RESEARCH ARTICLE

Genetic variability, heritability, and genetic advance for yield and yield related traits of food Barley (*Hordeum vulgare* L.) recombinant inbreed lines at Woreilu district, south Wollo, Ethiopia

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Abebe K, Mekonnen F, Zewdu D. Genetic variability, heritability, and genetic advance for yield and yield related traits of food Barley (*Hordeum vulgare* L.) recombinant inbreed lines at Woreilu district, south Wollo, Ethiopia. AGBIR.2024;40(1):787-791.

Barley is a multipurpose diploid (2n=14) and the most ancient cereal crop. Studying genetic variability and the magnitude of variation in barley is essential for improving the yields and enhancing production. The experiment was conducted on forty-nine six-row recombinant inbred line food barley genotypes in seven by-seven simple lattice design at Woreilu Farmer Training Center in the 2021/22 cropping season to estimate the extent of genetic variability, heritability, and genetic advance among the genotypes. Analysis of Variance (ANOVA) revealed that there was a significant difference ($p<0.001$) among forty-nine genotypes for all the traits studied. A high PCV and GCV were recorded for grain yield, fertile tiller per plant, and biomass yield. High GCV with high heritability and genetic advance as a percent of the mean recorded on grain yield, fertile tillers per plant, and biomass yield. Therefore, considering these traits for direct selection in barely breeding is important.

Key Words; Genetic advance; Heritability; PCV

INTRODUCTION

Food barley (*Hordeum vulgare* L.) is one of the most ancient crops among cereals and has played a significant role in the development of agriculture in the world. It has been cultivated in different continents since ancient times for its tremendous advantages. On the global scale the 2019/2020 cropping season, barley production amounted to approximately 141 million tons, from the total harvested area of 46.9 million ha with an average yield of 3.01-ton ha^{-1} [1]. According to the Central Statistical Agency [2], the area covered by barley in the 2019/2020 cropping season of Ethiopia was estimated to be 0.95 million ha, with a total production of 2.38 million tons, and its productivity is 2.51 tons per hectare.

Barley is one of the most important, economically valuable, and widely used cereal crops belonging to the family Poaceae with a diploid chromosome number (2n=14) [3]. Its grain is essential for preparing traditional food and beverages; the straw is used as animal feed [4]. It is also used as a cover crop to maintain soil quality, fertility, and productivity [5].

Even though barely has a tremendous advantage in the country production system is constrained by several factors, such as the dominant use of low-yielding farmers' varieties, inadequate number of improved varieties adapted to the different production systems, and varied agro-ecological zones [6]. In addition to this, the influence of several biotic and abiotic stresses contributes to reduced barley yields. Besides this, currently, many scholars in Ethiopia, Hitesh et al., [7], Temesgen et al., [8], and Geleta et al., [9] studied barley genetic variability and recorded wide variation in phenologic, morphologic and agronomic traits to generate new varieties, expand the genetic base of cultivars and discover parental lines, with the primary goal of developing of high yielding genotypes; However, there is still a significant gap of improved food barley availability. At the same time, there is still numerous barley genotypes in which their genetic variability did not study. So, further development and identification of desirable genotypes are essential for improving the crop. It depends on the extent of genetic variability in the population and the proportion of variation transmitted from parents to offspring.

Variation is the occurrence of differences among individuals due to differences in their genetic composition and the environment in which they are raised [10,11]. The knowledge of the nature and magnitude of variation in available breeding materials is essential for further crop improvement. Therefore, this study aimed to estimate the extent of genetic variability, heritability, and genetic advance among the food barley genotypes.

MATERIALS AND METHODS

Description of the study sites

The experiment was conducted in the 2021/2022 cropping season at the Woreilu farmer training center. The experimental site located at 10°49′N latitude and 39°28′E longitude, with an altitude of 2770 m.a.s.l. Its mean annual rainfall is 840 mm with a minimum temperature of 15.5°C and the maximum temperature of 22.5°C. The rainy months extend from June to the end of September, and the dominant soil types in the area are vertisol and clay soils [12].

