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Full length Research paper

Estimation of genetic variability, heritability and genetic advance among Ethiopian food barley (Hordeum vulgareL) landraces for yield and yield related traits

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Barley is the most important staple food crop due to early maturing and better adapted cereal in marginal areas. To launch an effective breeding program, it is essential to have information on the nature and magnitudes of genetic diversity. The objective was to assess genetic variability, heritability and genetic advance for yield and yield related traits. 100 barley landraces were arranged in 10 x 10 simple lattice designs at Haro Sabu Agricultural Research Center. Statistically, highly significant (p<0.01) and (p<0.05) variation was observed among materials for important quantitative traits. Genotypic variance of characters varied widely from 0.02 for grain weight per spike to 49.18 for plant height. Genotypic coefficient of variation ranged from 4.99% for days to maturity to 32.24% for number of spike lets per spike. Broad sense heritability ranged from 12.14% for harvest index to 81.70% for number of spike lets per spike. The highest genetic advance as percent of mean was recorded for number of spike lets per spike (60.03%) and the least for harvest index (4.38%). Generally, the magnitude of genetic variability among the studied materials showed great variations for desirable traits and thus confident enough to expect genetic progress if further breeding activities are carried out.

Key words: Barley, Coefficient of variation, Genetic advance, Heritability

INTRODUCTION

Barley (Hordeum vulgare L) (2n=2x=14) is one of the most important staple food crops in the highlands of Ethiopia. It is a cool season crop, the most dependable and early maturing cereal grain with relatively high yield potential including in marginal areas where other cereal crops cannot have adapted (Harlan,2008;Martin and Leonard,2010). The major barley production areas of the world include Europe, the Mediterranean fringe of North Africa, Ethiopia and the Middle East, former USSR, China, India, Canada and USA (Horsley and Hochhalter, 2004). Ethiopia is the 2nd largest barley producer in Africa, next to Morocco, accounting for about 25% of the total barley production in the continent (FAO, 2014).

However, there is great yield gap between national average yield (2.5.01 t/ha-1) (CSA, 2020) and world average yield (3.04 t/ha-1) (Foreign Agricultural Service/USDA April 2017 Office of Global Analysis). This production limitation may be attributed to primarily the low yielding ability of farmers' cultivars, which are the dominant varieties in use; the influence of several biotic and abiotic stresses; and poor promotion of improved barley production package technologies (Bayeh and Berhane, 2011).Ethiopian barley landraces are important source of genes for several traits like barley yellow dwarf virus resistance, powdery mildew, high lysine content, good vegetative vigor, drought resistance and resistance to several barley diseases (IBC, 2008). Although there exists high diversity of

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Ethiopian barley landraces in gene bank but the available genetic potential has not been effectively used. Increased agricultural production and productivity through development of high yielding varieties is the main goal of any breeding programs.

The prerequisite to achieve this goal is to find sufficient amount of genetic variability among plant populations from which desired lines are to be selected for further breeding activities. Identification of better genotypes with desirable traits and their subsequent use in breeding program and establishment of suitable selection criteria can be helpful for successful varietals improvement program (Al-Tabbal and Al-Fraihat, 2012). In order to launch an effective breeding program, it is essential to have information on the nature and magnitude of genetic variability; heritability and genetic advance present the breeding material at hand. Thus, selection of germplasm with wide genetic variation for yield and other desirable agronomic traits is an important activity of any plant breeder. Genetic variability which is due to genetic differences among individuals within a population, is the foundation of plant breeding since proper management of diversity can produce permanent gain in the performance of plant and can safeguard against seasonal fluctuations (Sharma, 2004; Welsh, 2008). Phenotypic variation, is the observable variation present in a character of a population, includes both genotypic and environmental components of variation and, as a result, its magnitude differs under different environmental conditions (Singh, 2006).

