

Genetic variability and association of traits in Ethiopian barley (*Hordeum vulgare* L.) genotypes at Holetta, Central Ethiopia

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Abstract. Ethiopia is the secondary center for diversity of barley, and has a large number of accessions preserved in its gene bank. To determine the genetic variability and to assess the associations among morpho-agronomic characters, three hundred and twenty Ethiopian barley genotypes were evaluated in 2017 main-season at Holetta Agricultural Research Centre using 20 × 16 Alpha Lattice design. The analysis of variance showed that there were significant differences among the genotypes in all traits except for days to emergence, indicating the presence of genotypic variation among the studied genotypes. Out of 320, one hundred and twenty three genotypes gave significantly higher yield than the grand mean (2772.45 kg/ha) with yield advantage of best performing genotypes ranging between 145.98% for genotype Shege to 100.66% for genotype HB-1963. Grain yield, biomass yield and kernels per spike had high phenotypic and genotypic coefficients of variation. The estimates of broad sense heritability and genetic advance were high for days to heading and maturity and thousand kernels weight. Grain yield exhibited positive and highly significant correlations with days to heading and maturity, number kernels per spike, biomass yield, harvest index, thousand kernels and hectolitre weights. Path coefficient analysis revealed that biomass yield followed by seed harvest index had high and positive direct effects on grain yield and negative direct effect was exerted by days to heading and scald disease. Therefore, there is a high possibility of developing new varieties from these genotypes.

Keywords: Barley, character, genetic variability.

INTRODUCTION

Barley is the most important food crop domesticated about 7,000 BC from its wild relative, *Hordeum vulgare* ssp *spontaneum*, in the area of the Middle East known as the Fertile Crescent (Zohary and Hopf, 1993; Badr *et al.*, 2000). Ethiopia was first considered as the center of origin for cultivated barley, although later it was regarded as a secondary center of diversity because of the absence of the wild relative (Vavilov, 1951).

Barley is the fourth most important cereal crop in the world after wheat, maize and rice (FAO, 2016), while in Ethiopia, it is fifth in yield (ton ha⁻¹) after Teff, Maize,

Sorghum and Wheat with productivity of 2.16 ton ha⁻¹ (CSA, 2018). Barley is a staple food grain, especially in the highlands of Ethiopia. It is used for food (bread, "injera"), beverages (local beer), livestock feed, and the straw are used for thatched roofing in the countryside of Ethiopia (USDA, 2015). Barley is grown twice a year from August to December (main season) and from March to July (short season) in altitudes from 1800 to 3400 m. a. s. l. (Berhane *et al.*, 1996; Muluken, 2013).

Among cultivated cereals in Ethiopia, barley has a large number of accessions preserved in the Ethiopian gene

Table 1. Zones, altitude ranges and number of accessions of the collected barley germplasm.

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

bank, with over 15,300 samples. This is approximately 23% of the total landraces in the gene bank (Abebe, 2006). The large diversity of Ethiopian barley landraces could be due to the diversity in soils, climate, altitude and topography together with social and geographical isolation for long periods (Harlan, 1968). The wide ecological ranges of barley crop can generate a high potential for adaptive genetic diversity against abiotic and biotic stresses, which is an excellent genetic resource for crop improvement (Ellis *et al.*, 2000; Nevo 1992).

Studying the genetic variability among the Ethiopian barley genotypes is crucial for developing high yielding varieties to satisfy the food demand of the increasing population in the highlands facing decrease in cultivated land. However, the conserved genotypes must be utilized for crop improvement in order to tackle the future global food and nutritional security challenges. Therefore, this study was conducted with the objectives of evaluating the genetic variability among Ethiopian barley genotypes and assessing the association among morpho-agronomic plant characteristics.

MATERIALS AND METHODS

The experiment was conducted at Holetta Agricultural Research Centre, which is located at 9°00'N and 38° 30' E at an altitude of 2400 m above sea level. Holetta Agricultural Research Centre has mean annual rainfall of

1044mm, mean relative humidity of 60.6%, and mean maximum and minimum temperatures of 22.10 and 6.20°C, respectively. The soil of the experimental field is clay classified as Nitosol, which was characterized with pH of 6.2.

Experimental materials and design

A total of 320 barley genotypes including 27 released varieties and 293 pure lines collected from the representative barley growing Zones of Ethiopia were used for the study (Table 1).

