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Genetic Variability and Character Association in Some Ethiopian Food Barley (*Hordeum vulgare* L.) Genotypes

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Abstract: Ethiopia is considered as one of the richest genetic resources centers in the world. The present study was conducted on thirty six food barley genotypes to estimate the genetic variability, broad sense heritability and genetic advance. The genotypes were grown in a simple lattice design at Holetta and Debark, Ethiopia. Data were collected on 11 morpho-agronomic quantitative characters. The analysis of variance at each location revealed highly significant ($p \leq 0.01$) to low significant ($p \leq 0.05$) difference for all the characters, except productive tillers in both testing locations. This indicated the existence of variability and hence the potential for selection and improvement for those characters. The mean performance of the genotypes indicated that IBON9045/05 at Holetta and BIFTU at Debark gave higher grain yield than the other genotypes. Grain yield, biomass, thousand kernel weight and kernel number per spike at Holetta were found to have high genetic advance as percent of mean with moderate heritability and genotypic coefficient of variability. At Debark, biomass, grain yield, harvest index and kernel number per spike have moderately high genotypic coefficient of variability with moderate heritability and high genetic advance as percent of mean. This means that effective and satisfactory selection for improvement of these important traits is possible. The present study generally implied the presence of significant genetic variability among the tested genotypes suggesting there is an opportunity to bring about improvement through direct selection and hybridization.

Key words: Character Association · Ethiopian Barley · Genetic Advance · Heritability

INTRODUCTION

Ethiopia, with its diverse agro-ecological and climatic features, is well known for being one of the 12 Vavilovian Centers of Diversity [1]. The altitudinal variation ranges from 110 m below sea level in areas of Kobar Sink to 4, 620 m.a.s.l. at Ras Dashen. Temperature and rainfall differences coupled with edaphic factors create a wide range of ecological conditions in the country. This complex topography and environmental heterogeneity provides a sustainable environment for a wide range of life forms. As a result, Ethiopia is considered as one of the richest genetic resources centers in the world. Crop plants such as coffee and tef (*Eragrostis tef*), a staple small cereal grain, are also known to originate in Ethiopia [2].

In Ethiopia, barley is produced mainly for human consumption and is one of the most important staple food crops. Barley grain is used in a diversity of recipes and deeply rooted in the culture and tradition of people's diets. The main cropping season, known locally as *meher,* relies on June-September rainfall, while the minor cropping season, known as *belg,* is during the short rainy season, March-April [3].

Early efforts in studying the agro-morphological variability of Ethiopian barley indicated the existence of a wide morphological variation. Since late 1960's, the breeding program besides hybridization and selection to develop varieties extensively used landraces and exotic germplasms and several hulled barley varieties have been released to farmers. Although some efforts to improve hull-less barley were made, it was found to have

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a generally lower kernel weight and were more susceptible to diseases than the hulled barley and no improved varieties of hull-less barley have been released [4]. The national average yield of barley is (1.4 t/h) which is still much below the world average (5.5t/h) [3]. Therefore, there is a need to improve the barley productivity in Ethiopia, by identifying barley varieties with desirable characteristics.

Knowledge regarding the amount of genetic variation in germplasm arrays and genetic relationships between genotypes are important considerations for efficient conservation and utilization of germplasm resources [5-7]. In the context of plant improvement, this information provides a basis for making decisions regarding selection of parental combinations that will maximize gain from selection and maintain genetic diversity. Farmers through centuries of experience have identified different landrace cultivars for each system of production and these cultivars are recognized by different local names. The lack of study of these landraces adapted to specific ecological conditions and utilized in the national breeding programs has been a concern of researchers, agricultural development workers and decision makers. The use of local landraces adapted to specific environments is still a topic of discussion at different forums because breeding for wide adaptation did not lead to desired objectives, especially in a country like Ethiopia where the diversity in barley growing environments is tremendous. There are still limitations to providing improved varieties adapted to specific environments and landraces are almost the sole sources of seed in the case of north Shewa for instance [8]. Some of the major food-barley production constraints are: low-yield capacity of farmers' varieties (landraces) and an inadequate number of improved varieties adapted to the different and varied agro-ecological zones of Ethiopia; lack of appropriate production practices (cultural practices and soil fertility management). In addition, biotic stresses such as disease (scald, net blotch, spot blotch and leaf rust), insect pests (Russian wheat aphid, barley shoot fly and chaffer grub) and weeds also contribute to the low yield performance of genotypes [9]. Therefore, the present study was conducted to estimate the extent of genotypic and phenotypic variability, heritability (in the broad sense) and genetic advance expected under selection.

