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Phenotypic diversity and population structure of Ethiopian barley (*Hordeum vulgare* L.) landrace collections

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Abstract

Landraces play a key role in crop breeding by providing beneficial trait for improvement of related crops and their genetic diversity studies are very important for breeding program and identification of parental lines. In this study, 585 barley (*Hordeum vulgare* L.) landraces collected from 13 agro-ecological zones of Ethiopia were evaluated along with 10 cultivars for their phenotypic diversity and population structure in relation to agronomic traits, resistance to major diseases and barley shoot fly. Data on 22 agronomic traits, three major diseases and barley shoot fly resistance-related traits were recorded. Univariate and multivariate approaches such as principal component and cluster analyses were applied to assess the genetic diversity and population structure. The analysis of variance indicated significant genotypic main, accessions x year and accession x environment interaction effects for almost all the traits evaluated. However, the accessions x environment interactions were mainly due to changes in magnitude rather than crossover types of interactions. The diversity analysis indicated that the population was highly structured according to kernel row-type, region (geographic) origin and altitude classes. Since the population is highly structured, appropriate statistical models will be needed when this population is used for association mapping studies. Eight principal components (PCs) in principal component analysis (PCA) accounted for the variation of 83.01%. The most related traits were included in the same PC, implying that results from PCA could give clues as to the relationship among traits. Though variability existed within and among clusters, useful germplasm clustered together. These materials are important sources of germplasm for the improvement of agronomic, disease and insect pest resistance traits.

Keywords: Barley, diseases, genetic diversity, landraces, multivariate, shoot fly

Introduction

Barley (*Hordeum vulgare* L.) is an important fourth cereal crop in Ethiopian cereal production and in food security. The country is considered as a major Vavilovian center of diversity and it is cultivated in a wide range of environments, from high altitude areas (>3000 masl) to low-rainfall environments (Addisu *et al*., 2015). A long history of barley cultivation, together with wide agro-ecological and cultural diversity in the country, has resulted in a large number of landraces of the crop which can adapt to different environmental conditions (Hadado *et al*., 2009). Among the important traits that could exist in the Ethiopian barley landraces include resistance to diseases (Woldeab *et al*., 2007). Other useful characteristics of Ethiopian barley landraces include tolerance to marginal soil conditions (Kebede *et al*., 2019), barley shoot fly (*Delia flavibasis* Stein) (Dido *et al*., 2020), tolerance to drought and other forms of abiotic stress and characters useful for low input agriculture (Yaynu, 2011).

In Ethiopia, barley landraces represent over 90% of the barley cultivation due to multiple food uses and adaptations to marginal environments (Hadado *et al*., 2009). In contrast to the genetic uniformity of modern cultivars, landraces exhibited variations both between and within populations. This within populations' diversity of barley landraces might allow them to cope with environmental stresses which is very important for achieving yield stability (Zhu *et al*., 2000).

Genetic diversity studies are important tools to identify diverse parental lines for hybridization and introgression of desirable genes into elite germplasm (Chakravorty *et al*., 2013). Knowledge of the phenotypic diversity and population structure of Ethiopian landraces together with a deeper understanding of the nature and extent of their variations is an important prerequisite for the efficient conservation and use of the existing plant materials.

Genetic variability can be assessed using univariate methods that measure dispersion, including calculation of population variances, the coefficients of variability (CV) and range estimates. However, multivariate techniques (cluster analysis, principal component analysis, principal coordinate analysis, and multi-dimensional scaling) used to studying genetic diversity in detail. Comparisons of mean differences among sub-populations that are created based on certain criteria can also be used to understand the extent of genetic diversity in a population.

As part of anassociation mapping study, field experiments were conducted on Ethiopian barley landraces to collect data on agronomic performance, disease and barley shoot fly resistance components. Thus, the research result presented in this paper described the phenotypic diversity and population structure of the Ethiopian barley landraces collected from differentbarley growing regions since 1979 to 2017. These results will also be utilized ultimately to identify germplasms that may be of use to the future Ethiopian barley improvement programs.

Materials and Methods

Plant materials

A total of 595 barley (*Hordeum vulgare* L.) accessions, consisting of 585 landraces, 9 standard varieties and 1 local check were used for this study. The landraces were obtained from the Ethiopian Biodiversity Institute (EBI) along with their passport data. The standard varieties and local check were obtained from Sinana and Holetta Agricultural Research Centers along with their relevant agronomic and disease response data. The 585 landraces were collections from different agro-ecological zones of Ethiopia and categorized in to two-rowed, six-rowed and irregular types based on kernel row number. The altitude of the collection sites for the landraces used in this study ranged from 1430 to 2950 meters above sea level.

Methods

For data analysis, the standard varieties were assigned to the different regions of Ethiopia based on regions for which they are normally recommended for cultivation. Accessions from regions with sample size less than 10 were also included in adjacent regions to reduce experimental error due to small sample size. This reduced the 42 agro-ecological zones of Ethiopia from which the landraces were originally drawn to thirteen zones. On the basis of altitude of the collection site of each accession, the 585 materials were categorized into four classes: altitude class I (< 1500m), altitude class II (1501-2000m), altitude class III (2001-2500m) and altitude class IV (>2500m).

Each accession was grown in a single row plot of 1.75 m long and 0.20 m between rows, in augmented design consisting of six blocks. The 10 checks were replicated six times (ones in each block) to estimate an error variance. Accessions were sown in field when

adequate moisture was available during 2018 and 2019 main cropping seasons at Sinana Agricultural Research Center (on-station) and Bale-Goba (on-farm), southeast Ethiopia. Fertilizer application and other agronomic practices undertake as recommended for barley production in Ethiopia.

Data Collection

Agronomic data

Phenological and morphological characteristics were determined according to barley descriptors (IPGRI,1994) based on plant based and plot based traits. For plant based traits i.e. plant height,awn length, total number of tillers per plant, number of effective tillers (seed-bearing) per plant, number of seeds per spike, spike length, spike density, spike weight, peduncle extrusion and peduncle length were considered. Ten randomly selected plants from central part of row were tagged at the early stage and measured timely according to the traits used. The averages were used for the analysis. For plot based traits, days to 50% heading and 95% physiological maturity, grain filling period, grain filling index, harvest index, 1000- seed weight, biomass yield and grain yield per plant were taken from the whole row for each accession and converted into per hectare bases for the analysis. Flag leaf length and width were taken by measuring scale and flag leaf area was calculated by following formula suggested by Muller (1991): flag leaf area (cm^2) = flag leaf length (cm) x flag leaf width (cm) x correction factor (0.75).

Disease data

Leaf rust, net blotch and barley yellow dwarf virus

Due to the continuous presence of the disease in the experimental areas (Bekele *et al*., 2018), natural infection with *Puccinia hordei* and *Pyrenophora teres* conidia, the causal agent of barley leaf rust and net blotch, respectively, was conducted under natural field conditions. The assessments of the disease were started after disease on-set and recorded five times during both seasons (at intervals of 14 days) on 10 randomly selected plants per row. The first assessment was started at the jointing stage (Zadoks *et al*., 1974) (GS 31-32) and the last at the soft-to-hard dough stage of kernel development (GS 85-87).

Two aspects of leaf rust development: incidence and area under the disease progress curve (AUDPC) and three aspects of net blotch development: percent severity index (PSI), AUDPC and apparent infection rate (AIR) were evaluated. Percent net blotch severity index was assessed near the end of the growing season at GS 85-87 and the disease severity scores were converted to percentage severity index (PSI) as suggested by Silvar *et al*. (2009).

$$PSI = \frac{Snr}{Npr\ x\ Msc}\ x\ 100$$

Where, Snr is the sum of numerical ratings, Npr is the number of plants rated and Msc is the maximum score on the scale.

AUDPC was computed using the following equation:

$$AUDPC = \sum_{i=1}^{n} [(Y_{i+1} + Yi)x\ 0.5][T_{i+1} - Ti)$$

Where, y_i = percentage of leaf area affected by net blotch at the i^{th} observation,
T_i = time (in days) at the i^{th} observation, and
n = total number of observation (scoring dates).
AUDPC is helpful because it combines the amount of disease over time.