The experiment was laid out in 20 × 16 Alpha Lattice Design with two replications, and each plot consisted of four rows spaced 0.2 m with 2.5 m length. The seed rate was 85 kg ha⁻¹ and fertilizers were applied during planting in the form of Urea and Diamonium phosphate (DAP) at the rate of 41 and 46 kg ha⁻¹ N and P₂O₅ respectively. The experiment was planted on 2017 planting time commonly practiced by farmers in the district and all field management practices were handled as required.

Data collection

Crop phenology like days to emergence (DTE), days to heading (DTH) and days to maturity (DTM) were counted from date of planting to 50% seedling emergence and

from date of emergence to 50% heading and 75% physiological maturity of plants in each plot respectively. The average plant height (PH) was measured from the ground to the tip of spikes of five main plants of the two middle rows of each plot. Disease scoring on barley leaf scaled and net blotch disease was assessed by visual examination using a scale of 0 to 9 according to (Saari and Prescott, 1975). Yield components such as fertile tillers per plant (FTP), spike length per plant (SLP) and kernels per spike (KPs) were determined from five random plants of the middle rows of each plot. After harvesting, indiscriminately counted thousand kernels weight (TKW) from each plot were weighted and adjusted to 12.5% standard grain moisture content of cereals, while hectoliter weight (HLW) was measured after drying the grain of each plot up to 12.5% moisture content. The total above ground biomass yield (BY) harvested from the middle two rows of each plot was dried out for some days under sun and then weighted. The grain yield (GY) was harvested from the middle two rows of each plot and adjusted to the standard grain moisture content (12.5%).

Analysis of variance (ANOVA)

Data were analyzed by restricted maximum likelihood (REML) to fit a mixed model with Genotypes, Replications and Blocks within replication as random effects. The REML model produced best linear unbiased predictors (BLUPs), which is a standard method for estimating random effects of a mixed model. PROC MIXED was conducted to estimate genotypes as well as residual variance components. The analysis of variance of quantitative traits was done using the general linear model:

$$Y_{ijk} = \mu + g_i + r_j + b_{kj} + \varepsilon_{ijk}$$

Where Y_{ijk} = the response of Y trait from the i^{th} genotype, grown in the k^{th} incomplete block of j^{th} replicate, μ = general mean, g_i = random effect of the i^{th} genotype, r_j = random effect of the j^{th} replicate, b_{kj} = random effect of k^{th} incomplete block in a j^{th} replicate, ε_{ijk} = experimental error.

Phenotypic and genotypic variance and estimation of broad sense heritability

The total phenotypic variance of each of the traits was partitioned into contributions due to genetic and non-genetic factors using the analysis of variance components method suggested by Singh and Chaudhury (1996). Genotypic variance and phenotypic variance were calculated as $\sigma^2_g = \frac{MS_g - MS_e}{r}$ and $\sigma^2_p = \sigma^2_g + \sigma^2_e / r$ respectively, where MS_g = mean squares of genotypes, MS_e = mean squares of experimental error, r = number of

replications, σ^2_p = phenotypic variance, σ^2_g = genotypic variance, and σ^2_e = error variance. Broad-sense heritability (H^2) is the proportion of phenotypic variance explained by genotypic variance. $H^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$.

Estimation of phenotypic and genotypic coefficient of variation

This is done using the following equations suggested by Singh and Chaudhury (1996).

$$PCV = (\sqrt{\sigma^2_p} / \bar{X}) * 100$$

$GCV = (\sqrt{\sigma^2_g} / \bar{X}) * 100$, where PCV = phenotypic coefficient of variation, σ^2_p = phenotypic variance, GCV = genotypic coefficient of variation, σ^2_g = genotypic variance and \bar{X} = the grand mean for the trait considered.

Phenotypic and genotypic correlation analysis

Estimation of genotypic and phenotypic correlations was done based on components of variances estimated from analyses of variance and co-variances, respectively (Dabholkar, 1992). Phenotypic correlation coefficient (r_p) = $Pcov_{xy} / \sqrt{(\sigma^2_{px} \cdot \sigma^2_{py})}$ and genotypic correlation coefficient (r_g) = $Gcov_{xy} / \sqrt{(\sigma^2_{gx} \cdot \sigma^2_{gy})}$, where $Pcov_{xy}$ = phenotypic covariance between variables x and y, $Gcov_{xy}$ = genotypic covariance between variables x and y, σ^2_{gx} = genotypic variance for trait X, σ^2_{gy} = genotypic variance for trait Y, σ^2_{px} = phenotypic variance for trait X and σ^2_{py} = phenotypic variance for trait Y.

