crop that is mainly grown by smallholder farmers [6]. It is grown in wide ranges of environments with altitudes varying from 1500 and 3500 m above sea level [7]. Barley is the fifth most important cereal crop after teff, wheat, maize and sorghum in area coverage in Ethiopia [8].

Farmers' varieties are largely an outcome of natural selection during centuries of cultivation. They usually exhibit genetic variation for qualitative and quantitative traits, have good adaptation for specific environmental condition and give dependable yield [9]. Also important sources of valuable genes for several traits such as

barley yellow dwarf virus resistance, powdery mildew resistance, high lysine content, vegetative vigour, drought tolerant and resistance to several barley diseases [10]. Besides, they have useful agronomic future such as good tillering, tolerance to marginal soil, resistance to barley shoot fly, aphids and frost resistance, vigorous seedling establishment and rapid grain filling period [11].

These farmers' varieties form potential parents for hybridization in crop improvement not only for yield productivity but also for resistance to diseases and pests. However, these farmers' varieties have not been fully utilized in modern breeding [12][13].

In order to effectively conserve, evaluate, and use germplasm, researchers must look into the estimate of genetic variation available. Genetic diversity is an integral aspect of any agricultural production system, in breeding, modification in germplasm effectively, the investigation of genetic diversity important, in the first part of the last century, recognized the importance of genetic variation in the germplasm of crop organisms [14].

More than 17000 barley accessions collected from barley growing regions of the country and maintained in the gene bank of the Ethiopian Institute of Biodiversity until 2021[15]. But majority of the accessions are not yet studied for their important agronomic traits. To make a wise decision on how to utilize and conserve the available barley genetic resource, studies have to be done on the genetic diversity of the crop[16].

Therefore characterizing this huge genetic resource is very essential for future crop improvement programme while our farmer is still straggling with low yielder varieties. Hence, the study aimed to assess the preliminary performance of barley accessions and genetic variabilityassociations for yield and yield relatedtraits of barley accessions.

II. Material And Methods

2.1.*Description of the Study Area*

The study was conducted at Lemo Wereeda in Hadiya Zone of Southern Nation Nationalities Peoples Region during 2019 main rainy season. The experimental station is located at an elevation of 2270 meters above sea level and is located at $7^0$32'44"N latitude and $37^0$52'50"E longitude. It is situated 230 km south of Addis Ababa, the capital of Ethiopia. It has a cool temperature range of 15-180C and an average rainfall of 1150mm [17].

2.2.*Plant Material*

Eightyfarmer'svarieties barley accessionsobtained from the Ethiopian Biodiversity Institute genebank and three standard checks (Awedo, Chefo and Bira,) were obtained from locally grown barley veritiesused for the study (Table 1).

2.3.*Experimental Design*

The experiment was laid down in augmented block design with no replication among the barley accessions and three standard checks repeated in every block.The accessions were sowed on 9 August 2018 in the main cropping season with diammonium phosphate (DAP) at the rate of 100 kg ha^{-1} and UREA at the rate of 100 kg ha^{-1} (complete application at sowing) and the other management practices were applied as per recommended for the research site. The gross plot size was 2 m x 0.8 m (1.6 m^2). Each plot accommodated four rows of 2 m length with distance of 20 cm between rows. The outer rows at both ends of plots were considered as borders.

The two middle rows were designated as sampling area. 0.5 m and 1 m distance kept between plots and blocks respectively.

Table 1. List of barley genotypes used for the study.