Experimental materials

A total of 49 six-row food barely genotypes including one released variety as a standard check used for the experiment and their pedigrees listed in Table 1.

Experimental design and agronomic practice

The experimental materials were laid out in 7 × 7 simple lattice designs and each genotype was planted on a plot size of 3 m^2 (2.5 m × 1.2 m). The distance between replications, blocks, and plots was 1.5 m, 1 m, and 0.5 m respectively. Each plot consisted of six rows with 20 cm spacing between rows. Planting was done by hand drilling using a seed rate of 100 kg ha^{-1} for each treatment keeping uniform stand counts at emergency. All other management practices were uniformly applied to all plots.

Description of the collected data

Fifteen phonological, agronomic and yield, and yield component data were collected on a plot and plant basis in each experimental unit. These traits were: Days to 50% Heading (DH), Days to 90% Maturity (DM), Biomass Yield in kg (BY), Grain Yield (GY), Thousand Kernels Weight in g (TKW), Harvesting Index (HI), Plant Height (PH), Number of Tillers Per Plant (TPP), Number of Fertile Tillers Per Plant (FTPP), Number of Spikelets Per Spike (SPS), Spike Length (SL), Number of Seed Per Spike (NSPS), Internode Per Plant (IPP), Peduncle Length (PL) and Awn Length (AL).

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Received: 05-Dec-2023, Manuscript No. AGBIR-23-120504; **Editor assigned:** 07-Dec-2023, Pre QC No. AGBIR-23-120504 (PQ); **Reviewed:** 25-Dec-2023, QC No. AGBIR-23-120504; **Revised:** 03-Jan-2024, Manuscript No. AGBIR-23-120504 (R); **Published:** 11-Jan-2024, DOI:10.35248/0970-1907.24.40.787-791

TABLE 1

Pedigree list of forty-nine six-row food barley genotypes including one standard check used for the experiment