Heritability can be defined in broad sense, as the proportion of the genotypic variability to the total variance (Allard, 2006). It refers to the portion of phenotypic ally expressed variation within a given environment and it measures the degree to which a trait can be modified by selection (Christianson and Lewis, 2003). Narrow sense heritability is the ratio of additive genetic variance to phenotypic variance (Falconer and Mackay,1996).Even though, estimates of heritability provide the basis of selection for phenotypic performance, estimates of heritability and genetic advance should be considered simultaneously because high heritability should not always associate with high genetic advance (Amin et al., 2004). Hence, high heritability coupled with genetic advance is more dependable, while for others, the intensity of selection should be increased; gives an idea of the possible improvement of new populations through selection and high heritability with low genetic advance indicates the presence of non-additive gene action (Vimal and Vishwakarma, 2009).To achieve at better choice of characters for selection of desirable genotypes under selection for high yield, a thorough knowledge on the nature and magnitude of genetic variability, extent of heritability and genetic advance present in the breeding material is necessary. In view of this, a total of 100 food barley landraces including three checks were evaluated. Therefore, the objective of the study was to assess the extent of genetic variability, heritability and genetic advance of barley landraces based on different agro-morphological traits.

MATERIALS AND METHODS

Study Area

The experiment was conducted during the main cropping season at Haro-Sabu Agricultural Research Center, Mata research sub-site, Western Oromia, Ethiopia. The area is located at 8°53'33"N latitude and 34°80'11"E longitude. Mata research sub-site is found with an elevation of 1900 meters above sea level. Soil types were classified as about 90% loam, 6% sand and 4% clay soil. Mean annual rainfall were 1219.15 mm. The minimum and maximum annual temperatures were 16.21and 27.77 °C, respectively. (Sayo district Agriculture and Natural Resource office, Demb Dollo. (Unpublished)

Breeding materials and Experimental Design

A total of 100 food barley landraces including two standard checks (HB 1307 and Abdane) and one local check were evaluated (Table 1). Materials were arranged in 10 x 10 simple lattice designs. Seed was drilled on 0.20m row spacing with1.65 m length and 1 m spacing between each block was used. Seed rate of 85kgha^{-1} and a combination of UREA and NPS fertilizer was applied at the recommended rate of 50kgha^{-1} and 100kgha^{-1}, respectively.NPS fertilizer was applied uniformly for all treatments equally at the time of sowing and split application was carried out for UREA (half at planting time and half at tiller initiation).

Method of data collection

Ten plants were selected randomly before heading from each row and tagged with thread and all the necessary plant based data were collected from these sampled plants (IPGRI, 1994). **Plant based data**: Peduncle length, grain weight per spike, plant height, and spike length, spike weight per plant, number of spike lets per spike, productive and total tillers per plant, flag leaf length and awn length. **Plot based data**: Days to heading, days to physiological maturity, thousand seed weight, grain yield, biological yield and harvest index.

Statistical data analysis

All measured agro-morphological traits were subjected to analysis of variance (ANOVA) using
Proc lattice and Proc GLM procedures of SAS version 9.2 (SAS, 2008)

