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Genetic Variability and Trait Association of Semi-Hulled Barley (*Hordeum vulgare* L.) Genotypes in North Western Ethiopia

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ABSTRACT

Barley is the fifth most important cereal crop and a secondary center of diversity in Ethiopia, with a large number of accessions preserved in its gene bank. To determine the genetic variability and to assess the associations among morpho-agronomic traits. 22 Semi-hulless genotypes were originated from ICARDA (International Center for Agricultural Research in the Dry Area) was evaluated in the 2022 and 2023 main cropping seasons at Debretabor sub-center agricultural research using a randomized complete block design with three replications. The analysis of variance revealed highly significant differences among semi-hulless barley genotypes in all traits except biomass yield, indicating the presence of genotypic variation among the studied genotypes. Fifty percent of the semi-hulless barley genotypes gave significantly higher yields than the grand mean (3349.58) kg ha^{-1}. The genotype (G13) (4392.67 kg ha^{-1}) showed the highest grain yield among all the semi-hulless barley genotypes. The number of grains per spike had a high phenotypic and genotypic coefficient of variation. Both higher heritability and higher genetic advance were observed for days to heading, number of grains per spike, thousand seed weight, and plant height. Grain yield exhibited positive, highly significant correlations with both genotypic and phenotypic traits, including the number of grains per spike, and harvest index. Both genotypic and phenotypic path coefficient analysis revealed that thousand-seed weight, harvest index, spike length, and number of grains per spike had positive direct effects on grain yield. Thus, these traits could be used as selection criteria for yield improvement in semi-hulless barley.

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Introduction

Barley (*Hordeum vulgare* L.) is an annual cereal crop, which belongs to the tribe *Triticeae* of family *Poaceae.* It is diploid (2n=14) and self-pollinated (Gepts, 1993). Barley is Ethiopia's fifth most important cereal crop in terms of area coverage and annual production, behind wheat, sorghum, maize, and tef (Bakala et al., 2022).

Ethiopia produces 2,024,921.70 tons of barley yearly on an area of about 959,273.40 hectares (Belete, 2023). More than 339,689 hectares of barley are grown in the Amhara region, yielding 633,115.4 tons. The national average of 2.11 tons/ha is higher than its productivity of 1.86 tons/ha (Birhanu et al., 2020).

Worldwide, barley is used as fodder and animal feed for animals and is a major food crop in highland regions where other grains cannot flourish (Bishnoi et al., 2022). Furthermore, it is essential for preserving food security. Glucan is a vital dietary fiber that dramatically reduces blood cholesterol, making up three to seven percent of barley grain (Agarwal, 2023; Hailu et al., 2015).

The genotypic correlation coefficient may serve as a crucial selection process criterion by providing a measure of the genetic correlation between traits (Van et al.,2019). The correlation coefficient is crucial in identifying the features that have a direct impact on grain yield, but it is not enough to assess the indirect effects of these traits on grain yield (Eleta et al., 2019). The correlation coefficient is divided by path analysis into the direct and indirect effects of independent features on yield (Khan et al., 2022). As a result, basic correlation coefficients are used to examine path coefficients. Understanding the degree and type of interrelationships between characters facilitates the development of an effective multiple-trait selection scheme by allowing for both direct and indirect selection of component characters (Patial et al., 2013; Gutierrez-Reinoso, 2021).

Before developing an appropriate breeding strategy for genetic improvement, estimation of variability for yield and potential yield attributes becomes crucial (Kumar et al., 2019;

Bailey-Serres et al., 2019). To determine the genetic variability and trait association of semi-hulled barley genotypes for a future breeding program, the current study was designed. Furthermore, by estimating the degree of association between trait pairs at the genotypic and phenotypic levels, the study compares the direct and indirect effects of the traits on yield improvement through yield-contributing traits, which may lead to the development of potential selection criteria for the creation of improved semi -hulless barley genotypes with increased yield.

Materials and Methods

Description of the Experimental Area

The experiment was carried out over the main cropping seasons of 2022 and 2023 at the Debretabor Agricultural Research Sub Center, which is located at 11.87 °N and 38.03 °E with an average annual rainfall of 1553 mm, it is at a mean elevation of 2630 m above sea level. The range of temperatures is 13.5 to 29.7 ^{0}C. The soil type is Luvisol, and its pH range is 4.5-5.6, making it an acidic soil.