The significance of phenotypic correlation coefficients was tested by the formula of Singh and Chaudhary (1996).

$$t' = r_{pxy} * \sqrt{\frac{g-2}{(1-rp^2xy)}}$$

t' value was tested against the tabulated t-value for (g-2) degree of freedom, where g is the number of genotypes studied, whereas the significance of genotypic correlation coefficient was tested using the formula described by

Robertson (1959) indicated as $t' = \frac{rg_{xy}}{SE_{g_{xy}}}$ and $SE = \sqrt{\frac{1-rg^2_{xy}}{2h_x \cdot h_y}}$,

where h_x = heritability of trait x, h_y = heritability of trait y, g = number of genotypes and rg_{xy} = genotypic correlation coefficient. Thus, the calculated value is compared with tabulated 't' value at g-2 degrees of freedom at 5% and 1% level of significance.

Path-coefficient analysis and expected genetic advance (GA)

Path coefficient analysis was computed to partition the

Table 2. Expected mean squares of some morphological and agronomic trait of barley genotypes grown at HARC, 2017.

Trait	Genotype (Df = 319)	Rep (Df = 1)	Block (rep) (Df = 38)	Error (Df = 281)	CV	Mean
DTE	0.07 ns	52.51 ns	0.13*	0.07	4.49	5.71
DTH	155.30**	954.41 ns	4.37*	3.64	3.16	60.29
DTM	176.54**	1154.69 ns	17.15 ns	16.37	3.97	101.90
SC	2.61**	13.86 ns	0.65**	0.53	11.13	6.56
N. Bloch	4.28**	12.80 ns	0.87**	0.79	17.57	5.05
FTP	0.77 **	16.83 ns	0.32**	0.28	11.80	4.48
SLP	1.73 **	110.30 ns	0.48**	0.39	8.72	7.18
PH	120.32 **	6177.08 ns	31.39**	23.19	4.60	104.79
KPS	266.79**	626.79ns	27.78**	25.24	14.67	34.23
GY	2400093.84**	19932974.00ns	266094.00*	242424.00	17.76	2772.45
BY	22638721.16**	741287174.00ns	4654534.00**	34832580.00	20.27	9203.91
HI	0.01**	0.36ns	0.03**	0.003	16.52	0.32
TKW	68.41 **	252.17 ns	5.61 ns	5.61	6.53	36.25
HLW	36.15 **	302.71 ns	10.87 ns	10.85	5.42	60.76

*, **=significant at 0.05 and 0.01 probability levels, ns= non-significant, Df= degree of freedom, DTE = Days to emergence, DTH = Days to heading, DTM = Days to maturity, SC = scald, N.Bloch= Net blotch, FTP = Number of fertile tillers per plant, SLP = Spike length (cm), PH = Plant height (cm), KPS = Number of kernels per spike, GY= Grain yield (kg/ha), BY= Biomass Yield(kg/ha), HI = Seed harvest index, TKW= Thousand kernel weight (g), HLW= Hectolitre weight (kg/hl),CV=coefficient of variation.

correlation coefficients to direct and indirect effects of the characters on yield as illustrated by Dewey and Lu (1959) using the formula $r_{ij} = P_{ij} + \sum r_{ik}p_{kj}$; where, r_{ij} =mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient, P_{ij} =component of direct effects of the independent character (i) on dependent character (j) as measured by the path coefficient and $\sum r_{ik}p_{kj}$ = summation of components of indirect effect of a given independent character (i) on the given independent character (j) via all other independent characters (k).

Genetic advance (GA) and genetic advance as percent of mean (GAM) were estimated with assumption that 5% of the genotypes was selected in accordance with the methods illustrated by Johnson *et al.* (1955).

$$GA = K * \delta_p * H \text{ and } GAM (\%) = \frac{GA}{\bar{X}} * 100$$

here, δ_p = phenotypic standard deviation on mean basis, H= Heritability in a broad sense, K =selection differential (where $k = 2.06$ at 5% selection intensity), \bar{X} = population mean of the quantitative character.

RESULTS AND DISCUSSION

Analysis of variance for some morpho-agronomic traits

The significant difference ($p < 0.01$) was observed among genotypes in all evaluated traits except days to

emergence (Table 2). This indicated the existence of significant genetic variability among the evaluated genotypes, and this in turn provides ample scope for selecting superior landraces to improve productivity of barley.