Further, disease data on symptomatic reactions (VSS-Visual Symptom Score) to the barley yellow dwarf virus (BYDV), serotypes PAV incidence (number of infected tillers/plot) and severity (percentage of foliage with symptoms) were recorded according to 0-9 scale as described by Singh *et al*. (1993). The disease scoring was undertaken at early stage due to the expression of BYD symptoms and peak activity period of its viruliferous aphid vectors (*Rhopalosiphum padi* L.) in the area (Bekele *et al*., 2018) at booting stage (41-49 Zadoks scale) (Zadoks *et al*., 1974). Presence or absence of leaf tip necrosis (*LTN*) on flag leaf of each accession was recorded over two years as mentioned by Shah *et al*. (2011) at anthesis stage. This stage corresponds to the stage 65-69 in the Zadoks scale (Zadoks *et al*., 1974).

Shoot fly data

Shoot fly resistance components were recorded from each row at seedling stage on the basis of whole plot (per row) as percent survival (PS) (ratio of live plants divided by the total number of plants), extent of leaf injury/infestation, incidence (ratio of infected plants divided by the total plant), crop recovery (CR) score (1-5 scale), dead heart (DHRT) percentage, oviposition (OVP) percentage and early seedling vigour (SVG).

Evaluation for seedling vigour (a combination of height, leaf growth, and robustness) was evaluated on a 1-5 scale at 30 days after emergence (DAE) according to Sharma *et al*. (1997). Oviposition percentage was calculated at 14 and 21 DAE by multiplying with 100 the ratio of number of plants with eggs to total number of plants. Similarly, the dead heart percentage was computed by calculating the ratio of number of plants with dead heart to total number of plants and multiplying with 100 at 14 and 21 DAE. Then, the rating scales were 1 = ≤ 10% infestation (highly resistant); 3 = 10 to 20% infestation (resistant); 5 = 20 to 35% infestation (moderately resistant); 7 = 35 to 50% infestation (susceptible); 9 = ≥50% infestation (highly susceptible).

Statistical analysis

The seed for the landrace collected from EBI were not enough to use replicated designs and it was obligatory to use augmented designs in such circumstances. As a result only the checks were replicated in each block and the landraces were not. The row data were adjusted to mean of zero and variance of one by using the means of checks in each block and the overall mean of checks in the whole plot. This was to minimize errors brought due to un-replicated landrace treatments. The formula used for the data adjustment was as follows (Federer and Ragavarao, 1975);

$$\bar{Y}_{ij} = Y_{ij} - X^{-}_{i} - X^{=}$$

Where, $\bar{Y}_{ij}$ = adjusted mean of each observation, Y_{ij} = original observation of each genotype, X^{-}_{i} = mean of checks in each block and $X^{=}$ = grand mean of checks in all blocks.

Further, the following procedures were used for combining the data from the three groups of accessions. First, we computed out environmental index for each character in each test site. According to Singh and Chaudhary (1985), the environmental index is defined as the deviation of the mean of all the accessions at a given test site from the overall mean and is given as

$$Ij = \frac{\sum_{i=1}^{t} Yij}{t} - \frac{\sum_{i=1}^{t}\sum_{j=1}^{s} Yij}{st}$$

Where, I_j is the environmental index of the j^{th} test site; Y_{ij} is the mean of the i^{th} accession in the j^{th} test site, 't' is the number of accessions and 's' is the number of test sites.

The statistical analyses for all traits were taken up using Genstat v15.0and SPSS v16.0. Means, ranges (minimum and maximum values), standard deviation, standard error and variance were analyzed. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2) and genetic advance as percentage of mean (GAM) were calculated according to procedure suggested by Singh and Chaudhary (1985). The combined analysis of variance was performed across test environments (location) and years.

The mean squares of the regions, altitude classes and kernel row numbers were tested against pooled mean squares of accessions within regions, altitude classes and kernel row number, respectively.

Multivariate analyses based on 22 quantitative and 13 diseases and barley shoot fly resistance component data such as Unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering based on similarity distance and principal component analysis (PCA) were performed in order to assess the degree of divergence and relatedness among the landraces and estimate the relative importance and contribution of traits to the overall variation using SPSS V16.

Results and Discussion

Univariate

The mean values, ranges and variation showed by the quantitative, diseases andshoot fly resistance component characters in this study are presented in Table 1. The result indicated that there was a wide range of variations among the landraces studied. The range of variability for most of the quantitative characters was relatively high. For instance, mean of days to heading and to physiological maturity ranged from 46.0 to 95.0 (with an average value 68.30) and

Table 1. Mean, range, standard deviation and coefficient of variation (%CV) estimates for different agronomic traits and diseases response at each location

Categories	Range		Mean	Std	Variance	CV (%)
	Min	Max				
Agronomic traits						
Days to heading	46.00	95.00	68.30	8.34	57.17	7.27
Days to maturity	90.00	145.00	108.60	10.70	75.42	9.85
Grain filling period	26.00	73.00	39.80	5.60	31.21	14.00
Grain filling index	21.19	56.67	37.01	4.62	21.31	12.47
Seedling vigour	1.00	5.00	2.06	1.17	1.37	17.17
Flag leaf length	4.80	26.80	15.24	2.44	5.93	15.98
Flag leaf width	0.20	2.40	0.76	0.24	0.06	31.49
Flag leaf area	1.81	50.96	8.80	4.07	16.53	38.70
Peduncle length	12.00	40.60	28.90	3.20	10.30	11.10
Peduncle extrusion	3.00	21.50	11.25	2.71	7.34	24.14
Plant height	75.10	139.30	104.10	7.46	55.64	7.170
Tiller per plant	0.70	9.80	4.20	1.10	1.15	26.10
Fertile tillers per plant	0.50	9.00	3.50	0.96	0.93	27.99
Seeds per spike	15.80	79.70	40.90	13.40	17.90	32.80
Awn length	8.10	44.90	12.00	0.90	0.90	18.30
Spike length	3.30	20.70	7.53	1.27	1.61	16.81
Spike weight	0.60	3.90	1.73	0.49	0.24	28.21
Spike density	1.70	19.10	5.82	2.69	7.25	46.26
Biomass yield	20.00	1580.00	361.80	164.2	2.60	45.40
Harvest index	4.20	64.40	22.41	8.77	76.96	39.15
Grain yield	1.80	251.30	73.95	34.98	13.60	35.70
Thousand seed weight	15.10	54.80	33.35	6.06	36.70	18.16
Leaf rust						
Incidence (%)	5.00	95.00	62.05	23.12	534.6	17.08
AUDPC	233.24	2314.02	1055.74	13.48	81.71	28.09
Net blotch						
Percent severity index	10.00	90.00	45.37	20.83	434.1	30.04
AUDPC	121.06	1087.03	406.05	7.08	50.13	10.78
Apparent infection rate	1.76	19.02	7.67	1.16	1.35	66.69
Barley yellow dwarf virus						
Nr. of infected tillers	0.00	11.3	1.44	0.71	0.50	49.23
% of foliage with symptoms	12.25	35.37	11.24	4.81	23.14	18.80
Leaf tip necrosis	0.10	0.90	0.35	3.58	12.82	29.82
Barley shoot fly						
Dead heart	1.00	68.20	11.14	5.38	28.93	48.26
Oviposition	0.20	3.50	1.44	0.71	0.45	34.29
Crop recovery rate	1.00	5.00	4.20	0.81	0.65	19.20
Percent survival	33.33	100.00	90.96	5.57	30.98	6.12
Shoot fly infection	13.00	93.00	41.35	11.04	121.90	26.70
Shoot fly incidence	3.77	53.78	37.20	21.51	462.91	57.83

90.0 to 145.0 days (with an average value 108.6). Leaf rust incidence ranged from 5.0% to 95.5% with average value of 62.05%. Dead heart formation due to barley shoot fly ranged from 1 to 68%. The highest coefficient of variation (CV) was shown by spike density, biomass yield per plant, harvest index and grain yield. The lowest values on the other hand were shown by days to heading, days to physiological maturity and plant height. From the results for combined analysis of agronomic traits it was observed that nearly all the sources of variations in the combined analysis were highly significant ($P \leq 0.01$) except for peduncle length, awn length and harvest index for accessions-year interaction.