MATERIALS AND METHODS

Description of the Study Area: The experiment was conducted in the 2010 main cropping season at two locations, namely, Holetta Agricultural Research Center (HARC) and Debark Agricultural Research Sub Center (DARSC). Holetta Agricultural Research Center (9° 3' N and 38° 30' E) is located 39 km west of Addis Ababa. It is one of the research centers known for highland crops and located at an altitude of 2400 m.a.s.l with annual average rainfall of 1274 mm most of which falling between March and October with peaks in July and August. The temperature ranges from 22°C to 7°C and the soil type is classified as Nitisol and Vertisol with a pH of 4.92.

Debark Agricultural Research Sub Center (DARSC) (14° 49' N and 37° 75' E) is located 830 km from Addis Ababa. It is a sub center of Gondar Agricultural Research Center located at an altitude of 2900 m.a.s.l with annual average rainfall of 1044mm most of which falling between April and September having peaks in July and August. The temperature ranges from 19.8°c to 8.6°c and the soil type is classified as cambisol.

Experimental Material: Twenty six released and 10 in pipe line food barley genotypes representing the germplasm of the crop were considered in this study. Descriptions of the genotypes are shown in Table 1.

Experimental Design and Trial Management: The experiment was laid out in 6 x 6 a simple lattice design with two replications. Each experimental plot measures 2.5m long and 1.2m wide. There were six rows on each plot with 0.2m row spacing. The middle four rows were used ($2m^2$ area) for data collection. In this study, fertilizer was applied at rate of 41 kg/h and 46 kg/h P_2O_5 and other crop management practices were undertaken as per the recommendation.

Data Collected

Plot Basis: Days to heading, Days to maturity, Grain filling period, Biomass yield (Kg/plot), Grain yield (Kg/plot), Harvest index (HI), Thousand -Kernel weight (g)

Plant Basis: Tiller number per plant, Plant height (cm), Spike length (cm), Kernel number per spike.

Statistical Analysis

Estimation of Genetic Parameters: Genotypic (V_g) and phenotypic (V_p) components of variances and coefficients of variation were estimated by the following formula [10]:

Genotypic variance

$$V_g = [MSG - MSE/r]$$

Table 1: Barley genotypes used in the experiment

Code no.	Genotype	Pedigree (Selection)	Source
1	HB- 1307	EH-1700/F71.B1.63	HARC
2	Dimtu	3369-19	HARC
3	Shege	3336-20	HARC
4	Tolese	Tolese	HARC
5	EH1642	EH1642	HARC
6	HB-42	-	HARC
7	ARDU12-60B	-	HARC
8	4748-16	MEZEZO	DBARC
9	4731-7	BASO	DBARC
10	Misrach	KULUMSA1/88	DBARC
11	Shedeho	3381-01	SARC
12	Yedogit	BI95IN 198	SARC
13	Estayish	218963-4	SARC
14	Trit	215235-2	SARC
15	Agegnehu	218950-08	SARC
16	Bentu	EMBSN5TH	KARC
17	IBCB-5/76/06	-	-
18	Mulu	3371-03	AARC
19	Setegn	3369-17	AARC
20	Abay	3357-10	AARC
21	Tilla	EMBSN 14/98	AARC
22	Guta	-	-
23	Biftu	SHASHO#22 Go-1(sn98B)	SARC
24	Dafo	ARUSO(42)4(sn99G)	SARC
25	Dinsho	WADAGO-4	SARC
26	Harbu	ARUSO	SARC
27	ACC.#220718	-	ICARDA (in pipe line)
28	IBON9163/05	-	ICARDA (in pipe line)
29	IBON9156/05	-	ICARDA (in pipe line)
30	BYT909//05	-	ICARDA (in pipe line)
31	IBON9045/05	-	ICARDA (in pipe line)
32	IBON9090/05	-	ICARDA (in pipe line)
33	IBON9098/05	-	ICARDA (in pipe line)
34	IBYT914/05	-	ICARDA (in pipe line)
35	IBON9114/05	-	ICARDA (in pipe line)
36	IBON9135/05	-	ICARDA (in pipe line)

HARC= Holetta Agricultural Research Center. DBARC= Debre Birhan Agricultural Research Center. SARC= Sirinka Agricultural Research Center. KARC= Kulumsa Agricultural Research Center. AARC= Adet Agricultural Research Center. SARC= Sinana Agricultural Research Center. ICARDA=International Center for Agricultural Research in the Dry Areas

Phenotypic variation

$V_p = [MSG/r]$

where MSG = mean squares of genotypes, MSE = mean squares of error and and *r* =number of replications.

