

Extent of Genetic and Phenotypic Variability in Food Barley (*Hordium vulgare* L.) Landraces from North Western Ethiopia

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Abstract

In Ethiopia, there are over 15 thousand barley landraces stored in biodiversity institute of the country. Knowing the phenotypic and genetic characteristics of landraces stored in the gene bank helps breeders to select best landraces based on tangible results for variety development. The study was conducted on 48 barley landraces with four standard checks in augmented block design at Adet agricultural research center in 2016/2017 cropping season. The objective was to know the extent of phenotypic and genetic variability, heritability and possibilities of genetic advancement of barley landraces. The data collected were days to 50% flowering, days to maturity, plant height, total tiller number per plant, effective tiller number per plant, number of spikes per plant, spike length, number of grains per plant, biomass yield, thousand-grain weight, grain yield and harvest index. Analysis of variance revealed highly significant differences ($P < 0.01$) among the landraces for the traits considered. Highest phenotypic coefficient of variance were 45.78, 42.8, 42.56 and 42.17 for biomass yield, grain yield, effective tiller number per plant and number of grains per plant respectively. Likewise the highest genotypic coefficient of variances were 47.87, 46.04, 45.9 and 44.65 for number of grains per plant, grain yield, biomass yield and effective tiller number per plant respectively. Highest heritability in the broad sense values were 99.44, 98.74, 95.27 and 93.49 for biomass yield, plant height, harvest index and total tiller number per plant respectively. The traits which had highest genetic advancement to be improved by selection were biomass yield, harvest index, total tiller number per plant and grain yield with the values 143.55, 81.26, 69.75 and 49.41 as percent of mean respectively. As a result, these traits could be improved by selection as there is ample variability in the landraces and the differences observed were due to genetic factors.

Keywords: Genetic advance; Genetic variability; Heritability; *Hordium vulgare*; Landrace

Introduction

Barley production in Ethiopia is ranking 21 in the world with a share of 1.2% and second in Africa next to Morocco. Barley is the fifth most important cereal crop next to tef, maize, wheat and sorghum in Ethiopia. Ethiopia is considered as one of the richest genetic resource centers for barley in the world. There are over 15 thousand barley landrace accessions collected and stored in the gene bank of Ethiopian Biodiversity Conservation. Most of these landraces are not well characterized with sufficient descriptors. It is believed that Ethiopian barley landraces have useful traits like disease resistance such as powdery mildew, yellow dwarf virus, net blotch, scald and loose smut, high tillering capacity, tolerance to marginal soil conditions, barley shoot fly, aphids and frost resistance, vigorous seedling establishment, and quick grain filling period. The landraces are also differing in productivity, phenotypic plasticity, seed color, maturity, height and other traits [1].

This indicates that most of Ethiopian barley landraces are not utilized in improved variety development programs. To exploit the landraces effectively, it is important to know the extent of variations among the landraces. According to, knowing genetic diversity and

agronomic potential of barley landraces enable to design utilization strategies for landraces [2].

Hence, lack of improved cultivars is an important limiting factor for low productivity of barley in Ethiopia. Productivity of barley in Ethiopia is around 1.63 ton/ha lagging far behind the world's average. So far about 41 improved food barley varieties have been released. These varieties could potentially provide 3 ton/ha⁵ at research fields. But the numbers of improved varieties are small (not more than 36) as compared to the vast agro-ecology of the country. Exploiting the existing landrace stocks in the gene bank for improved variety development that fit the vast agro-ecology is important. Therefore, this study was aimed to know the genetic variability, heritability of traits and possibility of genetic advancement of Ethiopian barley landraces by selecting for improved variety development programs [3].

Materials and Methods

Description of the study area

The study was conducted at Adet Agricultural Research Center (AARC). Adet is located 11016'N latitude and 37029'E longitude with

an altitude of 2240 m.a.s.l. The mean annual rainfall of AARC is 1250 mm ranging between 860 mm and 1771 mm. The average annual maximum temperature of the center is 25.5°C and the average

minimum temperature is 9.2°C. The soil type of Adet from which this experiment was conducted is red Nitosol with slight clay nature (Table 1) [4].

