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Genetic diversity of Ethiopian barley (*Hordeum vulgare* L.) genotypes based on multivariate statistical analysis for acid soil tolerance

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Abstract
Soil acidity is now a serious threat to barley production in most high lands of Ethiopia. Three hundred twenty (320) barley genotypes were evaluated in 2017 main-season, at Holeta Agricultural Research Center using 20x16 Alpha Lattice design under two-soil conditions (limed and unlimed). The objectives of the study were to evaluate the genetic variability among barley genotypes for soil acidity tolerance using multivariate analysis. Barley genotypes were classified into thirteen, sixteen and twelve clusters under unlimed and limed soil condition and by stress index cluster analysis, respectively. Principal component analysis exhibited 81% and 78% of total variation under unlimed and limed soil condition respectively. Phenotypic diversity index was very high for ear attitude, kernel row number and Kernel color and comparatively low for spike density.

Keywords: Barley, genetic variability, soil acidity stress

Introduction
Barley (*Hordeum vulgare* L.) is the most important cereal crop in Ethiopia, with productivity of 2.53 ton ha^{-1} [1]. It is an important crop grown in diverse agro-ecology from 1,500 to 3,500m altitude for many purpose in different seasons and production systems and a common food grain, especially for highlands of Ethiopia [2, 3].
Soil acidity is one of the most important constraints in barley production, mainly on Nitisols or Oxisols, of the Ethiopian highlands where the rainfall intensity is high and crop cultivation has been carried out for centuries [4, 5]. Barley is considered to be more sensitive to acidic soils than rye, oat, rice and wheat [6].
Among cultivated cereals, barley has several accessions preserved in the Ethiopian gene bank with more than 15, 300 collections. This is approximately 23% of the total landraces conserved in the gene bank of the country [7]. The large diversity in the Ethiopian barley landraces could be due to the diversity in soils, climate, altitude and topography together with geographical isolation for long periods [8]. Barley in gene bank serves as a reservoir of potentially useful genes for many purposes, including breeding for resistance to diseases, pests and other environmental stresses, as well as for traits that increase yield or food quality [9]. Most of acid tolerant crop varieties are usually obtained from highly acidic soils of the world. The most likely reasons for such associations are natural selection and adaptation or human selection by early agriculturalists. Hence, evaluation of germplasm collected from acid soil areas was considered as the logical and appropriate entry strategy in acid tolerance breeding [10].
Estimating genetic diversity and determining the relationship between the germplasm collections enhance efficient collection management and genetic improvement [11]. Multivariate statistical techniques are used by geneticists to estimate genetic diversity among cultivars within a crop under the presumption that cultivars within groups are genetically related whereas diverse cultivars are classified into different groups. The premise was that genotypes from different geographical regions would exhibit genetically diverse due to mutation, genetic drift and selection [12]. Hence, this study was done with the objective to evaluate the genetic variability among barley genotypes for soil acidity tolerance using multivariate analysis.

Materials and Methods

Description of the Study Area

The experiment was conducted at Holetta Agricultural Research Centre, which was located at 9º00'N, 38º 30'E at an altitude of 2400 m above sea level. It is 29 km away from Addis Ababa on the road to Ambo. Holetta Agricultural Research Centre had mean annual rainfall of 1044mm, mean relative humidity of 60.6%, and mean maximum and minimum temperature of 22.10°C and 6.20°C, respectively. The soil of the experimental field is clay classified as, Nitosol, which was characterized with pH of 4.58 and exchangeable acidity 2.50cmol/kg for unlimed experiment (HARC, 2017 Soil lab result).

Experimental Materials

A total of 320 barley genotypes including 27 released varieties and 293 pure lines collected from the representative acid soils in different Zones of Ethiopia (Table 1). The materials with their passport data were obtained from Holetta Agricultural Research Centre.

Table 1: Zones, altitude ranges and number of accessions of the collected barley germplasm used for the study

Zone of collection	Altitude classes				
	Class I	Class II	Class III	Class IV	Total
	<2000	2001-2500	2501-3000	>3000	
Agew Awi	1	4	5	_	10
Arssi	6	4	10	5	25
Bale	5	5	6	3	19
South Gondar	1	5	5	4	15
South wello	1	6	10	2	19
SouthTigray	5	8	10		24
Gurage	2	5	12	8	27
Hadya	2	6	3	_	10
Keficho Shekicho	1	1	_	_	2
West Shewa	2	5	8	2	17
East Gojam	_	5	6	2	13
Eastharerge	1	6	6	_	13
EastShewa	_	1	_	_	1
EastWellega	1	10	5	_	16
East Tigray	4	8	6	2	20
North Omo	3	5	15	3	26
North Shewa	4	10	11	11	36
Released varieties	_	_	_	_	27
Total	39	94	118	42	320

Soil Sample Collection, Chemical Analysis and Lime Application Procedures

Random soil samples were taken at a depth of 0-20 cm using a zigzag sampling pattern from experimental field before sowing and after harvest [13]. The collected samples were immediately air-dried and sieved to separate the roots and other unwanted materials from the soil and all samples were combined. Finally, composite sample was submitted for laboratory analysis. Soil pH was measured potentiometrically with a digital pH meter in the supernatant suspension of 1:2.5 soils to water ratio [14]. Exchangeable cations (Ca, Mg, K and Na) and cation exchange capacity (CEC) were determined after leaching the soil samples with 1 M ammonium acetate solution at pH 7 [15]. Exchangeable acidity (Al + H) was determined by saturating the soil samples with 1M KCl solution and titrated with 0.02 M NaOH [16].

Before sowing the acid soil was ameliorated by lime (CaCO3), to raise soil pH from acidic conditions to a target level that was optimized for the plant growth [17]. The amount of lime required was calculated based on the formula of [18].

$$\text{LR, } CaCO_3 \text{ (kg/ha)} = \frac{EA\ (\text{cmol /kg of soil}) * 0.15\text{m} * 104\ \text{m2} * \text{B.D (Mg/m3)} * 1000}{2000\ \text{cmol /kg}}$$

Where EA= exchangeable acidity, expressed in Cmol/kg of soil, 0.15 m plowing depth.

Total volume of hectares of soil = area (10000m^2)*Depth (0.15m), B.D = bulk density taken as 1.1 g/cm^3 for loam soil textural class.

Then multiplied by a crop coefficient factor for soil acidity which is 2.0 = for Al-sensitive crops (barley belongs to these groups).

Experimental Design and Procedures

The study was conducted on two soil acidity conditions (unlimed and limed soils) as two separate experiments laid out in 20x16 Alpha Lattice Design with two replications for each experiment. Plots consisted of four rows each 2.5m long by 0.8m width (2m^2). Each plot had 0.2m spacing between rows. The spacing between plots, blocks in each replication and between replications were 0.5m, 1.0m and 1.0m respectively. The seed rate was 85kgha^{-1} and fertilizers were applied during planting in the form of Urea and Diamonium phosphate (DAP) at the rate of 41 and 46kgha^{-1} respectively. The experiment was planted on the first week of July in 2017.All field management practices were handled as per the recommendation for barley production.

