

POTENTIAL OF ETHIOPIAN BARLEY (*Hordeum vulgare* (L.)) LANDRACES as gene source for MALTING QUALITY TRAITS

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Abstract: Eighteen landraces of barley (*Hordeum vulgare* (L)) and one standard & one local check were evaluated in four replications using RCBD at Bekoji (7° 32'N and 39° 15'E at an altitude of 2,810 masl) with the objectives of studying the genetic variability in yield and yield-related traits and identify landrace lines with high malt quality traits for the breeding program. The ANOVA showed a very highly significant difference between the genotypes in all the agronomic traits studied which indicated the existence of genetic variability which can be exploited in the breeding program. A wide range of variability was observed in morpho-agronomic traits of the studied barley genotypes. Biological yield varied between 5.5 and 12.17 t/ha, grain yield between 2.31 & 5.28 t/ha, number of seeds per spike between 26.38-68.83, and harvest index 35.13-63.6%. Two landraces Netchgebs (5.13) and Mixed Bati (5.28) out-yielded the standard check, EH1847 (5.11 t/ha) indicating the possibility of identifying superior genotypes to be released as varieties or to be used as a parent in the crossing program. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 0.53-28.08 and 0.44-27.63, respectively. The lowest PCV and GCV (0.53 and 0.44) were obtained for germination capacity while the highest PCV and GCV (28.08 and 27.63) values were obtained for the number of seeds per spike. High broad-sense heritability (>85%) was observed for most of the morpho-agronomic and quality traits such as awn length, spike length, protein content, harvest index, extract content, biological and grain yield indicating that these traits are governed mainly by a genetic factor and direct selection can give rapid progress. Biological yield, days to maturity, harvest index, plant height, and flag leaf length had a positive correlation with grain yield both at the genotypic and phenotypic levels. Similarly, hectoliter weight, thousand kernel weight, sieve test, friability, malt moisture content, germination energy, and capacity had a positive correlation with malt extract content both at the genotypic and phenotypic levels. This study showed the potential of the Ethiopian barley landraces to develop high quality malt barley.

Keywords: Ethiopian Barley Landraces, Correlation analysis, Malt quality.

1. INTRODUCTION

Barley (*Hordeum vulgare* L.) is grown as a commercial crop globally and is considered one of the most important cereal crops in the world (Yousufinia *et al.*, 2013). It is the fourth in total cereal production in the world after wheat, rice, and maize (FAO, 2013). Ethiopia, owing mainly to its diverse agro-ecological and climatic features, is recognized as one of the twelve Vavilovian centers of diversity of crops in the world which includes irregular rowed barley (Vavilov 1951; Harlan 1969 in Tiegist *et al.*, 2010). Barley is Ethiopia's fifth most important cereal crop after teff, maize, sorghum, and wheat, with yearly estimated harvests of about 2.1 million tons from over 1 million hectares of land (CSA, 2018). Suitable barley growing environments in Ethiopia are the highlands ranging from 2300 to 3000 meters above sea level (m.a.s.l). Barley is grown in Oromia, Amhara, Tigray, and Southern Nations Nationalities and Peoples Regional States (SNNPRS) (Wondimu *et al.*, 2014). In Ethiopia, research on barley improvement was started in the 1950s through the introduction of exotic germplasm and collections from local landraces to improve grain yield potential, and grain quality (Wondimu *et al.*, 2014).

The malt barley breeding program in Ethiopia is mainly used as a source of gene the European barley germplasm by importing with a bilateral agreement with European companies and CGIAR centers like ICARDA and CIMMYT (Mulatu and Grando, 2011). Till now the national barley breeding program released material from the crossing program and imported material from abroad (variety registration book). But not a single landrace variety was released as malt barley in the Ethiopian context even if Ethiopia is a center of diversity for barley (Vavilov 1951 and Harlan 1969). In the Ethiopian barley breeding program, the landrace genotypes use as a source of gene for resistance for leaf diseases (net blotch, scald, spot blotch) and BYDV (Bekele et al., 1997).