The analysis of variance showed that the mean squares for genotypes were significant ($p < 0.001$) for all agronomic, disease and shoot fly resistance component traits studied. This indicated the existence of a high degree of genetic variability in the material to be exploited in a breeding program and also reflected the broad ranges observed for each trait (Woldeab *et al*., 2007).

Phenotypic and genotypic variations

Phenotypic variance ($\boldsymbol{\delta}^2$p) and genotypic variance ($\boldsymbol{\delta}^2$g) were calculated to see the nature of variability among the landraces. Similarly, variability components, namely, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were also calculated to evaluate the extent of existing variability between the landraces in terms of agronomic traits and disease and shoot fly resistance component characters as shown in Table 2. To know the actual share of genotypic variance, the phenotypic variance divided into genotypic variance and environmental (error) variance. Then from the analysis, we observed that the share of genotypic variance for all characters were greater than 50% except for grain filling period, grain filling index, flag leaf length, peduncle extrusion, awn length and harvest index, indicating the genotypic effect on the phenotypic expression was greater than the effect of the environment. The values of estimated PCV were higher than the values of GCV for all the quantitative characters studied. The highest values of PCV and GCV were obtained for grain yield per plant followed by spike density, number of fertile (seed bearing) tiller per plant, number of seeds per spike, flag leaf area, leaf rust incidence, AUDPC (leaf rust and net blotch), number of infected tillers and leaf tip necrosis (BYDV), dead-heart formation and oviposition (Table 2).

The phenotypic and genotypic variances observed for these traits were also high, indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance of these traits. The result of the present study concurs with that reported by Woldeab *et al*. (2007), Hailu *et al*. (2016) and Bekele *et al*. (2018).Large differences between the PCV and GCV values were observed for the number of fertile tillers per plant and grain yield per plant indicating the high contribution of environmental variance to phenotypic variance. The phenotypic coefficients of variation were generally higher than the genotypic coefficients of variation for all traits studied, indicating the influence of growing environments. These findings were in agreement with those reported by Tahir *et al*. (2015) and Hailu *et al*. (2016).

Estimation of broad sense heritability (H^2)

The heritability estimates ranged from 18.31 to 92.55% for grain filling period and number seeds per spike, respectively. In this study, higher estimates of heritability (>75%) were recorded from number of seeds per spike, spike density, days to heading, lodging, days to maturity, grain yield per plant, 1000-seed weight, , whereas spike weight, number of fertile tillers per plant, and number of tillers per plant showed moderate estimates (Table 2).The highest estimated value of genetic advance (GA) (>20%) were recorded from grain yield, biomass yield, plant height, and number of seeds per spike. The moderate value were showed by thousand seed weight, lodging, days to maturity and days to heading, however, the remaining other quantitative characters had low genetic advances (Table 2). According to the result from this study, the expected genetic advance as percentage of mean of traits from agronomic traits, ranged from 8.30% for grain filling period to 66.62% for number of seeds per spike. For major diseases it ranged from 37.78% for net blotch percent severity index to 87.30% AUDPC (net blotch). Other characters that showed high estimates of genetic advance as a percentage of mean include flag leaf area, number of fertile tiller, total tiller per plant, spike density, grain yield per spike, thousand seed weight, plant height, spike length, peduncle extrusion and spike weight for agronomic traits and all diseases and shoot fly resistance component traits except leaf width from barley shoot fly resistance components (Table 2).

Table 2. Estimates of phenotypic (δ^2p), genotypic (δ^2g) variance, phenotypic (PCV) and genotypic (GCV) coefficients of variation of barley accessions based on agronomic data

Traits	Variance			% share of		Coefficient of variation		H^2	GA	GAM
	δg2	δp2	δe2	δg2	δe2	Phenotypic	Genotypic			
Days to heading	169.54	200.69	31.15	84.48	15.52	20.75	19.07	84.48	14.60	21.39
Days to maturity	183.10	239.38	56.28	76.49	23.51	14.25	12.46	76.49	16.88	15.55
Grain filling period	13.46	73.52	60.06	18.31	81.69	21.24	9.09	18.31	3.35	8.30
Grain filling index	24.89	54.16	29.27	45.96	54.04	19.89	13.48	45.96	5.97	16.14
Early growth vigor	0.93	1.48	0.55	62.84	37.16	59.06	46.81	62.84	1.52	73.63
Flag leaf length	5.05	12.37	7.32	40.82	59.18	23.08	14.75	40.82	2.46	16.14
Flag leaf width	0.13	0.17	0.04	76.47	23.53	54.97	48.07	76.47	0.41	54.69
Flag leaf area	26.15	36.65	10.50	71.35	28.65	68.79	58.11	71.35	5.99	38.08
Peduncle length	50.58	85.13	34.55	59.42	40.58	29.88	23.03	59.42	7.12	23.06
Peduncle extrusion	9.51	20.12	10.61	47.27	52.73	39.91	27.44	47.27	3.49	31.06
Plant height	84.87	168.69	83.82	50.31	49.69	12.49	8.86	50.31	22.58	12.10
Nr. of tillers per plant	3.26	4.83	1.57	67.49	32.51	62.08	42.79	67.49	2.13	50.48
Fertile tillers per plant	2.53	3.57	1.04	70.87	29.13	65.09	46.37	70.87	1.89	54.99
Nr. of seeds per spike	622.44	672.55	50.11	92.55	7.45	64.29	61.85	92.55	27.00	66.92
Awn length	1.08	2.56	1.48	42.19	57.81	13.34	8.67	42.19	1.15	9.58
Spike length	2.74	4.42	1.68	61.99	38.01	27.92	21.98	61.99	2.15	28.53
Spike weight	0.40	0.55	0.15	72.73	27.27	42.87	36.56	72.73	0.77	44.23
Spike density	21.51	24.96	3.45	86.18	13.82	85.69	79.55	86.18	5.46	33.62
Biomass yield per plant	209.00	515.00	306.00	40.55	59.45	62.40	39.73	40.55	25.01	48.08
Harvest index	36.10	139.30	103.20	25.92	74.08	55.54	28.27	25.92	5.69	26.79
Grain yield per plant	352.00	459.00	106.00	76.77	23.23	71.69	65.33	56.77	24.13	28.28
Thousand seed weight	86.74	115.23	28.49	75.28	24.72	32.20	27.93	75.28	11.31	33.91