Data collection

Crop phonology like days to emergence (DTE), days to heading (DTH) and days to maturity (DTM) were counted from date of planting to 50% seedling emergence and from date of emergence to 50% heading and 75% physiological maturity of plants in each plot respectively. The average plant height (PH) was measured from the ground to the tip of spikes of five main plants of the two middle rows of each plot. Disease scoring on barley leaf scaled and net blotch

disease was assessed by visual examination using a scale of 0 to 9 according to [19]. Yield components such as fertile tillers per plant (FTP), spike length per plant (SLP) and kernels per spike (KPS) were determined from five random plants of the middle rows of each plot. After harvesting, indiscriminately counted thousand kernels weight (TKW) from each plot were weighted and adjusted to 12.5% standard grain moisture content of cereals, while hectolitre weight (HLW) was measured after drying the grain of each plot up to 12.5% moisture content. The total above ground biomass yield (BY) harvested from the middle two rows of each plot was dried out for some days under sun and then weighted. The grain yield (GY) was harvested from the middle two rows of each plot and adjusted to the standard grain moisture content (12.5%). Stress susceptibility index (SSI) was calculating for each genotype using the formula developed by [20] and Stress tolerance index (STI) was calculated for each genotype using the formula developed by [21]. Qualitative traits (ear attitude, kernel row number, kernel color, spike density) were collected according to descriptors for barley [22].

Statistical Procedures

Cluster Analysis

Multivariate analysis computes two or more variables at a time. For this purpose the data will be standardized to mean of zero and a variance of one. Three hundred twenty genotypes and seventeen regions of origin were grouped into respective classes. The values of pseudo F statistic (PSF) and Hotellin's pseudo T^2 statistic were used for defining the optimum number of clusters. Hierarchical cluster analysis was computed using the PROC CLUSTER Procedure SAS Version 9.1.3 [23]. Unweighted Pair Group Method using Arithmetic Average linkage (UWPGMA) was employed. The results of the cluster analysis were presented in the form of a dendrogram to depict the degree of similarity and interrelationships among regions and genotypes.

Principal component analysis

The principal component analysis (PCA) was computed to reduce the number of variables in to a few correlated components that can explain much of the variability. It was performed using the correlation matrix to define the patterns of variation among genotypes based on the mean of quantitative characters. It also helps to identify characters that load the most in explaining the observed variation. The PROC PRINCOMP Procedure of SAS Version 9.1.3 [23] was used for principal component analysis.

Estimate of diversity index

The Shannon-Weaver diversity index (H′) was used to compute the phenotypic frequencies and to assess the phenotypic diversity for each character for all accessions. It is used in genetic resource studies as a convenient measure of both richness and evenness using quantitative data. It was computed using the phenotypic frequencies to assess the overall phenotypic diversity for each trait by zones and altitude ranges.

$$H = -\sum_{i-1}^{n} pi \ln(pi)$$

$$H' = {}^{H}/_{H_{max}}$$

$$H_{max} = \ln(n)$$

Where: H' = standardized relative diversity index, n = is the number of phenotypic classes per characters

Pi = is the proportion of the total number of entries in the i th class, ln = natural logarithm

Results and Discussion

Effect of Lime Application on Soil Acidity Related Chemical Properties of the Soil

The soil chemical analysis results after harvest for some chemical properties are presented in Table 2. The Soil acidity changed from strongly acidic to slightly acidic classes and the deficiency of certain plant nutrients were observed. The application of lime raised the soil pH to 6.24 and dropped exchangeable acidity from 1.71 to 0.21(cmol/kg) under unlimed and limed, respectively.

The organic carbon (OC) content was 1.29 and 1.54 % under unlimed and limed soil which is medium according to [24] who categorized OC content as very low (<0.06%), low (0.60–1.25%) and medium (1.26–2.50%). This have an impact on the availability of organic matter content in the soil. The values for total nitrogen (N) were 0.13 and 0.16% under limed and unlimed soil. According to [25], these values were rated as low. The available phosphorus (P) was 12.68 and 17.89 mg/kg under unlimed and limed soil, respectively. The available P categorized as high (> 50 mg/kg), as medium (15 – 50 mg/kg) and as low (< 15 mg/kg) [25]. Based on this classification, available P of limed soil was grouped as medium and unlimed as low.

The Cation Exchange Capacity (CEC) was 21.98 and 24.99 (cmol/kg) under unlimed and limed soil. According to [25], soils had optimum CEC values. Liming also affected exchangeable Al, exchangeable bases (Ca, Na, Mg and K), Available Micronutrient (Zn, Fe and Mn) (Table 2). This result was in agreement with the result of [26] indicated that an increase in the exchangeable bases as a result of lime application to soils. Reclaiming acid soils by liming had significant effect on selected soil chemical properties of soil [27].

Table 2: Selected chemical properties of the experimental soil

Soil properties	Limed soil	Un limed soil
pH(H_2O 1:2.5)	6.24	4.69
Nitrogen (%)	0.13	0.16
Organic carbon (%)	1.29	1.54
Available phosphorus (mg/ kg soil)	17.89	12.68
Exchangeable acidity (cmol/kg)	0.21	1.71
Cation exchangeable Capacity (cmol (+)/ kg)	24.99	21.98
Exchangeable Al (meq/100g soil)	0.09	1.25
Exchangeable Ca (cmol(+)/kg)	7.90	4.35
Exchangeable Mg (cmol(+)/kg)	3.09	0.78
Exchangeable Na (cmol(+)/kg)	0.07	0.04
Exchangeable K (cmol(+)/kg)	0.71	0.25
Micro nutrient Zn(ppm)	0.93	1.35
Micro nutrient Fe(ppm)	146.18	224.82
Micro nutrient Mn(ppm)	37.81	55.50

Cluster analysis for Genotypes under limed and unlimed soil

Cluster mean analysis was used to compare and classify the observed trait variation in the genotypes. Barley genotypes collected from wide eco-geographic range of the country had best adaptation to soil acidity [28]. Based on various phenotypic data, barley genotypes were grouped by cluster analysis on the basis of Euclidean distances of dissimilarity to their distinct groups under unlimed and limed soil conditions (Table 3 and 5).

Under unlimed soil condition, barley genotypes were classified into thirteen clusters (Table 3). Numbers of genotypes per cluster varied from one hundred eighty nine genotypes in cluster I to 1 genotypes in cluster XIII. Within cluster trait means (Table 7) and percent of genotypes in each cluster were shown in (Table 3, Figure 1). Cluster I hold 59.06% of the total experimental materials. Genotypes grouped under cluster I were scattered along all regions and more at altitude group between (2001 and 3000m.a.s.l). Majority of landraces were collected from zones North Shewa, East Tigray, South Tigray, North omo, South wello, Arssi and one released variety, whereas cluster II and III contained the second and third large number of barley genotypes, each of these cluster constitute eight released varieties and different number of landraces collected from different part of Ethiopia (Table 4). Furthermore cluster I has been characterized by early flowering and maturing, highly susceptible to scald and moderately susceptible for net blotch diseases, relatively lower number of fertile tillers per plant, relatively the lightest thousand seed weight, intermediate plant height, relatively shorter spike length, relatively lower grain yield and biomass yield as compared to grand mean of genotypes.

Cluster II include eighty three genotypes and characterized by intermediate flowering and maturing date, moderately susceptible to scald and net blotch diseases, relatively lower number of fertile tillers per plant, relatively longer spike length, intermediate plant height, higher number of kernel per spike, relatively the higher thousand seed weight, hectolitre weight, grain yield per hectare and relatively higher biomass yield per hectare as compared to grand mean of genotypes. Most of these landraces were collected at an altitude group between (2001 and 3000m.a.s.l) and all zones of collections except East Harerge, East Shewa and East Tigray. Relatively genotypes better in almost all performance were grouped under cluster IX which contribute 1.56% to the population these were Miscal-21, Travller, EH 1847, HB 1964 and Ibon174/03 (Table 4).