The existing high genetic variability in Ethiopian barley indicates the possibility of finding accession that can satisfy the quality standard of the malt barley set in the country. But until now extensive research activities was not done on Ethiopian barley concerning malt quality traits. This showed the importance of designing the experiment to study the genetic variability of the Ethiopian barley landraces on malt quality traits and identify potential lines for release and use as a parent for the malt barley crossing program of the country. Therefore, this work was designed and executed to study the genetic variability of the Ethiopian barley landraces for malt quality traits and identify potential landrace lines for the future breeding program in the country.

2. MATERIALS AND METHODS

Description of the study area

The Bekoji experimental site, is a sub-station of Kulumsa Agricultural Research Center, located in Arsi Zone at 7° 32'N and 39° 15'E. The station soil is classified as Eutric Nitosol, exhibiting a clay content of approximately 48.5% (Tanner *et al.*, 1993) and is relatively deficient in phosphorus with pH of 5.3. The site receives an annual average rainfall of 1020 mm which occurs from June-October. The station is situated at an altitude of 2,810 m.a.s.l. with an annual average temperature minimum of 8°C and maximum of 20°C, but the last 10 years average temperature minimum 4.095°C and maximum 19.5°C.

Experimental Material

The materials for this study consisted of a total of 20 genotypes of which 18 are landraces (accessions) collected from various districts of Arsi zone in south eastern Ethiopia and two released malt barley varieties. The landraces were collected and maintained by Kulumsa Agricultural Research Center. The original samples were collected from farmers' fields purposely.

Experimental Design and cultural practices

The field experiment was conducted at Bekoji, Arsi zone in 2014/15 using a randomized complete block design (RCBD) with four replications. Sowing was done by hand drilling at the rate of 100 kg ha⁻¹ in plots of 3 m² (2.5 m x 1.2 m) with six rows; 0.2 m between row spacing, 0.5m between plots and 1 m between blocks. The four middle rows with an area of 2 m² were harvested. Fertilizer application at a rate of 41 kg N as (Urea) ha⁻¹ and 46 kg P₂O₅ (Di -Ammonium Phosphate as (DAP)) ha⁻¹ at planting (100 kg DAP and 50 kg urea ha⁻¹) was used. Two hand weeding were done (18-20 and 35-40 days) after planting.

Data collection

Data were recorded for fourteen quantitative characters in the field using barley Descriptors (IPGRI, 1994) and nine quality parameters were assessed at Asella Malt Factory laboratory.

Data on plant height, number of tillers/plant, flag leaf length, awn length, spike length, number of fertile tiller and number of seed/spike were recorded from 10 randomly taken plants from each plot, and the average values were used for subsequent statistical analysis. Days to heading, days to maturity, stand %, 1000-kernel weight (TKW), biological yield, harvest index, grain moisture content, friability, hectoliter weight, wort color, germination energy, germination capacity, protein content, sieve test and grain yield/m² were determined on a whole-plot basis.

Data Analysis

To reveal the total variability present within the tested genotypes in randomized complete block design, ANOVA was conducted for all the characters evaluated as per Gomez and Gomez, 1984. For the analysis of variance, the following mathematical model was adopted.

$$Y_{ij} = \mu + \tau_i + r_j + \varepsilon_{ij}$$

Where, Y_{ij} is the observed value of genotype i on replication j , μ is the grand mean, τ_i the effect of the i^{th} genotype, r_j is the effect of j^{th} replication and ε_{ij} is the residual.

The data have been subjected to the analysis of variance using SAS software version 9.0 (SAS, 2002). Variance components and genetic parameters were computed using the same software. The phenotypic and genotypic correlation coefficient was calculated using the GENES statistical software (Cruz, 2013).