Leaf rust										
Incidence (%)	415.70	652.10	236.40	63.75	36.25	90.11	85.10	63.75	30.41	41.82
AUDPC	250.29	387.20	136.91	64.64	35.36	88.44	71.10	64.64	30.96	39.17
Net blotch										
Percent severity index	431.30	707.30	276.00	60.98	39.02	38.34	29.94	60.98	26.20	37.78
AUDPC	1.06	1.67	0.61	63.47	36.53	74.27	59.17	63.47	1.52	87.30
Apparent infection rate	595.40	987.90	392.50	60.27	39.73	50.58	39.27	60.27	34.42	55.38
Barley yellow dwarf virus										
Nr. of infected tillers	0.73	1.21	0.48	60.33	39.67	74.32	57.73	60.33	1.12	75.69
% foliage with symptoms	0.54	0.92	0.38	58.70	41.30	68.51	52.49	58.70	1.11	79.57
Leaf tip necrosis	0.71	1.12	0.41	63.39	36.61	71.03	56.55	63.39	1.15	77.24
Degree of attack	0.53	1.05	0.52	50.48	49.52	74.25	52.75	50.48	0.86	62.63
Barley shoot fly										
Dead heart formation	27.61	44.36	16.75	62.24	37.76	79.79	67.17	72.24	6.91	62.01
Oviposition percentage	0.15	0.28	0.13	53.57	46.43	76.75	56.90	63.57	0.78	54.49
Shoot fly infestation	130.70	222.51	91.81	58.74	41.26	36.07	27.65	58.74	13.38	32.35
Shoot fly incidence	67.00	251.60	184.60	26.63	73.37	42.64	22.00	26.63	11.82	31.77
Early growth vigour	0.93	1.48	0.55	62.84	37.16	59.06	46.81	62.84	1.52	53.63
Seedling color	0.36	0.38	0.02	94.74	5.26	55.04	53.57	64.74	0.63	55.84
First leaf width	1.36	1.85	0.49	73.51	26.49	19.21	16.47	53.51	1.65	23.35
Second leaf width	1.74	2.42	0.68	71.90	28.10	20.85	17.68	61.90	1.74	53.26
Crop recovery rate	0.60	1.06	0.46	56.60	43.40	74.46	68.40	76.60	0.95	52.47
Percent survival	17.45	39.70	22.25	43.95	56.05	76.93	64.59	73.95	5.05	55.55
Stand count	1427.00	3766.00	2339.00	37.89	62.11	41.16	25.34	37.89	66.69	44.73

AUDPC = area under the disease progress curve; H^2 = broad sense heritability, GA = Genetic advance, GAM = Genetic advance expressed as mean

Variability components, namely, phenotypic and genotypic coefficient of variabilities were also calculated to evaluate the extent of existing variability between the landraces in terms of resistance to major diseases and barley shoot fly. Accordingly, high and moderately high PCV and GCV were observed for leaf rust and barley yellow dwarf virus, respectively. For net blotch moderately high PCV for estimated AUDPC values. On the other hand, for barley shoot fly resistance, moderately high PCV and GCV estimated values were observed for dead heart, oviposition percentage, crop recovery and percent survival. High heritability and genetic advance estimates computed showed variability (Table 2).

Variation within regions of origin

Analyses of variance revealed highly significant differences ($P \leq 0.01$) between regions of origin of the barley accessions for the 22 agronomic characters and between accessions pooled over the regions for agronomic characters studied (Table 3). The results suggested the occurrence of significant regional differentiation and existence of significant phenotypic variation between the accessions as a whole. Region-wise partitioning of the variance indicated significant within-region differences ($P \leq 0.05$) among the populations within Arsi for 20 characters; for 19 characters within Gojam; for 18 characters within Bale and Gonder; for 17 characters within Shewa and Sidama; for 16characters within Gemo Gofa, Hararghe, Jimma, Tigray, Wellega and Wello and for 13 characters for Hadiya (Table 3).

In terms of altitude classes, for 21 characters within altitude classes II (1501-2000m) and III (2001-2500m); for 20 characters within altitude class IV (>2500m) and for 18 characters within altitude class I (<1500m) were observed. On the other hand, based on kernel row number, among population within two- and six-rowed barley types for 21 characters and for 16 characters within irregular barley types were observed (Table 4).

In general, within region variation was greater for days to heading and maturity, number of tillers per plant, number of seeds per spike, spike weight, spike density and flag leaf width for all the regions. Assuming that a significant portion of the phenotypic variation is genetic, it would be possible to make selection for any of the first group of characters within a particular region. It was apparent that between regions variance was greater than between accessions pooled over regions and the latter was greater than that between accessions in some regions. Within altitude classes and kernel row number variation was greater for all phenological characters, tillers per plant, number of fertile tillers per plant, spike weight and density, 1000-seed weight and grain yield per plant.

The mean square of accessions response to diseases based on regions of origin, altitude classes and kernel row number is shown in Table 5. Accessions from all regions except those from Bale, Hadiya, Jimma and Sidama showed highly significant variations in resistance to disease and barley shoot fly. On the other hand, accessions from low altitude areas had non-significant variations in response to barley yellow dwarf virus. For barley shoot fly resistance components, accessions from 10 regions had showed highly significant variations (Table 6). In terms of altitude classes, on the other hand, highly significant variations were observed among accessions except those from altitude class I (<1500m), however, highly significant variations were observed for all resistance component traits for barley shoot fly (Table 6).

Bivariate statistics

Principal component analysis

The principal component analysis (PCA) based on 23agronomic characters studied revealed that the first eight principal components (PCs) with Eigen values greater than one accounted for 83.01% of the total variations among landraces as shown in Table 7. The relative magnitude of Eigen values from the first PCs (20.32%) indicated that, the traits such as days to heading and maturity, flag lead width and area, number of seeds per spike, spike weight and density from agronomic traits and leaf rust incidence, net blotch infection rate, oviposition, dead-heart formation, stand-count and leaf width from disease and shoot fly components, respectively posed the greater contribution in the positive direction while days to early seedling vigour, 1000-seed weight, grain filling index, spike length, shoot fly incidence, early seedling vigour, net blotch percent severity index and grain yield loaded heavily in the negative direction. Similarly, biomass yield per plant, plant height, flag leaf length, and spike length contributed major variation in the second PC which accounted 15.20% (Table 7). Peduncle length and extrusion, spike length, BYDV leaf tip necrosis and percent foliage with symptoms loaded greater contribution in the third PC and grain filling period and index, flag leaf length and AUDPC due to leaf rust posed higher contribution in forth PC. For PC-5 and PC-6, the contribution of

Table 3. Mean square estimates for different agronomic traits of barley landraces based on regions of origin

Traits¥	Regions of origin												
	Arsi	Bale	G/Gofa	Gojam	Gonder	Hadiya	Hararghe	Jimma	Shewa	Sidama	Tigray	Wellega	Wello
DTH	109.11**	57.00**	22.41ns	274.56**	396.36**	84.54**	28.57**	47.06**	205.33**	161.03**	97.06**	165.29**	101.54**
DTM	170.37**	118.23**	95.54**	263.28**	343.24**	138.68**	133.07**	46.63ns	210.81**	190.25**	147.47**	232.25**	151.26**
GFP	77.65ns	70.74**	73.90*	63.74ns	91.27ns	63.13ns	78.75**	30.04ns	72.08ns	74.62ns	56.59ns	61.22ns	60.05ns
GFI	40.29*	31.42*	28.95ns	68.13**	108.50**	31.81ns	25.03ns	17.84ns	54.87**	45.32*	34.05ns	38.23ns	34.71ns
VIG	1.36**	1.88**	1.26**	1.47**	1.92**	1.44**	1.15**	1.49**	1.21**	1.80**	1.06**	0.90**	1.18**
FLL	12.45**	7.07ns	11.98**	11.04**	16.62**	4.64ns	12.00**	14.33**	10.84ns	10.99*	8.94ns	9.65ns	10.75ns
FLW	0.12**	0.10**	0.04**	0.08**	0.22**	0.11**	0.14**	0.12**	0.16**	0.18**	0.12**	0.63**	0.07**
FLA	28.97**	18.50**	11.08**	16.23**	59.44**	22.52**	35.20**	36.34**	35.49**	27.24**	24.06**	106.29**	18.01**
PDL	21.32ns	16.74ns	15.53ns	26.62ns	17.14ns	29.40ns	13.47ns	25.16ns	24.16ns	29.42ns	19.32ns	21.75ns	33.81ns
PEX	17.31**	21.10**	7.25ns	20.02**	14.06**	15.91ns	7.29ns	17.65**	17.37**	21.73**	14.73**	8.69ns	18.79*
PLH	126.95**	87.27**	135.31**	139.96**	166.30ns	119.99ns	76.49ns	129.40**	106.96ns	257.32**	193.07**	187.13**	170.15*
NTPP	3.73**	3.61**	3.32**	5.47**	5.91**	2.49**	3.49**	2.94**	6.41**	1.74ns	6.10**	5.36**	4.36**
NFTPP	2.66**	2.35**	2.53**	4.32**	3.74**	2.58**	1.95**	2.09**	4.89**	1.36ns	5.36**	3.25**	4.06**
NSPS	509.12**	324.82**	497.06**	251.58**	505.06**	684.61**	402.35**	808.28**	489.25**	515.03**	243.97**	505.24**	524.27**
AWL	2.56**	1.43**	2.64**	1.59*	0.91ns	1.79**	3.26ns	0.93*	1.49*	0.63ns	3.43ns	2.05**	6.02ns
SPL	4.32**	1.99**	4.24**	2.47**	2.30**	6.19**	3.01**	5.12**	3.91**	2.56*	5.22*	2.25ns	3.74**
SPW	0.39**	0.25**	0.30**	0.23**	0.51**	0.71**	0.57**	0.50**	0.50**	0.31**	0.38**	0.36**	0.29**
SPD	22.25**	11.63**	14.76**	9.84**	14.81**	24.60**	19.12**	28.66**	19.41**	16.05**	80.00**	12.46**	18.97**
BYPP	588.57**	485.99**	857.93**	321.90ns	534.09**	263.51ns	443.24**	452.05ns	349.87**	713.29**	459.81*	263.83ns	223.07**
HI	103.73**	123.30ns	144.60ns	167.35**	176.15**	90.67ns	81.65ns	81.51ns	99.36ns	97.71**	105.66*	158.16**	89.03ns
GYPP	292.00**	272.00ns	700.00**	301.00**	276.00**	301.00ns	278.00**	386.00**	241.00**	365.00**	364.80**	211.11**	180.10*
TSW	91.94**	59.47**	162.74**	91.50**	88.67**	114.18**	36.70*	93.60**	63.99**	102.41**	46.34ns	107.66**	98.16**