No	Genotype	Pedigree
1	HB1966	Standard check
2	IBON46	Carbo/Hamra/4/Rhn-08/3/DeirAlla106//DL71/Strain205/5/ICB_116132
3	IBON47	Rhn/Lignee527/3/Arar//Hr/Nopal/4/Alanda//Lignee527/Arar/5/Maknusa
4	IBON1	ADABELLA/esmeralda/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia1
5	IBON10	CIRU/BGCLM 157.MBV
6	IBON11	CIRU/TOCTE
7	IBON12	CIRU/TOCTE
8	IBON13	CIRU/TOCTE
9	IBON14	CIRU/TOCTE
10	IBON15	CIRU/TOCTE
11	IBON16	CIRU/ZIGZIG
12	IBON17	CIRUELO/LACEY
13	IBON18	GLORIA-BAR/COPAL/3/LBIRAN/UNA80//LIGNEE640
14	IBON19	Gloriabar/copal/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia1
15	IBON2	ATACO/COMINO//ALELI/3/PETUNIA 1
16	IBON20	Gloria-bar/copal/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia 1
17	IBON21	Gloria-bar/copal/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia 1
18	IBON22	KASKADE/LEGACY
19	IBON23	KASKADE/LEGACY
20	IBON24	LACEY/ATILIR
21	IBON25	LBIRAN/UNA80//LIGNEE640/3/PETUNIA 1
22	IBON26	LBIRAN/UNA80//LIGNEE640/3/PUNGSANCHAPSSALBORI
23	IBON27	Lbiran/una80//lignee640/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia 1
24	IBON28	Lbiran/una80//lignee640/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia 1
25	IBON29	LEGACY/CHAMICO/4/BREA/DL70//TOCTE/3/BREA/DL70//CABUYA
26	IBON3	BLLU/3/BREA/DL70//3*CABUYA
27	IBON30	M104/PFC 88210//DOÑA JOSEFA
28	IBON31	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/LEGACY
29	IBON32	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/LEGACY
30	IBON33	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/M104
31	IBON34	P.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia1/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia
32	IBON35	P.sto/3/lbiran/una80//Pignee640/4/bllu/5/Petunia1/6/p.sto/3/Lbiran/una80//Lignee640/4/bllu/5/petunia
33	IBON36	P.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia1/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia
34	IBON37	Penco/chevron-bar/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia 1
35	IBON38	Penco/chevron-bar/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia 1
36	IBON39	Rihane03/3/As46/Aths*2//Aths/Lignee686/6/Rhn//Bc/Coho/3/DeirAlla106//Api/EB89-8-2-15-4/5/CM67/3/Apro//Sv02109/Mari/4/Carbo
37	IBON4	BLLU/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1
38	IBON40	Rhn-03/Eldorado/5/Rhn-03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda/6/QB813-2/5/Aths/Lignee686/4/Rhn-03/3/Bc/Rhn//Ky63-1294
38	IBON40	Rhn-03/Eldorado/5/Rhn-03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda/6/QB813-2/5/Aths/Lignee686/4/Rhn-03/3/Bc/Rhn//Ky63-1294
39	IBON41	Manel/1USWBSI
40	IBON42	Rhn-03/Eldorado/5/Rhn-03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda/6/Rihane-03/3/As46/Aths*2//Aths/Lignee686
41	IBON43	Aths/Lignee686//Mari/Aths*2/3/Lignee527/NK1272//Alanda/4/Maknusa
42	IBON44	ALISO/CI3909-2//FALCON-BAR/3/HIGO/4/Giza130
43	IBON45	Encino/tocte//Manel
44	IBON 48	Rhn-03/Eldorado/5/Rhn-03//Lignee527/NK1272/4/Lignee527/Chn 01/3/Alanda/6/Lignee527/Aths//Lignee527/NK1272
45	IBON5	Brea/dl70//cabuya/6/p.sto/3/lbiran/una80//lignee640/4/bllu/5/petunia 1
46	IBON6	Canela//e.acacia/defra/4/cli18/e.quebrancho//e.quebrancho/ncl95109/3/canela
47	IBON7	CIRU//6B89.2027/CHAMICO
48	IBON8	CIRU//6B89.2027/CHAMICO
49	IBON9	CIRU/3/LEGACY//PENCO/CHEVRON-BAR

Data analysis

Analysis of variance was done using Proc GLM procedures of SAS *version* 9.0, (SAS, 2014) after testing the ANOVA assumptions.

The model for lattice design is:

Where, $Pijk$ =phenotypic value of ith genotype under jth replication and kth incomplete block within replication j, m=grand mean; g_i =the effect of ith genotype; $eijk$ =effect of random error.

bk(j) =the effect of incomplete block k within replication j; rj=the effect of replication j.

Estimation of phenotypic and genotypic parameters

The phenotypic and genotypic variances and coefficients of variation were estimated according to the statistical procedure of SAS software (SAS, 2014) using fixed model (proc fixed) generated the genotypic and error variance, and also other components were calculated with excel by using the formula, adopted by Burton et al., [13] as follow:

Environmental variance $(\sigma_g^2) = MS_e$

Genotypic variance $(\sigma_g^2):(\sigma_g^2) = \frac{MS_g - MS_e}{r}$

Phenotypic variance $\sigma_p^2:(\sigma_p^2) = \sigma_g^2 + \sigma_e^2$

Where, r=number of replication, σ_g^2=Genotypic variance and σ_e^2= Environmental variance

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$

Where, σ_p^2=phenotypic variance, σ_g^2=Genotypic variance and $\bar{x}$=mean of character being evaluated

Heritability (In the broad sense)

Heritability in the broad sense for quantitative characters where computed using the formula developed by Allard [10] as follows:

$$H^2 = \left[\frac{\sigma_g^2}{\sigma_p^2}\right] \times 100$$

Where, H^2=heritability in the broad sense, σ_p^2 =phenotypic variance and

σ_g^2 =genotypic variance

Genetic advance (GA) and genetic advance as a percent of the mean (GAM)

Estimated with the assumption that 5% of the genotypes were selected following the methods illustrated by Johnson et al., [14].