Genotypic coefficient of variability (GCV)

$$GCV = \left(\sqrt{V_g}/x\right)X100$$

Phenotypic coefficient of variability (PCV)

$$PCV = \left(\sqrt{V_p}/x\right)X100$$

where Vp, Vg and x are the phenotypic variances, genotypic variances and grand mean,

Heritability (H^2) in the broad sense was computed for each character [11] as follows:

where σ^2_G and σ^2_P are genotypic and phenotypic variance components respectively,

Genetic Advance (GA): Expected genetic advance and GA as percent of the mean assuming selection intensity of 5% was computed [12].

where: GA = expected genetic advance, K = is a constant (k = 2.056 at 5% selection intensity) and σ_p= is phenotypic standard deviation on mean basis.

Genetic advance (as % of mean) (GAM) was computed to compare the extent of predicted genetic advance of different traits under selection using the formula:

$$GAM = \frac{GA}{(x)} X100$$

where: x = mean of the quantitative character and GAM = genetic advance as percent of mean

Principal Component Analysis: PCA is defined as a method of data reduction to explain the relationships between two or more characters and to divide the total variance of the original characters into a limited number of uncorrelated new variables [13]. This will allow visualization of the differences among the individuals and identify possible groups. The general formula to compute scores on the first component extracted (created) in a principal component analysis

$$Pc1 = b\backslash 11(X1) + b\backslash 12 + \ldots b1p(Xp)$$

where, PC1 = the subject's score on principal component 1 (the first component extracted),
b1p = the regression coefficient (or weight) for observed variable p, as used in creating principal component 1and
Xp = the subject's score on observed variable p.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA): The analysis of variance for Holetta is given in Table 2. At Holetta, the analysis of variance revealed highly significant ($p \leq 0.01$) difference for days to heading, grain filling period; days to maturity, plant height, spike length, kernel number per spike, biomass, grain yield and thousand-kernel weight among genotypes. Difference for harvest index was also significant ($p \leq 0.05$). However, productive tillers showed non-significant differences among genotypes. The significant differences among genotypes indicated the existence of variability among the genotypes considered in this study. At Debark, the analysis of variance showed highly significant differences for days to heading, grain filling period, days to maturity, spike length, kernel number per spike, biomass, harvest index and grain yield. Plant height and thousand-kernel weight also revealed significant difference among genotypes. This shows that there is high genetic variability among genotypes (Table 3). On the other hand, differences among genotypes for productive tillers were non-significant indicating that genotypes have the same performance for productive tillers at both locations.

Phenotypic and Genotypic Variations: At Holetta, the amount of genotypic and phenotypic variability that exists in a species is of utmost importance in breeding for better varieties. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population [10]. At Holetta, the present finding showed that the magnitude of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all characters studied similar to Debark. This indicates that the apparent variation was not only due to genotypes but also due to influence of environment which was also reported by other authors [14, 15].

Among the characters productive tillers, harvest index and biomass showed larger difference between genotypic and phenotypic coefficient of variation. This indicated that, the great influence of environment on these characters (Table 4). However, minimum difference between phenotypic and genotypic coefficients of variation was observed for the rest of the characters. According to previous work [16] the PCV and GCV values are considered as low (<10%), medium (10-20%) and high (>20%). Accordingly, biomass and grain yield revealed high genotypic and phenotypic coefficients of variation.

This finding is in agreement with that of previous works [8, 17] which reported high values of GCV for grain yield and biomass. On the other hand thousand kernel weight, kernel number per spike and harvest index showed medium GCV and highest PCV values. Genotypic and phenotypic coefficient of variation values suggests that there is a good scope for yield improvement through phenotypic selection for the characters. Among characters days to heading, grain filling period, plant height, spike length and productive tiller per plant indicated lowest GCV values. This implies in the phenotypic expression of these traits, the effect of genotypic factors is low. Therefore, the low GCV values of these characters are not suggest for improving these trait through selection.

At Debark, all values of genotypic coefficient of variances are lower than the values of phenotypic coefficient variance. These indicated that the variations were not due to genotypes but also due to environmental