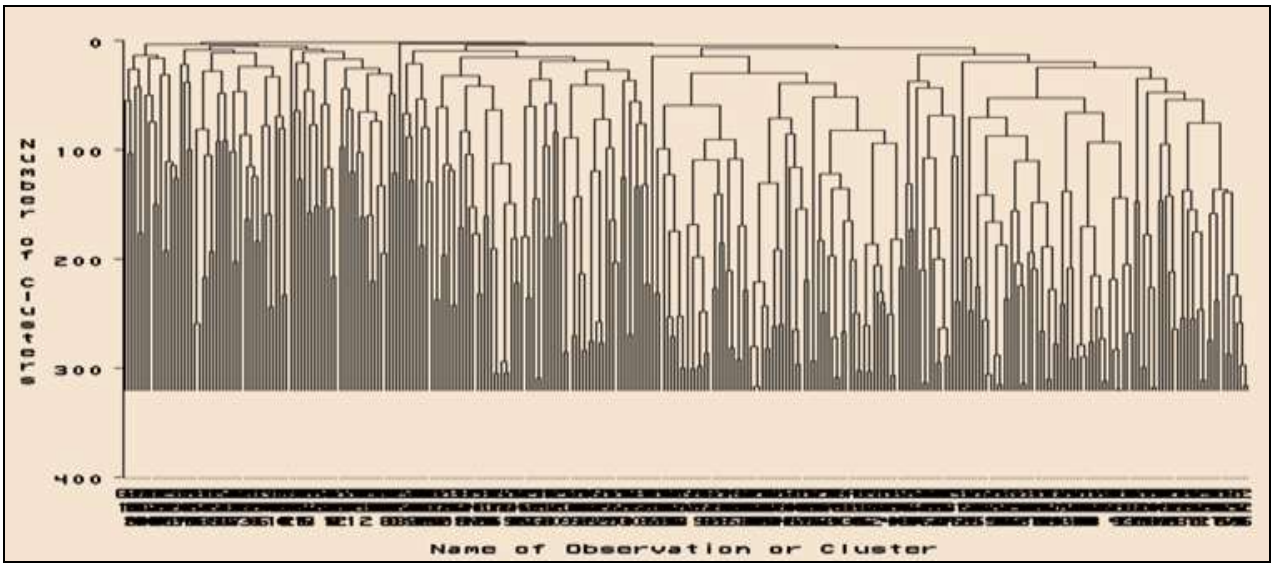

Fig 1: Dendrogram of barley genotypes under unlimed soil revealed by UPGMA cluster analysis based on 14 quantitative traits

Table 3: Clustering pattern of 320 Barley genotypes under unlimed soil

Cluster	Genotypes number														Total	%
I	1	2	3	6	8	9	10	11	12	16	17	18	19	20	189	59.06
	21	22	29	30	38	39	40	41	44	45	46	47	48	49		
	50	51	53	57	58	59	60	62	63	65	66	68	69	70		
	71	72	73	74	76	79	83	84	90	91	92	96	101	102		
	104	105	106	107	108	109	110	112	113	114	115	116	117	118		
	119	121	126	129	130	133	138	140	141	142	143	145	146	147		
	149	150	151	152	153	155	158	159	161	162	163	165	166	167		
	168	169	170	171	172	173	174	176	178	179	180	184	185	186		
	190	193	194	195	196	197	198	199	200	203	205	206	207	208		
	209	210	211	212	213	214	215	216	217	218	219	223	224	226		
	227	228	229	230	232	234	235	236	237	238	244	246	248	250		
	251	252	253	254	255	256	258	259	260	261	262	264	265	266		
	267	268	269	271	272	273	274	275	276	277	278	279	281	283		
	286	287	288	290	291	293	316									
II	4	5	7	13	14	15	23	24	27	28	28	31	32	33	83	25.94
	34	35	36	37	42	54	55	56	61	67	75	77	78	80		
	81	82	83	85	86	88	89	94	95	98	99	100	103	111		

	120	122	123	124	131	132	136	137	144	154	156	157	181	183		
	188	192	201	204	220	233	239	240	242	243	245	247	249	263		
	270	280	282	284	285	289	294	296	298	299	303	314	319	320		
III	26	175	64	97	148	231	189	87	135	315	134	307	177	305	23	7.19
	317	127	191	312	313	187	257	311	309							
IV	43	128	225	93											4	1.25
V	52	164	202	222	292										5	1.56
VI	125														1	0.31
VII	139	221													2	0.63
VIII	160	182	241	302											4	1.25
IX	295	318	308	304	310										5	1.56
X	297														1	0.31
XI	300														1	0.31
XII	301														1	0.31
XIII	306														1	0.31

Table 4: Distribution of barley genotypes under unlimed soil over thirteen clusters by eighteen zones of origin and four altitude groups based on 14 quantitative traits

Zone	**Clusters**													**Total**
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	
Agew Awi	7	2	_	1	_	_	_	_	_	_	_	_	_	10
Arssi	15	7	2	_	1	_	_	_	_	_	_	_	_	25
Bale	11	7	1	_	_	_	_	_	_	_	_	_	_	19
South Gondar	9	4	_	1	1	_	_	_	_	_	_	_	_	15
South wello	15	3	_		1	_	_	_	_	_	_	_	_	19
South Tigray	19	2	1	_	1	_	_	1	_	_	_	_	_	23
Gurage	8	17	1	_	_	1	_	_	_	_	_	_	_	27
Hadya	3	5	2	_	_	_	_	_	_	_	_	_	_	11
Keficho Shekicho	1	1	_	_	_	_	_	_	_	_	_	_	_	2
West Shewa	7	10	_	_	_	_	_	_	_	_	_	_	_	17
East Gojam	9	4	_	_	_	_	_	_	_	_	_	_	_	13
East harerge	13	_	_	_	_	_	_	_	_	_	_	_	_	13
East Shewa	1	_	_	_	_	_	_	_	_	_	_	_	_	1
East Wellega	10	5	_	_	1	_	_	_	_	_	_	_	_	16
East Tigray	19	_	_	1	_	_	_	_	_	_	_	_	_	20
North Omo	18	3	1	1	_	_	2	1	_	_	_	_	_	26
North Shewa	23	5	7	_	_	_	_	1	_	_	_	_	_	36
Rleased varieties	1	8	8	_	_	_	_	1	5	1	1	1	1	27
Total	**189**	**83**	**23**	**4**	**5**	**1**	**2**	**4**	**5**	**1**	**1**	**1**	**1**	**320**
% of population	59.06	25.94	7.19	1.25	1.56	0.31	0.63	1.25	1.56	0.31	0.31	0.31	0.31	
Group	**Altitude Group**													
<2000	34			1	2	_	1	_	_	_	_	_	_	38
2001-2500	71			18	1	_	3	_	_	1	_	_	_	94
2501-3000	65			37	10	3	1	1	2	_	_	_	_	119
>3000	18			19	2	1	_	_	_	2	_	_	_	42
Total	188			75	15	4	5	1	2	3	_	_	_	293

Under limed soil conditions, barley genotypes were assigned to sixteen clusters (Table 5). Numbers of genotypes per cluster varied from One hundred fifteen genotypes in cluster I to two genotypes in cluster XVI. Cluster means (Table 7) and percent of populations in each cluster were shown in (Table 5, Figure 2). One hundred fifteen genotypes were found in cluster I, which was 35.93% of the total experimental materials. Landraces grouped under cluster I were scattered along all zones and at altitude group between (2001and 3000m.a.s.l). This cluster containing the majority of landrace from zones of Arssi, North Shewa, East Tigray and South Tigray and released varieties, followed by cluster VIII and VI (Table 6). Furthermore cluster I had been characterized by early flowering and maturing, highly susceptible to scald and moderately susceptible for net blotch diseases, relatively lower number of fertile tillers per plant, relatively higher thousand seed weight, intermediate plant height, relatively shorter spike length, relatively lower grain yield and biomass yield as compared to grand mean of genotypes.