From the three hundred and twenty genotypes, one hundred and twenty three of them gave higher grain yields than grand mean (2772.45 kg/ha). Biomass yield exhibited the widest range (4341.17 to 18625.25 kg/ha) followed by grain yield (1402.32 to 6819.78 kg/ha), plant height (74.37 to 121.12 cm) and days to heading (41.49 to 87.07 days). Genetic diversity of barley has also been reported by Seid *et al.* (2015) which indicates that grain yield exhibited the widest range (2258 to 6202 kg/ha) followed by biomass yield per plot (1483 to 2733 g), plant height (82.9 to 118.1 cm) and days to maturity (110.3 to 137 days).

Genotypes Shege, HB-1307, Acc-24970, Acc-233040-A, HB -1966, HB - 42, Ardu 12-60B, Ahore 880/61, EH - 1847 and HB -1963 produced significantly higher grain yield than other genotypes (Table 3). These high yielding genotypes were emerged after 5.7 days. Their days to heading were ranged from 60.6 days for genotype EH-1847 to 80.1 days for genotype HB-42 and they were matured within 103.2 days for genotype EH-1847 to 117.2 days for genotype Shege. Their plant height was ranged from 99.96 cm for genotype EH-1847 to 117.32 cm for genotype Shege. The mean of best performing genotypes were showed that they were late for days to heading and maturity and taller than the remaining genotypes.

Severity of scald (SC) and net blotch (N. blotch) diseases was ranged from 2.78 for resistance genotype

Table 3. Mean of traits of top ten yielding barley genotypes grown at HARC, 2017.

Geno	DTE	DTH	DTM	SC	N.bloch	FTP	SLP	PH	KPS	GY	BY	HI	HLW	TKW
HB -1963	5.71	68.75	109.95	3.81	4.90	4.37	6.75	100.02	28.20	5563.37	14406.20	0.35	67.56	45.43
EH -1847	5.71	60.57	103.24	4.79	4.98	5.22	7.52	99.96	27.74	5571.93	14637.40	0.36	67.35	44.32
Ahore 880/61	5.72	71.10	116.68	4.22	5.04	4.51	4.94	107.71	52.53	5635.02	17296.00	0.33	62.90	44.51
Ardu 12-60B	5.71	75.31	114.46	3.55	5.06	5.31	7.31	115.20	54.08	5800.80	18625.80	0.32	63.80	37.31
HB – 42	5.71	80.05	117.12	2.78	4.98	4.11	6.88	113.67	52.42	5856.52	14222.50	0.38	63.30	50.05
HB -1966	5.71	65.47	111.99	4.93	4.76	4.67	6.33	111.17	43.82	5927.98	15259.90	0.36	60.78	41.19
Acc-233040-A	5.72	72.20	112.91	7.09	4.90	4.15	8.33	102.22	36.28	5951.85	15411.30	0.38	63.09	39.34
Acc-24970	5.71	65.50	112.19	4.73	5.39	4.68	5.99	106.91	43.49	6221.37	16511.50	0.35	62.47	43.03
HB-1307	5.71	65.51	111.30	3.00	5.04	5.28	6.87	109.09	44.66	6446.37	16392.70	0.36	64.21	41.19
Shege	5.71	76.78	117.23	5.53	4.90	4.34	8.47	117.32	54.48	6819.78	18103.90	0.35	60.65	41.74
Mean of best	5.71	70.12	112.71	4.44	4.99	4.66	6.94	108.33	43.77	5979.50	16086.74	0.35	63.61	42.81
Grand Mean	5.71	60.29	101.90	6.56	5.05	4.48	7.18	104.79	34.23	2772.45	9203.91	0.32	60.76	36.25
Mean of Landrace	5.71	59.70	101.12	6.69	5.06	4.48	7.19	105.01	33.98	2621.90	8913.21	0.32	60.42	35.65
Mean of released	5.71	66.81	110.49	5.31	5.01	4.48	7.19	102.51	37.00	4406.30	12358.45	0.35	64.37	42.71

Geno = Genotype , DTE = Days to emergence, DTH = Days to heading, DTM = Days to maturity, SC = scald, N.Bloch= Net bloch, FTP = Number of fertile tillers per plant(count), SLP = Spike length (cm), PH = Plant height (cm), KPS = Number of kernels per spike (count), GY= Grain yield (kg/ha), BY= Biomass Yield (kg/ha), HI = Seed harvest index, HLW= Hectolitre weight (kg/hl),TKW= Thousand kernel weight (g)

HB - 42 to 7.09 for susceptible genotype Acc-233040-A and from 4.76 for genotype HB -1966 to 5.39 for genotype Acc-24970 respectively.