Table 2: Analysis of variance (ANOVA) of barley genotypes tested at Holetta

		Mean squares										
Source of variation	Df	DHE	GFP	DMA	PLH	SPL	PT/PL	KN/SP	BM	GY	HI	TKW
Replication	1	22.2*	5.0*	48.3**	4.6^{ns}	1^{ns}	0.01^{ns}	14.2^{ns}	17013889*	1121378^{ns}	16.9^{ns}	2.9^{ns}
Trt.(adj.)	35	89.5**	53.6**	35.3**	157.4**	1.1**	1^{ns}	113.2**	9949603**	1810332**	89.5*	53**
Block w/rep	10	9.9*	14.2^{ns}	8.1^{ns}	133.4**	0.4^{ns}	0.8^{ns}	52.8^{ns}	7580556**	799108**	32ns	36*
Intra b/error	25	4.3	8.5	5.7	44.9	0.4	0.6	29.5	2747222	290853	43.1	16.4
RCBD error	35	5.9	10.1	6.4	70.2	0.4	0.7	36.1	4128175	436069	39.9	22.1
R^2 (%)	-	97.5	91.7	91.5	88.3	84.8	75	88	89	93.7	80.3	85.7
Effic. (%)	-	118.1	106.9	103.1	131.3	100	101	108.9	127	126.8	92.6	116
CV (%)	-	2.9	6.2	2.1	6.9	7.9	14.7	13.1	17.8	17.7	20.3	11.8

*, ** indicates significance at 0.05 and 0.01 probability levels, respectively. DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height, Spl= Spike length, PTI/PL=Number of Productive tillers, KN/SP= Number of Kernels/ Spike, BMA=biomass, HI= Harvest Index and TKW=1000Kernel Weight. Trt.(adj= treatment adjusted, RCBD= randomized complete block design, Intra b/error = intra block error, Effic.= efficiency relative to RCBD, CV= coefficient of variance and W/rep= with in replication.

Table 3: Analysis of variance (ANOVA) of barley genotype tested at Debark

		Mean squares										
Source of variation	Df	DHE	GFP	DMA	PLH	SPL	PT/PL	KN/SP	BM	GY	HI	TKW
Replication	1	1.1^{ns}	0.5^{ns}	0.1^{ns}	17.3^{ns}	0.5^{ns}	0.05^{ns}	11.7^{ns}	8890139**	578529^{ns}	14.3^{ns}	7.1^{ns}
Trt.(adj.)	35	23.5**	40.4**	49.5**	102**	1.1**	0.9^{ns}	71.3**	3435853**	995223**	80**	28**
Block w/rep	10	12.7^{ns}	19.6^{ns}	35.6^{ns}	109.7*	0.4^{ns}	0.58^{ns}	13.4^{ns}	3775139**	432818^{ns}	24.3^{ns}	64.8**
Intra b/error	25	6.4	15.9	16.9	49.9	0.34	0.72	10.4	1159639	263666	20.8	14.8
RCBD error	35	8.2	17	22.3	66.9	0.35	0.68	11.2	1906925	311995	21.8	29.1
R^2 (%)	-	88.7	80.8	86.6	84.8	84.6	73.1	92	88.2	79	78.6	86.2
Effic. (%)	-	111.9	101	114.4	116	100.7	94.7	101.7	137.3	106	100.6	161
CV (%)	-	3.4	8.7	3.4	7.1	7.7	19.7	7.3	10.9	12.4	10.8	9.8

*,** indicates significance at 0.05 and 0.01 probability levels, respectively. DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height, Spl= Spike length, PTI/PL=Number of Productive tillers, KN/SP= Number of Kernels/ Spike, BMA=biomass, HI= Harvest Index and TKW=1000Kernel Weight. Trt. (Adj= treatment adjusted, RCBD= randomized complete block design, Intra b/error = intra block error, Effic.= efficiency relative to RCBD, CV= coefficient of variance and W/rep= with in replication.

Table 4: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variation and genetic advance as percent of mean for characters of barley genotypes studied at Holetta 2010/11

Character	R/ge mean	Mean±SEM	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	ECV (%)	H^2 (%)	GA	GAM (%)
DHE	55.3-81.25	70.05 ± 2.07	42.6	4.3	46.9	9.3	9.7	2.9	90.8	12.9	18.5
GFP	39.3-59.4	46.9 ±2.9	22.5	8.5	31	10.1	11.8	6.2	72.5	4.6	9.8
DMA	112-125.5	117.01 ± 2.4	14.8	5.8	20.6	3.3	3.8	2.0	71.8	6.6	5.6
PLH(cm)	81.3-124.3	97.68 ± 6.7	56.2	44.9	101.1	7.6	10.3	6.8	55.5	11.4	11.6
SPL(cm)	6.6-9.75	7.96 ± 0.63	0.4	0.4	0.8	8.0	11.3	8.0	50.0	0.9	11.3
PTI/PL	3.5-7.0	5.4 ± 0.79	0.2	0.6	0.8	8.2	16.5	14.3	25	0.5	9.2
KN/SP	22.52-54.7	41.47 ± 5.42	41.8	29.5	71.3	15.5	20.3	13.1	58.6	10.1	24.3
BM(kg/h)	3803-3862	9277.7 ± 1657	3601190	2747222	6438412	20.4	27.1	17.8	56.7	2519.6	27.1
HI (%)	13.65-48.1	32.33 ± 6.56	23.2	43.1	66.3	14.9	25.2	20.3	34.9	5.8	17.9
TKW(gm)	22.2-49.5	34.44 ± 4.05	18.3	16.4	34.7	12.4	17.1	11.7	52.7	9.5	27.6
GY(kg/h)	982.3-5083	3040.1 ± 539	759739	290853	1050592	28.6	33.7	17.7	72.3	1523.5	50.1