S.N	Accession Number	S.N	Accession Number	S.N	Accession Number	S.N	Accession Number	S.N	Accession Number
1	242068	18	238648	35	242579	52	238657	69	242091
2	241684	19	243188	36	244910	53	238373	70	242577
3	244940	20	243554	37	244909	54	241681	71	238845
4	242584	21	239512	38	239523	55	239519	72	238639
5	239529	22	239532	39	237820	56	243180	73	238366
6	237843	23	239510	40	243591	57	239517	74	237821
7	239521	24	244937	41	239538	58	242582	75	243186
8	243189	25	243302	42	239531	59	244912	76	241120
9	243194	26	239075	43	239818	60	244922	77	238817
10	243193	27	244924	44	239518	61	237817	78	237816
11	238823	28	242573	45	231857	62	239511	79	237811
12	242060	29	243581	46	243570	63	239515	80	237856
13	243590	30	242581	47	241682	64	237859	81	Awedo
14	237854	31	238651	48	243305	65	236809	82	Bira
15	244935	32	243608	49	241680	66	241676	83	Chefo
16	239513	33	242069	50	238812	67	237822		
17	238821	34	243556	51	243410	68	237823		

Note: The Ethiopian Biodiversity Institute genebank database assigned an accession number to each germplasm sample; Awedo Bira and Chefo are barley varieties that have been produced in the research area.

2.4.*Data Collection*

Data were recorded for eight quantitative characters using barley descriptors [18]. Data for plant height, spikelet per spike, kernel per spike and spike length were recorded based on randomly selected and tagged 20 individual plants from each plot. Whereas traits recorded based on plot basesday to 50% flowering, days to 75% maturity, thousand seed weight and grain yield were taken from the whole row for each accession and grain yield per plot converted into hectare for the analysis.

2.5.*Statistical Analysis*

2.5.1.*Analysis of Variance*

R statistical software was used to perform analysis of variance on eight quantitative traits (version 4.0.5; augmented RCBD package).

2.5.2.*Principal Component Analysis*

To avoid differences in measurement scales, the data were standardized to mean zero and variance of one before computing principal component analysis. R statistical software was being used to calculate the principal component based on the correlation matrix (version 4.0.5; Facto Mine R package).

2.5.3.*Euclidean Distance and Clustering of Genotypes*

Euclidean Distance (ED) was computed from all traits after standardized as established by Sneath and Sokal (1973). The distance matrix from phenotypetraits was used to construct dendrogram based on the Unweighted Pair Group Method with Arithmetic Means(UPGMA). The results of the cluster analysis were presented in the form of dendrograms. R statistical software (version 4.0.5; factoextra package) used for the analysis of distance matrix and constructing Dendrogram.

III. RESULT AND DISCUSSION

3.1.*Analysis of Variance*

The analysis of variance of eightquantitative traits understudy indicated that therewerehighly significant differences($P < 0.01$) betweentested genotypes for days to 50% flowering and days to 75% maturity(Table 2). Thus, the study showed that the presence ofvariability for the character considered which can be exploited for further barley improvement program through selection breeding programmes.

The genotypes had a range of 57 to 92 days to 50% flowering and 89 to 134 days to 75% maturity(Table 3). The three genotypes 244910, 244909 and 243305 were attaining 50% within 57 days but genotypes 242091 and 239075were delayed for 50% flowering. Genotypes 244924, 243305, and 242575, on the other hand, reach 75 % maturity in 89 days, but genotype 239075 takes 134 days to reach 75% maturity. The presence of a wide range of maturity within the genotypes will allow breeders to develop varieties for short growing season areas and extended rainfall season areas. According to Ebrahim et al. (2015), the time it takes for 20 Ethiopian barley genotypes to reach 50% flowering varies between 75 and 100 days.

On the other hand, spike length, spikelets per spikeand kernel per spike showed highly significant ($P< 0.01$) variations observed between tested genotypes. The value ranges from 6.08 to 10.29 cm, 18.47 to 52.18 and 17.16 to 52.11 for spike length, number of spikelets per spike and number of kernels per spike, respectively. The highest number of spikelets per spike and number of kernels per spike were recorded from 24168 and 241682 genotypes, respectively. On the contrary, genotype 242068 exhibited the smallest number for spikelets per spike and number of kernels per spike.Ebrahim et al. (2015) observed a huge variety of spike lengths from Ethiopian barley genotypes, ranging from 3.82 to 9.38 cm.