Experimental Materials and designs

The experiment was laid out in a randomized complete block design with three replications, and each plot consisted of six rows spaced 0.2 m with 2.5 m length with the total plot size were 1.2 m × 2.5 m. The seed rate was 125 kg ha^{-1} and fertilizers were applied during planting in the form of Urea and NPS at the rate of 41,0 and 46,0 kg ha^{-1} N and P_2O_5 respectively. For data collection, the middle four rows were used. All management including weeding and other cultural practices were achieved uniformly to the entire plot according to the local recommendation.

Data Collection

Plant height (cm): Was measured as the height in centimeter from the soil surface to the tip of spike excluding the awn at maturity and expressed as an average of randomly taken ten plants per plot.

Spike length (cm): Spike length of the main plant was measured in centimeter from base to the tip excluding the awns and expressed as the average of randomly taken ten plants in a plot.

Number of grains per spike: Was determined by counting the number of grains produced on the main tiller of each plant and expressed as an average of randomly taken ten plants in each plot.

Days to heading: Was recorded as the number of days from seedling emergence to the date on which 50% of a plot has produced heads.

Days to maturity: Was recorded as the number of days from seedling emergence to the stage when 90% of a plot reached maturity.

Biomass yield (kg ha^{-1}): Was determined by weighing the total dried above ground biomass from the four central rows of each plot and expressed in kilogram per hectare.

Grain yield (kg ha-1): Grain yield of the four central rows adjusted to 12.5% moisture content and expressed in kilogram per hectare.

Harvest index (%): Was calculated on plot bases from the four rows as the ratio of dry weight of the grain to the dry weight of the above ground biomass and expressed as a percentage.

Thousand seed weights (g): Weight in gram of random samples of thousand seeds per plot adjusted to 12.5% moisture content.

Table 1. List of six rowed and spring nature semi-hulless genotypes.

Genotype Code	Pedigree
G1	ATAH92/GOB//MERIT, BICB09-1323-0AP-0TR-1MR
G2	Arupo'S'12/PI002325Maf102//Cossack/4/ Viringa's'/5/Litani ICB03-0186-6AP-0AP
G3	N09084 F3 10/030587 N09084 F3 10/030587-0TR-4MR
G4	V Morales/6/LEGACY//PENCO/CHEVRON-BAR M06356 F6 08/030377-0TR-4MR
G5	H98029005/199049003G08092 F3-0TR-9MR
G6	G09143 F3 10/030637G09143 F3 10/030637-0TR-9MR
G7	Atahualpa/6/Rhodes's'//TB/Chzo/3/Gloria'S'/Copal'S'/4/ESC-11-72-83-3E-7E-5E-1E/5/Aleli ICB02-0537-0AP-8TR-1AP-0AP-0TR-0MR
G8	PENCO/CHEVRON-BAR 101067 04/D00163-0AP-0TR-6MR
G9	Alanda-0112/Petunia 1 ICB03-0302-12AP-0AP-0TR-0MR
G10	W13167/6/ANCA/2469//TOJI/3/SHYRI/4/ATACO/5/ALELI/7/LEO-B/CANELA//GOB96DHICB06-1179-34-AP-0AP-0TR-0MR
G11	W13167/6/ANCA/2469//TOJI/3/SHYRI/4/ATACO/5/ALELI/7/Schooner/Babunji//Noor68/Kataf ICB06-1181-17AP-0AP-0TR-0MR
G12	Aths/Lignee686//Orge905/Cr289-53-2/3/F6Vnb4_Khomes ICB02-0149-0AP-0TR-0MR
G13	Atahualpa//Alanda-01/Hamra/3/Keel ICB03-0170-26AP-0AP-0TR-0MR
G14	VMorales/6/LEGACY//PENCO/CHEVRON-BAR M06356 F6 08/030377-0TR-4MR
G15	Alanda-0112/Petunia 1 ICB03 -0302-12AP-0AP-0TR-0MR
G16	N09084 F3 10/030587 N09084 F3 10/030587-0TR-2MR
G17	PETUNIA 2/3/ AGAVE /SUMBARD400//MARCO/4/PETUNIA 1/5/TRA-B/1038//PETUNIA 1/3/PENCO/6/BLLU CBSS01Y00848T-A-0Y-2M-1M-2Y-0M
G18	Arupo'S'12/3/P1002325/Maf102//Cossack/4/Viringa'S'/5/Litani ICB03-0186-6AP-0AP
G19	Viringa'S' Tarida ICB01-1130-8AP-0AP-0TR-0MR
G20	101067/H96009015001 G0810 F3-0TR-16MR
G21	VMorales/6/LEGACY//PENCO/CHEVRON-BAR M06356 F6 08/030377-0TR-5MR
G22	Store