Expected Genetic Advance (GA)

$$GA = K \times \sqrt{H^2(\mathrm{b})}$$

Where, K=the standardized selection differential at 5% selection intensity (K=2.063).

^{2}=heritability in the broad sense, b=phenotypic standard deviation on a mean basis.

The genetic advance as % of means (GAM)

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Where, GAM=genetic advance as a percent of the mean, GA=genetic advance under selection and =Grand mean of the population

RESULTS AND DISCUSSION

Analysis of variance

The result of the analysis of variance revealed, the presence of highly significant variation among genotypes (P<0.01) for days to heading, days to maturity, plant height, tiller per plant, fertile tiller per plant, number of spikelet's per spike, spike length, number of seed per spike, internode per plant, peduncle length, awn length, biomass yield, grain yield, thousand kernel weight, and harvesting index Table 2. It indicates the presence of adequate variability among genotypes for those traits and improve through selection and hybridization. Similarly, Hitesh et al., [7] reported significant genetic variability among food barley genotype (P<0.01) for days to heading, days to maturity, number of tillers plant^{-1}, plant height, spike length, 1000 kernel weight, biomass yield, harvest index, and grain yield and number of spike per plant. Temesgen et al., [8] and Tigist et al., [15] indicated the presence of highly significant variation among food barley genotypes for days to heading, days to maturity, plant height, grain yield, and harvest index.

Range and mean of different characteristics

Based on Table 3, it appears that there was a significant range in various traits, such as grain yield ranging from 1763 kg for IBON27 to 5743 kg for IBON9. Biomass yield ranged from 5464 kg for IBON22 to 15143 kg for IBON29. Plant height spanned from 58.54 cm for IBON7 to 93.09 cm for HP1966. Additionally, the number of seeds per spike ranged between 48.5 for IBON24 to 83. The thousand-kernel weight ranged from 33.43 g for IBON1 to 60.93 g for IBON14. Previous studies by Jimera et al., [16], Temesgen et al., [8], and Geleta et al., [9] also observed a wide range of variations in grain yield, thousand kernel weight, and biomass yield, respectively. Let me know if you need further assistance with this topic.

TABLE 2

Mean squire for 15 quantitative traits of 49 barley genotypes grown at Woreilu Woreda farmer training center in 2021/2022 main cropping season)

Traits	Replication (df=1)	Block (df=12)	Genotypes df=48	Error (df=36)	R^2	CV
DTH	0.26	12.85	71.67**	5.72	0.95	3.42
DTM	1.72	5.25	69.98**	7.12	0.93	2.38
PH	2.55	14.33	126.65**	26.16	0.87	7.18
TPP	6.9	0.39	1.33**	0.3	0.87	15.54
FTPP	11.11	0.4	1.54**	0.26	0.9	16.18
SPS	232.66	0.73	14.58**	2.14	0.92	6.59
SL	14.12	0.35	2.23**	0.38	0.9	8.64
NSPS	2244.5	6.82	130.06**	18.46	0.93	6.48
IPP	0.37	0.28	0.68**	0.18	0.85	8.63
AL	0.83	0.39	2.10**	0.2	0.94	3.49
PDL	11.48	1.92	31.40**	1.12	0.98	4.3
BY	22959.2	752125.9	11896471.10**	1029904	0.94	9.78
GY	4114.54	35365.73	1537674.88**	20700.96	0.99	4.01
TKW	2.3	6.22	57.30**	6.18	0.93	5.46
HI	0.09	11.95	50.84**	12.68	0.85	10.2

Note: ** significant different at P<0.01, df=degree of freedom, CV=Coefficient of Variation, R^2=coefficient of determination, DH=days to 50% heading, DM=days to 90% maturity, PH=Plant Height, TPP=number of Tillers Per Plant, FTPP=number of Fertile Tillers Per Plant, SPS=number of Spiklets Per Spike, SL=Spike Length, NSPS=Number of Seed Per Spike, IPP=number of Inter node Per Plant, AL=Awn Length, PDL=Peduncle Length BY=Biomass Yield, GY=Grain Yield, TKW=Thousand Kernel Weight and HI=Harvest Index.