Thousand seed weight ranges from 31.01.6 to 52.21 g with a mean of 43.3 g. The thousand grain weight of 18 Ethiopian barley accessions ranged from 21.2 to 52.7 g, with a mean of 36.2 g, according to Alemayehu and Parlevliet (1997).A wide range of variation was also observed among examined genotypes in grain yield. The yield ranges from 10.2 to 44.63 quintals ha^{-1}. The highest grain yield was harvested from Awedo(released variety) and the lowest yield was from the farmers' varieties accession 243590. Even though the highest grain yield was measured from the one improved variety; 35 farmer's varieties were able to produce higher grain yield than the Chefo improved variety. On the other hand, 65 farmer's varieties were able to produce higher grain yield than bira improved variety. This show that the unrevealed potential of farmers' varieties in improvingyield

through the utilization of conserved germplasm. In addition, the presence of such wide variation in yield will help in developing of new barley variety.Since increasing the production of grain yield is the ultimate goal of plant breeding. Grain yields of Ethiopian Barley genotypes ranged from 22.58 to 62.02 quintals ha^{-1}, according to Ebrahim et al. (2015).

Table 2. Mean square values of eight quantitative characters of 83 barley accessions along with the three standard checks.

Source of Variation	df	Mean Square							
		DF	DM	PH	SL	SPS	KPS	TSW	GY
Block	4	4.17^{ns}	6.67^{ns}	1.67^{ns}	0.12^{ns}	16.65^{ns}	16.08^{ns}	4.92^{ns}	14.52^{ns}
Genotypes	82	50.12**	171.88^{**}	38.92^{*}	0.63**	93.4**	106.35**	17.28*	53.91**
Accessions	79	50.57**	135.92^{**}	30.63^{*}	0.75**	70.72**	80.86**	15.18*	40.25^{ns}
Checks	2	74.4**	667.27**	354.43**	2.1**	912.76**	1062.99**	98.89**	678.35**
Checks vs Accessions	1	366.65^{ns}	2896**	82.11*	0.09^{ns}	546.7**	563.41**	66.27**	267.93**
Error	8	3.57	4.77	8.87	0.1	12.4	12.21	4.65	14.21
CV		2.9	2.1	3.7	3.8	10.7	10.9	5	13.5

*, **,ns, Significant at ($p<0.05$ and ($p<0.01$), and non-significantrespectively. df= degree of freedom; DF= days to 50% flowering; DM= days to 75% maturity; PH= plant height (cm); SPS=number of spikelet per spike; KPS = number of kernels per spike; SL= spike length (cm); TSW = thousand seed weight (g); GY = grain yield (quintals/ha); CV, coefficient of variation (%).

Table 3. Minimum, maximum and Mean values of eight quantitative traits of 83 barley genotypes.

Traits	Min	Max	Mean
Days to 50% flowering	57.00	92.00	64.65
Days to 75% maturity	89.00	134.00	104.92
Plant height (cm)	63.45	92..65	81.26
Spike length (cm)	6.08	10.29	8.35
Spikelet per spike	18.47	52.18	32.76
Kernel per spike	17.16	52.11	32.04
Thousand seed weight (g)	31.01	52.21	43.34
Grain yield (quintal/ha)	10.20	44.63	27.84

3.2. *Principal Component Analysis*

The principal component analysis (PCA)was used for the reduction of the data set and to transform the available data set into principal components. In this study eight phenotypic quantitative traits were used and analysis of PCA was performed and presented in table 4. PCA transformed eight data set into eight factors loadings that the first principal component (PC1) contributed the highest variability and the last principal component (PC8) contributed the lowest variability, which accounted for the entire (100%) variability.