Statistical Analysis

R4.4.0 program performed an analysis of variance for the genotype by year combined data. At a significance level of 5% and 1%, mean separation was performed using the least significant difference (LSD).

Estimation of Genetic Parameters

A formula adapted from Johnson et al. (1955) was used to estimate various genetic parameters, such as genotypic variance (σ^2g), phenotypic variance (σ^2p), phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV).

Genotypic variance (σ^2g) = $\frac{MSg-MSe}{r}$

where: σ^2g = genotypic variance
MSg = mean square due to genotypes.
MSe = environmental variance (error mean square)
r = number of replications

Phenotypic variance (σ^2p) = $\sigma^2g + \sigma^2e$

Where:
σ^2p = phenotypic variance
σ^2e = error variance

Genotypic Coefficient of Variation (GCV)

It was calculated using the following formula suggested by Burton and De Vane (1953) and Johnson et al. (1955): formula:

$$GCV = \frac{\sqrt{\sigma 2g}}{\bar{x}} * 100;$$

Where: GCV = Genotypic coefficient of variation

Phenotypic Coefficient of Variation (PCV)

$$PCV = \frac{\sqrt{\sigma 2p}}{\bar{x}} * 100$$

PCV =Phenotypic coefficient of variation
$\bar{x}$ = Grand mean of the characters under study.

PCV and GCV (Whan et al., 1991): >20% - high; 10 - 20%- moderate; <10% – low

Heritability

Heritability is, in general, defined as the ratio of genotypic variance to the total observed variance in the entire population. Heritability (H^2) in the broad sense was determined using Allard's formula (1960).

$$H^2 = \left[\frac{\delta^2 g}{\delta^2 p}\right] x100$$

H^2 = heritability in a broad sense
σ^2g = genotypic variance
σ^2 p = phenotypic variance (σ^2g) + (σ^2e)
σ^2e= environmental variance

Genetic Advance

Genetic advance (GA) was calculated with the method suggested by Allard (1960):

GA=k. σ^2p. H^2
Where: GA genetic advance.
constant = 2.06 at 5% selection intensity.
σ^2p= phenotypic standard deviation.
H^2=Heritability in a broad sense.

Genetic Advance as a Percent of the Mean (GAM)

Genetic advance as a percent of the mean was calculated to compare the extent of the predicted advance of different traits under selection, using the following formula.

GAM = GA x100 / $\bar{x}$.

Where:
GAM=Genetic advance as a percent of the mean.
GA=Genetic advance under selection.
$\bar{x}$ = the Grand mean of the trait.

Genetic advance (Johnson et al., 1955): >20% - high; 10- 20% - moderate; <10% - low

Genotypic coefficient of correlation

$$r_g = \frac{gcov \rightleftarrows x.y}{\sqrt{\delta^2 gx.\delta^2 gy}}$$

Phenotypic coefficient of correlation

$$r_g = \frac{gcov \rightleftarrows x.y}{\sqrt{\delta^2 gx.\delta^2 gy}}$$

Where:
r_g= Genotypic correlation coefficient
r_p = Phenotypic correlation coefficient
$Gcov_{xy}$ = Genotypic covariance between variables x and y
$Pcov_{xy}$ = Phenotypic covariance between variables x and y
$\sigma^2_g x$= Genotypic variance for variable x
$\sigma^2_g y$ = Genotypic variance for variables y
$\sigma^2_p x$ = Phenotypic variance for variables x
$\sigma^2_p y$= Phenotypic variance for variables y

Path Coefficient Analysis

The analysis was done following the method suggested by Dewey and Lu (1959):

rij= pij +∑ rik +pkj

Where:
rij = mutual association between the dependent character,
i= (yield-related trait) and independent character,
j= (grain yield) as measured by the correlation coefficients;
Pij= is the components of direct effects of the independent character (i),
Σ rik +pkj = summation of components of the indirect effect of a given independent character (i) on the given dependent character (j) via all other independent characters (k).