Cluster VIII include forty nine genotypes which accounts 15.31% of the population and characterized by genotypes which had early flowering and maturing, relatively lower number of fertile tillers per plant, shorter plant height and spike length, higher kernel per spike, lightest thousand seed weight, relatively the lower hectolitres weight, grain yield and biomass yield as compared to grand mean of genotypes. Most of these genotypes were collected from altitude group between (2001 and 3000 m.a.s.l) and zones except Agew Awi, Hadya, East Shewa and Keficho Shekicho. On the other hand genotypes better in almost all trait performance were grouped under cluster V which contributes 9.06% to the population (twenty nine genotypes). These had intermediate flowering and maturing date, relatively higher number of fertile tillers per plant, relatively longer spike length, intermediate plant height, relatively, higher number of kernel per spike, thousand seed weight, hectolitres weight, grain yield and biomass yield as compared to grand

mean of genotypes. Most of these landrace were collected at an altitude group of (2501-3000m.a.s.l) and zones except South Tigray, Hadya, East Harerge and East Shewa.

The result above showed that number of cluster under limed is greater than number of cluster under un limed soil these was due to under unlimed soil genotypes were exposed to nutritional toxicity and deficiency that found in growing soil environments. Soil acidity could prevent barley genotypes from expressing its maximum genetic potential and plant responses affected by the stresses. Under acidic stress large number of genotypes found under similar groups owing to little variation on their quantitative traits as a result of stress. Under both unlimed and limed soil condition cluster I had larger number experimental materials which account 59.06% and 35.94%, respectively. Similarly much of the material from Arssi, South Tigray, East Tigray and North Shewa had greater contribution to cluster I but the number of genotypes under un limed was larger than that of limed soil condition. Comparatively small numbers of released varieties were found under both unlimed and limed soil condition but relatively greater number found under limed soil condition this implied that landraces ecological amplitudes may exceed those of the varieties derived from them in terms of evolution and adaptation to change in agricultural systems under specific cultural and environmental stresses [29].

Based on the altitudinal clustering under both unlimed and limed soil condition cluster I had larger number experimental materials which account 64.16% and 37.88% respectively for total population. Under both soil conditions much of the materials grouped under altitudinal range between 2000-3000 m.a.s.l. similar results were indicated that landraces ecological amplitude may exceed those of the varieties derived from them [29]. Abiotic stress factors could prevent the plant from expressing its maximum genetic potential [30]. Altitude range between 2000-3000 m.a.s.l. was affected by soil acidity and barley genotypes collected from these areas were grouped to gather in response to stress than normal growing environments [31].

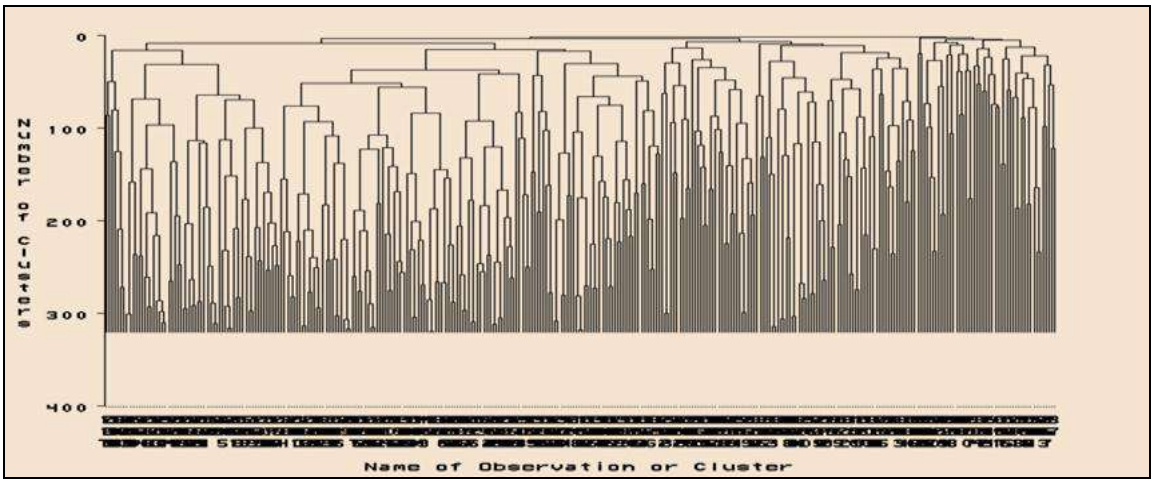

Fig 2: Dendrogram of barley genotypes under limed soil revealed by UPGMA cluster analysis based on 14 quantitative traits

Table 5: Clustering pattern of 320 Barley genotypes under limed soil

Cluster	Genotypes									Total	%
I	1	2	8	9	10	13	17	19	20	115	35.94
	29	30	33	39	40	41	45	48	49		
	52	54	59	64	68	69	70	72	73		
	74	84	96	97	104	105	107	108	112		
	114	116	118	119	121	129	130	136	138		
	140	142	144	147	149	150	151	152	153		
	155	162	163	165	166	172	173	174	180		
	185	186	187	188	189	196	197	200	202		
	204	205	207	208	211	213	214	218	222		
	225	226	227	228	231	232	233	236	237		
	246	248	250	253	256	258	260	262	264		
	267	271	272	273	274	276	277	278	279		
	280	281	292	300	306	307	317				
II	3	19	117	143	190	230	286			7	2.19
III	4	61	111	137	192	284				7	2.19
IV	5	28	88	99	270	297				6	1.88
V	6	7	11	14	23	26	27	31	32	29	9.06
	57	95	98	103	110	120	122	123	127		
	139	143	159	193	194	245	304	311	313		
	316	318									
VI	12	16	46	51	63	71	77	91	102	33	10.31
	109	115	125	126	134	135	158	161	176		
	178	184	191	198	221	249	255	269	293		
	296	309	315								

VII	15	25	34	37	55	86	87	131	181	14	4.38
	201	241	243	247	257	263					
VIII	18	21	22	38	50	58	60	62	66	49	15.31
	76	79	83	90	93	106	113	141	145		
	146	164	167	168	169	170	171	175	199		
	203	206	209	210	212	215	217	219	223		
	224	229	234	236	251	252	254	259	261		
	265	266	268	275	283	290	291				
IX	24	35	36	47	56	67	78	80	85	23	7.19
	89	100	101	124	128	160	182	183	216		
	239	240	242								
X	42	220	295	299	302	308	310	319		8	2.50
XI	44	53	65	75	92	132	133	148	179	14	4.38
	238	244	282	287	288	289	312				
XII	81	154	314							3	0.94
XIII	82	294	303							3	0.94
XIV	94	156	157	285						4	1.25
XV	177	305	320							3	0.94
XVI	298	301								2	0.63

Table 6: Distribution of barley genotypes under limed soil over thirteen clusters by eighteen zones of origin and four altitude groups based on 14 quantitative traits