TABLE 3

Range, mean, variance, genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance as a percent of the mean for 15 characters of barley genotypes in 2021/22 main cropping season

Trait	Mean ± SE	Range	σ^2g	σ^2p	PCV	GCV	h^2b	GA	GAM
DTH	69.93 ± 1.88	58-82	32.97	35.83	8.55	8.21	92.01	11.35	32.97
DTM	112.19 ± 2.10	101-126	31.43	34.99	5.28	5.00	89.85	10.97	32.97
PH	71.26 ± 4.04	54.8-98.6	50.25	63.33	11.17	9.95	79.35	13.03	32.97
TPP	3.63 ± 0.45	2-6	0.51	0.66	22.31	19.56	76.02	1.27	32.97
FTPP	3.19 ± 0.41	2-5	0.64	0.77	27.59	25.08	82.64	1.50	32.97
SPS	22.21 ± 1.16	16-29	6.22	7.29	12.16	11.21	85.30	4.75	32.97
SL	7.01 ± 0.48	3.8-9.8	0.93	1.12	15.12	13.69	83.58	1.83	32.97
NSPS	66.32 ± 3.39	48-87	55.80	65.03	12.15	11.26	85.82	14.27	32.97
IPP	4.82 ± 0.33	3-6	0.25	0.34	12.03	10.37	74.62	0.89	32.97
AL	12.88 ± 0.36	10.6-14.8	0.95	1.05	8.00	7.61	90.38	1.92	32.97
PDL	24.60 ± 0.85	16.4-34	15.14	15.70	16.08	15.80	96.43	7.88	32.97
BY	10372.45 ± 800.66	4500-16000	5433283.5	5948235.55	23.51	22.47	91.34	4595.87	32.97
GY	3589.44 ± 113.51	1815-5900	858948.03	869298.51	25.98	25.82	98.81	1900.56	32.97
TGW	45.56 ± 1.96	32-66	25.56	28.65	11.74	11.19	89.21	9.85	32.97
HI	34.90 ± 2.81	24.45-50.22	19.08	25.42	14.44	12.52	75.06	7.80	32.97

Note: DH=days to 50% heading, DM=days to 90% maturity, PH=Plant Height, TPP=number of Tillers Per Plant, FTPP=number of Fertile Tillers Per Plant, SPS=number of Spiklets Per Spike, SL=Spike Length, NSPS=Number of Seed Per Spike, IPP=number of Inter node Per Plant, AL=Awn Length, PDL=Peduncle Length BY=Biomass Yield, GY=Grain Yield, TKW=Thousand Kernel Weight and HI=Harvest Index.

Estimates of phenotypic and genetic variance and coefficient of variation

Table 3 provides estimates of genotypic and phenotypic variance, as well as genotypic and phenotypic coefficient of variation. It's worth noting that in this study, PCV values were greater than GCV values for all traits, albeit only slightly. This suggests that environmental influence had a low effect on trait expression. Burton and Devane [13] classify GCV and PCV values as low, medium, or high based on whether they fall below 10%, between 10-20%, or above 20%, respectively. Based on this classification, grain yield, fertile tiller per plant, and biological yield all showed high GCV and PCV. Tiller per plant, on the other hand, showed moderate GCV and high PCV. This suggests that phenotypic expression is a good indicator of genotypic potential, making these characters effective for selection. Similar results were reported by Jimera et al., [16] for grain yield, biomass yield, and fertile tillers per plant, as well as by Azeb et al., [17] for grain yield and biological yield.