The contribution of the remaining unknown characters is measured as the residual effect (R^2) which is calculated as: √1-R^2, Where R^2=∑ pij +rij.

Results and Discussion

Analysis of Variance for Some Morpho-Agronomic Traits

The significant difference ($P \leq 0.01$) was observed among genotypes in all evaluated traits except biomass yield (Table 2). The year was highly significant ($P \leq 0.01$) for days to heading, days to maturity, plant height, number of grains per spike, biomass yield, and harvest index. The genotype-by-year interaction was highly significant for days to maturity, plant height, grain yield, and harvest index. The year was highly significant ($P < 0.01$) for days to heading, days to maturity, plant height, number of grains per spike, biomass yield, and harvest index. The genotype-by-year interaction was highly significant for days to maturity, plant height, grain yield, and harvest index. This indicated the existence of significant genetic variability among the evaluated semi-hulless barley genotypes, and this in turn provides ample scope for selecting superior genotypes to improve production and productivity. Previous studies have reported highly significant differences in genotypes for grain yield and yield-related traits in barley (Aklilu et al., 2020). Similarly, Tiegist (2010) reported the existence of highly significant variations for days to heading, days to maturity, thousand seed weight, spike length, number of grains per spike, and plant height, in Ethiopian barley landrace collections. Similar findings have also reported significant differences in genotypes by environment interaction effect for plant height, number of grains per spike, and grain yield in barley (Dyulgerova et al., 2021). This finding in agreement with those who reported a highly significant variation among food barley genotypes for all traits considered in the study (Geleta et al., 2019).

Based on the mean values of 22 semi-hulless barley genotypes the range of various traits days to heading varied from (52.67-73 days), days to maturity (102.33-113.00 days), plant height (68.18-101.85 cm), spike length (6.54-9.73 cm), number of grains per spike (21.1-60.13), thousand seed weight (34.00-56.07 g) and grain yield (2244.92-4392.67 kg ha^{-1}). A comparative study of semi-hulless barley genotypes for eight traits showed a clear distinction among genotypes. G12 (52.67 days) was the earliest to head. Regarding days to maturity, G20 (102.33 days) was the earliest to mature compared to other genotypes. For plant height, the genotype G22 (101.85cm) had the tallest plant height. Regarding spike length, G3 (9.73cm) had the longest spike length. G1 (60.13) had the highest number of grains per spike. G13 (4392.67 kg ha^{-1}) showed the highest grain yield among all the genotypes, regarding thousand seed weights, and G22 (56.07 g) had the highest thousand seed weights among all genotypes tested in the experiment (Table 3).

Phenotypic and genotypic variations

Genetic variability is an important tool that helps in the formulation of breeding strategies for crop improvement, based on the information on the genetic properties of the population (Pandey et al., 2011; Swarup, Cargill et al., 2021). Total variation based on the genotypic effects is a measure of genotypic and phenotypic variance, which is known as broad-sense heritability (Allard, 1960). Parida et al. (2018). The highest genotypic coefficient of variation (GCV) was observed for the number of grains per spike (46.02). Moderate genotypic coefficient of variation was observed by grain yield (17.98), plant height (14.66), thousand seed weight (16.19), and spike length (14.97) similar result was also obtained from the previous finding (Necdet, 2016) (Table 4). These characters with high GCV values indicate greater potential for selection.

A high phenotypic coefficient of variation (PCV) was recorded for the number of grains per spike (47.98), grain yield (29.62). biomass yield (20.34). Whereas, moderate (PCV) values were observed for traits like plant height (18.00) and spike length (17.97). Days to maturity showed the lowest PCV and GCV values (4.54) and (3.29), respectively. In this study, higher PCV values were observed than GCV, indicating environmental influence for trait expression. A similar fashion has also been reported by Dyulgerova (2021) in barley.