ns, *, ** = non-significant, Significant at P≤0.01 levels of significance, respectively.

¥ DTH = days to heading, DTM = days to maturity; GFP = Grain filling period; GFI = Grain filling index; EVG = Early vigour growth; INL = Internode length; FLL = Flag leaf length; FLW = Flag leaf width; FLA = Flag leaf area; PDL = Peduncle length; PEX= Peduncle extrusion; PLH = Plant height; NTPP = Number of tillers per plant; NFTPP = Number of fertile tillers per plant; NSPS = Number of seeds per spike; AWL = Awn length; SPL = Spike length; SPW = Spike weight; SPD = Spike density; BYPP = Biological yield per plant; HI = Harvest index; GYPP = Grain yield per plant; TSW = Thousand seed weight; LDG = Lodging.

Table 4. Mean square estimates for different agronomic traits of barley landraces based on Altitude classes and kernel row number

Traits¥	Altitude classes				Kernel row number		
	<1500m	1501-2000m	2001-2500m	>2500m	Two-rowed	Six-rowed	Irregular
DTH	389.29**	99.62**	161.19**	181.48**	134.00**	176.61**	243.37**
DTM	303.30**	134.96**	200.72**	221.19**	139.81**	234.17**	345.60**
GFP	84.20ns	71.21**	72.77**	62.20ns	66.75**	77.44**	83.16ns
GFI	96.26**	45.42**	50.38**	43.34*	51.76**	47.51**	48.28*
VIG	1.63**	1.35**	1.40**	1.04**	1.27**	1.55**	1.89**
FLL	8.24ns	10.99**	12.01**	12.24**	10.05**	13.81**	12.58ns
FLW	0.17**	0.11**	0.18**	0.15**	0.15**	0.17**	0.16**
FLA	15.21*	28.45**	39.94**	31.56**	28.27**	37.75**	37.57**
PDL	37.34ns	24.15ns	24.27ns	24.38ns	28.04ns	22.67ns	27.05ns
PEX	42.44**	19.08**	18.44**	15.43**	20.71**	19.40**	22.19*
PLH	387.63**	137.29**	163.94**	162.50**	128.04**	139.02**	209.70ns
NTPP	3.90*	4.38**	4.87**	5.56**	5.17**	4.10**	4.67**
NFTPP	3.15*	3.38**	3.45**	4.00**	3.88**	2.99**	2.85**
NSPS	316.07**	620.19**	637.56**	581.79**	65.40**	282.33**	182.00ns
AWL	1.21ns	3.13**	2.51**	1.68**	2.99**	2.37**	1.77*
SPL	2.02**	5.32**	3.99**	3.09**	3.05**	3.84**	1.62ns
SPW	0.38**	0.42**	0.48**	0.56**	0.19**	0.38**	0.26**
SPD	9.21**	23.87**	22.62**	20.32**	1.76**	15.47**	3.91**
BYPP	788.70*	500.74**	471.20**	533.49**	464.66**	547.10**	471.01ns
HI	169.52**	111.63*	119.70**	132.52**	115.71**	140.90*	138.65*
GYPP	380.80**	403.50**	306.90**	279.50**	346.30**	337.20**	306.10**
TSW	125.23**	121.72**	116.86**	81.20**	47.18**	77.23**	96.69**

ns, *, ** = non-significant, Significant at P≤0.01 levels of significance, respectively.

¥ DTH = days to heading, DTM = days to maturity; GFP = Grain filling period; GFI = Grain filling index; EVG = Early vigour growth; INL = Internode length; FLL = Flag leaf length; FLW = Flag leaf width; FLA = Flag leaf area; PDL = Peduncle length; PEX= Peduncle extrusion; PLH = Plant height; NTPP = Number of tillers per plant; NFTPP = Number of fertile tillers per plant; NSPS = Number of seeds per spike; AWL = Awn length; SPL = Spike length; SPW = Spike weight; SPD = Spike density; BYPP = Biological yield per plant; HI = Harvest index; GYPP = Grain yield per plant; TSW = Thousand seed weight; LDG = Lodging.

Table 5. Mean square for leaf rust, net blotch, barley yellow dwarf virus of barley landraces estimated from field experiments conducted from 2018 to 2019 based on regions

Region	Leaf rust		Net blotch			BYDV			
	Inc (%)	AUDPC	PSI	AUDPC	AIR	NIT	FWS	LTN	DA
Arsi	62.1**	849.4**	14.42**	22.06**	10.81*	1.32**	33.31**	0.64*	55.82**
Bale	61.4*	651.3**	20.09*	35.96ns	7.67**	1.34**	34.0**	0.7*	49.8**
Gamo Gofa	68.4**	1059.3**	34.01**	47.01*	14.32**	1.6**	36.9**	0.7**	40.7**
Gojam	65.3*	975.4**	30.14**	38.17**	11.34**	1.3*	34.3**	0.6*	74.4**
Gonder	63.1**	755.8**	30.34*	39.66**	12.20**	1.3**	34.7**	0.7**	55.3**
Hadiya	65.3**	1925.3**	37.34**	43.44**	13.92ns	1.4**	38.9**	0.7*	68.7**
Hararghe	68.5**	1357.0**	35.06**	45.45**	14.75**	1.6**	39.7**	0.7**	59.3**
Jimma	66.1*	2006.4*	35.17ns	44.51*	13.66**	1.6**	38.4ns	0.7**	96.4**
Shewa	67.5**	975.4**	25.87**	38.82**	12.42d**	1.5*	37.3**	0.7**	75.4**
Sidama	69.6**	1437.3**	33.75*	41.45*	14.33ns	1.6**	37.6**	0.6**	21.4**
Tigray	75.6**	1991.9*	33.90**	41.82*	16.03**	1.7**	35.6**	0.7**	25.3**
Wellega	74.3**	1038.8**	33.42**	39.82**	12.80*	1.5**	35.7**	0.6**	79.2**
Wello	68.0**	1051.7**	31.65**	400.16*	13.93**	1.5*	39.0**	0.7**	38.8**
Altitude classes									
I (<1500)	74.31ns	2104.3**	41.27*	66.41**	21.02*	1.93**	41.3*	0.81*	81.5*
II (1501-2000)	67.32*	2047.02*	39.23**	54.2**	19.28*	1.9**	37.84*	0.8**	73.25**
III (2001-2500)	66.19**	1974.31**	36.52**	46.2**	13.10**	1.7ns	34.27**	0.73**	49.25**
IV (>2500)	61.24**	1389.07**	35.09**	38.27**	12.87**	1.6**	33.51**	0.7**	27.92**
Kernel row number									
Two-rowed	67.21**	1907.53**	47.28**	53.04**	17.81*	1.91**	43.02**	0.8*	57.24**
Six-rowed	63.03**	1769.37**	42.02**	44.67**	14.23**	1.72**	39.7**	0.7**	43.05**
Irregular	65.02*	1481.54**	37.34**	43.28**	13.66**	1.65*	38.03ns	0.7*	49.23*

ns, *, ** = non-significant, Significant at P≤0.01 levels of significance, respectively.
Inc = Incidence, AUDPC = Area under the disease progress curve, PSI = Percent severity index, AIR = Apparent infection rate, NIT = Number of infected tillers (Incidence) , FWS = % of foliage with symptom (Severity), LTN = Leaf tip necrosis, DA = Degree of attack