Zone	**Clusters**																**Total**
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**XI**	**X**	**XI**	**XII**	**XIII**	**XIV**	**XV**	**XVI**	
Agew Awi	3	_	1	_	1	2	_	_	1	_	1	_	_	1	_	_	10
Arssi	14	1	1	1	2	2		3	_	_	_	_	_	1			25
Bale	9	_	_	_	2	1	1	4	2	_	_	_	_	_	_	_	19
South Gondar	3	_	1	_	2	3	_	4	_	_	2	_	_	_	_	_	15
South wello	7	1	1		1	3	_	4	2	_	_	_	_	_	_	_	19
South Tigray	11	_	_	1	_	1	1	7	_	1	1	_	_	_	_	_	23
Gurage	5	_	_	1	3	1	5	3	6	_	1	1	1	_	_	_	27
Hadya	4	_	1	1	_	1	2	_	2	_	_	_	_	_	_	_	11
Keficho Shekicho	1	_	_	_	1	_	_	_	_	_	_	_	_	_	_	_	2
West Shewa	7	_	2	1	1	_	2	1	1	_	1	_	_	1	_	_	17
East Gojam	8	_	_	_	1	1	_	1	_	_	1	1		_	_	_	13
East harerge	4	1	_	_	_	_	_	7	1	_	_	_	_	_	_	_	13
East Shewa	1	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	1
East Wellega	4	_	_	_	3	3	2	1	1	_	2	_	_	_	_	_	16
East Tigray	11	1	_	_	2	1	_	5	_	_	_	_	_	_	_	_	20
North Omo	8	1	_	_	4	5	_	3	4	1	_	_	_	_	_	_	26
North Shewa	11	2	_	_	1	6	1	6	3	_	4	_	_	1	1	_	36
Rleased varieties	4	_	_	1	5	3	_	_	_	6	1	1	2	_	2	2	27
Total	115	7	7	6	29	33	14	49	23	8	14	3	3	4	3	2	320
% of population	35.94	2.19	2.19	1.88	9.06	10.31	4.38	15.31	7.19	2.5	4.38	0.94	0.94	1.25	0.94	0.63	
Group	**Altitude Group**																
<2000	15	_	_	1	_	3	2	13	1	_	1	_	_	_	_	_	36
2001-2500	41	4	4	1	4	6	2	19	5	_	5	2	_	1	_	_	94
2501-3000	43	1	2	1	15	15	7	15	8	2	5	_	1	3	1	_	119
>3000	12	2		2	5	3	4	5	7	_	4	_	_	_	_	_	44
Total	111	7	6	5	24	27	15	52	21	2	15	2	1	4	1		293

Table 7: The summary of cluster mean of barley genotypes under unlimed (upper) and limed soil condition (lower) for 14 quantitative traits

Trait	**Clusters under unlimed**												
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**
DE	6.9	6.9	6.9	6.9	7.1	6.9	6.9	7.0	6.9	7.0	6.9	6.9	7.3
DTH	56.8	71.0	65.9	64.4	54.2	68.2	75.4	68.2	62.0	73.4	76.9	75.2	64.1
DTM	100.0	119.0	112.6	109.6	98.3	119.8	119.5	114.5	114.4	122.8	113.3	119.9	111.3
SC	7.6	5.7	5.9	7.4	8.2	6.0	6.8	5.9	5.0	2.7	6.8	4.9	7.2
Net	4.8	6.0	4.6	4.5	4.6	4.8	6.5	5.1	3.9	2.4	2.3	2.6	2.7
FT	2.7	2.6	2.5	2.8	2.9	3.0	3.4	3.3	3.1	2.4	2.6	2.1	2.9
SL	6.9	7.0	6.4	6.4	7.4	6.5	8.1	6.8	7.1	7.1	5.7	7.9	5.7
PHT	94.2	101.1	90.6	94.3	96.0	92.7	94.4	96.1	91.3	111.8	67.7	113.9	79.7
SPS	28.5	35.8	33.6	32.0	25.6	39.8	45.4	23.1	23.5	49.0	20.4	51.3	20.7
YLD	1822.0	3416.0	2746.2	2237.6	1956.3	3031.6	2507.3	3240.1	4506.1	4916.6	1111.1	4989.1	1246.6
BM	7053.4	12234.7	8299.8	8391.7	7551.5	6706.4	12604.9	10372.3	12257.5	16186.3	4182.9	14103.8	6181.9
HI	0.3	0.3	0.4	0.3	0.3	0.5	0.2	0.3	0.4	0.3	0.2	0.4	0.2
HLW	57.7	62.0	61.6	73.0	57.0	61.1	59.3	64.2	66.0	64.6	59.6	61.1	62.6

TKW	33.9	39.7	38.2	30.4	34.7	38.0	32.8	43.2	48.0	37.6	35.6	42.7	46.8

Trait	Clusters under limed															
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
DE	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7
DTH	56.8	55.9	75.4	73.1	63.4	58.9	69.4	54.6	66.7	67.1	62.4	76.6	67.4	67.9	67.5	76.0
DTM	98.4	97.1	113.6	113.3	106.9	102.0	111.7	94.5	108.1	110.7	103.6	114.8	113.4	111.9	109.3	115.8
SC	6.8	7.0	6.4	5.0	6.4	6.7	6.2	7.0	6.4	4.9	6.5	5.4	4.0	5.6	4.9	4.5
Net	4.46	4.38	5.99	5.37	4.91	4.79	5.74	4.29	6.01	4.00	4.64	5.57	4.88	5.99	3.93	4.44
FT	4.5	4.2	4.7	4.3	4.6	4.5	4.5	4.4	4.4	4.5	4.6	4.6	4.8	4.5	4.4	4.8
SL	7.1	6.8	7.6	7.5	7.4	7.2	7.5	6.8	7.5	7.4	7.4	7.2	5.9	7.9	7.2	7.9
PHT	105.1	99.0	109.6	107.2	104.7	104.7	105.8	102.9	106.0	104.0	103.3	109.8	107.9	106.8	105.5	116.3
KPS	32.7	32.7	40.5	46.6	33.8	35.7	38.0	31.0	35.4	35.9	35.0	37.7	46.9	32.2	43.1	54.3
YLD	2235.7	1644.3	3906.1	4833.0	3464.8	3111.8	3895.5	1878.6	3128.8	5636.4	2423.1	3308.7	6100.9	2745.2	4929.6	6310.3
BM	7607.8	4781.9	14914.6	16441.6	10888.3	8893.7	13266.5	6013.5	12004.3	14709.8	10061.4	15927.2	16733.4	13437.6	11754.1	18364.9
HI	0.3	0.4	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.4	0.3	0.3	0.3	0.3	0.4	0.3
HLW	60.0	58.1	62.6	62.5	62.7	60.8	61.7	59.5	61.7	64.3	60.7	62.7	63.2	61.6	63.8	62.2
TKW	34.4	29.4	42.1	38.9	39.2	37.5	39.1	33.2	38.5	45.7	36.4	44.4	42.9	41.8	38.5	39.5

DTE = Days to emergence, DTH = Days to heading, DTM = Days to maturity, SC = scald, N.Bloch= Net bloch, FT = Number of fertile tillers per plant(count), SL = Spike length (cm), PHT = Plant height (cm), KPS = Number of kernels per spike (count), YLD= Grain yield (kg/ha), BM= Biomass Yield(kg/ha), HI = Seed harvest index, TKW= Thousand kernel weight (gm), HLW= Hectoliter weight (kg/hl)

Cluster analysis for genotypes by SSI and STI

Based on grain yield data under both soil conditions, genotypes were grouped according to their acid susceptible and tolerance index on the basis of Euclidean distances of dissimilarity. Under index cluster analysis, barley genotypes were subdivided into twelve clusters (Figure 3). The greatest number of genotype was found under Cluster VI and I had sixty five and fifty eight genotypes per cluster, respectively and characterized by high susceptibility and low tolerance index (Table 9).