The number of fertile tillers per plant was ranged from 4.11 for genotype HB - 42 to 5.31 for genotype Ardu 12-60B with mean of 4.48, and the spike length per plant (SLP) was ranged from 4.94 (cm) for genotype Ahore 880/61 to 8.47 (cm) for genotype Shege with mean of 7.18 (cm). The number of kernels per spike was ranged from 27.74 for genotype EH -1847 to 54.48 for genotype Shege with mean of 34.23, while the thousand kernel weight was ranged from 37.31 (g) for genotype Ardu 12-60B to 50.05 (g) for genotype HB-42 with mean of 36.25 (g)). The hectolitre weight of the grain of genotypes was ranged from 60.65 (kg/hl) for genotype Shege to 67.56 (kg/hl) for genotype HB -1963 with mean of 60.76 (kg/hl).

High variability in biomass yield, grain yield and harvest index of best performing genotypes was also observed. The biomass yield was ranged from 14222.50 (kg/ha) for genotype HB-42 to 18625.80 (kg/ha) for genotype Ardu 12-60B with mean of 9203.91 (kg/ha), and the grain yield was ranged from 5563.37 (kg/ha) for genotype HB-1963 to 6819.78 (kg/ha) for genotype Shege with mean of 2772.45 (kg/ha). Seed Harvest index was ranged from 0.32 for genotype Ardu 12-60B to 0.38 for genotype Acc-233040-A with mean of 0.32 (Tables 3).

The yield advantage of the best performing genotypes was ranged from 145.98% for genotypes Shege (6819.78 kg/ha) to 100.66% for genotypes HB-1963 (5563.37 kg/ha) from grand mean (2772.45 kg/ha) (Table 3). The mean performance of landrace as compared to released varieties shows that landraces were earlier by

7.11 and 9.37 days for days to heading and maturity respectively. Girma *et al.* (2015) had reported similar finding that improve varieties were late for days to heading and maturity as compared to farmers varieties

The severity of scald also show that landrace were more susceptible to disease than released varieties, as this was due to released varieties that were developed with the objective of resistance to scald in hot spot areas like Holeta. Landraces were taller and had weak straw than released varieties. The variation among the mean of spike length of landrace and released varieties showed no difference among them. Girma *et al.* (2015) had similar finding that most of the farmers varieties were tall with weak stem, which was the common character of the local farmers varieties and improved varieties were relatively short with strong stem. Variation in spike length among the

Table 4. Means, estimates of phenotypic (σ^2p), genotypic (σ^2g), and environmental variance (σ^2E); phenotypic (PCV) and genotypic (GCV) coefficients of variations, broad sense heritability (H^2), genetic advance (GA) and genetic advance as percentage of means (GAM) for various traits of barley genotypes grown at HARC, 2017.

Trait	Mean	σ^2e	σ^2g	σ^2p	σ^2E	H^2	PCV	GCV	GA	GAM
DTH	60.29	3.64	80.77	82.71	1.94	97.66	15.08	14.91	18.3	30.35
DTM	101.90	16.37	85.29	94.02	8.72	90.72	9.52	9.06	18.12	17.78
SC	6.56	0.53	1.10	2.89	1.79	38.10	25.91	15.99	1.33	20.34
N.Bloch	5.05	0.79	1.85	2.27	0.42	81.58	29.85	26.96	2.53	50.16
FTP	4.48	0.28	0.27	0.42	0.15	63.83	14.42	11.52	0.85	18.96
SLP	7.18	0.39	0.71	0.92	0.21	77.35	13.36	11.75	1.53	21.29
PH	104.79	23.19	51.73	64.08	12.35	80.73	7.64	6.86	13.31	12.70
KPS	34.23	25.24	120.77	133.38	12.62	90.54	33.74	32.10	21.54	62.92
GY	2772.45	242424.00	1160723.99	1291136.61	130412.61	89.90	40.98	38.86	2104.31	75.90
BY	9203.91	3483258.00	10682875.00	12625464.93	1942589.93	84.61	38.61	35.51	6193.44	67.29
HI	0.32	0.003	0.004	0.01	0.002	70.00	23.37	19.56	0.12	36.53
TKW	36.25	5.61	33.50	36.49	2.99	91.81	16.66	15.97	11.42	31.51
HLW	60.76	10.85	13.94	19.92	5.98	69.98	7.35	6.15	6.43	10.59

DTH = Days to heading, DTM = Days to maturity, SC = Scald, N.Bloch = Net bloch, FTP = Number of fertile tillers per plant (count), SLP = Spike length (cm), PH = Plant height (cm), KPS = Number of kernels per spike (count), GY= grain yield (kg/ha), BY= Biomass Yield(kg/ha), HI = Seed harvest index, TKW= Thousand kernel weight (g), HLW= Hectoliter weight (kg/hl).

farmers and improved varieties were small.