R/ge mean=range of mean, SEM= Standard error of the mean, ^{2}g= Genotypic variance, ^{2}e = Environmental variance, ^{2}p= Phenotypic variance, H^2 (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean. DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height (cm), SPL= Spike length (cm), PTI/PL=Number of Productive tillers per plant, NK/SP= Number of Kernels per spike, BM=biomass (kg/h), GY= Grain yield (kg/h), HI= Harvest index (%), TKWt=1000Kernel Weight (gm)

Table 5: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variation and genetic advance as percent of mean for characters of barley genotypes studied at Debark 2010/11

Traits	Range of mean	Mean ±SEM	σ^2g	σ^2e	σ^2P	GCV (%)	PCV (%)	ECV (%)	H^2 (%)	GA	GAM (%)
DHE	67.47 - 86.95	75.23 ± 2.54	8.3	6.4	14.7	3.8	5.6	3.3	56.4	4.4	5.8
GFP	37.5- 56.5	45.91.± 3.98	12.5	15.9	28.4	7.7	8.6	8.6	42.2	4.5	10.0
DMA	112.42 – 132.88	121.15± 4.11	16.3	16.9	33.2	3.3	4.7	3.4	49.0	5.7	4.7
PLH	81.31 - 115.05	99.18± 7.06	26.0	49.9	75.9	5.1	8.7	7.1	34.2	6.1	6.2
SPL	6.0 - 9.0	7.61± 0.58	0.4	0.4	0.8	8.3	11.7	8.3	50.0	0.9	11.8
PT/PL	3.0- 6.0	4.3± 0.85	0.1	0.7	0.8	7.3	20.8	19.4	12.5	0.2	4.6
KN/S	31.0 - 60.0	44.07± 3.22	30.4	10.4	40.8	12.5	14.5	7.3	74.5	9.6	21.8
BM	7072.73 - 12373	9870±1076	1138107	1159639	2297746	10.8	15.3	10.9	49.5	1542	15.6
GY	3004.31 - 6129.5	4142± 513.5	365778	263666	6299444	15.6	18.1	12.3	58.1	947.6	22.8
HI	28.65 - 53.85	42.32± 4.56	29.6	20.8	50.4	12.8	16.7	10.7	58.7	8.5	20.1
TKW	31.0-47.15	39.24±3.84	6.6	14.8	21.4	6.5	12.0	9.8	30.8	2.9	7.4

SEM= Standard error of the mean, ^{2}g= Genotypic variance, ^{2}e = Environmental variance, ^{2}p= Phenotypic variance, H^2 (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation (%), GA= Genetic advance, GAM= Genetic advance as percent of mean. DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height (cm), SPL= Spike length (cm), PTI/PL=Number of Productive tillers per plant, NK/SP= Number of Kernels per spike, BM=biomass (kg/h), GY= Grain yield (kg/h), HI= Harvest index (%), TKWt=1000Kernel Weight (gm)

influence (Table 5). The characters like productive tiller per plant, biomass and thousand-kernel weight showed larger difference between genotypic coefficient of variance and phenotypic coefficient of variance indicating that a great influence of environment on these characters. Phenotypic coefficient of variation (PCV) was quite higher for grain yield per plant and number of grains per spike [18] in barley. But the present study indicated the PCV values of grain yield and kernel number per spike was not much higher than GCV values this impaling that the contribution of genotype for phenotypic expression was high.

Among characters days to heading, grain filling period, days to maturity, plant height, productive tiller per plant and spike length showed lowest GCV values as similar as Holetta. This implies that characters with low GCV values are not important for yield improvement through selection. However, characters like, kernel number per spike, biomass, grain yield, harvest index indicated moderately high GCV values impaling that the genotype contribution for phenotypic expression was high and less environmental influence on these characters. The genotypic variance at Debark was found to be relatively greater than its corresponding environmental variance days to heading, kernel number per spike, grain yield and harvest index this implies in the phenotypic expression of these traits, the effect of environmental factors is low.