Cluster III, IX, XI, VII and II contained three, one, three, eight, and nine genotypes per cluster and had lower susceptible index of -5.22, -3.45, -2.06, -1.91 and -1.82, respectively for grain yield (Table 8 & 9). Cluster VII and II had genotypes collected from almost all acid soil affected zones of country and released varieties and grouped under attitude groups suitable for barley production, reflecting their higher yields in the unlimed than in the limed environment, indicating that they are less vulnerable to acidic soil stress and hence acid soil tolerant. Cluster V, VIII, and XII, had high susceptible index of 3.09, 2.87 and 2.52, indicating that they were highly vulnerable to acid soil stress. These are genotypes with specific adaptation to more favourable environments and they gave higher yield under limed environment, but gave low yields under unlimed environment.

Cluster XII, XI, X, IX,VIII,VII and VI contained one, three, eight, one, eight, eight and sixty five genotypes per cluster and had high tolerance index of 4.43, 3.64 , 3.35, 2.81, 2.64, 1.86 and 1.47, respectively, for grain yield, indicating that they could tolerate soil acidity stress (Table 8). The greatest number of genotype was under Cluster VI and VII. Cluster VII had genotypes collected from acid soil affected zones of Bale, South Gondar, South wello, Gurage, West Shewa, North Shewa and realised varieties and grouped under attitude groups suitable for barley production, characterized by low susceptibility and high tolerance index (Table 8, 9, 10).

Table 8: The summary of cluster mean of barley genotypes by stress indices

Trait	Clusters											
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
SSI	1.33	-1.82	-5.22	0.66	3.09	1.05	-1.91	2.87	-3.45	1.44	-2.06	2.52
STI	0.35	0.38	0.43	0.62	0.97	1.47	1.86	2.64	2.81	3.35	3.64	4.43

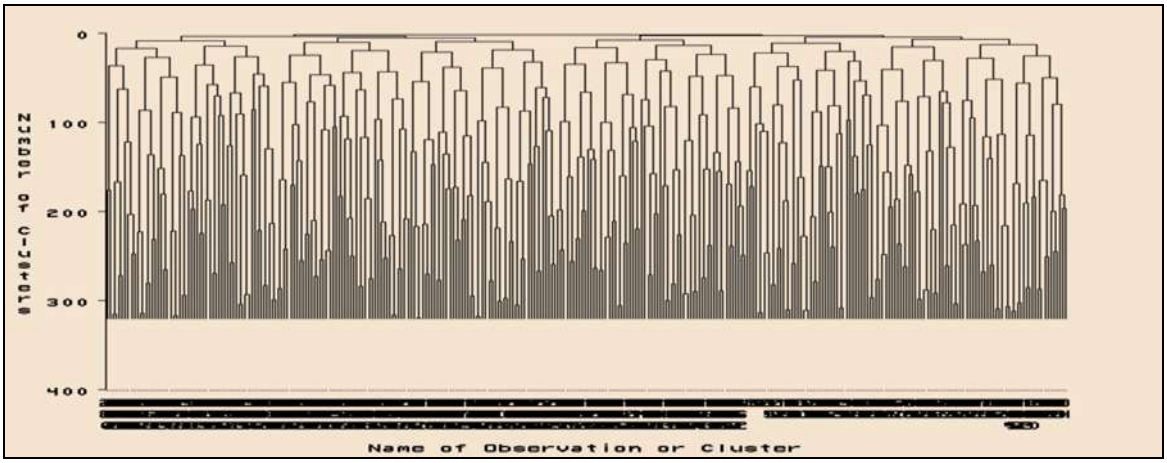

Fig 3: Dendrogram of barley genotypes by stress index revealed by UPGMA cluster analysis based on yield

Table 9: Clustering pattern of 320 Barley genotypes by stress indices

Clusters	Genotypes									Total	%
I	1	2	3	4	5	6	7	8	9	58	18.13
	10	11	12	15	16	17	18	19	20		
	21	23	24	25	26	27	28	29	30		
	31	32	34	35	37	38	39	40	42		
	44	45	46	47	48	49	50	51	53		
	54	55	56	57	59	60	61	62	63		
	64	66	68	71							
II	13	14	22	41	43	52	58	85	94	9	2.81
III	33	36	136							3	0.94
IV	65	67	69	70	72	73	74	75	76	129	40
	77	78	79	80	81	82	83	84	86		
	87	88	89	90	91	92	93	95	96		
	97	98	99	100	101	102	103	104	105		
	106	107	108	109	110	111	112	113	114		
	115	116	117	118	119	120	122	123	124		
	125	126	127	128	129	130	131	132	133		
	134	135	137	138	139	140	141	142	143		
	145	146	147	148	150	151	152	153	154		
	155	156	157	158	159	160	161	162	163		
	164	165	166	167	168	169	170	171	172		
	173	174	175	176	178	179	180	181	182		
	183	185	186	187	188	189	191	195	196		
	197	199	202	204	207	209	210	217	219		
	221	252	284								
V	121	144	149	177	184	193	194	198	200	27	8
	205	208	211	212	213	216	220	223	226		
	227	228	231	232	234	236	237	238	258		
VI	190	192	201	203	206	214	215	218	222	65	20.31
	224	225	229	230	233	235	239	241	242		
	243	244	245	246	248	249	250	251	253		
	254	255	256	257	259	260	261	262	263		
	264	265	266	267	268	269	270	271	272		
	273	274	275	276	277	278	279	281	283		
	285	287	288	289	290	292	293	294	295		
	297	298									
VII	240	247	280	282	286	291	296	304		8	2.50
VIII	299	300	301	302	303	305	306	311		8	2.50
XI	307									1	0.31
X	308	309	310	312	313	315	316	319		8	2.50
XI	314	317	318							3	0.94
XII	320									1	0.31

Table 10: Distribution of barley genotypes by stress index over 14 clusters by eighteen zones of origin and four altitude groups based on yield traits

Zone	Cluster												Total
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	
Agew Awi	6	1	_	2	_	1	_	_	_	_	_	_	10
Arssi	3	1	_	15	2	4	_	_	_	_	_	_	25
Bale	2	_	1	8	4	3	1	_	_	_	_	_	19
South Gondar	2	1	_	6		5	1	_	_	_	_	_	15
South wello	_	_	_	7	2	9	1	_	_	_	_	_	19
South Tigray	2	1	_	3	4	13	_	_	_	_	_	_	23
Gurage	11	_	2	8	1	4	1	_	_	_	_	_	27
Hadya	_	1	_	10	_	_	_	_	_	_	_	_	11
Keficho Shekicho	1	_	_	1	_	_	_	_	_	_	_	_	2
West Shewa	6	_	_	7	_	3	1	_	_	_	_	_	17
East Gojam	4	_	_	9	_	_	_	_	_	_	_	_	13
East harerge	_	_	_	8	1	4	_	_	_	_	_	_	13
East Shewa	1	_	_	_	_	_	_	_	_	_	_	_	1
East Wellega	11	2	_	3	_	_	_	_	_	_	_	_	16
East Tigray	4	1	_	1	8	6	_	_	_	_	_	_	20
North omo	_	_	_	24	1	1	_	_	_	_	_	_	26
North Shewa	5	1	_	17	4	8	1	_	_	_	_	_	36
Rleased varieties	_	_	_	_	_	4	2	8	1	8	3	1	27
Total	58	9	3	129	27	65	8	8	1	8	3	1	320

Group	Altitude Group												
<2000	3	1	_	17	7	10	_	_	_	_	_	_	38
2001-2500	22	4	_	37	8	21	2	_	_	_	_	_	94
2501-3000	27	4	2	53	9	23	1	_	_	_	_	_	119
>3000	6	_	1	22	3	7	3	_	_	_	_	_	42
Total	58	9	3	129	27	61	6	_	_	_	_	_	293

Principal Component Analysis

Principal component analysis was performed with the standardized mean values for each of the fourteen quantitative traits used to observe the general pattern for variation of traits and to determine relationships among traits.