The principal component analysis indicated that the two principal components PC1 and PC2 with eigenvaluesranged from 2.05 to 3.48 containing variability of 43.59% and 25.68% respectively (Table 4, Figure 1). The first

two PC contain total variability of 69.27% (Table 4).These PC1 and PC2 hadeigenvalue more than 1 (Hair et al., 1998); while the rest (PC3 to PC8) had eigenvalue less than 1 (Chatfied and Collin, 1980) andwould not be considered in the interpretation of the results obtained due to that they werenot significantly influencing and contributing to the variability among the barley genotypes.

Spikelet per spike (0.48) and kernel per spike (0.48) contributed significant positive variability loading in the PC1 compared to the rest of the traits whereas spike length (-0.38) and thousand seed weight (-0.38) provided negative loading to the rest of the traits(Table 4,Figure 2). The PC2 accounted for 25.68% of the total variation and was mainlyimpacted bydays to 50% flowering (0.48) and days to 75% maturity (0.48) with positive loading.But, grain yield (-0.55) and plant height (-0.42) influenced with negative loading(Table 4, Figure 2).Therefore, most of the variations among genotypes in PC1 and PC2 was brought due to these major traits indicated above.

Table 4.Principal component factors, eigenvalues, individual, and cumulative variability of eight quantitative traits of 83 barleygenotypes.

Traits	PC 1	PC 2	PC 3	PC4	PC 5	PC 6	PC 7	PC 8
Days to 50% flowering	0.31	0.48	-0.23	-0.28	0.12	-0.09	0.71	0.01
Days to 75% maturity	0.35	0.40	-0.38	-0.25	0.11	-0.14	-0.68	-0.03
Plant height (cm)	0.09	-0.42	-0.76	0.35	-0.14	-0.28	0.13	0.00
Spike length (cm)	-0.38	-0.03	-0.23	-0.61	-0.64	0.11	0.01	-0.01
Spikelet per spike	0.48	-0.21	0.02	-0.06	-0.17	0.42	-0.01	0.71
Kernel per spike	0.48	-0.21	0.03	-0.04	-0.14	0.45	0.03	-0.69
Thousand seed weight (g)	-0.38	0.16	-0.42	0.11	0.39	0.69	-0.01	0.01
Grain yield (quintals/ha)	-0.01	-0.55	-0.02	-0.02	0.58	-0.12	0.02	0.00
Eigenvalue	3.48	2.05	0.85	0.57	0.52	0.37	0.14	0.003
Variability (%)	43.52	25.58	10.64	7.18	6.45	4.69	1.81	0.03
Cumulative (%)	43.52	69.11	79.76	86.94	93.44	98.14	99.96	100.00

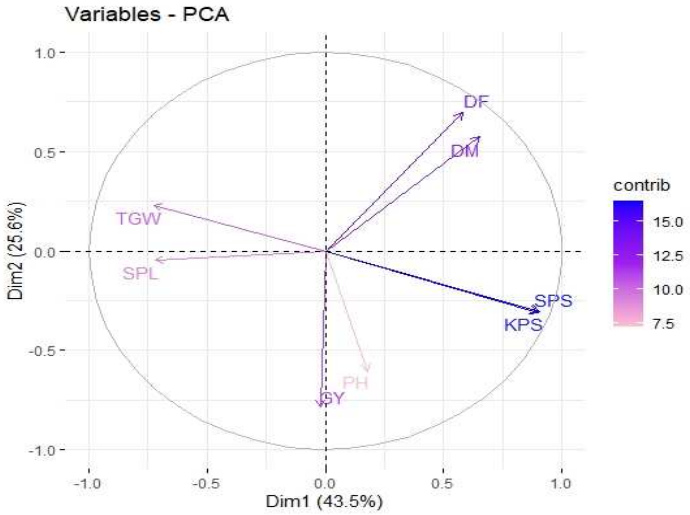

Fig. 1. The length of arrows shows the proportion of contributionin the principal components and the direction of arrows indicate whether the proportion is positive or negative in 83 barley genotypes.