Analysis of variance components

Table 1: List of barley landraces and checks used for experimental purpose

Entry code	Acc. No	Region	Latitude	Longitude	Altitude (m.a.s.l)	Entry code	Acc. No	Region	Latitude	Longitude	Altitude (m.a.s.l)
1	64197	Amara	12-24-00-N	37-05-00-E	2090	51	219311	Oromiya	04-52-00-N	38-05-00-E	1870
2	3239	Amara	12-23-00-N	37-17-00-E	1830	52	219316	Oromiya	05-53-00-N	39-11-00-E	1820
3	3240	Amara	12-18-00-N	37-10-00-E	1830	53	219317	Oromiya	05-44-00-N	39-20-00-E	1800
4	4560	Oromiya	09-10-00-N	35-42-00-E	1900	54	220677	Amara	08-48-00-N	39-21-00-E	2000
5	3465	Oromiya	08-57-00-N	37-46-00-E	1800	55	221312	SNNP	07-13-00-N	37-46-00-E	2130
6	3583	SNNP	07-00-00-N	37-53-00-E	2140	56	221313	SNNP	07-13-00-N	37-46-00-E	2130
7	3612	Oromiya	07-14-00-N	36-55-00-E	1810	57	221324	SNNP	06-09-00-N	37-36-00-E	2150
8	3617	Oromiya	07-55-00-N	37-24-00-E	1890	58	223192	Tigray	13-43-00-N	39-28-00-E	1930
9	3632	Oromiya	09-32-00-N	35-28-00-E	1800	59	223194	Tigray	12-42-00-N	39-31-00-E	1940
10	3638	Amara	11-49-00-N	37-37-00-E	1780	60	225179	SNNP	06-57-00-N	37-51-00-E	2100
11	3763	Amara	12-31-00-N	37-10-00-E	1870	61	225992	Amara	12-22-00-N	37-17-00-E	1830
12	3940	Oromiya	08-54-00-N	40-46-00-E	1830	62	229997	Oromiya	06-64-00-N	39-01-00-E	1940
13	3941	Oromiya	08-54-00-N	40-46-00-E	1890	63	230614	Oromiya	07-01-00-N	40-29-00-E	1870
14	3943	Oromiya	09-05-00-N	40-50-00-E	1870	64	230620	Oromiya	07-05-00-N	40-36-00-E	1800
15	235286	Tigray	13-38-00-N	39-17-00-E	1780	65	219307	Oromiya	05-39-00-N	38-13-00-E	1880
16	4193	Oromiya	09-02-00-N	40-44-00-E	1870	66	230622	Oromiya	07-05-00-N	40-36-00-E	1820
17	4194	Oromiya	09-03-00-N	40-44-00-E	1840	67	225176	SNNP	06-57-00-N	37-51-00-E	2100
18	4195	Oromiya	09-26-00-N	41-02-00-E	1800	68	230624	Oromiya	07-08-00-N	40-42-00-E	1800
19	202561	Oromiya	07-32-00-N	40-42-00-E	2090	69	230628	Oromiya	07-11-00-N	40-44-00-E	1790
20	239513	Oromiya	07-04-77-N	40-31-71-E	2050	70	232372	Oromiya	09-22-00-N	41-47-00-E	2020
21	64022	SNNP	06-53-00-N	37-48-00-E	2140	71	231223	Oromiya	08-35-00-N	39-53-00-E	1780
22	64053	SNNP	06-12-00-N	37-35-00-E	2150	72	232373	Oromiya	09-22-00-N	41-47-00-E	2020
23	64248	SNNP	07-02-00-N	37-54-00-E	1900	73	233028	SNNP	05-55-00-N	37-20-00-E	2050
24	64260	Oromiya	07-29-00-N	39-15-00-E	1910	74	234337	Tigray	14-05-00-N	38-57-00-E	1810
25	237021	Amara	08-50-00-N	39-20-00-E	1750	75	235264	Tigray	12-58-00-N	39-34-00-E	1850
26	64344	Oromiya	07-33-00-N	36-36-00-E	1880	76	235274	Tigray	13-31-00-N	39-07-00-E	1620
27	64345	SNNP	07-10-00-N	36-21-00-E	2140	77	235283	Tigray	13-38-00-N	39-15-00-E	1900
28	202536	Amara	12-47-00-N	37-40-00-E	1750	78	235284	Tigray	13-40-00-N	39-15-00-E	1840
29	202537	Amara	12-47-00-N	37-40-00-E	1750	79	233030	SNNP	05-58-00-N	37-17-00-E	2030
30	202538	Amara	12-47-00-N	37-40-00-E	1750	80	235299	Tigray	13-23-00-N	39-21-00-E	1860
31	202539	Amara	13-03-00-N	37-47-00-E	1810	81	235635	SNNP	05-17-00-N	37-39-00-E	2150
32	202540	Amara	13-03-00-N	37-47-00-E	1810	82	235636	SNNP	05-17-00-N	37-39-00-E	2150
33	202541	Amara	12-23-00-N	37-17-00-E	1830	83	235637	SNNP	05-17-00-N	37-39-00-E	2150
34	202542	Amara	12-18-00-N	37-10-00-E	1830	84	235651	Oromiya	04-56-00-N	38-11-00-E	1780
35	202660	Oromiya	07-41-00-N	36-58-00-E	1810	85	235652	Oromiya	04-56-00-N	38-11-00-E	1780
36	202661	Oromiya	07-41-00-N	36-58-00-E	1810	86	235654	Oromiya	05-28-00-N	38-15-00-E	1880
37	202670	Oromiya	07-55-00-N	37-24-00-E	1890	87	235746	Amara	12-24-00-N	37-07-00-E	1920
38	202676	Amara	11-49-00-N	37-37-00-E	1780	88	237021	Amara	08-50-00-N	39-20-00-E	1750
39	202820	Oromiya	09-09-00-N	41-07-00-E	1910	89	237022	Oromiya	08-50-00-N	39-00-00-E	1800
40	202536	Amara	12-47-00-N	37-40-00-E	1750	90	239514	Oromiya	07-09-00-N	40-40-88-E	2050
41	12970	SNNP	37-36-00-N	06-09-00-E	2150	91	241675	Oromiya	07-17-36-N	38-22-98-E	1720
42	212972	Oromiya	37-44-00-N	05-01-00-E	1850	92	242098	Amara	11-06-00-N	39-47-00-E	1760
43	217010	Amara	12-38-00-N	37-06-00-E	2090	93	242574	Tigray	13-52-10-N	39-35-24-E	1820
44	217173	Oromiya	07-33-00-N	36-36-00-E	1880	94	242581	Oromiya	07-00-00-N	40-27-40-E	1828
45	217175	Oromiya	07-33-00-N	36-36-00-E	1880	95	243182	Oromiya	07-00-00-N	40-27-40-E	1828
46	217176	SNNP	07-10-00-N	36-21-00-E	2140	96	243184	Oromiya	06-59-44-N	40-28-04-E	1830
47	219151	Oromiya	09-19-00-N	41-03-00-E	2020	97	243614	Amara	10-39-00-N	36-38-00-E	1815
48	219152	Oromiya	09-11-00-N	41-03-00-E	2100	98	HB1307	Oromiya			
49	219148	Oromiya	08-49-00-N	40-28-00-E	1800	99	Abdane	Oromiya			
50	219307	Oromiya	05-39-00-N	38-13-00-E	1880	100	Local	Oromiya	08-53-33-N	34-80-11-E	1700