3. RESULTS AND DISCUSSIONS

Analyses of variance have been done for grain yield and other agronomic traits, biological yield, seed physical traits, and malting quality attributes. Phenotypic, genotypic, and environmental correlations have been computed between different pairs of quantitative traits. The results generated from these analyses are presented in the following sections.

Analysis of Variance

The analysis of variance for the thirteen characters studied is given in Table 1. All characters showed a very highly significant ($p < 0.001$) difference among the tested genotypes. The significance of genotypic difference indicates the presence of some genotypes with higher values for each of the characters among the tested entries.

The significance of genotype difference indicates the presence of variability for each of the characters among the tested entries. Germination energy, however; was highly significant at a 1% probability level. Similarly, previous studies on collections of barley landraces from different regions of the country indicated that significant variations existed for many of these traits like days to heading (DH), days to maturity (DM), flag leaf length (FLL), awn length (AL), spike length (SL), number of seeds per spike (NSS), plant height (PLH), and number of fertile tillers per plant (NFTP) Tiegist *et al.*, (2010). Berhane and Alemayehu (2011) also reported a large amount of variation between populations for days to heading, days to maturity, and plant height.

Table 1: Analysis of variance for grain yield and other agronomic traits in twenty barley landraces (genotypes) grown at Bekoji in 2014

Traits	Mean Squares			
	Replications	Genotypes	Error	CV (%)
	Df 3	19	57	
DH	10.3	57.04***	1.52	1.40
DM	6.37	78.8***	2.44	1.05
PLH	9.03	267.73***	4.88	1.80
AL	6.49	4.62***	0.75	5.72
FLL	7.66	19.61***	1.42	7.00
NSS	56.84	952.92***	30.53	10.05
SL	1.05	1.87***	0.21	5.52
NFTP	9.68	11.14***	3.00	14.78
NTP	16.28	15.31***	4.71	16.45
BY	0.62	11.54***	0.44	7.54
GMC	0.38	1.06***	0.13	2.60
GY	0.007	2.45***	0.0064	1.94
HI	31.35	261.54***	14.29	7.95

DH= Days to heading, DM= Days to maturity, PLH= Plant height, AL= Awn length, FLL= Flag leaf length, NSS= Number of seeds per spike, SL= Spike length, NFTP= Number of fertile tillers per plant, NTP= Number of tillers plant, BY= Biological yield, GMC= Grain moisture content, GY= Grain yield, HI= Harvest index.

***= Very highly significant at $P \leq 0.001$

Range and Means of Different Characters

The accessions called Mixed bati (5.28 t/ha) and Nech gebs (5.13 t/ha) better than the standard check EH1847 (5.1 t/ha) and the local check Holkr (4.58 t/ha). According to our objectives accessions Mixed bati and Sheneka fulfilled the malting quality parameters like hectoliter weight, thousand kernel weight, sieve test, germination energy, germination capacity, extract content, friability, malt moisture content, the color of wort, and protein content. These landraces are also attained

the minimum standards of the Ethiopian Standards Agency and Asella Malt Factory and can be advanced further in the breeding program for release as new varieties. The broad difference apparent among the barley landraces tested would provide ample opportunities for the genetic improvement of the crop through selection directly from the landraces and/or can be used in traits recombination through hybridization.

A wide range of values had been observed in morpho-agronomic traits of the studied barley genotypes (Table 2). Biological yield exhibited the widest range (6.67 - 12.67 t/ha) followed by grain yield (3.2 - 5.28 t/ha), number of seeds per spike (26.38 - 69.45), harvest index (35.13 - 63.59), plant height (104.5 - 136.25), and thousand kernel weight (36.55 - 66.05). This result is in agreement with that of Berhane *et al* (1997) who reported a wide range of variation for days to heading (96 - 116), days to maturity (137 - 174), plant height (80 -140), and grain yield (4202 - 5705 kg/ha) in an experiment conducted at Sheno.