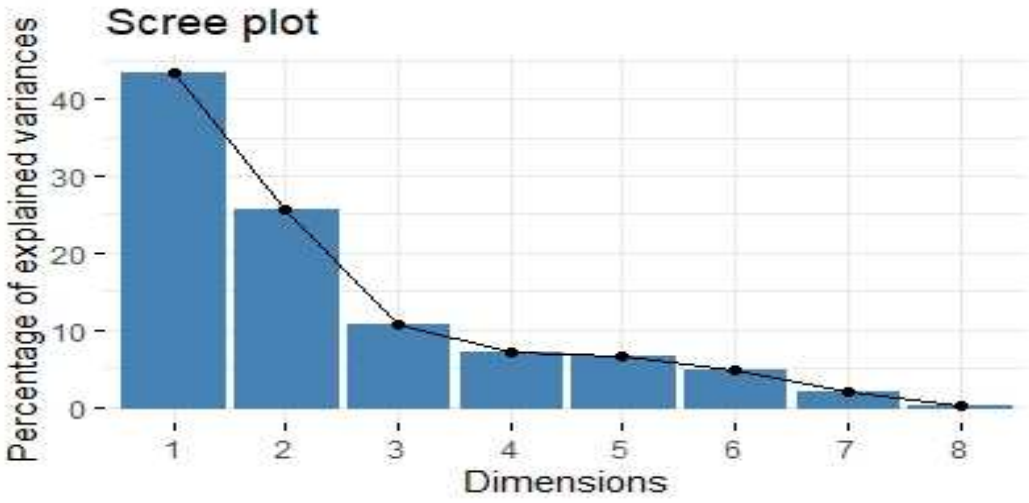

Fig. 2. Scree plot of data showing maximum variability explained by first and second principalcomponents in 83 barley genotypes.

3.3.*Cluster Analysis*

The distance matrix from eight quantitative traits was used to construct dendrograms basedon the Unweighted Pair Group Method with ArithmeticMeans (average).The Euclidean distances of all possible pairs of 83 barley genotypes were estimated by Euclidean distance from eight quantitative traits and the results as Euclidean distancematrix. The genotypes were broadly grouped into four distinct clusters. The first cluster contains 38 (45.78%) genotypes including one improved variety (Bira). The second cluster was also constructed by 26 (31.33%) genotypes including two of the improved varieties (Chefo and Awedo) (Table 5; Figure 3). The third and fourth clusters comprises 11 (13.25%) and 8 (9.64%) genotypes, respectively. After evaluating a different number of farmers' varieties of barley accessions and categorizing them into a different number of clusters based on the morphological traits, Angassa and Mohammed (2021), Mekonnon et al. (2015), and Addisu and Shumet (2015) reported similar results.

The constructed dendrogram showed that theexistence of variability among the studied barley genotypes.Characterization of such genotypes and clustering them basedon their morphological traits and genetic similarity will helpin the identification of best performer parents forhybridization/ crossing. Grouping of genotypes by usingmultivariate analysis based on their similarity inthe present study would be valuable for barley breeders inthat the most important accessions in the population may beselected from different clusters for barley improvementprograms.

Table 5.Clusters, number of genotypes and list of genotypes in each cluster of evaluated 83 barley genotypes.

Cluster	Number of Genotypes	List of Genotypes
I	38	243590, 242579, 242577, 243305, 242060, 242069, 238366, 242584, 238648, 242573, 242581, 238373, 242582, 237818, 237811, 243591, 237817, 237820, 238639, Bira, 239532, 243608, 243193, 243581, 239538, 239529, 239523, 238816, 239531, 239518, 239519, 239512, 238817, 239521, 239515, 238823, 239513, 239510
II	26	241684, 241680, 241120, 237859, 241676, Chefo, 241682, 241681, 243554, 243570, 238812, 239517, 243186, 238821, 237856, 243194,243189, 237822, 243188, 243180, 238657, Awedo, 243556, 243410, 237854, 239511
III	11	238651, 244922, 244910, 244909, 244937, 244924, 237843, 244935, 244940, 242068, 243302
IV	8	244912, 239075, 242091, 236809, 238845, 237821, 237857, 237823