With regards to number of kernels per spike, landraces had lower number of seeds per spike than released varieties. The number of kernels per spike had relation with the final grain yield. The yield advantages of released varieties were 1.78 tones more than landraces. Biomass yield, harvest index, Hactoliter weight and thousand seed weight of released varieties were higher than landraces. Abteu *et al.* (2015) had similar finding that improved varieties that had higher grain yield than landrace. Acc-233040-A (5951.85kg/ha) and Acc-24970 (6221.37 kg/ha) had better grain yield than recently released variety HB-1966 (5927.98 kg/ha).

Phenotypic and genotypic variations

For almost all studied traits, the genotypic (σ^2g) and phenotypic (σ^2p) variance were larger than error variance (σ^2e) (Table 4). This indicated that the number of blocks within replication used in evaluating these genotypes were adequate to give a better estimation for the error variance. The estimated phenotypic variance (σ^2p) was higher than genotypic variance (σ^2g). A wide range of σ^2p was observed for biomass yield followed by grain yield and plant height, because these traits are quantitative traits which are highly influenced by environmental factors. The estimates of genotypic variance were higher than the corresponding environmental variance except for severity of scald diseases. This signified the existence of sufficient genetic variability among the studied genotypes for these traits (Table 4). Jaya (2017) had reported similar results which indicate that the estimates of phenotypic variance were higher than genotypic variance.

Phenotypic (PCV) and genotypic (GVC) coefficients of variation

GCV ranged from 6.15% for hectolitre weight to 38.86% for grain yield and PCV from 7.35% for hectolitre weight to 40.98% for grain yield (Table 4). The coefficients of variation revealed that, grain yield, biomass yield, net blotch disease, number of kernels per spike and scald disease had the highest variation. Such traits were the most indicative and responsive barley traits. Deshmukh *et al.* (1986) reported that genotypic and phenotypic coefficients of variation greater than 20% are considered as high. Jamshidi and Javanmard (2017) reported that grain yield, biological yield and harvest index had the highest rate of variation. Therefore these traits are essential for selecting superior barley genotypes. However, traits hectolitre weight and plant height had the least rate of variation and are not much suitable traits for selecting superior barley genotypes. The difference between PVC and GVC for scald diseases, number of kernels per spike, harvest index and biomass yield was large. This showed that the influence of the environment on their expression was large. The difference between PVC and GVC was small for days to heading and maturity, thousand-kernel weight and plant height. This indicated the existence of enormous inherent variability that remain less affected by environment, and useful for indirect selection of genotypes in improving barley genotypes. Jaya (2017) reported similar findings of GVC and PVC for barley genotypes, which indicates high estimates of variation that were observed for number of effective tillers per plant, spike length and biological yield. Low GCV and PCV were observed for days to flowering and maturity.

Broad sense heritability and genetic advance

Broad sense heritability was ranged from 38 for Scald disease to 98% for days to heading. Highest broad sense heritability was observed for days to heading, days to maturity, thousand-kernel weight, grain yield, scald diseases, number of kernels per spike, biomass yield, number of fertile tillers per plant, hectolitre weight, spike length, seed harvest index, plant height and Net blotch diseases.

Genetic advance as percent of mean (GAM) was estimated in order to determine the relative merits of different characters that could be further utilized in the selection program of crop improvement. According to Johnson *et al.* (1955), genetic advance as percent of mean was categorized as high (>20%), moderate (10 to 20%) and low (0 to 10). High GAM were obtained from grain yield, biomass yield, net blotch diseases, number of kernels per spike, harvest index, thousand-kernel weight, days to heading, spike length and scald diseases, while moderate were obtained for fertile tillers per plant, days to maturity, plant height and hectolitre weight (Table 4).

Relative comparison of heritability along with genetic advance as percent of mean of the traits indicated that days to heading, days to maturity, thousand kernel weight, grain yield, scald diseases, number of kernels per spike, biomass yield, number of fertile tillers per plant, hectolitre weight, spike length, harvest index, plant height and net blotch diseases had high heritability estimates along with high genetic advance as percent of mean. Jalal (2012) had reported that number of kernels per main spike, grain yield, biological yield, plant height, thousand kernels weight and number of fertile tillers per plant had high heritability accompanied with high genetic advance. Jaya (2017) also indicated that plant height, number of effective tillers, spike length, biological yield and grain yield had high heritability estimates along with high genetic advance as percent of mean.