Accession	Genus/ species	Zone	District	Latitude	Longitude	Altitude
IC-1276	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-32-00-N	37-30-00-E	2210
IC-1479	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-35-00-N	37-30-00-E	2230
IC-3472	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-45-00-N	37-06-00-E	2350
IC-3474	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-47-00-N	37-06-00E	2475
IC-3483	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-58-00-N	37-13-00-E	2880
IC-3484	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-58-00-N	37-13-00-E	2780
IC-3485	<i>H. vulgare L.</i>	W.Gojjam	Wemberma	10-43-00-N	37-04-00-E	2110
IC-3507	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-37-00-N	37-29-00-E	2415
IC-4372	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-34-00-N	37-25-00-E	2220
IC-4374	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-41-00-N	37-10-00-E	2050
IC-4375	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-41-00-N	37-10-00-E	2050
IC-4376	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-42-00-N	37-10-00-E	2030
IC-4377	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-42-00-N	37-10-00-E	2030
IC-4393	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-59-00-N	37-10-00-E	2940
IC-4394	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-59-00-N	37-10-00-E	2900
IC-4395	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-59-00-N	37-10-00-E	2900
IC-4396	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-59-00-N	37-10-00-E	2840
IC-4397	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-59-00-N	37-13-00-N	2700
IC-4398	<i>H. vulgare L.</i>	W.Gojjam	Sekela	11-00-00-N	37-30-00-E	2750
IC-4399	<i>H. vulgare L.</i>	W.Gojjam	Sekela	11-00-00-N	37-30-00-E	2760
IC-4400	<i>H. vulgare L.</i>	W.Gojjam	Sekela	11-00-00-N	37-30-00-E	2770
IC-4401	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-57-00-N	37-17-00E	2600
IC-4402	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-57-00-N	37-19-00E	2630
IC-4403	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-54-00-N	37-14-00-E	2580
IC-4404	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-57-00-N	37-19-00-E	2650
IC-4405	<i>H. vulgare L.</i>	W.Gojjam	Sekela	11-00-00-N	37-30-00-E	2720
IC-4406	<i>H. vulgare L.</i>	W.Gojjam	Sekela	11-00-00-N	37-30-00-E	2700
IC-4407	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-54-00-N	37-14-00-E	2500
IC-4408	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-57-00-N	37-19-00-E	2490
IC-4392	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-59-00-N	37-10-00-E	2940
IC-4639	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-33-00-N	37-40-00-E	2600
IC-4640	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-30-00-N	37-38-00-E	2400
IC-64194	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-27-00-N	37-03-00-E	2400

IC-64195	<i>H. vulgare L.</i>	W.Gojjam	Wemberma	10-42-00-N	37-03-00-E	2107
IC-64196	<i>H. vulgare L.</i>	W.Gojjam	Adet	11-30-00-E	37-30-00-E	2030
IC-64197	<i>H. vulgare L.</i>	W.Gojjam	Merawi	11-24-00-N	37-05-00-E	2090
IC-202595	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-43-00-N	37-10-00-E	2360
IC-202596	<i>H. vulgare L.</i>	W.Gojjam	Jabi Tehnan	10-43-00-N	37-10-00-E	2360
IC-202609	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-31-00-N	37-27-00-E	2100
IC-202610	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-31-00-N	37-27-00-E	2100
IC-219772	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-53-00-N	37-01-00-E	2560
IC-219773	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-56-00-N	37-06-00-E	2550
IC-219774	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-51-00-N	37-07-00-E	2550
IC-219775	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-51-00-N	37-07-00-E	2550
IC-219776	<i>H. vulgare L.</i>	W.Gojjam	Sekela	10-53-00-N	37-10-00E	2590
IC-219777	<i>H. vulgare L.</i>	W.Gojjam	Sekela	11-00-00-N	37-13-00-E	2680
IC-223952	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-37-00-N	37-25-00-E	2020
IC-223953	<i>H. vulgare L.</i>	W.Gojjam	Dembecha	10-34-00-N	37-25-00-E	2220

Table 1: Experimental materials and the entry codes.