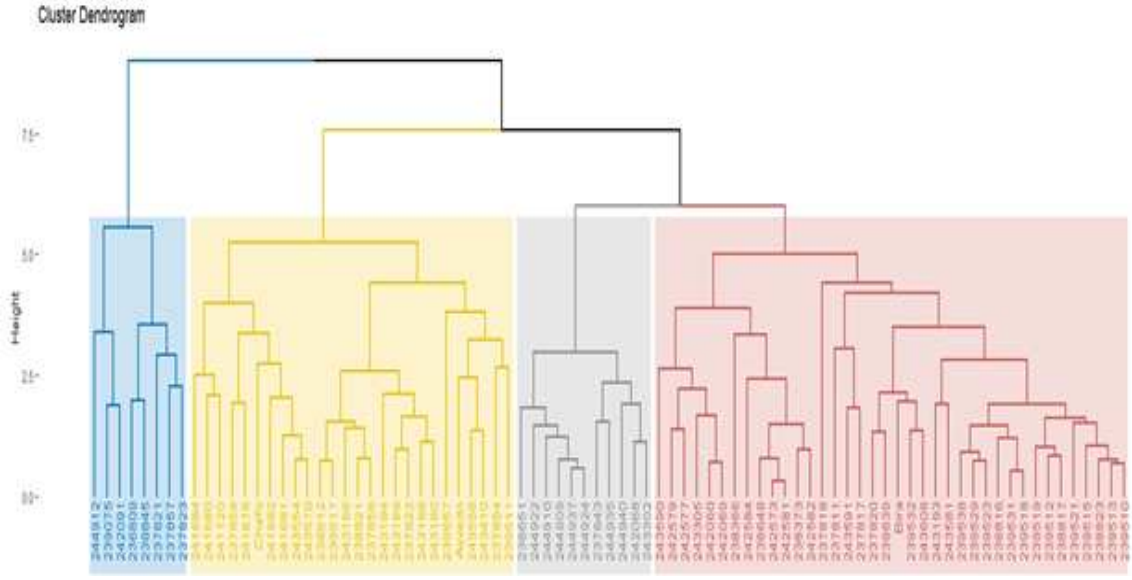

Fig. 3. Dendrogram of 83 barley genotypes based on eight quantitative traits.

Genotypes clustered in the first cluster were characterized by having lowest days for 50% flowering and 75% maturity. Cluster two characterized by greater grain yield, plant height, spikelet per spike kernel per spike. Contrary, genotypes clustered in the fourth cluster took the highest days for 50% flowering and 75% maturity and lowest ingrain yield (Table 6).

Table 6.Cluster means value for eight quantitative traits of 83 barley genotypes grouped in four clusters.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV
Days to 50% flowering	61.60	65.42	80.50	84.00

Days to 75% maturity	98.6	108.50	127.5	128.00
Plant height (cm)	80.56	84.29	77.17	69.05
Spike length (cm)	8.67	7.51	7.66	8.17
Spikelet per spike	27.70	45.26	34.43	42.20
Kernel per spike	26.74	45.12	34.11	42.00
Thousand seed weight (g)	45.17	38.75	43.86	33.20
Grain yield (quintal/ha)	27.12	31.54	19.01	13.82

IV. CONCLUSION

The study was conducted to assess the preliminary performance of barley accessions and genetic variability associations for yield and yield related traits of barley accessions. Eighty barley accessions and three standard check types were tested for eight quantitative traits. Analysis of variance showed very significant differences between tested genotypes for days to 50% flowering and days to 75% maturity, spike length, spikelets per spike, kernel per spike, and grain yield. Also significant variability observed between genotypes for plant and thousand grain weight.The principal component analysis showed that the two principal components PC1 and PC2 with eigenvalues greater than one containing variability of 43.59% and 25.68% respectively. The genotypes were broadly grouped into four distinct clusters C1, C2, C3 and C4 constitutes 45.78%, 31.33%, 13.25% and 9.64% of genotypes, respectively. In general, the study convincingly demonstrated great potential of farmer's varieties for the studied traits. As a result, the accessions were divergent and had a lot of genetic variation, which might be utilized in future barley breeding projects to improve productivity and production of barley crop.