Broad Sense Heritability and Genetic Advance: Heritability estimate for characters under study at Holetta is indicated in Table 4. According to a report of Singh [19] heritability values are classified as very high (≥ 80%), moderately high (60-79%), moderate (40-59%) and low (≤ 40%). At Holetta, days to heading (90.8%) indicated very high heritability while grain yield (72.3%) grain filling period (72.5%), days to maturity (71.8%)) revealed moderately high heritability. It was also reported high heritability estimates for grain yield which support the present findings [20, 21]. Heritability for the other characters was moderate except for productive tillers (25%) and harvest index (34.9%). This showed the environmental effect constitute a major portion of the total phenotypic variation [22].

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone [23]. Among the characters, productive tillers showed relatively low heritability and it has low value for genetic advance. Therefore, selection of superior genotypes based on this character would not be as effective as selection for days to heading, grain yield, kernel number per spike, biomass and thousand-kernel weight. This result is supported by another finding [24] for thousand-kernel weight.

At Holetta, genetic advance ranged from 5.6% for days to maturity to 50.1% for grain yield (Table 4). Expected genetic advance as percent of the mean was high for kernel number per spike (24.3%), biomass (27.1%), thousand kernel weight (27.6%) and grain yield (50.1%). Similar findings were, reported for kernel number per spike and thousand-kernel weight [17]. The rest of the characters indicated moderate genetic advance as percent

of mean while days to maturity, grain filling period and productive tillers per plant had low genetic advance as percent of mean. This low estimate of genetic advance as a percent mean arises from low estimate of genotypic variance.

Genetic coefficient of variation is not sufficient for determination of the extent of variation that perpetuate from one generation to the next. Genetic coefficient of variation coupled with heritability estimates would give a better picture of the extent of genetic advance that can be made through selection [25]. Low genetic advance indicates slight changes of improvement of these traits in subsequent generations [26, 27].

Among characters studied biomass and grain yield had high GCV, high genetic advance as percent of mean with moderate heritability. Thousand-kernel weight and Kernel number per spike indicated moderate GCV, heritability and high genetic advance as percent of mean. Hence, they can be used as a selection criterion, but ultimate evaluation must be in the target environment prior to using them. Other characters showed similar fashion except productive tillers. It has low values for measurement of all variables.

In general, days to heading showed the highest heritability with moderately high genetic advances percent of mean. On the other hand, grain filling period and days to maturity revealed that moderately high heritability but accompanied with low genetic advance as percent of mean. Therefore, selection may not be effective based on these traits. Among characters kernel number per spike, biomass, thousand kernel weight and grain yield sowed that moderate heritability with high genetic advance as percent of mean. Hence, selection based on these traits can be effective for further breeding purpose. Similarly, kernel number per spike, thousand-kernel weight and grain yield were also reported [28-30].

At Debark, broad sense heritability showed moderately high values for kernel number per spike (74.5%) (Table 5). Similar finding was reported in wheat which obtained high heritability for kernel number per spike [31]. Other characters such as days to maturity (49.0%), spike length (50.0%) and biomass (49.5%), grain filling period (42.2%), spike length (50.0%), grain yield (58.1%) and harvest index had moderate heritability values. Similar findings have been reported for characters like days to maturity, spike length, number of kernels per spike [20, 21] and have also reported high heritability in broad sense for most of these characters. Productive tillers (12.5.0%) and thousand-kernel weight (30.8.0%) and plant height (34.2%) indicated low heritability. The heritability value alone provides no indication of the amount of genetic progress that would result in selecting the best individual, but considering heritability estimates along with the genetic advance is more useful. The pattern of heritability is similar to that of Holetta but higher at Holetta than at Debark.

Genotypic coefficient of variation along with heritability would determine the extent of genetic advance that can be made through selection for estimating genetic gain under selection [25]. Based on this context, harvest index and grain yield characterized by moderately high genotypic coefficient of variation, moderately high heritability and high genetic advance as percent of mean can be considered for selection. Therefore, these characters are governed by additive gene effects and less influenced by environment at this location (Table 6). Similar findings were also reported [15, 31].

At Debark, the range of genetic advance as percent of mean ranged from 4.6% for productive tiller per plant to grain yield (22.8%). At this location, kernel number per spike (21.8%), grain yield (22.8%) and harvest index (20.1%) had high genetic advance as percent of mean. Spike length (11.8%), grain filling period (10.0) and biomass (15.6%) indicated moderately high genetic advance as percent of mean. The lowest genetic advance as percent of mean were observed for days to heading (5.8%), days to maturity (4.7%), plant height (6.2%) and thousand kernel weight (7.4%). Among the characters studied, kernel number per spike and grain yield had high genetic advance as percent of mean with moderate heritability and genotypic coefficient of variance at Holetta. Nevertheless, it is not always true that high estimates of heritability are always associated with high genetic gain [32]. Although days to maturity and days to heading, had moderate heritability, but the recorded genetic advance as percent of mean were lowest values among characters. Therefore, selection of superior genotypes based on this trait would not be effective for future breeding program under Debark environmental condition.