Peduncle length, spike length, harvesting index, number of seeds per spike, thousand kernel weight, and internode per plant all showed moderate GCV and PCV. It suggests the existence of enough genetic variation on the studied genotypes to perform a selection for improvement. Similarly, Shegaw et al., [18] reported similar results for spike length and thousand kernel weights. Temesgen et al., [8] also reported similar results for the number of seeds per spike and 1000-kernel weight. Plant height showed low GCV and moderate PCV, Suggesting the presence of considerable environmental influence on the phenotypic expression of this trait has low responsiveness to selection. Days to maturity, awn length, and days to 50% heading showed low GCV and PCV. Indicates minimum genetic variation among the genotypes for these traits and practically impossible to improve these traits through selection. Similarly, Shegaw et al., [18] observed low GCV and PCV for days to maturity. Temesgen et al., [8] and Geleta et al., [9] also reported similar results for days to heading, days to 90% maturity, and awn length.

Heritability is a good index of the transmission of characters from parents to offspring. Table 3 provides an estimation of heritability. High heritability values indicated the genotypic variance constitutes a large portion of the total phenotypic variations, and low heritability values indicated a relatively high contribution of the environment to the phenotype. Based on this delineation in the present experiment, all studied traits showed high heritability values, indicating that the observed variation was mainly under genetic control and less influenced by the environment. Hence, the success of crop improvement through selection could be possible. Similarly, Jimera et al., [16] and Mohammad et al., [19] reported high heritability values for grain yield and 1000 kernel weight. Tigist et al., [15] also observed similar results for days to heading, days to maturity, thousand-kernel weight, grain yield, number of seeds per spike, and biomass yield.

Table 3 provides expected genetic advance and genetic advance as a percent of the mean. Improvement of characters in genotypic value for the new population compared with the base population under the single cycle selection at a given selection intensity refers to genetic advance [20]. In the present study, the expected genetic advance as a percent of the mean showed a wide range of variation from 9.78 % for days to maturity to 52.95 % for grain yield.

The effectiveness of selection depends upon the genetic advance of the character selected along with heritability [14]. Grain yield, fertile tiller per plant, biomass yield, peduncle length, spike length, thousand kernel weight, number of seeds per spike, spike lets per spike, tiller per plant, and harvesting index had high heritability with high GAM in this study which indicates the presence of additive gene action for the inheritance of these traits and simple selection would be effective for improving these traits. Similarly, Tigist et al., [15] reported similar results for thousand kernel weight, grain yield, number of kernels per spike, biomass yield, fertile tillers per plant, and spike length. Adhikari et al., [21] also reported similar results for grain yield. Days to heading, plant height, internode per plant, and awn length showed high heritability with moderate genetic advance as a percent of the mean, indicating that these traits were controlled by both additive (genes transmitted from parents to offspring) and non-additive (interaction between genes of the same or different loci) gene actions. Similarly, Shegaw et al., [18] and Azeb et al., [17] reported high heritability with moderately high genetic advance as a percent of the mean in barley. On the other hand, days to maturity showed high heritability estimates with low genetic advance as a percent of the mean, indicating that this trait controlled by non-additive gene action and genotype × environment interaction plays significant roles in the expression of this trait, so selection may not be effective.

Al-tabbal and Al-fraihat [22] reported a similar result. High GCV with high heritability and genetic advance provide better information than other parameters alone [23].

Grain yield, fertile tiller per plant, and biomass yield had high heritability, GCV, and GAM value in the present study, which indicates a large portion

of genetic variation, is attributable to additive gene action. Similarly, Shegaw et al., [18] reported high heritability, GCV, and GAM for grain yield [24,25].

CONCLUSION

The result of the analysis of variance suggests that the presence of genetic variability among genotypes for all tested traits. This result shows the presence of variation in genetic constituent among the genotypes for the concerned traits. It suggests the present of significant opportunity for improving barley genotypes through selection. The findings of this study should be utilized by breeders who are interested in enhancing the quantity of food barley recombinant inbred line genotypes. Furthermore, it is recommended that these barley materials be evaluated in various agro-ecologies during different seasons to draw more dependable conclusions and recommendations.

ACKNOWLEDGEMENTS

The authors would like to thank Mekdela Amba University for its financial support, and we are also grateful to Holeta Agricultural Research Institute for its support in providing seeding materials to conduct this study.