Phenotypic and Genotypic Variations

The amount of genotypic and phenotypic variability that exists in a species is of utmost importance in breeding better varieties and in a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population (Burton and De Vane, 1953). The estimated variance component, phenotypic coefficient of variability (PCV), and genotypic coefficient of variability (GCV) of the characters studied at Bekoji are presented in Table 2.

In general, the PCV values were greater than GCV values among all characters investigated although the differences were small. This indicated that the environmental effect was small for the expression of most characters. Among all characters, higher GCV and PCV values (>10%) were observed for flag leaf length, number of seeds per spike, number of tiller per plant, biological yield, grain yield, harvest index, thousand kernel weight, friability, and color of wort. The lowest GCV and PCV values (<5%) were observed for extract content, germination capacity, germination energy, grain moisture content, days to heading, and days to maturity. Plant height, awn length, spike length, sieve test, hectoliter weight, malt moisture content, and protein content were showed intermediate (>5% and <10%) coefficients of variability. Among the big variations; the number of seeds per spike, biological yield, and grain yield had considerable variation than the other traits.

Table 2: Estimates of mean, range, variance components, and coefficients of variability, heritability, genetic advance and genetic advance as percent of mean of the twenty three characters studied at Bekoji in, 2014

Traits	Mean±SE	Range	σ^2_g	σ^2_e	σ^2_{ph}	GCV (%)	PCV (%)	h^2_b (%)	GA	GA as % Mean
DH	88.2±1.23	82.50-95.25	13.88	1.52	14.26	4.22	4.28	97.33	7.67	8.70
DM	148±1.56	142.25-156.50	19.09	2.44	19.70	2.94	2.99	96.91	9.00	6.06
PLH	122.55±2.2	104.50-136.25	65.97	4.86	67.18	6.63	6.69	98.19	16.73	13.65
AL	15.16±0.86	13.38-18.07	0.97	0.75	1.16	6.49	7.09	83.76	2.03	13.67
FLL	17.02±1.19	12.88-20.93	4.55	1.42	4.90	12.53	13.01	92.75	4.39	25.8
NSS	54.96±5.52	26.38-69.45	230.60	30.53	238.23	27.63	28.08	96.80	31.28	56.92
SL	8.38±0.46	6.8-9.4	0.41	0.21	0.47	7.67	8.15	88.55	1.32	15.81
NFTP	11.73±1.73	7.7-14.75	2.03	3.00	2.79	12.16	14.23	73.04	2.94	25.05
NTP	13.19±2.17	9.03-16.93	2.65	4.71	3.83	12.33	14.82	69.20	3.35	25.40
BY	8.81±0.66	6.67-12.17	2.77	0.44	2.88	18.91	19.28	96.18	3.43	38.96
GMC	13.76±0.36	12.85-14.77	0.23	0.13	0.27	3.51	3.74	87.94	0.99	7.23
GY	4.12±0.08	3.20-5.28	0.61	0.01	0.61	18.98	19.00	99.74	1.61	39.10
HI	47.57±3.78	35.13-63.59	61.81	14.29	65.38	16.53	17.00	94.54	16.20	34.04
ST	91.88±0.93	77.05-99.63	36.89	0.86	37.11	6.61	6.63	99.42	12.51	13.62
TKW	44.27±0.84	36.55-66.05	50.44	0.71	50.62	16.04	16.07	99.65	14.63	33.05
HLW	59.05±0.87	55.13-66.42	10.50	0.75	10.69	5.49	5.54	98.24	6.67	11.30
GE	97.94±0.71	96.75-99.00	0.20	0.50	0.32	0.45	0.58	61.11	0.91	0.93
GC	98.52±0.58	97.50-99.50	0.18	0.34	0.27	0.44	0.53	68.46	0.88	0.90
MMC	4.35±0.49	3.70-5.03	0.11	0.24	0.17	7.74	9.56	65.52	0.69	15.93
PC	10.60±0.47	8.29-12.64	0.86	0.22	0.91	8.74	9.01	94.06	1.91	18.01
FR	61.93±0.99	49.35-77.13	56.53	0.98	56.78	12.14	12.17	99.57	15.49	25.01
EC	75.38±0.81	70.43-78.90	3.02	0.65	3.18	2.30	2.37	94.90	3.58	4.75
WC	3.64±0.38	3.13-5.00	0.88	0.14	0.91	25.72	26.24	96.08	1.93	52.98