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REFERENCES

[1] S.E, Ullrich," Significance, adaptation, production, and trade of barley," in Barley: Production, Improvement and Uses, ed S.E. Ullrich (Oxford. UK: Wiley-Blackwell), 2010, 3-13.
[2] V. Kumar, A. Khippal, J. Singh, R. Selvakumar, R. Malik, D. Kumar, Barley research in India: Retrospect and prospects J.Wheat Res., 6, 2014, 1-20.
[3] J.R. Harlan, D. Zohary, Distribution of wild wheats and barley. Science153, 1966, 1074-1080. doi: 10.1126/science.153.3740.1074
[4] S.Ceccarelli, S. Grando, V. Shevstov, H. Vivar, A.Yahayaoui, M. El-bhoussini, The ICARDA strategy for global barleyimprovement. Barley Wheat Newslett18, 1999, pp. 3–12.
[5] A.Badr, K.Müller, R. Schäfer-Pregl, H. Rabey, S. Effgen, On theorigin and domestication history of barley (Hordeumvulgare). Mol. Biol. Evol. 17, 2000,pp. 499–510. doi: 10.1093/oxfordjournals.molbev.a026330
[6] T. Zeleke, Evaluation of host reaction and yield performance of malt barley cultivars toNet Blotch, Pyrenophora teres in Bale. Journal of Plant Sciences. 2017;5(1):43–7.
[7] S. Bekele, T. Yoseph, T. Ayalew, Growth, Protein Content, Yield and yield components of malt barley (*Hordeum vulgare L.*) Varieties in Response to Seeding Rateat Sinana District, Southeast Ethiopia. International Journal of Applied AgriculturalSciences. 6. (4), 2020, pp. 61-71.
[8] Central Statistical Agency, Report on Area and Production of Crops. Statistical Bulletin 584, 2017, Volume I, Addis Ababa.
[9] J.R. Harlan, Crops & Man. 2nd Edition, American Society of Agronomy, Crop Science Society of America, Inc., Madison,1975.
[10] C. Qualset, Sampling germplasm in a center of diversity: an example of disease resistance in Ethiopian barley. Frankel OH, Hawkes JG (eds), Crop Genetic Resources for Today and Tomorrow, Cambridge University Press, Cambridge,1975, pp. 81-96.
[11] B. Birhanu, A. Fekadu, L. Berhane, Food barley in Ethiopia. In: S. Grando and M. H. Gomez (Eds), Food barley: importance, uses and local knowledge. Proceedings of the International Workshop on Food Barley Improvement, 14-17 January 2002, Hammamet,Tunisia. Aleppo: ICARDA,pp. 53-81.
[12] D. Fischbeck, Diversification through breeding. In: von Bothmer R., van Hintum T.,Knupffer H., Sato K., editors. Diversity in barley (Hordeum vulgare). Amsterdam: Elsevier Science BV; 2003. pp. 29-52.