Under un limed soil condition, the principal component analysis exhibited variances of 35%, 15%, 10%, 8%, 7% and 6%, for the first six principal components and accounts for about 81% of total variation. The first two principal components (PCA1and PCA2) contributed about 50.0% of the total variation (Table 11). Characters with relatively larger absolute values of eigenvector weights in principal component had the largest contribution to the variation of the genotypes into clusters, as it was normally assumed that characters with larger absolute values closer to unity within the principal component influence the clustering more than those with lower absolute values closer to zero [32]. Based on the Eigen values and Eigen vectors, it is possible to indicate which traits are mainly responsible to explain the variation [33].

The first principal component analysis (PCA1) clarified 35% of the variation. Characters with relatively greater positive weights of eigenvectors in PCA1 includes, grain yield, days to maturity, biomass yield and days to heading showed greater loading for the variation in the first principal components, Traits like incidence of scald, fertile tiller per plant, incidence of net blotch, days to emergence and spike length had smaller negative/ positive eigenvector values contributed least loadings for the first principal component. Kernel per spike, days to heading, harvest index and days to maturity had relatively larger positive contribution to the second principal component. Besides, spike length, fertile tiller per plant and thousand kernel weights had smaller negative eigenvector values contributed least loadings for the second principal component (Table 11).

Under limed soil condition, the principal component analysis exhibited variances of 31%, 15%, 10%, 8%, 7% and 6%, were extracted for the first six principal components and accounts about 78% of total variation. The first two principal components (PCA1 and PCA2) contributed about 46% of the total variation. Characters with relatively greater positive weight of eigenvectors in PCA1 include biomass yield, days to maturity, days to heading and grain yield had a greater contribution to variation in PCA1. However, the incidence of scald, harvest index, incidence of net blotch and fertile tiller per plant had the least contribution to variation in PCA1. Kernel per spike, days to maturity, days to heading and harvest index had relatively larger positive contribution to the second principal component and traits spike length, fertile tiller per plant, hectolitre weight and plant height had smaller negative eigenvector values contributed least loadings for the second principal component (Table 11). The PCA based on data from stressed and non-stress treatments revealed that PCA1 account for 47.9% of variation and showed the larger loading value of yield related and morphological characters [34]. Traits such as days to heading and days to maturity and seed per spike contributed major variation and traits fertile tiller per plant had least loadings for the first principal component [35].

Table 11: Eigenvalue, variance, cumulative variance, and eigenvalues for 14 quantitative traits of barley genotypes grown under unlimed (left) and limed soil conditions (right)

	Unlimed						Limed					
Variable	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
DE	0.00	-0.16	-0.21	0.31	0.69	-0.53	0.16	0.07	0.29	0.34	0.26	-0.39
DTH	0.36	0.18	0.11	0.24	0.07	0.10	0.40	0.17	-0.14	0.19	-0.03	0.00
DTM	0.40	0.14	0.04	0.17	0.07	0.06	0.41	0.19	-0.09	0.15	0.02	0.04
SC	-0.34	0.01	0.20	-0.01	0.07	-0.11	-0.33	-0.09	-0.18	0.19	0.00	-0.16
Net	-0.03	-0.01	0.00	-0.50	0.66	0.55	-0.01	-0.07	-0.13	-0.08	0.89	-0.23
FT	-0.10	-0.44	-0.18	-0.23	0.00	-0.28	0.00	-0.41	0.09	-0.23	0.27	0.56
SL	0.02	-0.49	0.39	-0.15	-0.13	-0.03	0.13	-0.44	-0.26	0.09	-0.18	-0.31
PHT	0.24	-0.19	0.47	-0.28	0.03	-0.22	0.08	-0.16	-0.46	-0.51	-0.11	-0.40
KPS	0.22	0.46	0.23	-0.22	0.10	-0.27	0.19	0.54	-0.23	-0.14	0.05	0.00
YLD	0.40	-0.03	-0.12	-0.24	-0.03	-0.16	0.39	0.01	0.17	-0.37	0.01	0.06
BM	0.38	-0.12	0.17	-0.03	0.03	-0.09	0.42	-0.08	-0.13	-0.08	0.04	0.22
HI	0.10	0.15	-0.55	-0.51	-0.20	-0.22	-0.07	0.17	0.58	-0.48	-0.07	-0.32
HLW	0.31	-0.18	-0.25	0.16	-0.01	0.19	0.26	-0.23	0.26	0.26	-0.03	-0.08
TKW	0.26	-0.41	-0.21	0.14	-0.06	0.26	0.29	-0.40	0.20	0.00	-0.10	-0.17
Eigenvalue	4.90	2.05	1.33	1.12	1.00	0.90	4.40	2.13	1.39	1.17	1.03	0.84
Variance	0.35	0.15	0.10	0.08	0.07	0.06	0.31	0.15	0.10	0.08	0.07	0.06
Cumulative var (%)	0.35	0.50	0.59	0.67	0.74	0.81	0.31	0.47	0.57	0.65	0.72	0.78

DTE = Days to emergence, DTH = Days to heading, DTM = Days to maturity, SC = scald, N.bloch= Net bloch, FT = Number of fertile tillers per plant(count), SL = Spike length (cm), PHT = Plant height (cm), KPS = Number of kernels per spike (count), YLD= Grain yield (kg/ha), BM= Biomass Yield(kg/ha), HI = Seed harvest index, TKW= Thousand kernel weight (gm), HLW= Hectoliter weight (kg/hl)

Diversity Index

Estimates of Shannon Weaver diversity index over zones of origin and altitude groups showed high diversity index for the four qualitative traits studied. Phenotypic diversity was very high for ear Attitude (H′=1.13), kernel row number (H′=0.78) and Kernel color (H′=0.65) and comparatively spike density (H′=0.53) had low phenotypic diversity (Table 13) at zone of origin. For ear attitude, semi erect (122 genotypes) and semi re-curved (90 genotypes) had larger contribution for phenotypic diversity, contrary erect (22 genotypes) and re-curved (19 genotypes) had lower contribution for phenotypic diversity. Zonal distribution of trait ear attitude showed that North Shewa, Gurage and East Tigray had large number of genotypes with semi erect ear attitude and North Omo, North Shewa and Gurage had large number of genotypes with semi re curved ear attitude (Table 12).

Phenotypic diversity was very high for Ear Attitude (1.32), Kernel color (H′=0.99) and kernel row number (H′=0.96), comparatively spike density (H′=0.65) had low Phenotypic diversity for altitude groups (Table 13). This was due to high ecological heterogeneity of the country, which was favourable condition for barley cultivation. All characters were high in phenotypic diversity over all zones of origin and altitude groups for this study. The same results were reported by Berhane and Alemayehu [36], polymorphism was high for kernel row type (H' = 0.80), spike density (H' = 0.76) and kernel colour (H' = 0.75). Abebe and Bjornstad [37] also had The highest mean diversity index (H) pooled over traits was shown by populations from Arsi and Welega, whereas the lowest is for individual populations from Bale,Shewa, Tigray and Gamu Gofa**.**

Regional diversity index

Estimate of diversity index (H') pooled over zone of origin showed high phenotypic diversity among four qualitative characters. The mean H' ranged from 0.35 for Keficho Shekicho to 1.06 for Arssi zone. Arssi, Gurage, North Omo, Agew Awi, North Shewa, South Welo, West shewa, East Gojam, South Gonder and Bale showed greater diversity index followed by Misrak harerge and Keficho Shekicho zones showed lower phenotypic diversity index (Table 13).