Table 6. Estimates of genotypic variances for barley shoot fly resistance components based on regions of origin, altitude classes and kernel row number

Categories	DHRT	OVP	INF	INC	SVG	SC	LW-1	LW-2	CR	PS
Region										
Arsi	24.99**	0.10**	105.35*	300.30**	2.33**	0.24**	1.11**	1.18**	1.20**	52.17**
Bale	8.66*	0.09*	94.10*	257.20**	2.30**	0.30**	0.86*	1.51**	0.88**	19.13**
Gamo Gofa	15.91ns	0.11**	116.30ns	305.20ns	2.37**	0.22**	1.18ns	1.31ns	1.57ns	44.28*
Gojam	18.15**	0.13**	122.88**	327.30*	2.14**	0.22**	1.24**	1.40*	1.15**	34.10*
Gonder	22.16**	0.08**	58.33**	166.40*	2.76**	0.14**	0.93*	0.92*	1.07**	40.95**
Hadiya	23.41ns	0.10**	143.50*	396.80*	2.70**	0.16**	0.77ns	1.11ns	1.27ns	43.24ns
Hararghe	16.08**	0.14**	90.70**	270.00*	1.63**	0.04**	1.41**	1.27**	0.77**	41.57**
Jimma	14.05ns	0.07ns	160.02*	369.20**	2.36**	0.00ns	0.56ns	1.39ns	0.31ns	20.35*
Shewa	39.04**	0.15**	81.90**	299.30**	2.03**	0.16**	0.58**	1.22**	1.38**	57.30**
Sidama	8.41*	0.17**	93.25**	225.30*	2.94**	0.38**	12.88*	1.12*	0.88*	13.31*
Tigray	18.44*	0.12**	124.34*	305.30*	1.89**	0.10**	0.74*	1.22*	0.79**	35.09*
Wellega	20.55**	0.26**	84.88**	503.40**	1.39**	0.11**	0.64**	0.98**	1.16**	33.11**
Wello	14.88*	0.14**	88.90**	218.30*	1.94**	0.21**	1.12*	1.15ns	1.36**	27.15*
Altitudinal classes										
I (<1500)	4.32ns	0.11*	112.12ns	341.70ns	1.82**	0.04ns	0.75ns	1.14*	0.14*	32.55ns
II (1501-2000)	17.15**	0.10**	100.84*	271.90**	2.21**	0.20**	0.98*	1.15ns	0.88**	37.18*
III (2001-2500)	20.94**	0.13**	103.00**	278.80**	2.11**	9.30**	1.04**	1.43**	1.05**	39.11**
IV (>2500)	26.74**	0.13**	101.40*	346.20*	1.83**	0.13**	0.78**	1.02*	1.43**	41.55*
Kernel row number										
Two-rowed	35.78**	0.29**	204.37**	245.80**	1.27**	0.35**	2.04**	2.53**	0.83**	31.67**
Six-rowed	51.36**	0.27**	217.40**	244.40*	1.55**	0.42**	1.76**	2.40**	1.18**	44.64**
Irregular	35.81**	0.39**	292.05*	346.30**	1.89**	0.18**	1.36**	2.15**	1.26**	42.60*

*, **, ns = significant at P = 0.05; P = 0.01 level, and non-significant respectively.
DHRT = Dead heart, OVP = Oviposition, INF = Infection, INC = Incidence, SVG = Seedling vigour, SC = Seedling colour, LW-1 = First leaf width, LW-2 = Second leaf width, CR = Crop recovery, PS = Percent survival

number of tillers per plant and productive tillers per plant was high. Peduncle length and extrusion posed greater contribution in positive direction and dead-heart formation in the negative direction to seventh principal component. Eigen values from eighth PC accounted 4.94% for which the traits such as harvest index, grain yield per plant and 1000-seed weight posed the greater contribution (Table 7).

Cluster analysis

Hierarchical cluster analysis technique was used to see the aggregation patterns of 585 barley landraces. Because the results of cluster analyses based on mean phenotypic data and loading scores of genotypes in the extracted principal components from PCA were more or less the same, the cluster analyses results based on principal components were selected as the most suitable methods to calculate cluster. Cluster analysis based on Euclidean dissimilarity using the between-

Table 7. Eigen values, explained variation, communality values, and Eigen vectors in PCA for barley landraces estimated using LS means over two years (2018-2019).