[13] P. Langridge, R. Waugh, Harnessing the potential of germplasm collections. Nat Genet. 2019;51:200-1. doi: 10.1038/s41588- 018-0340-4.
[14] P. Smýkal, M.N. Nelson, J.D. Berger, E.J. Von Wettberg,. The impact of genetic changes during crop domestication. Agronomy, 8(7): 119, 2018.
[15] A. Delessa, M. Jemal, Genetic diversity assessment of Ethiopian Landrace Barley (Hordeum Vulgare (L.)) GenotypesthroughMultivariate Analysis. American Journal of Biological and Environmental Statistics. Vol. 7, No. 3, 2021, pp. 67-73. doi: 10.11648/j.ajbes.20210703.12
[16] W.G. Abtew, Characterization of genetic variation among Ethiopian barley (Hoerdeum vulgare L.) genotypes. PhD dissertation. Institute of Plant Breeding, Seed Science and Population Genetics, Hohenheim University, Stuttgart Germany, 2020.
[17] Y. Horamo, M. Chitakira,K. Yessoufou, Farmers' Knowledge Is the Basis for Local Level Agro-Forestry Management: The Caseof Lemo Woreda in Hadiya Zone, Ethiopia.Front. Sustain. Food Syst. 5:739061. doi: 10.3389/fsufs.2021.739061
[18] IPGRI (International Plant Genetic Resource Institute), Description of barley (*Hordeum vulgare* L.). International Plant Genetic Resources Institute, Rome, Italy, 1994.
[19] P. H. Sneath, R. R. Sokal, *Numerical taxonomy. The principles and practice of numerical classification*, 1973.
[20] S. Ebrahim, E. Shiferaw F. Hailu, Evaluation of genetic diversity in barley (Hordeum vulgare L.) from Wollo high land areas using agromorphological traits and hordein. *African Journal of Biotechnology*, *14*(22), 2015, pp.1886-1896. DOI: 10.5897/AJB2014.14258.
[21] F. Alemayehu,J.E. Parlevliet, Variation between and within Ethiopian barley landraces. *Euphytica*, *94*(2), 1997, pp.183-189. https://doi.org/10.1023/A:1002946004268.
[22] J.F Hair, J.R. Andrson, R.E. Tatham, W.C. Black, Multivariate Data Analysis. 5th ed. London: Prentice-Hall international, Inc; 1998.
[23] C. Chatfied, A.J. Collin, Introduction to multivariate analysis. New York, NY: Published in the USA by Chapman and Hall in Associationwith Methuen, Inc.; 1980. pp. 733.
[24] B. Mekonnon, B. Lakew and T. Dessalegn, Morphological diversity and association of traits in Ethiopian food barley (Hordeum vulgareL.) landraces in relation to regions of origin and altitudes. *Journal of Plant Breeding and Crop Science*, *7* (2), 2015, pp. 44-54.https://doi.org/10.2135/cropsci2009.10.0564.
[25] F. Addisu, T. Shumet, Variability, heritability and genetic advance for some yield and yield related traits in barley (Hordeum vulgare L.) landraces in Ethiopia. *International Journal of Plant Breeding and Genetics*, *9*(2), 2015, pp.68-76. DOI: 10.3923/ijpbg.2015.68.76.

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Delessa Angassa, was born on March 12, 1968 in Wonchi District, South-West Shoa Zone of Oromia Region, Ethiopia from his father, Angassa Kussa, and his mother, Birki Erko. He attended elementary and junior secondary education atChitu elementary and secondary schools and his senior secondary at Dejazmach Geresu Duki comprehensive secondary school from 1975 to 1986. After successfully passing the Ethiopian School Leaving Examination, he joined Haramaya University in September 1987 and graduated with a B.Sc. degree in Plant Sciences in December 1991. Immediately after graduation, he was employed by the Ministry of Agriculture and worked in the Amhara and Oromia Regions as an expert in crop production and protection, Head of Agricultural Development Office, Team Leader of Extension and Natural Res--ource Development and Protection, and Coffee Agronomist at wereda and zonal level from January 1991 up to August 2005. He joined the school of graduate studies at Haramaya University in September 2005 to pursue his studies for a Master of Science degree in Agronomy. After graduating in 2007, he joined the Ethiopian Biodiversity Institute, working as an associate researcher and researcher.Author of eight scientific papers and participated in various national and international workshops and training on genetic resource conservation and sustainable utilization.