SNNP= south nation and nationality of the people, m.a.s.l= matter above sea level, Acc. No= accession number

Quantitative traits variances (phenotypic, genotypic and environmental variances) and the respective coefficient of variations were calculated following the formula suggested by Burton and DeVane (1953) as follows;

Genotypic variance ($\square^2$g) $\square^2 g = \frac{Msg - Mse}{r}$

Where MSg = mean square of genotypes, MSe = error mean square, r = number of replications.

Environmental variance or error variance ($\square^2$e): $\square^2$e=MSe

Phenotypic variance ($\square^2$p): $\square^2 p = \square^2 g + \square^2 e$

Estimates of coefficient of variation were carried out as follows.

Phenotypic coefficient of variation (PCV %): $\frac{\sqrt{\alpha^2 p}}{\overline{X}} * 100$

Genotypic coefficient variation (GCV %): $\frac{\sqrt{\alpha^2 g}}{\overline{X}} * 100$

Environmental coefficient of variations (ECV%): $\frac{\sqrt{\alpha^2 e}}{\overline{X}} * 100$

Broad sense heritability (H^2) and genetic advances

Heritability (H^2): Heritability in broad sense for all characters was computed using the formula given by Falconer (1996). $H^2 = (\delta^2 g/\delta^2 p) \times 100$
Where H^2 = heritability in broad sense $\delta^2 g$ = genotypic variance and $\delta^2 p$ = phenotypic variance.
Genetic advance under selection (GA): Expected genetic advance for each character assuming a selection intensity at 5% (K =2.056) were computed using the formula developed by Johnson *et al.* (2010a) as: $GA = k(\sqrt{\delta^2 p})\, H^2$
Where GA = expected genetic advance, k is constant (selection differential (K=2.056 at 5% selection intensity), $\sqrt{\delta^2 p}$ = is the square root of the phenotypic variance.
Genetic advance as percent of mean (GAM) was calculated to compare the extent of predicted advance of different traits under selection using the formula.

$$GAM = \frac{GA}{\overline{X}} * 100$$ (Johnson *et al.*, 2010a)

Where $\bar{x}$ = mean for the trait considered; $\square^2$p$\square$phenotypic variance; $\square^2 g$ =genotypic variance; $\square^2$e= environmental variance, PCV (%) = Phenotypic coefficient of variation; GCV (%) = Genotypic coefficient of variation, ECV (%) =Environmental coefficient of variations.