Phenotypic and genotypic correlation of yield with other traits

Genotypic correlation coefficient values were greater for most of the traits than their corresponding phenotypic correlation coefficient values, indicating the inherent association of the traits.

Grain yield had positive and highly significant phenotypic correlation with days to heading, days to maturity, number of kernels per spike, biomass yield, thousand kernel weight and hectolitre weight. Additionally, grain yield had significant correlation with fertile tillers per plant, plant height, harvest index and spike length. Similarly at genotypic level, days to heading, days to maturity, number of kernels per spike, biomass yield, thousand kernel weight and hectolitre weight exhibited positive and highly significant correlation

with grain yield. Plant height, harvest index and spike length exhibited positive and significant genotypic correlation with grain yield (Table 5). This indicates that selecting for higher values of these traits could lead to grain yield improvement of barley. Zerihun (2007) reported that grain yield per plot had positive and highly significant association with days to heading, days to maturity, number of kernels per spike, biomass yield, harvest index and thousand kernel weight at both phenotypic and genotypic level. Jalal (2012) and Temesgen (2014) had also similar findings.

Genotypic path coefficient analysis

Genotypic path coefficient analysis revealed that biomass yield followed by seed harvest index had high and positive direct effects on grain yield. In addition to this, their association with grain yield was highly significant and positive (Table 6). Positive association and direct effect suggested that these traits were good contributors of grain yield and significantly help as selection criteria in barley breeding programs. The minimum direct effect was exerted by plant height, spike length, thousand kernel weight, hectolitre weight, days to maturity and number of kernels per spike and negative direct effect was exerted by days to heading and scald disease; but, had positive association with grain yield except scald disease at genotypic levels. Zerihun (2007) had similar report which stated that positive direct effect on grain yield per plot was exerted by harvest index per plot (0.65) followed by biomass yield per plot (0.64). Days to maturity, Days to heading, Thousand kernel weight, Hectolitre weight, Spike length and Number of kernels per spike (0.26) and scald disease(-0.54) and Seed harvest index(-0.38) had exerted positive and negative indirect effects respectively on grain yield through biomass yield.

CONCLUSIONS

Studying the genetic variability of plant germplasm, association of traits with grain yield and their heritability is the first step in plant breeding programs to select plants having the required characters. In this line, 320 barley genotypes were evaluated and the analysis of variance showed that there were significant differences among genotypes for all traits except days to emergence, which is mainly influenced by available soil moisture. Better phenological, yield and yield components responses of barley were observed from genotypes; Shege, HB-1307, Acc-24970, Acc-233040-A, HB -1966, HB - 42, Ardu 12-60B, Ahore 880/61, EH -1847 and HB -1963. Genotypic and phenotypic coefficients of variation were ranged from 6.15 % for hectolitre weight to 38.86% for grain yield and from 7.35% for hectolitre weight to 40.98% for grain yield, respectively. Broad sense heritability was in the range of

Table 5. Estimates of Phenotypic (below diagonal) and genotypic (above diagonal) correlation coefficients among various traits of barley genotypes grown at HARC, 2017.