Generally, there was no appreciable difference between two locations as far as heritability and genetic advance as percent of mean is considered. Those traits with high heritability and genetic advance as percent of mean at Holetta exhibited same behavior at Debark. Moreover, having medium to low heritability and genetic advance at Holetta showed almost similar pattern at Debark.

Table 6: Eigenvectors, Proportion, Cumulative and eigenvalues of the first four principal components (PCs) of barley genotypes evaluated at Holetta and Debark 2010/11 Cropping season

Eigen vectors								
	Holetta				Debark			
Characters	PCA1	PCA2	PCA3	PCA4	PCA1	PCA2	PCA3	PCA4
DHE	0.418	-0.244	-0.046	0.123	0.254	-0.406	0.329	0.189
GFP	-0.254	0.328	0.390	-0.374	0.409	0.300	-0.220	-0.193
DMA	0.366	-0.015	0.379	-0.228	0.509	-0.019	0.039	-0.067
PLH	0.102	-0.422	0.533	-0.297	0.116	-0.459	0.294	0.364
SPL	0.044	-0.291	0.249	0.705	0.017	-0.009	0.528	-0.366
NT/PL	0.028	0.451	0.255	0.334	0.083	0.044	0.404	-0.647
KN/S	0.345	-0.148	-0.364	-0.174	0.187	0.063	0.351	0.215
BM	0.401	-0.018	0.160	-0.059	0.472	-0.021	0.057	-0.069
HI	0.304	0.406	-0.233	-0.066	0.858	0.555	0.283	0.342
TKW	0.235	0.380	0.273	0.234	0.366	-0.056	-0.132	0.003
GY	0.429	0.185	-0.059	-0.056	0.295	0.463	0.297	0.261
Eigen Value	4.38	1.98	1.52	1.15	3.15	1.98	1.46	1.18
Proportion	39.7	18.08	13.87	10.47	28.68	18.08	13.28	10.76
Cumulative	39.7	57.78	71.65	82.12	28.68	46.76	60.04	70.8

DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height (cm), SPL= Spike length (cm), PTI/PL=Number of Productive tillers per plant, NK/SP= Number of Kernels per spike, BM=biomass (kg/h), GY= Grain yield (kg/h), HI= Harvest index (%), TKWt=1000Kernel Weight (gm)

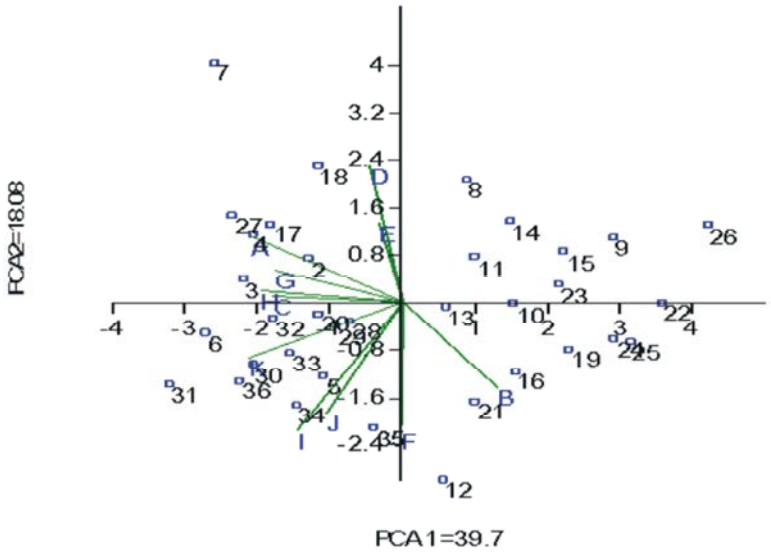

Fig. 1: Diagram showing the pattern among 36 barley genotypes based on the first two Principal components at Holetta. Genotypes codes are shown in Table 1

Principal Component Analysis: Eigenvectors, Proportion, Cumulative and eigenvalues of the first four principal components (PCs) of barley genotypes evaluated at Holetta and Debark are shown in Table 6. The variation studied through principal component analysis revealed that four principal components having greater than 1 eigenvalues contributed 82.12% and 70.8% of the total variation at Holetta and Debark, respectively. At Holetta, the relative magnitude of Eigenvectors from the first principal component (39.7%) characters that contributed more to the first principal component (vriables with largest coefficients) are days to heading, days to maturity and kernel number per spike, biomass, harvest index and grain (Figure 1, Table 6). From the second principal component, which contributed (18.08%) of the total variation, the most pre dominant characters which contributed positively are grain filling period, productive tillers, harvest index and thousand kernel weight. On the other hand, plant height contributed negatively to PCA2. The third principal component explained 13.87% of total variation. Among all positively contributing characters plant height, grain filling period and days to maturity contributed the