Parameters		PC_1	PC_2	PC_3	PC_4	PC_5	PC_6	PC_7	PC8
Eigen Values		4.47	3.34	2.71	3.04	1.69	1.57	1.34	1.09
Individual variation explained (%)		20.32	15.20	12.36	9.27	7.70	7.13	6.10	4.94
Cumulative variation explained (%)		20.32	35.51	47.88	57.15	64.85	71.98	78.07	83.01
Traits	Communalities								
Days to heading	0.939	0.729	0.101	0.043	-0.339	0.418	-0.141	-0.283	0.076
Days to maturity	0.940	0.539	0.027	0.373	0.198	0.603	-0.185	-0.251	-0.106
Grain filling period	0.988	-0.142	-0.090	0.492	0.723	0.351	-0.092	-0.006	-0.252
Grain filling index	0.978	-0.518	-0.105	0.320	0.720	0.030	0.006	0.153	-0.231
Early growth vigour	0.391	-0.741	0.180	0.113	0.160	-0.171	0.063	0.058	-0.066
Flag leaf length	0.777	0.198	0.600	-0.315	0.412	-0.124	0.017	0.239	0.190
Flag leaf width	0.808	0.561	0.531	-0.217	0.219	0.234	-0.072	-0.078	0.223
Flag leaf area	0.930	0.507	0.637	-0.291	0.319	0.127	-0.054	-0.262	-0.224
Peduncle length	0.754	-0.007	0.073	0.640	-0.414	0.157	-0.217	0.279	0.134
Peduncle extrusion	0.751	-0.239	0.073	0.580	-0.203	-0.026	-0.176	0.499	0.173
Plant height	0.628	0.239	0.486	0.350	-0.165	-0.130	-0.147	0.382	0.034
Nr. of tillers per plant	0.937	-0.369	0.285	-0.128	-0.220	0.500	0.619	0.125	-0.076
Nr. of fertile tillers per plant	0.930	-0.417	0.282	-0.146	-0.179	0.430	0.634	0.165	-0.099
Nr. of seeds per spike	0.904	0.760	-0.048	0.261	0.175	-0.251	0.355	0.187	-0.040
Awn length	0.249	0.026	0.093	0.105	-0.007	0.304	-0.064	0.358	0.056
Spike length	0.633	-0.470	0.437	-0.264	0.226	0.054	-0.182	0.199	0.159
Spike weight	0.686	0.553	-0.084	0.486	0.033	-0.012	0.353	0.008	0.108
Spike density	0.928	0.772	-0.238	0.323	0.050	-0.183	0.350	0.042	-0.103
Biomass yield per plant	0.981	-0.146	0.806	0.329	-0.091	-0.268	0.054	-0.262	-0.224
Harvest index	0.910	-0.327	0.301	0.313	0.240	-0.047	0.275	-0.222	0.656
Grain yield per plant	0.893	-0.410	0.413	0.451	0.093	-0.255	0.269	-0.362	0.273
Thousand seed weight	0.751	-0.571	0.116	0.363	-0.165	0.283	-0.228	-0.318	0.138
Leaf rust									
Incidence (%)	0.679	0.412	-0.086	0.052	-0.167	0.307	0.272	0.013	0.128
AUDPC	0.922	-0.414	0.447	0.251	0.504	0.109	-0.038	0.079	-0.244
Net blotch									
Percent severity index	0.739	-0.630	0.118	0.148	-0.454	0.246	-0.117	0.070	0.090
AUDPC	0.899	-0.480	-0.249	0.243	0.426	0.430	0.104	0.034	-0.394
Apparent infection rate	0.668	0.665	-0.009	0.110	-0.147	0.152	0.217	-0.061	-0.096
Barley yellow dwarf virus									
Nr. of infected tillers (%)	0.552	-0.381	-0.111	0.231	0.122	0.212	-0.151	0.061	0.449
Foliage with symptoms (%)	0.698	0.125	0.535	0.574	-0.141	0.093	-0.072	0.046	-0.007
Leaf tip necrosis	0.413	0.104	0.467	0.702	-0.265	0.190	-0.056	0.046	-0120
Degree of attack	0.447	-0.467	-0.298	0.407	-0.307	0.031	-0.143	.040	0.027
Barley shoot fly									
Dead hear formation	0.821	0.459	0.066	0.178	-0.073	-0.195	0.348	-0.602	-0.081
Oviposition	0.784	0.831	-0.025	0.032	-0.146	-0.005	0.116	-0.126	-0.171
Shoot fly infestation	0.616	0.056	0.065	0.325	0.061	0.038	0.313	-0.379	0.295
Shoot fly incidence	0.813	-0.730	0.014	0.296	0.208	-0.048	0.158	-0.197	0.245
Early growth vigour	0.634	-0.714	0.180	0.113	0.160	-0.171	0.063	0.058	-0.066
Seedling color	0.391	0.062	0.093	0.149	0.059	-0.210	-0.171	0.002	-0.144
First leaf width	0.471	0.590	0.089	-0.023	-0.052	-0.009	0.012	-0.022	-0.207
Second leaf width	0.509	0.489	0.017	-0.075	-0.214	-0.320	-0.076	-0.033	-0.229
Crop recovery rate	0.568	0.325	-0.269	-0.071	-0.089	0.394	-0.029	-0.002	0.311
Percent survival	0.825	0.398	-0.055	-0.291	-0.110	0.260	-0.332	0.572	-0.047
Stand count	0.773	0.818	0.031	-0.170	-0.154	0.078	0.008	0.023	-0.099

AUDPC = Area under the disease progress curve, PC = Principal component

groups linkage method categorized the germplasm into eight clusters at a 15% linkage distance as shown in Table 8. Numbers of landraces per cluster varied from 2 landraces in cluster II to 200 landraces in cluster III. Cluster I consists of 66 landraces, which is 11.2% of the total experimental materials. It is characterized as having landraces with early heading, large number of tillers per plant and medium plant height. Landraces grouped under cluster I were distributed over all regions and majority of them found in altitudinal class III (2001-2500m) and IV (>2500m). Cluster II comprised only 2 landraces with smaller number of tillers per plant, heavier biomass yield and moderately long grain filling period. Landraces with vigorous seedling, relatively long maturity and grain filling period, larger number of tillers and seed bearing tillers, long spikes and short plant height were grouped in cluster III which account 34.2% (200 landraces) materials. Cluster VI had ninety eight landraces (16.8% of population) and characterized by landraces with longer grain filling period, moderate peduncle length, large tiller per plant, high spike density and relatively lighter seed. Cluster VII included 77 landraces (13.2% population) which had long plant height, large seeds per spike, moderate number of tillers per plant, longer peduncle and spike length (Table 8).On the other hand, landraces included in cluster I characterized as having high recovery rate, relatively low oviposition percentage and dead-heart formation. Cluster II comprised of landraces with high oviposition and net blotch apparent infection rate. Landraces included in Cluster IV have higher AUDPC for both leaf rust and net blotch diseases (Table 8).

In this study, the variation exhibited by the 585 landraces along with 10 check cultivars, in 22 agro-morphological traits, three major barley diseases and barley shoot fly resistance responses showed that selection for several of these traits may be effective. We found highly significant location x accessions and year x accessions interactions for most of the traits studied. The interaction effects were always due to differences in magnitude of the means from different environments rather than differential responses of the genotypes in different environments. The genotypic effects were also significant for all traits considered, indicating that variability existed among the genotypes for each of the traits studied. The large variation observed in this study and previous studies (Bekele *et al*., 2018) in Ethiopian barley germplasm could be ascribed to many factors. One important factor is the fact that barley is grown in many different environmental conditions. These include rainfall, temperature, altitude, growing period, and edaphic factors. Other factors are linguistic, cultural, historical and economic system differences among the people who are cultivating barley (Hadado *et al*., 2009), which contribute to its variation. The various physical, biological and human factors as well as complex interactions among such factors all seem to have contributed to the wide range of variation of the crop in the country.

The detected high morphological, disease and shoot fly resistance variation for regions of origin, altitude classes and kernel row number suggested that the structure of morphological variation in Ethiopian barley landraces strongly influenced by environmental factors so that the degree of variation of characters differ with regions and altitude classes from where the accessions collected. Phenotypic diversity in Ethiopian barley was also reported by Tahir *et al*. (2015). The different levels of regional variability of a particular character could be due to differences in forces of selection and/or differences in the intensity of a particular selecting force. High genetic variation was observed in an altitude class II and III, which included the major barley growing areas in the country. Similar result was reported by Demisse and Bjornstad, (1998), where they found high variation concentration in areas between 2,000-3,000 and 2,400 and 3,000 m a.s.l., respectively.

In general, results obtained from analysis of regions of origin and different altitude class showed wide variation with regions of high altitude, humid and cooler temperature. From this result it was concluded to reject the null hypothesis and accept the alternative hypothesis, which was stated as there was no or low genetic variation between regions.

The two multivariate approaches utilized in the current study, principal component and cluster analyses, revealed the involvement of a number of traits in contributing towards the overall observed diversity. In the current study, eight PCs were observed with Eigen value greater than 1 accounted 83.01% of the variability in the original data. The most related traits were placed in the same principal component (PC) and hence the results from PCA provided clues as to the relationship among traits. The well adapted traits like 1000-seed weight, plant height days to head and days to maturity were the traits which contribute relatively high for the variation exists. Hence from the combined principal component analysis it was detected that altitude played a major role in discriminating accessions based on morphological traits as compared to regions of collection.