Treatments and experimental design

The experiment was conducted in 2016/2017 cropping season on 48 Ethiopian barley landraces and four standard checks. The experimental design was augmented randomized complete block design. The design had six blocks in a size of 2.5 m × 4.8 m each. The block to block distance was 1 meter. Each block contains eight landraces and four standard checks. The total experimental area was 4.8 m × 20 m [5].

Data collection

In this study both plant-based and plot-based traits were taken. For plant-based traits i.e. plant height, total number of tillers per plant, number of effective tillers per plant, number of spikes per plant, spike length and number of grains per plant. Five randomly selected plants were tagged at the seedling stage and measured timely according to the traits used. The average was used for the analysis. Plot-based traits i.e. thousand-grain weight, biomass and grain yield, and harvest index were taken from the whole plot and converted into hectare bases for analysis. In addition, days to 50% flowering and days to maturity were counted from emergence to 50% flower setting and maturity, respectively [6].

Data analysis

Analysis of variance: The values of each observation were adjusted in each block by means and grand means of the checks to minimize errors as the landraces has not been replicated.

The collected data was analyzed by using SAS version 9.2 software program for Analysis of Variance (ANOVA) to split the source of variations into genotype, block and environmental or error variance [7].

Variance estimations: Phenotypic variance, genotypic variance and environmental variances has been estimated according to the method.

$$(\delta^2_g) = \text{MST-MSE}; (\delta^2_p) = \delta^2_g + \delta^2_e;$$

$$\text{PCV \%} = \frac{\sqrt{\delta^2_p}}{\bar{x}} \times 100 \text{ and } \text{GCV \%} = \frac{\sqrt{\delta^2_g}}{\bar{x}} \times 100$$

Where PCV: Phenotypic Coefficient of Variance; GCV: Genotypic Coefficient of Variance; MST: Mean Square of Treatments; MSE: Mean Square of Error (environmental variance; δ^2_e); δ^2_g : Genotypic Variance and δ^2_p : Phenotypic Variance [8].

Heritability and expected genetic advance: Broad sense heritability (H^2) was estimated with the formula suggested by (Falconer, D.S. and T.F.C. Mckay. 1996).

$$\text{Heritability } (H^2) = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Genetic Advance (GA) at 5% selection intensity and Genetic advance as percent of mean of genotypes (GAM %) were estimated by the formula suggested.

$$\text{GA} = \text{GA} (\%) = K.H^2b \times \sigma_p$$

H^2 =Heritability in broad sense, σ_p =Phenotypic standard deviation, GA=Expected Genetic Advance and k=the standardize selection differential at 5% selection intensity ($K=2.063$). Selection was estimated using the formula suggested by Lush and Johnson (1955) [9].

Results

Analysis of Variance (ANOVA) results

Analysis of variance results revealed highly significant differences

($P < 0.01$) among the landraces ensuring existence of genetic variability in the studied landraces for the 12 quantitative traits. In the contrast analysis there is a highly significant difference among the 48 barley landraces showing variability to be used in selection for crop improvement. The contrast analysis among checks also indicated highly significant differences in the 11 characters excluding effective

peduncle extrusion, thousand seed weight, number of seeds per spike, days to 50% flowering and days to maturity [11].