DH= Days to heading, DM= Days to maturity, PLH= Plant height, AL= Awn length, FLL= Flag leaf length, NSS= Number of seeds per spike, SL= Spike length, NFTP= Number of fertile tillers per plant, NTP= Number of tillers plant,

BY= Biological yield, GMC= Grain moisture content, GY= Grain yield, HI= Harvest index, ST = Sieve test, TKW = Thousand kernel weight, HLW = Hectoliter weight, GE = Germination energy, GC = Germination capacity, MMC = Malt moisture content, PC = Protein content, FR = Friability, EC = Extract content, WC = Wort color. σ^2_g = Genotypic variance, σ^2_e = Error variance, σ^2_{ph} = Phenotypic variance, GCV= Genotypic coefficient of variability, PCV=Phenotypic coefficient of variability, h^2_b = Broad sense heritability, GA= genetic advance, GA % Mean= genetic advance as percent of mean.

Heritability

Estimated heritability for the characters studied is presented in Table 2. Heritability provides a numerical value to define the level of genetic and environmental effects on the expression of a trait. High heritability values indicate a high level of genetic variance as a component of the total variance. The genotypic variance (σ^2_g) accounted for the highest proportion of the total phenotypic variance (σ^2_p) as compared to the variances due to error (σ^2_e) in most of the traits studied (Table 2). This shows that the observed phenotypic differences were due to real genetic differences among the genotypes.

The heritability values were sufficiently high for most of the traits studied indicating the possibility of progress from selection in both the agronomic and malt quality traits. The high heritability values for most of the characters could be attributed to the favorable environment at the study site and the big difference between the genotypes in most of the traits. Moderate high heritability values were obtained for most of the traits studied including grain yields as reported by previous workers (ICARDA, 1990; Whan *et al.*, 1991; Desalegn *et al.*, 2000).

According to (Singh *et al.*, 1990), the heritability of a character is considered very high if the value is more than 80%, so selection for such a character should be fairly easy because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of the environment to phenotype. But for a character with low heritability, say less than 40%, selection may be considered difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Heritability is moderate when it is between 40 and 80%.

In this study high heritability traits were observed for grain yield (99.74%), thousand kernel weight (99.65%), friability (99.57%), sieve test (99.42%), hectoliter weight (98.24%), plant height (98.19%), days to heading (97.33%), days to maturity (96.91%), a number of seeds per spike (96.8%), wort color (96.08%), extract content (94.9%), harvest index (94.54%), protein content (94.06%), flag leaf length (92.75%), spike length (88.55%), grain moisture content (87.94%), and awn length (83.76%). Therefore, it can be assumed that the phenotypes of these traits are mainly determined by their genetic constitution than environmental factors. Similarly, moderate heritability was observed for germination energy (61.11%), malt moisture content (65.52%), germination capacity (68.46%), number of tillers per plant (69.2%), and number of fertile tillers per plant (73.04%). The heritability of malt barley traits is more influenced by genetic factors, indicating the possibility of a positive response for genetic gain and the fact that the barley collections are amenable to genetic improvement in the study area. Eshghi and Akhundova (2010) indicated that additive effects were important for protein content in the generation mean and variance analysis of barley material they have studied. Burton (1953) indicated that the genotypic coefficient of variability together with heritability estimates would give a clear picture about the extent of advance to be expected from selection

Genetic advance

The estimated genetic advance and expected genetic advance as percent of the mean for the characters considered at Bekoji in 2014 are presented in Table 2. Expected genetic advance as percent of the mean was generally high for most characters. Among the characters, the highest genetic advance as percent of mean was recorded for the number of seeds per spike, wort color, grain yield, and biological yield. Since the number of seeds per spike, wort color, grain yield, and biological yield had high genetic advance as percent of the mean and high heritability, they can be used as a selection criterion to improve grain yield and malt quality.