Among all characters, Ear Attitude shows high polymorphic in all zone of origin except Keficho Shekicho, followed by kernel row number from West Shewa,South Gonder, Bale,Arssi, Gurage, Agew Awi, North Omo,and South Welo, showed high phenotypic diversity index. Genotypes from East Tigray and Hadeya showed lower phenotypic diversity index for kernel row number. Spike density from Gurage, Agew, Awi, East Tigray showed high phenotypic diversity index. Genotypes from East Welega, South Gonder, West Shewa, South Tigray, South Wello, and North Shewa showed lower phenotypic diversity index. Kernel color from Arssi, West Shewa, North Omo, Gurage, North Shewa, South Wello, Hadeya, Misrak Gojam, East Welega and East Tigray showed high phenotypic diversity index. Genotypes from Agew Awi, Bale and released varieties, showed lower phenotypic diversity index. Similarly a previous report found among all characters, kernel row number from Gonder, grain color from Gojam, Shewa, and Wellega, spike density from Arssi and Tigray showed high phenotypic diversity index [38].

Altitudinal diversity index

Altitude groups showed high phenotypic diversity among four qualitative characters. The mean H' pooled over characters for four altitude groups varied from 1.01 for altitude between 2000 and 3000 to 0.95 for altitudes group greater than 3000 m.a.s.l with total mean value of 0.98±0.14. Altitude groups between 2500-3000 m.a.s (119 genotypes) followed by altitude groups 2001-2500 m.a.s (94 genotypes) had a large number of genotypes with the highest mean diversity index of 1.01±0.14. Ear Attitude and kernel color showed the highest altitudinal diversity index in all altitude and relatively spike density showed lower altitudinal diversity index (Table 13). Similarly reported to mean diversity index for characters increases with altitude reaching a maximum between 2400-2800 m.a.s.l and decreasing beyond that altitude [9, 37, 39]. This indicates high phenotypic diversity in barley was related to high rainfall and lower temperature at high altitudes, which shows barley that is a cool season crop.

According to Bedasa *et al* [38] difference in altitude gradient and agro ecological setting gave high diversity variation in barley genotypes and found that Kernel row number from altitude group between 2001and 3000 m.a.s.l, grain color from altitude group 1500-2000 and 2501-3000 m.a.s.l and spike density from altitude group 2501 and 3500 m.a.s.l showed the highest diversity index.

Table 12: Distribution of three qualitative traits under seventeen zone of the country

	No of Geno	Row type			Spike density			Kernel color			Ear Attitude				
		2	Irr	6	Lax	Inter	Dense	White	Purple	Black	Erect	Sami erect	Horizontal	semi-recurved	Recurved
Agew Awi	10	6	2	2	3	6	1	1	9	_	1	3	2	3	1
Arssi	25	10	3	12	1	6	18	10	8	7	2	7	8	6	2
Bale	19	3	7	9	1	16	2	17	2	_	1	9	3	5	1
South Gondar	15	7	3	5	1	14	_	2	11	2	1	7	2	4	1
South wello	19	3	4	12	_	17	2	12	5	2	1	6	4	7	1
South Tigray	23	16	1	6	_	21	2	15	8		1	9	5	7	1
Gurage	27	12	3	12	7	13	7	15	6	6	2	13	4	8	_
Hadya	11	3		8	_	8	3	3	1	7	1	7	2	1	_
Keficho Shekicho	2	1	1	_	1	1	_	2	_	_	_	_	_	2	_
West Shewa	17	7	4	6	3	12	2	4	7	6		7	6	2	2
East Gojam	13	9	1	3	3	10		4	8	1	1	4	2	6	_
East harerge	13		5	8		10	3	13	_	_	1	6	1	4	1
East Shewa	1	1	_	_	1	_	_	_	1	_	_	_	1	_	_
East Wellega	16	11	4	1	1	15	_	5	10	1	_	6	4	5	1
East Tigray	20	18	_	2	2	13	5	14	4	2	_	11	4	5	_
North omo	26	9	3	14	1	22	3	14	6	6	_	1	8	11	6

North Shewa	36	5	6	25	1	31	4	20	12	4	2	16	7	9	2
Released varieties	27	13	1	13	1	16	10	25	2	_	8	10	4	5	_
Total	320	134	48	138	27	231	62	176	100	44	22	122	67	90	19

Table 13: Estimate of Shannon-Weaver diversity index (H') of Ethiopian barley genotypes for seventeen zone of origins and four altitude groups by four qualitative traits

Zone		Row type	Spike density	Kernel color	Ear Atitude	Mean± SE
Agew Awi		0.95	0.9	0.33	1.5	0.92+0.24
Arssi		0.97	0.71	1.09	1.47	1.06+0.16
Bale		0.99	0.54	0.34	1.31	0.80+0.22
South Gondar		0.99	0.24	0.76	1.34	0.83+0.23
South wello		0.91	0.34	0.88	1.37	0.88+0.21
South Tigray		0.74	0.3	0.65	1.33	0.76+0.21
Gurage		0.96	0.99	0.99	1.19	1.03+0.05
Hadya		0.59	0.59	0.86	1.03	0.77+0.11
Keficho Shekicho		0.69	0.69	0	0	0.35+0.20
West Shewa		0.99	0.26	0.99	1.24	0.87+0.21
East Gojam		0.79	0.54	0.86	1.2	0.85+0.14
East harerge		0.67	0.54	0	1.31	0.63+0.27
East Wellega		0.78	0.23	0.83	1.25	0.77+0.21
East Tigray		0.33	0.86	0.8	1	0.75+0.15
North omo		0.95	0.52	1.01	1.19	0.92+0.14
North Shewa		0.83	0.47	0.94	1.35	0.90+0.18
Released variety		0.83	0.8	0.26	1.32	0.80+0.22
Total Mean		0.78	0.53	0.64	1.13	0.77+0.17
Altitude class	Total	Row type	Spike density	Kernel color	Ear Atitude	Mean± SE
<2000	38	0.99	0.59	0.99	1.33	0.98±0.15
2001-2500	94	0.99	0.71	0.94	1.38	1.01±0.14
2501-3000	119	0.98	0.71	0.97	1.38	1.01±0.14
>3000	42	0.89	0.61	1.09	1.2	0.95±0.13
Total Mean		0.96	0.65	0.99	1.32	0.98±0.14

Conclusion

Soil acidity is now a serious threat to barley production in most high lands of Ethiopia. The extent of acidity is increased in 2.1% within the past three decades mainly due to increase in continuous cropping and use of acidifying fertilizers in parity with increased in demand for barley production without expansion of the cultivated area. However, the assessment of genetic diversity among barely genotypes using multivariate statistical analysis is indispensable for plant breeding purposes, since it provides selection and screening tolerant genotypes available in germplam collections.

Results from the field evaluation of barley genotypes under acidic (unlimed) and non-acidic (limed) soil condition demonstrated that there were genetic diversity between genotypes collected from different barley growing acid prone areas. Better responses of barley phonological and yield components were observed under limed environments. Acidic soil had severe impact on growth, development and genetic diversity of barley genotypes from early seedling emergence to final harvest by depleting soil nutrient and make barley growing Ethiopian highland unproductive.

Although better yield and yield components also observed under acidic environment from tolerant genotypes that gave indication of Ethiopia had wide genetic diversity of barley genotypes that could tolerance to soil acidity stress.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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