REFERENCES

1. Food and Agriculture Organization of the United Nation. 2020.
2. CSA R. The Federal Democratic Republic of Ethiopia Report on Area and Production of Major Crops. Addis Ababa, Ethiopia. 2016.
3. Alnarp. Doctoral Thesis on Barley Genetic Resources Swedish University of Agricultural Sciences. 2013.
4. Abraha A, Uhlen AK, Abay F, et al. Genetic variation in barley enables a high quality *injera*, the Ethiopian staple flat bread, comparable to tef. Crop Sci. 2013;53(5):2040-2050.
5. Magdoff F, van Es H. Building soils for better crops. Beltsville: Sustainable Agriculture Network; 2000.
6. Gebeyaneh AA. Genetic variability and breeding potential of barley (*Hordeum vulgare* L) landraces from north Shewa in Ethiopia.
7. Yadav HC, Singh SK, Gupta PK, et al. Studies on path coefficient analysis and genetic divergence in feed barley (*Hordeum vulgare* L.). J Pharmacogn Phytochem. 2018;7(2):613-616.
8. Dinsa T, Mekbib F, Letta T. Genetic variability, heritability and genetic advance of yield and yield related traits of food barley (*Hordeum vulgare* L.) genotypes in Mid Rift valley of Ethiopia. Adv Crop Sci Technol. 2018;6(5):1000401.
9. Negash G, Lule D, Jalata Z. Estimation of genetic variability, heritability and genetic advance among Ethiopian food barley (*Hordeum vulgare* L.) landraces for yield and yield related traits. Int J Agric Sci. 2021;6(3):185-192.
10. Allard RW. Principles of plant breeding. Soil Sci. 1961;91(6):414.
11. Falconer DS. Introduction to quantitative genetics. Pearson Education India; 1996.
12. Arage K. Environmental profile of woreilu woreda.
13. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1953;45(10):478-481.
14. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans1. Agron J. 1955;47(7):314-318.
15. Shiferaw T, Abate B, Lakew B. Genetic variability and association of traits in Ethiopian barley (*Hordeum vulgare* L.) genotypes at Holetta, Central Ethiopia. J Agric Crop Res. 2020;8(1):11-19.
16. Haile J, Legesse H, Rao CP. Genetic variability, character association and genetic divergence in barley (*Hordeum vulgare* L.) genotypes grown at Horo district, Western Ethiopia. Sci Technol Arts Res J. 2015;4(2):1-9.
17. Hailu A, Alamerew S, Nigussie M, et al. Genetic variability, heritability and genetic advance for yield and yield related traits in barley (*Hordeum vulgare* L.) germplasm. Middle East J Sci Res. 2016;24(2):450-458.
18. Derbew S, Elias U, Hussein M. Genetic variability in barley (*Hordeum vulgare* (L.)) landrace collections from Southern Ethiopia. Int J Sci Res. 2013;12(2):125-131.
19. Matin MQ, Amiruzzaman M, Billah MM, et al. Genetic variability and path analysis studies in barley (*Hordeum vulgare* L.). Int J Appl Sci Biotechnol. 2019;7(2):243-247.
20. Singh. Plant breeding principles and methods. 2001;896.
21. Adhikari BN, Joshi BP, Shrestha J, et al. Agronomic performance and correlation study in barley (*Hordeum vulgare* L) Genotypes. Sch J Agric Vet Sci. 2018;5(12):658-663.
22. Al-Tabbal JA, Al-Fraihat AH. Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. J Agric Sci. 2012;4(3):193.
23. Manju PR, Sreelathakumary I. Genetic variability, heritability and genetic advance in hot chilli (*Capsicum chinense* Jacq.).
24. Lakew B, Semeane Y, Alemayehu F, et al. Exploiting the diversity of barley landraces in Ethiopia. Genet Resour Crop Evol. 1997; 44:109-116.
25. Sharma JR. Statistical and biometrical techniques in plant breeding. Indian J Genet Plant Breed. 2001;61(04):391-392.