Estimates of Heritability and Expected Genetic Advance

Heritability, estimates can be grouped in to the following categories: low heritability (<40%), medium heritability (40-59%), moderately high (60-79%) and very high heritability (>80%) according to Allard,(1960, very high heritability was observed for days to heading (88.00), number of grains per spike (92.00), thousand seed weight (84.00), while moderately high heritability was displayed for plant height (66.00), and spike length (69.00). Similar results showed very high heritability for plant height and thousand-seed weight by Madhu Patial et al. (2023), Eshghi and Akhundova (2010) also reported very high heritability for these traits, indicating that those traits are inherited from the parents to offspring. Moderate heritability values were recorded for days to maturity (53.00) and grain yield (36.00). All the traits showed high genetic advance except days to maturity, which showed low genetic advance as a percentage of the mean. A Higher heritability coupled with higher genetic advance was observed for days to heading, number of grains per spike, thousand seed weight, and plant height.

Table 2. The mean square of the combined analysis of variance for all the traits studied of 22 semi-hulless genotypes

SOV	DH	DM	PH	SL	NGS	BY	GY	TSW	HI
Genotype (G)	218.71**	47.40**	477.92**	4.87**	1156.14**	3018488.46^{ns}	1709464.47**	137.70**	163.49**
Year (Y)	528.00**	334.09**	498.12**	0.35^{ns}	1138.13**	25047348.48**	52560.27^{ns}	0.00^{ns}	332.29*
G x Y	0.0^{ns}	12.68*	106.95**	0.83^{ns}	20.96^{ns}	2936237.37^{ns}	1092309.33**	0.0^{ns}	102.10*
MSE	5.42	6.90	37.18	0.59	22.61	2033098.85	479080.78	10.26	55.01

SOV=Source of variation, MSE=mean square error, ** and * = Significant at 0.01 and 0.05 probability levels, respectively and ^{ns}=non-significant difference, DH=days to heading, DM=days to maturity, PH=plant height, SL= spike length, NGS=number of grains per spike, BY=biomass yield, GY= Grain yield, TSW= Thousand seed weight, HI= harvest index

Table 3. The mean performance of the combined analysis for yield and yield components of 22 semi-hulless genotypes tested at Debretabore agricultural research sub-center in the 2022 and 2023 cropping seasons.

GN	DH	DM	PH	SL	NGS	GY	TSW	HI
G1	69.67	106.00	86.25	7.75	60.13	3879	37.00	44.84
G2	69.00	106.50	75.63	7.93	29.47	3924.83	43.33	47.67
G3	73.00	113.00	82.30	9.73	29.57	3175.58	35.33	41.06
G4	66.00	104.83	68.18	7.50	59.27	3585.25	37.60	45.80
G5	59.67	105.67	84.77	7.75	21.10	2787.42	47.73	49.02
G6	70.33	107.33	75.87	8.05	27.73	2873.42	37.60	35.65
G7	54.33	103.33	66.72	7.31	48.30	3587.5	44.33	42.23
G8	65.67	105.83	80.72	7.60	55.97	3333.58	37.13	41.84
G9	56.67	103.33	80.72	6.80	52.13	3873.75	39.13	44.00
G10	65.67	106.33	88.22	7.19	51.53	3852.33	42.27	45.29
G11	64.33	106.83	69.07	6.54	49.13	3405.5	43.07	39.61
G12	52.67	104.00	71.02	7.40	51.77	3724.67	36.93	46.23
G13	62.67	103.67	93.73	7.25	46.60	4392.67	40.13	48.56
G14	66.67	103.83	68.75	7.55	51.93	2900.08	39.80	37.74
G15	53.33	104.83	82.57	7.03	53.53	3860.17	39.20	43.02
G16	72.00	110.33	79.10	9.41	29.80	3063.67	34.00	44.04
G17	66.67	103.83	78.63	9.47	22.10	2244.92	41.20	30.43
G18	67.00	106.17	74.17	8.20	27.40	3636.17	41.40	49.48
G19	58.00	103.33	89.25	9.43	24.23	2462.75	43.40	32.61
G20	62.00	102.33	81.95	7.92	49.23	3105.92	40.27	38.97
G21	67.00	104.83	72.08	8.30	58.13	3059.58	36.13	39.04
G22	69.67	112.17	101.85	8.67	26.07	2961.92	56.07	36.87
Mean	64.18	105.83	79.62	7.94	42.05	3349.58	40.59	42.00
CV (%)	3.63	2.48	7.66	9.65	11.31	20.66	7.89	17.66
LSD	0.81	0.91	2.11	0.27	1.65	239.61	1.11	2.57