Discussion

Range of phenotypic values

The 52 barley genotypes (48 landraces and four standard checks) exhibited

Character	Block	Treatment	Error	Among treatment	Among Checks	Checks vs. treatment	CV (%) among treatments
	(DF=5)	(DF=51)	(DF=15)	(DF=2)	(DF=1)	(DF=1)	
DF	145.208**	220.692**	20.375	67.2474**	475.3472**	272.25**	7.0575
DM	44.5**	118.26**	31.12	38.6129**	53.39**	25.84**	6.1577
PH (cm)	9.1478**	247.07**	3.1206	78.0717**	868.75**	1.8**	1.984
TTNPP	0.7724**	2.505**	0.163	0.3813**	0.1335**	0.4556**	7.62
ETNPP	0.506**	3.363**	0.3069	0.4755**	0.02347ns	0.544ns	13.488
NSPP	1.532**	4.3805**	1.9691	2.2616**	1.9339**	7.6544**	28.269
SL (cm)	0.2060ns	5.0184**	1.0569	2.7587**	1.5022**	9.2011**	12.25
NGPP	1.3427**	105.13**	23.537	4.7834**	47.0450**	464.4025**	5.8489
BM (t/ha)	0.004**	0.997**	0.0056	0.6377**	0.1089**	3.8025**	3.427
TGW (gm)	27.523**	100.868**	16.15	63.9215**	12.7513**	261.6306**	13.867
GY (t/ha)	0.00174**	0.1823**	0.0015	0.05811**	0.01492**	0.0436**	5.5844
HI	0.00041**	0.0093**	0.0004	0.0011**	0.0032**	0.05855**	7.0428

Note: **: Significant at 1% probability level; ns: non-significant; CV: Coefficient of variation; DF: Days to 50% flowering; DM: Days to Maturity; PH: Plant Height; TTNPP: Total Tiller Number Per Plant; ETNP: Effective Tiller Number Per Plant; NSPP: Number of Spikes Per Plant; SL: Spike Length; NGPP: Number of Grains Per Plant; BM: Biomass Yield; TGW: Thousand-Grain Weight; GY: Grain Yield and HI: Harvest Index on hectare bases.

Table 2: Analysis of variance for 48 barley landraces and 4 standard checks.

number of tiller per plant which was not significant. Contrast analysis of checks against test treatments had also highly significant differences except for effective number of tillers per plant. The landraces did not show significant differences from block to block for spike length (Table 2) [10].

In agreement with the present finding a study conducted by revealed highly significant differences for days to 50% flowering, plant height, number of effective tillers, days to maturity, biomass yield, grain yield, harvest index, thousand-grain weight and number of seeds in the evaluation of 20 barley landraces. One hundred and two barley accessions and five checks showed highly significant differences among landraces of barley for plant height, awn length,

wide range of variations. Grain yield showed wide range (0.43 t/ha - 1.459 t/ha) followed by plant height (57.00 cm-112.00 cm), days to 50% flowering (48-94) and days to maturity (74-115) [12].

The highest standard error was observed for days to maturity (5.5787), days to 50% flowering (4.5139) and thousand-grain weight (4.019) in their descending order indicating the extent of environmental impact. The lowest standard error was for grain yield (0.0385), biomass yield (0.0745) and harvest index (0.021) showing less environmental impact. This indicates that grain yield, biomass yield and harvest index were less affected by the environment (Table 3) [13].

Character	Mean	± SE	Range	
			Minimum	Maximum
DF	63.958	4.5139	48	94
DM	90.597	5.5787	74	115

PH (cm)	89.036	1.7665	57	112
TTNPP	5.292	0.403	2.6	11.2
ETNPP	4.107	0.554	1	10.6
NSPP	4.964	1.4033	1.2	11.6
SL (cm)	8.394	1.028	2.1	13.4
NGPP	21.417	1.2526	4.1	42
BM (t/ha)	2.175	0.0745	0.1	4
TGW (gm)	28.98	4.019	8.6	42.1
GY (t/ha)	0.6902	0.0385	0.43	1.459
HI	0.2984	0.021	0.0893	0.43

Note: DF: Days to 50% flowering, DM: Days to Maturity; PH: Plant Height; TTNPP: Total Tiller Number Per Plant; ETNPP: Effective Tiller Number Per Plant; NSPP: Number of Spikes Per Plant; SL: Spike Length; NGPP: Number of Grains Per Plant; BM: Biomass Yield; TGW: Thousand-Grain Weight; GY: Grain Yield and HI: Harvest Index on hectare bases.

Table 3: Mean, Standard Error (SE) and Ranges for 48 barley landraces and 4 checks.

In line, that high ranges of grain yield (2258 kg/plot-6202 kg/plot), plant height 82.9 cm-118.1 cm), days to 50% heading (75 days-100 days) and days to heading (110.3 days-137 days) were found in a study conducted on 20 varieties [14].