Trait	DTH	DTM	SC	N.Bloch	FTP	PH	SLP	KPS	GY	BY	HI	TKW	HLW
DTH		0.89**	-0.47**	-0.06 ns	-0.14*	0.05 ns	0.14*	0.50**	0.51**	0.62**	-0.19**	0.36**	0.37**
DTM	0.86**		-0.46**	-0.02 ns	-0.12*	-0.01 ns	0.08 ns	0.52**	0.59**	0.65**	-0.14*	0.34**	0.38**
SC	-0.45**	-0.43**		0.05 ns	-0.07 ns	-0.1 ns	-0.02 ns	-0.26**	-0.59**	-0.53**	-0.02 ns	-0.32**	-0.25**
N.Bloch	-0.03 ns	-0.01 ns	0.01 ns		0.07 ns	0.05 ns	-0.01 ns	-0.03 ns	-0.03 ns	0.01 ns	-0.05 ns	-0.02 ns	-0.02 ns
FT	-0.08*	-0.06 ns	-0.10*	0.02 ns		0.11*	0.25**	-0.30**	0.09 ns	0.16*	-0.13*	0.16*	0.08 ns
PHT	0.07 ns	0.03 ns	-0.13*	0.04 ns	0.17*		0.32**	0.09 ns	0.14*	0.22**	-0.17*	0.11*	-0.04 ns
SL	0.16**	0.12*	-0.07 ns	0.01 ns	0.27**	0.38**		-0.26**	0.13*	0.30**	-0.30**	0.40**	0.22**
KPS	0.47**	0.49**	-0.24**	-0.02 ns	-0.23**	0.14*	-0.15*		0.31**	0.26**	0.04 ns	-0.38**	-0.11*
YLD	0.49**	0.56**	-0.53**	-0.02 ns	0.10*	0.18*	0.15*	0.31**		0.82**	0.18**	0.48**	0.38**
BM	0.58**	0.61**	-0.47**	0.01 ns	0.17**	0.28**	0.33**	0.25**	0.79**		-0.38**	0.48**	0.37**
HI	-0.2**	-0.17*	0.04 ns	-0.03 ns	-0.16*	-0.23**	-0.35**	0.01 ns	0.13*	-0.46**		-0.01 ns	-0.03 ns
TKW	0.32**	0.30**	-0.26**	-0.02 ns	0.10*	0.07 ns	0.28**	-0.36**	0.44**	0.39**	0.05 ns		0.51**
HLW	0.31**	0.32**	-0.19**	-0.05 ns	0.02 ns	-0.07 ns	0.11*	-0.11*	0.32**	0.27**	0.04 ns	0.50**	

*, ** = significant at 0.05 and 0.01 levels of probability, respectively, ns = non-significant, DTH = Days to heading, DTM = Days to maturity, SC = scald, N.bloch= Net Bloch, FTP = Number of fertile tillers per plant(count), SLP = Spike length (cm), PH = Plant height (cm), KPS = Number of kernels per spike (count), GY= Grain yield (kg/ha), BY = Biomass Yield(kg/ha), HI = Seed harvest index, TKW = Thousand kernel weight (g), HLW = Hectolitre weight (kg/hl).

Table 6. Estimates of genotypic path coefficient analysis among various traits of barley genotypes grown at HARC, 2017.

	DTH	DTM	SC	PHT	SLP	KPS	BY	HI	TKW	HLW	rg
DTH	-0.11	0.03	0.02	0.00	0.00	0.03	0.62	-0.10	0.01	0.01	0.51**
DTM	-0.10	0.04	0.02	0.00	0.00	0.03	0.66	-0.08	0.01	0.01	0.59**
SC	0.05	-0.02	-0.05	0.00	0.00	-0.02	-0.54	-0.01	0.00	-0.01	-0.59**
PHT	-0.01	0.00	0.00	0.01	0.00	0.01	0.22	-0.09	0.00	0.00	0.14*
SLP	-0.02	0.00	0.00	0.00	0.01	-0.02	0.31	-0.17	0.01	0.01	0.13*
KPS	-0.06	0.02	0.01	0.00	0.00	0.06	0.26	0.02	-0.01	0.00	0.31**
BY	-0.07	0.02	0.02	0.00	0.00	0.02	1.01	-0.21	0.01	0.01	0.82**
HI	0.02	-0.01	0.00	0.00	0.00	0.00	-0.38	0.55	0.00	0.00	0.18**
TKW	-0.04	0.01	0.01	0.00	0.00	-0.02	0.48	0.00	0.02	0.02	0.48**
HLW	-0.04	0.01	0.01	0.00	0.00	-0.01	0.38	-0.01	0.01	0.03	0.38**

*, ** = significant at 0.05 and 0.01 of probability levels, respectively, DTH = Days to heading, DTM = Days to maturity, SC = scald, SLP = Spike length (cm), PHT = Plant height (cm), KPS = Number of kernels per spike (count), BY = Biomass Yield (kg/ha), HI = Seed harvest index, TKW= Thousand kernel weight (g), HLW= Hectolitre weight (kg/hl), rg= Genotypic correlation coefficient.

38 for scald diseases to 98% for days to heading, and the highest genetic advances as percent of means were obtained from grain yield, biomass yield and number kernels per spike.

Both phenotypic and genotypic correlations of grain yield with days to heading and maturity, number of kernels per spike, biomass yield, thousand kernel weight, hectolitre weight, plant height and harvest index were positive and significantly high. Based on the results obtained, it is concluded that the studied barley genotypes have high genetic variation in the studied traits, and the significantly correlated traits with grain yield are good yield contributors. Thus, they could be used as indirect plant selection criteria for grain yield improvement of the studied barley genotypes.

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