GN=Genotype name, CV (%) =Coefficient of variation, DH=days to heading, DM=days to maturity, PH (cm)=plant height, SL (cm)= spike length, NGS=number of grains per spike, BY (kgha^{-1}) =biomass yield, GY (kgha^{-1}) = Grain Yield, TSW= Thousand seed weight, HI (%) = harvest index

Table 4. Estimates of mean, variance components, and coefficients of variability, heritability, and genetic advance of the 22 semi-hulless barley traits.

Traits	DH	DM	PH	SL	NGS	GY	TSW
GM	64.18	105.83	79.62	7.94	42.1	3349	40.59
Range	50-76	99-122	49.6-117	5.4-11.6	16.2-73	1259-5684	29.6-57
σ^2g	69.86	12.15	136.24	1.42	374.52	363014	43.24
σ^2p	78.97	23.1	205.43	2.04	407.11	983435	51.22
σ^2e	9.12	10.95	69.20	0.62	32.59	620420	7.98
GCV	13.02	3.29	14.66	14.97	46.02	17.98	16.19
PCV	13.84	4.54	18.00	17.97	47.98	29.62	17.63
ECV	4.7	3.12	10.44	9.93	13.57	23.51	6.95
H^2	0.88	0.53	0.66	0.69	0.92	0.36	0.84
GA	16.2	5.21	19.6	2.04	38.24	754	12.5
GAM	25.23	4.92	24.6	25.71	90.93	22.51	30.66

GM=grand mean, σ^2g = Genotypic variance, σ^2e = Environmental variance, σ^2p= Phenotypic variance, GCV = Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, H^2 (%)= Broad-sense heritability, GA= Genetic Advance, GAM(%) = Genetic advance as percent of mean, and K = Selection intensity, DH=days to heading, DM=days to maturity, PH=plant height, SL= spike length, NGS=number of grains per spike, GY= Grain yield, TSW= Thousand seed weight, HI(%)= harvest index.

Moderate heritability, along with high genetic advance as a percentage of the mean, was observed for grain yield. Moderate heritability and low genetic advance were observed for days to maturity. Genetic advance as a percent mean ranged from (7.62 %) for days to maturity to (23.62 %) for 1000 grain weight, indicating that selecting the top 5% of the genotypes could result in an improvement range of 7.62% for days to maturity to 23.62% for 1000 grain weight (g). According to Kobir et al. (2023) high genetic advance was obtained for both plant height and grain yield.

Phenotypic and genotypic correlation

Genetic associations between different traits can be identified, providing a helpful tool in the selection process. At the genotypic level, days to heading (0.28*), number of grains per spike (0.3), biomass yield (0.53**), and harvest index (0.33**) exhibited a highly significant positive correlation with grain yield whereas, spike length and thousand seed weight were exhibited non-significant negative correlation with grain yield. Among yield-contributing traits, at the genotypic level, plant height had a highly significant positive correlation with both spike length and thousand seed weight (0.42**); Similar results of positive correlation of plant height with spike length by Shiferaw et al. (2020); Maduhu Patial *et al* (2023 positive correlation of plant height with spike length. Plant height had a highly significant positive correlation with days to heading (0.30**).