RESULTS AND DISCUSSIONS

Analysis of variance

Analysis of variance (ANOVA) showed that significant ($P<0.01$) differences were obtained for all traits evaluated (Table2). Thus highly significant differences among different landraces for parameters like days to heading, days to maturity, plant height, peduncle length, spike length, awn length, flag leaf length, productive tillers per plant, grain yield, grain weight per spike, spike weight per plant, number of spike lets per spike, thousand seed weight and biological yield. This indicated that there was high potential variability among the barley landraces for various traits which would be helpful for effective selection.
Similarly, Assefa (2003) reported that, barley landraces showed significant variations for many traits like thousand seed weight, spike length, heads per square meter, grain yield per spike, days to heading, and days to maturity and plant height in Ethiopian barley landraces. Study by Oettler *et al.*(2009) showed significant differences among nine barley genotypes for grain yield, spikes/m², thousand seed weight, dry matter, days to an thesis and plant height.

Table 2: Mean squares, degrees of freedom and some of statistical parameters of all studied traits of barley landraces

	Source of variation							The ranges and mean values for agro-morphological characters				
Traits	Replication	Blocks within Replications	Treatments	Error	R^2 (%)	CV%	Efficiency Relative to RCBD (%)	Min	Max	Mean	SE(±)	LSD (5%)
	DF=1	DF=18	DF=99	DF=81								
DH	33.62*	11.04	50.62**	7.83	89.79	4.63	102.1	49.5	86	60.36	0.52	5.75
DM	206.04**	13.15**	50.15**	8.21	90.04	3.12	103.9	82	111	91.8	0.53	5.99
PH	2288.26**	37.37**	134.18**	35.83	86.02	7.17	100	46.5	100.8	83.54	0.87	11.92
PDL	34.53*	6.03**	27.98**	5.77	87.2	16.92	103	2.7	22.1	14.19	0.39	4.78
SL	19.16**	1.19*	1.51**	0.64	80.6	9.52	106.6	5.63	10.93	8.43	0.09	1.71
AL	4.65*	1.3	7.02**	1.21	88.54	8.81	100.1	4	15.6	12.46	0.19	2.19
FLL	62.16**	7.38*	7.69**	3.73	76.86	12.99	108.1	10.03	21.73	14.87	0.2	4.16
PTPP	27.16**	1.01*	1.29**	0.58	79.77	16.88	105.3	2.31	6.53	4.51	0.08	1.61
TTPP	27.23**	1.05	1.09*	0.68	74.81	16.45	103.2	3.4	7	5.02	0.08	1.72
YLD	16.3**	0.36	1.25**	0.5	78.17	19.67	94.63	1.4	5.55	3.58	0.08	1.37
GWPS	0.37**	0.03	0.07**	0.03	77.74	16.73	99.11	0.4	1.75	1.06	0.02	0.35
SWPP	1.48**	0.04	0.13**	0.04	82.37	14.82	99.41	0.6	2.3	1.39	0.03	0.41
NSTPS	54.71*	10.82	72.90**	7.34	93.34	15.26	102.6	7	31.3	17.76	0.64	5.6
TSW	2751.34**	57.4	110.10**	54.24	76.9	23.8	100.1	7.85	46.4	30.94	0.74	14.69
BYLD	60.72**	1.4	8.37**	1.86	87.03	15.27	95.48	3.6	14.25	8.93	0.22	2.64
HI	10.95*	42.02*	58.47.*	45.81	60.82	18.61	94.81	28.1	58.65	41.21	0.58	14.82

Key: *, ** indicates significance at 0.05 and 0.01 probability levels, respectively. DF= degree of freedom RCBD=randomized complete block design, R^2= R- square, CV= Coefficient of variation, DH = days to heading, DM= days to maturity, PH=plant height, PDL= peduncle length, SL= spike length, AL =awn length, FLL =flag leaf length, PTPP =productive tillers per plant, TTPP=total tillers per plant, YLD = grain yield, GWPS =grain weight spike^{1}, SWPP, =spike weight plant^{-1}, NSTPS=number of spike lets spike^{-1}, TSW =thousand seed weight, BYLD=biomass yield, HI=harvest index

The mean values and ranges of agro-morphological traits.