Character associations

Grain yield is the most complex trait and is influenced by many factors (known and unknown) that determine productivity. Therefore, understanding the inheritance and interrelationships of grain yield and characters influencing it is very important for formulating selection criteria. Thus, estimation of the correlations of grain yield with its components and among yield-related traits is essential to utilize the existing variability through selection. The analyses for the measured traits were performed using the GENES statistical software (Cruz, 2013).

Correlations of grain yield and yield-related traits

Correlations of grain yield and related traits are presented in Table 3. The characters studied were days to heading, days to maturity, flag leaf length, awn length, spike length, grain yield, number of seeds per spike, plant height, number of fertile tillers per plant, biological yield, harvest index, and grain moisture content.

Days to maturity, flag leaf length, awn length, plant height, number of tillers per plant, biological yield, grain moisture content, and harvest index had a positive correlation with grain yield t/ha both at the genotypic and phenotypic level. The genotypic correlations of grain yield t/ha with days to maturity (0.390 vs 0.385), flag leaf length (0.286 vs 0.265), biological yield (0.645 vs 0.635), and harvest index (0.437 vs 0.424) were slightly higher than their respective phenotypic correlation coefficients which are in agreement with the findings of Johnson *et al.* (1955) and Wasihun (2007) who explained their results of low phenotypic correlation due to the masking and/ or modifying effects of the environment on the phenotypic association among traits. Singh (1993) stated also that if the value of the genotypic correlation coefficient is higher than the phenotypic correlation coefficient, it means that there is a strong association between these two characters genetically but the phenotype value is lessened by the significant interaction of the environment. Alemayehu (2003) reported that grain yield was strongly and positively associated with plant height, spike length, number of heads per unit area, and harvest index. Grain yield t/ha was negatively correlated with days to heading, crop stand percent, spike length, and the number of seeds per spike both at the genotypic and phenotypic levels. Characters are also highly related among themselves as they are with yield. Positive and significant association of pairs of characters justified the possibility of correlated response to selection and the negative and significant correlations prohibit the simultaneous improvement of those traits (Singh *et al.*, 1990).

Days to heading was positively correlated with days to maturity, the number of seeds per spike, and plant height but negatively correlated with flag leaf length, spike length, and harvest index both at genotypic and phenotypic level (Table 3). Moreover, correlations of days to heading with these traits were greater than the corresponding phenotypic correlation, indicating the existence of a strong association. Similar to this Zaheer (2005) and Zaheer *et al* (2008) found that days to heading showed a significant positive relationship with days to maturity.

Plant height was positively correlated with days to heading, days to maturity, flag leaf length, awn length, number of tillers & fertile tillers per plant, biological yield and grain moisture content but negatively correlated with crop stand percent, number of seeds per spike, spike length and harvest index both at the genotypic and phenotypic level.

The biological yield was positively associated with days to heading, days to maturity, flag leaf length, awn length, number of seeds per spike, number of tillers & fertile tillers per plant but negatively correlated with crop stand percent, spike length, and harvest index. Harvest index was positively associated with crop stand percent, spike length, and grain moisture content, but negatively associated with days to heading, days to maturity, flag leaf length, awn length, number of seeds per spike, plant height, number of tillers & fertile tillers per plant and biological yield at both genotypic and phenotypic level.