At the phenotypic level, the number of grains per spike (0.58**), and harvest index (0.58**) showed a highly significant positive correlation with grain yield. Spike length (-0.55**), thousand seed weight (-0.58**), and days

to maturity (-0.26) showed a highly significant negative correlation with grain yield. Negative association of days to maturity with grain yield was reported by Shubham et al. (2023). Days to heading had a highly significant positive correlation with days to maturity (0.38), plant height (0.77**), and the number of grains per spike (0.5*). Days to maturity had a significant positive correlation with plant height (0.49*) and spike length (0.51*). However, days to maturity had a significant negative correlation with the harvest index (-0.48*). In the other side, plant height had a significant positive correlation with thousand-seed weight (0.47*). Spike length also had a highly significant correlation with plant height (0.42**), while a negative significant correlation with number of grains per spike (-0.69*). Thousand-seed weight also had a significant positive correlation with plant height (0.42*). However, there was a non-significant negative correlation with the harvest index (-0.41^{ns}).

Table 5. Genotypic correlation coefficient (r_g) (upper diagonal) and phenotypic correlation coefficient (r_p) (below diagonal) of eight semi-hulless barley traits.

Traits	DH	DM	PH	SL	NGS	TSW	HI	GY
DH		0.38**	0.77**	0.3^{ns}	0.5*	-0.27^{ns}	-0.13^{ns}	0.16^{ns}
DM	0.28*		0.49*	0.51*	-0.37^{ns}	0.15^{ns}	-0.48*	-0.26^{ns}
PH	0.39**	0.24*		0.35^{ns}	-0.37^{ns}	0.47*	-0.23^{ns}	-0.09^{ns}
SL	-0.26*	0.25*	0.42**		-0.69**	-0.11*	-0.23^{ns}	-0.55**
NGS	-0.11^{ns}	-0.12^{ns}	-0.38**	-0.56**		-0.47*	0.006^{ns}	0.58**
TSW	0.12^{ns}	0.14^{ns}	0.42**	-0.004^{ns}	-0.33**		-0.41^{ns}	-0.58**
HI	-0.02^{ns}	-0.05^{ns}	-0.07^{ns}	-0.006^{ns}	-0.04^{ns}	-0.19^{ns}		0.58**
GY	0.28*	0.002^{ns}	0.009^{ns}	-0.17^{ns}	0.3*	-0.12^{ns}	0.33**	

PH (cm)=plant height, SL (cm)= spike length, NGS=number of grains per spike, BY (kg ha^{-1}) =biomass yield, GY (kg ha^{-1}) = Grain Yield, TSW= Thousand seed weight, HI (%) = harvest index.

Table 6. Genotypic path coefficients of direct (bold diagonal) and indirect (off-diagonal) effects of 22 Semi-hulless barley genotypes.

Traits	DM	PH	SL	NGS	TSW	HI	r_g
DM	-0.138	-0.08	0.27	-0.16	0.07	-0.53	-0.26^{ns}
PH	-0.068	-0.17	0.19	-0.16	0.2	-0.25	-0.09^{ns}
SL	-0.07	-0.06	0.53	-0.3	-0.05	-0.26	-0.55**
NGS	0.07	0.06	-0.37	0.44	-0.2	0.006	0.58**
TSW	-0.02	-0.08	-0.05	-0.21	0.4	-0.46	-0.58**
HI	0.06	0.04	-0.12	0.003	-0.18	1.1	0.58**
Residual	0.01						

PH (cm)=plant height, SL (cm)= spike length, NGS=number of grains per spike, BY (kgha^{-1}) =biomass yield, GY (kgha^{-1}) = Grain Yield, TSW= Thousand seed weight, HI (%) = harvest index

Table 7. Phenotypic path coefficients of direct (bold diagonal) and indirect (off-diagonal) effects of 22 Semi-hulless barley genotypes.

Traits	DM	PH	SL	NGS	BY	TSW	HI	r_p
DM	-0.02	-0.004	0.006	-0.001	0.06	0.006	-0.05	0.002^{ns}
PH	-0.005	-0.02	0.01	-0.004	0.15	0.02	-0.06	0.009^{ns}
SL	-0.005	-0.006	0.02	-0.006	-0.11	-0.0002	-0.06	-0.170^{ns}
NGS	0.003	0.006	-0.01	0.01	0.35	-0.02	-0.4	0.300*
BY	-0.001	-0.002	-0.003	0.004	1.03	0.0009	-0.5	0.530**
TSW	-0.003	-0.006	-0.0001	-0.004	0.02	0.05	-0.2	-0.120^{ns}
HI	0.001	0.001	-0.002	-0.0005	-0.54	-0.008	0.9	0.330**
Residual	0.08							