The mean values and ranges for 16 agro-morphological characters are presented in Table 2. Mean of days to heading ranged from 50 to 86 days (with an average of 60 days). Similarly, Wosene *et al.* (2015) reported that genotypes differ in days to 50 % heading. Physiological maturity ranged from 82 to 111 days (with an averageof 92 days). These variations deal great flexibility for developing improved varieties suitable for various agro-ecologies with variable length of growing period and also can be recommended for various cropping systems. Early maturing is desirable for areas where the terminal moisture is the limiting factor for barley production. It also guides breeders to develop a variety which can escape late season drought by improving traits which relate to days to maturity in the required direction. Thomas and Fukai (1995) reported that barley plants took between 105-157 days to maturity. Total time to maturity depends on variety, location and planting date.

Similarly, plant height, peduncle length, awn length and flag leaf length varied from 47 to 101cm (with an average of 84), 3to 22cm (with an average of 14), 4to 16cm (with an average of 13) and 10 to 22cm (with an average of 15), respectively. Briggs (1978) reported barley stands from 60-120 cm tall. Number of productive and total tillers per plant were recorded the mean values ranged between 2 to 7 (with an average 5) and 3 to 7 (with an average 5), respectively. The variation in plant height, number of productive and total tillering capacity per plant indicated the possibility to develop tolerant variety against lodging problems and varieties with variable biomass and grain yield. Similarly, Gomez-Macpherson (2001) reported field grown barley typical plant produced 2-5 tillers per plant. Similar result reported by Grcíadel *et al.* (2003) that the magnitude of the difference in tillering was more affected by the environment. That means, at common seeding rates, a single plant usually develops from one to five stems but under favorable conditions it may have several times that number (Reid, 1979).

Spike length is a character of considerable importance, as the larger spike is likely to produce more grains and eventually higher yield. Spike length ranged from 5.6 to 10.9cm (with an average of 8.4). This variability was resulted from morphological character of the landraces. That is, two-row barley had a relatively long spike as compared to the six-row barley (Eid, 2009; Xue *et al*., 2010). Grain yield, grain weight per spike, spike weight per plant and number of spike lets per spike ranged from 1.40 to 5.55 tons per hectare (with an average of 3.58), 0.40 to 1.75 gm (with an average 1.06 gm), 0.60 to 2.30 gm (with an average 1.39 gram) and 7.00 to 31.30 (with an average 17.76) respectively. Parameters like thousand seed weight, biological yield and harvest index ranged between 7.9 to 46.4 gm (with an average 30.9 gm), 3.60 to 14.25 tons per hectare (with an average 8.93) and 28.10 to 58.65 % with an average of 41.21% respectively (Table 2). Variation in grain yield, grain weight per spike, spike weight per plant and number of spike lets per spike, thousand seed weight, biological yield and harvest index implied that, it is possible to create a variety with high grain yield and/or other biological yields.

Therefore, wider ranges of variations were observed among barley landraces for all quantitative traits (Table2). This variation is fundamental for effective selections and sustainable improvement of barley by combining the desirable traits. The ANOVA showed that variation among the landraces was significant for all the characters measured. This indicated the existence of high degree of genetic variation in the material to be exploited in breeding programs and reflected in the broad ranges observed for each character.

Phenotypic and genotypic coefficient of variation

The genotypic variance was found to be comparatively greater than its corresponding environmental variance for days to heading, days to maturity, plant height, peduncle length, awn length, and spike weight per plant, number of spike lets per spike and biomass yield (Table3). Similarly, Ahmed *et al.* (2008) reported high level of genotypic variance for days to heading, days to maturity and spike lets per spike, grains per spike, plant height and biomass. This implied that, in the phenotypic expression of these traits, the effect of environmental factors was low compared to the genetic component and so that selection will be more effective when the genetic variation in relation to environmental variation is high (Poehlman and Sleeper, 2005).In addition, both genotypic and phenotypic variance were observed to be reasonably greater than its corresponding environmental variance for days to heading, days to maturity, plant height, peduncle length, awn length, number of spike lets per spike and biomass yield (Table3) indicating selections may be more effective and efficient upon these attributes and their phenotypic expressions would be a good indication of genotypic potential. This result is in agreement with the findings of Ahmed *et al.* (2008).