Table 3: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among fourteen traits of 20 barley genotypes studied at Bekoji in 2014

	DH	DM	STD	FLL	AL	SL	NSS	PLH	NTP	NFTP	BY	GY	GMC	HI
DH		0.716**	-0.130	-0.103	-0.037	-0.325	0.552	0.421	0.472	0.506	0.434	-0.021	0.141	-0.519
DM	0.696**		-0.289	0.316	0.147	-0.609*	0.297	0.409	0.498	0.331	0.723**	0.390	0.578	-0.360
STD	-0.120	-0.272		0.033	0.372	0.673*	0.375	-0.506	-0.349	-0.190	-0.430	-0.364	-0.384	0.066
FLL	-0.018	0.286	0.057		0.343	-0.457	-0.212	0.048	-0.083	-0.205	0.287	0.286	0.581	-0.062
AL	-0.028	0.134	0.382	0.328		0.023	0.181	0.349	0.163	0.302	0.343	0.026	-0.138	-0.389
SL	-0.312	-0.592**	0.646**	-0.397	0.041		0.370	-0.697*	-0.401	-0.305	-0.585	-0.369	-0.577	0.241
NSS	0.536**	0.295	0.367	-0.179	0.172	0.362		-0.260	-0.223	-0.146	0.057	-0.291	-0.396	-0.390
PLH	0.355	0.333	-0.403	0.887**	0.250	-0.581**	-0.201		0.481	0.490	0.774**	0.558	0.432	-0.254
NTP	0.379	0.401	-0.257	-0.047	0.140	-0.334	-0.176	0.370		0.898**	0.486	0.273	0.472	-0.230
NFTP	0.420	0.281	-0.141	-0.149	0.247	-0.262	-0.111	0.401	0.894**		0.325	-0.040	0.201	-0.435
BY	0.416	0.691**	-0.402	0.253	0.322	-0.565**	0.055	0.625**	0.413	0.270		0.645**	0.620*	-0.391
GY	-0.021	0.385	-0.353	0.265	0.022	-0.362	-0.288	0.476*	0.232	-0.030	0.635**		0.780**	0.437
GMC	0.141	0.527**	-0.368	0.511*	-0.131	-0.532**	-0.371	0.343	0.328	0.116	0.574**	0.727**		0.206
HI	-0.493**	-0.336	0.056	-0.046	-0.363	0.233	-0.376	-0.185	-0.207	-0.361	-0.416	0.424	0.181	

DH = days to heading, DM = days to maturity, STD = crop stand percent, FLL = flag leaf length, AL = awn length, SL = spike length, GY = grain yield, NSS = number of seeds per spike, PLH = plant height, NFTP = number of fertile tillers per plant, BY = biological yield, HI = harvest index and GMC = grain moisture content, * = p < 0.05 ** = p < 0.01.

4. SUMMARY AND CONCLUSION

Eighteen barley landraces collected from different districts of Arsi zone, Oromia region, along with one standard and one local check were tested in RCBD with four replications at Bekoji during the 2014 main growing season (June – December). The Analysis of variance showed very significant differences among the tested genotypes for all traits considered in the study. A wide range of values was observed in morpho-agronomic traits of the studied barley genotypes.

The phenotypic coefficient of variability was greater than the genotypic coefficient of variability, with a small difference between them. This indicated that the environmental effect was small for the expression of most characters. Flag leaf length, number of seeds per spike, number of tillers per plant, number of fertile tillers per plant, biological yield, harvest index, and grain yield had high phenotypic and genotypic coefficients of variability.

The results from this study showed that there was a moderate to a high level of heritability for all traits. The broad-sense heritability estimate ranged from 61.11% for germination energy to 99.74% for grain yield. By selecting appropriate parents, genetic improvement can be achieved in all these traits. Grain yield was positively correlated with biological yield, days to maturity, harvest index, awn length, plant height, number of tillers per plant, and flag leaf length.

The result of this study showed that the potential of the Ethiopian barley landraces for malt barley traits and can be used in the breeding program. Besides, there is a possibility of selecting landrace lines with good malt quality traits for direct release.

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