Phenotypic and genotypic variance

Genotypic variance (δ^2g), phenotypic variance (δ^2p), Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are indicated. PCV and GCV values >20% regarded as high, PCV and GCV values between 10% and 20% medium, PCV and GCV values <10% low.

The genotypic variance ranged from (0.00886 to 243.949) and phenotypic variance (0.0093 to 247.07) for harvest index and plant height, respectively. Genotypic and phenotypic coefficient of variances ranged (10.3037% to 62.8%) and (12.0034 to 63.04876) respectively; the lowest corresponding for days to maturity and the highest for biomass yield [15].

In agreement with this investigation a study on 36 barley landrace populations in southern Ethiopia indicated high genotypic variance for plant height, biomass yield per plant, days to maturity, number of grains per plant and thousand-grain weight. They also reported that there were corresponding high phenotypic variances for plant height, biomass yield, days to maturity, number of grains per spike and thousand-grain weight. High GCV and PCV values for productive tillers, biological yield and for harvest index.

In this study phenotypic coefficient of variation was slightly higher than genotypic coefficient of variation for most of the traits indicating less environmental impacts on the estimated differences. The highest error variance was for days to maturity (31.12) followed by number of grains per plant (23.5367) and days to 50% flowering (20.375). This indicates that these traits were highly influenced by environment. The error variance for harvest index (0.0004), Grain yield (0.00149) and biomass yield were small showing these traits are less influenced by the environment rather the differences are due to genetic variations (Table 4) [16].

Character	δ^2g	δ^2p	δ^2e	GCV%	PCV%
DF	200.32	220.69	20.375	22.129	23.227
DM	87.14	118.26	31.12	10.304	12.003
PH (cm)	243.95	247.07	3.1206	17.542	17.654
TTNPP	2.342	2.505	0.163	28.918	29.908
ETNPP	3.0561	3.363	0.3069	42.566	44.652
NSPP	2.4114	4.3805	1.9691	31.283	42.163
SL (cm)	3.9615	5.0184	1.0569	23.712	26.688
NGPP	81.593	105.13	23.537	42.176	47.875
BM (t/ha)	0.9914	0.997	0.0056	45.779	45.908

TGW (gm)	84.718	100.87	16.15	31.761	34.656
GY (t/ha)	0.1864	0.1794	0.0015	42.8	46.049
HI	0.0089	0.0093	0.0004	31.544	32.318

Note: DF: Days to 50% flowering; DM=Days to Maturity; PH: Plant Height; TTNPP: Total Tiller Number Per Plant; ETNPP: Effective Tiller Number Per Plant, NSPP: Number of Spikes Per Plant; SL: Spike Length; NGPP: Number of Grains Per Plant; BM: Biomass Yield; TGW: Thousand-Grain Weight; GY: Grain Yield and HI: Harvest Index on hectare bases.

Table 4: Phenotypic and genotypic variances and coefficients of variations.

Broad sense heritability and expected genetic advance

Selection in conjunction with genetic advance is more effective than heritability estimates alone. If heritability of a character is very high, selection for such characters could be easy. Heritability estimates can be placed in the following categories: Low heritability (<40%), medium heritability (40%-59%), moderately high (60%-79%) and very high heritability (80% or more).

In the current study, heritability in the broad sense ranged from (55.0485 to 99.4383), number of spikes/plant being the lowest and biomass yield the highest. Accordingly, days to 50% flowering, plant height, total tiller number per plant, effective tiller number per plant, biomass, thousand-grain weight and harvest index had high heritability values. GAM ranged from 2.29 for plant height to 143.55 for biomass. Higher values of GAM were also recorded for spike length, total tiller number per plant, effective tiller number per plant, number of spikes per plant, grain yield and harvest index indicating better response to selection.