On the other hand, the degree of genotypic variances was smaller than that of environmental variance or considerable environmental influences were observed for spike length, flag leaf length, productive tiller per plant, total tiller per plant, grain yield, grain weight per spike, thousand seed weight and harvest index indicating that, the effect of environmental factors on the phenotypic expression of these traits were high. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values are considered as low (<10%), medium (10-20%) and high (>20%) (Deshmukh *et al.,* 1986). Accordingly, in this study high PCV recorded for number of spike lets per spike (35.66%),thousand seed weights (29.30%), peduncle length (28.95%), grain yield, (25.91%), biomass yield (25.33%), productive tillers per plant (21.44%), grain weight per spike (21.09%) and spike weight per plant (20. 97 %) (Table3). Similarly, Chand *et al.* (2008) reported higher PCV for grain yield per plant and number of grains per spike in barley. Similarly, high GCV recorded for number of spike lets per spike (32.24%), peduncle length (23.48%) and biomass yield (20.20%). This indicated that the genotypic contribution to phenotypic expression was high and less environmental effects on these traits. Similarly, Jalata *et al.* (2010) and Chand *et al.* (2008) reported high values of GCV for grain yield and biomass. The lowest GCV values stated for days to heading (7.66%), days to maturity (4.99%), plant height (8.39%), spike length (7.82%), flag leaf length (9.46%), total tiller per plant (9.02%) and harvest index (Table3). The selection for these traits would not be effective to improve grain yield. Correspondingly, Assefa (2003) reported low GCV values for days to heading, days to maturity and plant height, and the highest GCV value for grain yield per spike. High PCV and GCV for grain yield, biomass, harvest index, thousand seed weight and plant height were reported in barley (Sharma *et al.,* 2005; Amsal *et al.,* 2006; Bekele *et al.,* 2008)

Table 3: Estimation of different variance parameters, heritability and genetic advance for 16 traits in barley

Characters	Range of mean	Mean ±SEM	δ^2e	δ^2g	δ^2p	PCV (%)	GCV (%)	ECV (%)	H^2 (%)	GA*	GAM (%)
DH	49.5-86	60.36±1.98	7.83	21.4	29.23	8.96	7.66	4.64	73.21	8.15	13.51
DM	82-111	91.80±2.03	8.21	20.97	29.18	5.88	4.99	3.12	71.86	8	8.71
PH	46.50-100.8	83.54±4.23	35.83	49.18	85.01	11.04	8.39	7.17	57.85	10.99	13.15
PDL	2.70-22.10	14.19±1.69	5.77	11.11	16.88	28.95	23.48	16.93	65.81	5.57	39.24
SL	5.63-10.93	8.43±0.57	0.64	0.44	1.08	12.3	7.82	9.49	40.47	0.86	10.25
AL	4.00-15.60	12.46±0.78	1.21	2.91	4.12	16.28	13.68	8.83	70.6	2.95	23.68
FLL	10.03-22.00	14.87±1.37	3.73	1.98	5.71	16.07	9.46	12.99	34.68	1.71	11.48
PTPP	2.31-6.53	4.51±0.54	0.58	0.36	0.94	21.44	13.21	16.89	37.97	0.76	16.77
TTPP	3.40-7.00	5.02±0.58	0.68	0.21	0.89	18.74	9.02	16.43	23.16	0.45	8.94
YLD	1.40-5.55	3.61±0.50	0.5	0.38	0.88	25.91	16.96	19.59	42.86	0.83	22.88
GWPS	0.40-1.75	1.06±0.12	0.03	0.02	0.05	21.09	13.34	16.34	40	0.18	17.38
SWPP	0.60-2.30	1.39±0.14	0.04	0.05	0.09	20.97	15.26	14.39	52.94	0.32	22.87
NSTPS	7.00-31.30	17.76±1.92	7.34	32.78	40.12	35.66	32.24	15.25	81.7	10.66	60.03
TSW	7.85-46.40	30.94±5.21	54.24	27.93	82.17	29.3	17.08	23.8	33.99	6.35	20.51
BYLD	3.60-14.25	8.93±0.96	1.86	3.26	5.12	25.33	20.2	15.27	63.64	2.96	33.2
HI	28.10-58.65	41.21±4.79	45.81	6.33	52.14	17.52	6.11	16.42	12.14	1.81	4.38