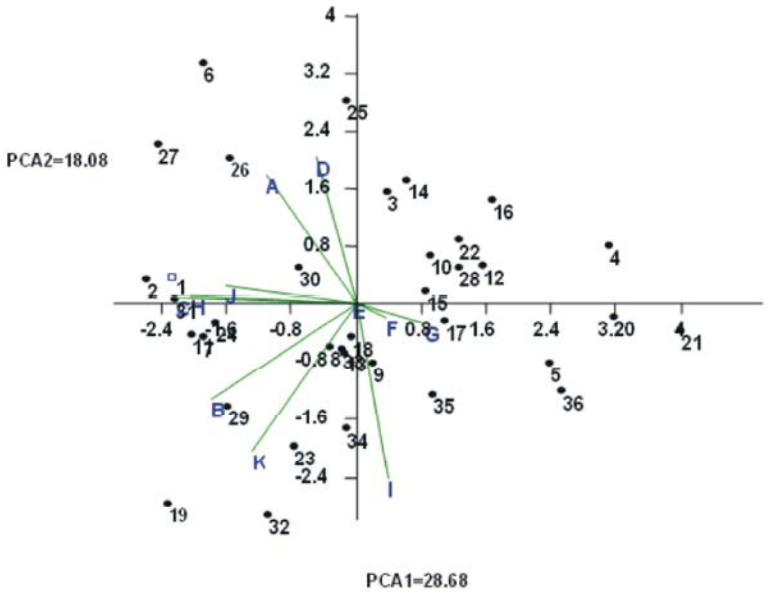

Fig. 2: Diagram showing the pattern among 36 barley genotypes based on the first two principal components at Debark. Genotypes codes are shown in Table 1

highest positive value respectively. Characters like kernel number per spike contributed more negative to PCA3. Similarly, 10.47% of the variation was accounted by the fourth principal components. Characters like spike length and productive tillers contributed more positive to PCA4. Grain filling period contributed more negative to PCA4.

At Debark, among the eleven principal component analyses only the first four PC had greater than 1 Eigen values and they contributed 70.8% of the total variation. Principal component 1 contributed 28.68% of the total variation (Figure 2). All characters contributed positively for principal component one. Among these traits grain filling period, days to maturity, biomass, harvest index and thousand-kernel weight contributed high positive values. Harvest index contributed the highest positive values among the entire characters.

The traits, which contributed more positively to PC2, were harvest index, grain yield per hectare and grain filling period (Table 6). Days to heading and plant height, which were, contributed negative direction to PCA2. The third principal component displayed 13.28% of the total variation. All traits contributed positively except grain filling period and thousand-kernel weight for PC3. Among positively contributed characters spike length, productive tillers per plant and days to heading contributed the highest positive values respectively.

The last and the fourth principal components contributed 10.76% of the total variation. Days to heading, plant height, kernel number per spike, harvest index, thousand-kernel weight and grain yield per plant contributed positively for PC4. Along with positively contributed characters plant height and harvest index had values that are more positive. Spike length and productive tillers contributed negatively. The negative value of spike length, productive tillers showed their negative association with other traits.

CONCLUSION

As evidenced by evaluation of yield and yield components, the performance of the genotypes under the study was higher at Debark than Holetta. At both locations, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) which indicates the observed variation was not only due to genotypes but also environment. The expected genetic advance as percent of mean varied from 5.6% for days to maturity to 50.1% for grain yield at Holetta and 4.6% for productive tiller per plant to22.8% for grain yield at Debark. At Holetta, productive tillers have low heritability and low genetic advance as percent of mean. Therefore, selection of genotypes based on this character would not be effective for yield improvement. Genotypic coefficient of variation with heritability would be determining the extent of genetic advance. Based on this context, kernel numbers per spike, harvest index and grain yield had moderately high GCV, broad sense heritability and high genetic advance as percent of mean

at Debark. Similarly, at Holetta kernel number per spike, thousand-kernel weight, biomass and grain yield indicated high GCV, with moderate heritability and the highest genetic advance as percent of mean. Therefore, these traits were governed by additive gene action and less influenced by environment. The principal component analysis and cluster diagram based on Euclidian dissimilarity using group average method indicated that there was high variability among genotypes. Therefore, this variability would be high potential for genetic improvement of food barley.

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