In this study high heritability values were combined with high GCV and PCV values indicating the variations observed were due to genetic variation but not due to environment influence and the expected genetic gain from selection could be high. Biomass yield, harvest index, total number of tillers/plant and effective tiller number/plant had high heritability, GCV, PCV and GAM values. This shows that these traits could be improved by selection as there is ample variability in the landraces and the differences observed in the tested genotypes were due to genotypic variations but not due to environmental impact. Number of spikes/plant and spike length have moderately high values of heritability, PCV, GCV and GAM values showing good probabilities to be improved by selection. Plant height had high heritability but low PCV, GCV and GAM values so that it has

low probability of improvement by selection.

In consistent with the results in the current study, high broad sense heritability values of biomass yield per plant, plant height, days to maturity, thousand-grain weight, number of grains per spike and grain yield were recorded. He also indicated moderate heritability values of harvest index, total tiller number and number of spikes per plant.

In line, sixty four Ethiopian barley genotypes and reported high heritability values in the broad sense as 95.93%, 93.82%, 92.89% and 91.27% for number of kernels per spike, days to maturity, germination percentage and days to heading respectively.

Likewise a study on 225 genotypes indicated that high broad sense heritability values of 89%, 83%, 82% and 76% for susceptibility to lodging, days to maturity, days to heading and number of spike groups per spike. They also reported that the lowest heritability values were r40% for susceptibility to scaled disease. According to their report the highest GAM% values were 116.92%, 32.34%, 32.25% and 32.06 for susceptibility to lodging, number of spikelet groups per spike, susceptibility to scaled disease and flag leaf width respectively. These values for GAM% were followed by 21.92% for grain yield per plant. The lowest GAM% value was 14.59% for head length indicating low probability of improvement by selection. The highest PCV values were 63.49%, 39.61%, 23.25 and 20.57 for susceptibility to lodging and scaled disease, flag leaf width and number of spike groups per spike. The highest GCV values were 60.03%, 24.90%, 19.03% and 17.97% for susceptibility to lodging and scaled disease, flag leaf width and number of spike groups per spike. Number of grains per plant had GCV value of 14.57%. They reported that the PCV, GCV, heritability values coincide with high GAM% value for the barley landrace accessions indicating high probability of improvement by selection (Table 5) [17].

Character	H2 (%)	GA	GAM (%)
DF	90.768	27.818	2.3899
DM	73.685	16.531	3.438
PH (cm)	98.737	32.018	2.2902
TTNPP	93.493	3.0527	69.748
ETNPP	90.874	3.438	55.135
NSPP	55.049	2.3769	35.195
SL (cm)	78.94	3.6482	38.06
NGPP	77.612	16.417	3.8541

BM (t/ha)	99.438	2.0483	143.55
TGW (gm)	83.989	17.402	4.1357
GY (t/ha)	59.213	0.4905	49.408
HI	95.269	0.1895	81.26

Note: DF: Days to 50% flowering; DM: Days to Maturity; PH: Plant Height; TTNPP: Total Tiller Number Per Plant; ETNPP: Effective Tiller Number Per Plant; NSPP: Number of Spikes Per Plant; SL: Spike Length; NGPP: Number of Grains Per Plant; BM: Biomass Yield; TGW: Thousand-Grain Weight; GY: Grain Yield and HI: Harvest Index on hectare bases.

Table 5: Heritability in the broad sense and expected genetic advance.

The characters like number of spikes per plant, spike length, thousand-grain weight and showed moderately high heritability, PCV, GCV and GAM values showing these traits could be improved by selection for the studied genotypes. Likewise high heritability, genotypic coefficient of variation and phenotypic coefficient of variation were reported for number of kernels per spike in barley [18].

Conclusion

The result of the analysis of variance showed highly significant differences ($P < 0.01$) among the genotypes for the 12 quantitative traits ensuring the presence of appreciable genetic variability in the studied barley landraces. This also further demonstrated by the presence of higher range of values and higher level of PCV and GCV for most of the traits considered. The higher heritability values estimated for most of the traits signifies that the differences observed in the barley landraces were due to genotypic variations but not due to environmental factors.

Recommendations

From the traits investigated, biomass yield, harvest index, total number of tillers/plant and effective tiller number/plant had high heritability, GCV, PCV and GAM values. Consequently, these traits could be improved by selection as there is ample variability in the landraces and the differences observed were due to genetic factors.

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