Table 8. Summary of cluster mean of regions of origin of barley accessions for agronomic characters

Traits	Cluster							
	1	2	3	4	5	6	7	8
Days to heading	66.15	69.33	69.08	68.69	71.13	66.86	66.97	67.19
Days to maturity	104.67	111.83	113.01	107.17	109.55	109.48	101.59	103.24
Grain filling period	38.51	42.50	43.93	38.48	38.43	42.62	34.62	36.05
Grain filling index	36.64	38.08	38.77	35.91	35.19	38.64	34.11	34.93
Early seedling vigour	1.71	1.33	2.82	1.22	1.28	2.36	1.20	1.16
Flag leaf length	15.74	18.87	15.48	16.77	17.50	14.92	14.32	14.88
Flag leaf width	0.72	1.07	0.74	0.89	1.06	0.71	0.69	0.74
Flag leaf area	8.75	15.48	8.68	11.34	14.20	8.17	7.61	8.44
Peduncle length	34.09	37.18	27.86	33.55	34.39	32.22	31.25	32.18
Peduncle extrusion	12.57	13.88	10.39	11.96	12.04	12.25	10.71	11.34
Plant height	108.76	124.28	95.31	116.33	120.99	101.53	107.79	112.33
Tiller per plant	4.56	3.42	4.04	4.42	4.40	4.35	4.09	4.30
Fertile tillers per plant	3.71	2.67	3.14	3.86	3.85	3.33	3.62	3.79
Seeds per spike	36.33	49.50	38.24	42.68	43.49	36.19	42.77	43.11
Awn length	11.96	11.05	12.12	12.03	12.29	11.95	11.81	11.80
Spike length	7.79	7.97	8.27	7.43	7.67	7.75	6.44	6.83
Spike weight	1.72	1.77	1.55	1.79	1.77	1.64	1.88	1.84
Spike density	4.98	6.60	4.98	6.04	5.94	4.90	7.17	6.73
Biomass yield per plant	573.10	1476.67	171.52	738.31	989.26	352.37	302.43	471.16
Harvest index	20.00	12.12	23.03	17.29	16.25	22.80	20.43	18.23
Grain yield per plant	114.80	175.80	41.31	128.64	162.95	80.07	62.23	86.50
Thousand seed weight	36.87	39.17	29.29	37.34	37.03	34.76	33.57	35.38
Leaf rust								
Incidence (%)	71.49	70.00	64.21	75.75	74.26	65.08	76.28	76.79
AUDPC	1573.10	1476.67	1171.52	1738.31	989.26	1352.37	1302.43	1471.16
Net blotch								
Percent severity index	13.72	16.13	38.32	11.58	14.08	22.38	7.42	7.91
AUDPC	114.80	175.80	141.31	1028.64	162.95	180.07	162.23	186.50
Apparent infection rate	1.81	2.83	1.17	2.79	2.66	1.28	2.35	2.40
Barley yellow dwarf virus								
Nr. of infected tillers (incidence)	11.02	15.41	13.20	18.83	11.34	12.34	17.29	14.33
% foliage with symptoms (Severity)	12.25	6.52	21.52	23.54	9.11	13.73	14.38	16.01
Leaf tip necrosis	1.74	1.17	1.67	1.38	1.53	1.84	.84	1.08
Barley shoot fly								
Dead heart formation	9.09	12.00	11.07	14.48	14.91	9.53	13.04	13.24
Oviposition	1.01	2.32	0.95	2.14	2.16	1.58	1.99	2.06
Shoot fly infestation rate	42.18	46.00	40.18	45.09	45.17	40.17	40.34	40.96
Shoot fly incidence rate	39.27	21.57	49.98	21.76	24.89	47.98	18.43	18.21
Crop recovery rate	4.47	4.33	3.95	4.33	4.17	4.31	4.44	4.42
Percent survival	91.03	94.28	89.00	93.17	91.91	89.29	94.00	94.15
Number of accession	**66**	**2**	**200**	**40**	**12**	**98**	**90**	**77**

In summary, our results showed that there was a wide range of variation residing in the studied materials at regional and within region levels. Therefore, future germplasm collection should concern all levels of variation. The enormous variation would continue to provide breeders with good opportunities for breeding and selection. In conclusion, the current study revealed the pattern of population structure and genetic diversity of barley genotypes sampled from landraces as well as cultivars from Ethiopian. The study also identified potential germplasm for improvement of agronomic and quality traits particularly for the Ethiopian barley-breeding program.

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References

Addisu, F. and Shumet, T. (2015). 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**): 68-76.

Bekele, B., Abraham, A., Kumari, S.G., Ahmed, S., Fininsa, C. and Yusuf, A. (2018). Ethiopian barley landraces: useful resistant sources to manage Barley yellow dwarf and other foliar diseases constraining productivity. *Eur J Plant Pathol* https://doi.org/10.1007/s10658-018-01644-4.

Chakravorty, A., Ghosh, P.D. and Sahu,P.K. (2013). Multivariate Analysis of Phenotypic Diversity of Landraces of Rice of West Bengal. *American Journal of Experimental Agriculture* **3**(1): 110-123.

Demissie, A., Bjornstad, A. and Kleinhofs, A. (1998). Restriction fragment length polymorphisms in landraces from Ethiopia in relation to geographic, altitude, and agro-ecological factors. *Crop Sci*. **38**: 237-243.

Dido, A.A., Singh, B.J.K., Degefu, D.T., Tesfaye, K.and Krishna, M.S.R. (2020). Diversity and resistance components analysis of barley landraces to barley shoot fly (*Delia flavibasis*). *Journal of Plant Diseases and Protection.* https://doi.org/10.1007/s41348-020-00364-4

Federer, W.T. and Ragavarao, D. (1975). On Augmented Designs. *International Biometric Society* **31**: 29-35.

Hadado, T.T., Rau, D., Bitocchi, E. and Papa, R. (2009). Genetic diversity of barley (*Hordeum vulgare* L.) landraces from the central highlands of Ethiopia: comparison between the Belg and Meher growing seasons using morphological traits. Genetic Resource Crop Evolution **56**: 1131-1148.

Hailu, A., Alamerew, S., Nigussie, M.and Assefa, E. (2016). Genetic variability, heritability and genetic advance for yield and yield related traits in barley (*Hordeum vulgare* L.) germplasm. *World Journal of Agricultural Sciences* **12**(**1**): 36-44.

IPGRI, (1994). Description of barley (*Hordeum vulgare* L.). International Plant Genetic Resources Institute (IPGRI), Rome, Italy.

Kebede, A, Kang, M.S. and Bekele, E. (2019). Advances in mechanisms of drought tolerance in crops, with emphasis on barley. *Advances in Agronomy* **156**: 265-314.

Muller, J. (1991). Determining leaf surface area by means of linear measurement in wheat and triticale (brief report). *Archiv Fuchtungsforsch* **21**: 121-123.

Shah, S.J.A., Hussain, S., Ahmad, M., Farhatullah, A.I. and Ibrahim, M. (2011). Using leaf tip necrosis as a phenotypic marker to predict the presence of durable rust resistance gene pair Lr34/Yr18 in wheat. *Journalof General Plant Pathology* **77**:174-177.

Sharma, G.C., Jotwani, M.G. Rana, B.S. and Rao N.G.P. (1977). Resistance to the sorghum shoot fly, *Atherigona soccata* (Rondani) and its genetic analysis. *J. Entomol. Res*. **1**: 1-12.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical Methods in Quantitative Analysis. Kalayani Publishers. New Delhi, pp 39-78.

Singh, R.P., Burnett, P.A., Albarran, M. and Rajaram, S.(1993). Bdv1: a gene for tolerance to Barley yellow dwarf virus in bread wheats. *Crop Science***33**:231-234.

Silvar, C., Casas, A.M., Kopahnke, D., Habekub, A., Schweizer, G., Gracia, M.P., et al. (2009). Screening the Spanish barley core collection for disease resistance. *Plant Breeding* **129**: 45-52.

Tahir, Z., Assefa, A., Sentayehu, A. and Gebresellasie, W. (2015). Phenotypic diversity in Ethiopian food barley (*Hordeum vulgare* L.) genotypes. *World Journal of Agricultural Sciences***12**: 308-314.

Yaynu, H. (2011). Response of Barley Landraces to Low-Moisture Stress in a Low-Rainfall Environment. In: Barley Research and Development in Ethiopia, Mulatu, B. and S. Grando (Eds.). International Center for Agricultural Research in the Dry Areas, Holetta, Ethiopia, pp: 47-56.

Woldeab, G., Fininsa, C., Singh, H., Yuen, J. and Crossa, J. (2007). Variation in partial resistance to barley leaf rust (*Puccinia hordei*) and agronomic characters of Ethiopian landrace lines. *Euphytica* **158**:139-151.

Zadoks, J.C., Chang, T.T. and Konzak, C.F. (1974). A decimal code for the growth stages of cereals. *Weed Research* **14**(**6**): 415-421.

Zhu, Y., Chen, H., Fan, J., Wang, Y. and Li, Y., et al. (2000). Genetic diversity and disease control in rice. *Nature* **406**: 718-722.

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