Key: ***** 2.06 at 5% selection intensity, DH = days to heading, DM= days to maturity, PH=plant height, PDL = peduncle length, SL=spike length, AL =awn length, FLL=flag leaf length, PTPP =productive tillers per plant, TTPP=total tillers per plant, YLD= grain yield GWPS =grain weight per spike, SWPP, =spike weight per plant, NSTPS=number of spikelet per spike , TSW = thousand seed weight , BYLD =biomass yield , HI=harvest index, SEM= Standard error of the mean, δ^2g= Genotypic variance, δ^2e = Environmental variance, δ^2p = 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.

Broad sense heritability and genetic advance

Heritability values classified as very high (≥ 80 %), moderately high (60-79 %), Moderate (40-59 %) and Low (≤ 40 %) (Singh, 2001) Thus if heritability of a character is very high, selection for such characters could be easier and would be more effective. In this study heritability (H^2) estimates ranged from 12.14 % for harvest index to 81.70 % for number of spike lets per spike (Table 3). Moderately high heritability values recorded for days to heading (73.21 %), days to maturity (71.86 %), peduncle length (65.81 %), awn length (70.60 %) and biomass yield (63. 64 %) indicating that, they were mainly controlled by additive gene effect and fixable through selection Plant height (57.85%), spike length (40.47%) grain yield (42.86%) and spike weight per plant (52.94%) were recorded as moderate heritability in broad sense. Similar findings were reported by Khan *et al*. (2003) and Kumar *et al*. (2003). Highest heritability with highest variability was observed for number of spike lets per spike but moderately high heritability with highest variability were recorded for days to heading, days to maturity and plant height as well (Table 3). This indicates that high opportunity for improvement can be succeeded through selection.

Flag leaf length (34.68%), productive tillers per plant (37.97%), total tillers per plant (23.16%), grain weight per spike (40.00%), thousand seed weight (33.99%) and harvest index (12.14%) scored lower heritability values (Table3). This revealed the environmental effect constitutes a major portion of the total phenotypic variation (Moghaddam *et al.,* 1997). For traits with low heritability, selection may be considerably difficult or impractical due to the masking effect of the environment.

The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. Expected genetic advance as percent of mean was categorized as low (<10%), moderate (10-20%), and high (>20%) (Johnson *et al.,*2010a) Accordingly, number of spike lets per spike (60.03%), peduncle length (39.24%), biomass yield (33.20%), awn length (23.68%), grain yield (22.88%), spike weight per plant (22.87%) and thousand seed weight (20.51%) recorded high genetic advance as per cent of mean (Table 3). This result is in agreement to Jalata *et al.* (2010). These traits were governed by additive gene actions since high values of genetic advance are indicative of additive gene action while low values are indicative of non-additive gene action (Singh and Narayanan, 1993).

High heritability together with high genetic advance is an important factor for predicting the resultant effect for selecting the best individual since the effectiveness of selection depends upon genetic advance of the character selected along with heritability (Manju and Sreelathakumary, 2002). Therefore, in this study, days to heading, peduncle length, awn length, number of spike lets per spike and biological yield had high heritability accompanied with genetic advance as percent of mean (Table 3) indicating selection will be effective considering these characters. It is not necessarily true that, high estimates of heritability are always associated with high genetic gain (Ghuttai *et al.,*2015). Low to moderate heritability and moderate to high genetic advance as percent of means were recorded for grain yield, grain weight per spike, spike weight per plant and thousand seed weight (Table 3). Similar results were reported by Chand *et al.* (2008) and Kahrizi *et al.* (2010)

CONCLUSION ANDRECOMMENDATION

It was concluded that, there are comprehensive genetic variability among the studied materials with better agronomic performance that can provide basic information for further breeding activities for improvement and thus confident enough to expect genetic progress if further breeding activities are carried out.

CONFLICT OF INTERESTS

The authors declare that there is no any conflict of interest

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