PH (cm)=plant height, SL (cm)= spike length, NGS=number of grains per spike, BY (kgha^{-1}) =biomass yield, GY (kgha^{-1}) = Grain Yield, TSW= Thousand seed weight, HI (%) = harvest index

Phenotypic and genotypic *path coefficient*

Yield is generally considered a polygenic character controlled by various other traits or components; therefore, selection based solely on correlation analysis could overlook other indirect causes that may lead to misleading results (Uddin et al., 2015). Path analysis splits correlation coefficients into direct and indirect effects, which may not be provided by simple correlation estimates of yield and other traits. Path coefficient analysis revealed that at the phenotypic level, biomass yield (0.103) had the highest positive direct effect on grain yield, followed by harvest index (0.9). In this case, phenotypic correlations were also positive and highly significant (r = 0.59** and r = 0.58**), respectively. Aklilu et al. (2020) reported similar results of direct effect for biomass yield and harvest index.

At the genotypic level, harvest index (1.1), followed by biomass yield (1.02), spike length (0.53), number of grains per spike (0.44), and thousand seed weight (0.4), showed high positive direct effects. However, spike length and thousand-seed weight showed negative highly significant genotypic correlation coefficients of -0.55**, and -0.58**, respectively. As a result, it was indicated that there is a real relationship between the number of grains per spike, biomass yield, and harvest index at the base of grain yield.

Similarly, Aklilu et al. (2020) reported that a positive direct effect of harvest index, biomass yield, and number of grains per spike. however, the days to maturity and plant height showed a negative genotypic direct effect. Similarly, maximum of the indirect effect of genotypic level at different traits on grain yield was contributed by days to maturity and number of grains per spike. a negative direct effect, similarly reported for days to maturity and plant height by Aklilu et al. (2020). The residual effect at the phenotypic level was observed as (0.08) and (0.01) at the genotypic level. This means the characters in the path analysis expressed the variability in grain yield by 92% and 99% at phenotypic and genotypic levels, respectively, and the remaining 8% and 1% need additional characterization for the future breeding program.

Conclusion

Studying the genetic variability of semi-hulless barley, association of traits with grain yield, and their heritability is the first step in plant breeding programs to select crops having the required characters. In this study, 22 semi-hulless barley genotypes were evaluated, and the analysis of variance revealed highly significant differences among semi-hulless barley genotypes in all traits except biomass yield, indicating the presence of genotypic variation among the studied genotypes, which is mainly influenced by available soil moisture. The best performance on phenological, grain yield, and yield component traits of semi-hulless barley were observed from genotypes G1, G3, G12, G13, G15, G20, and G22. The highest genotypic and phenotypic coefficient of variation was observed for the number of grains per spike. Very high heritability was observed for days to heading, number of grains per spike, thousand seed weight, plant height, and spike length. Both phenotypic and genotypic correlations of grain yield with number of grains per spike, and harvest index were positive and significantly correlated. In general, the study discovered that direct selection system would be more priority and inspiring than indirect selection for improving yield. This could be the nature of genotypes because of their better adaptive traits to variable environmental conditions which have important implications for sustainable crop production.

Declarations

Ethics Statement

The study does not need ethical approval.

Author Contributions Statement

All the authors have approved the final version of this manuscript.

Conceptualization: AA; Data curation: SS.; DB., Formal analysis: AA., DB.; Investigation: AA., DB., SS.; Methodology: AA., DB; Resources: AA., SS., DB., Software: AA.; Supervision: AA., DB.; SS., Validation: AA., DB.; SS., Visualization: AA., DB., SS.; Writing-Original Draft Preparation: AA.; Writing- Review and Editing: SS.; DB.

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Conflict of Interest Statement

The authors are under no obligation to disclose any relevant financial or non-financial interests. According to the authors, they have no conflicting interests.

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References

Agarwal, A. K. (2023). The Vital role of millets in sustainable agriculture: ensuring food security and enhancing environmental sustainability.

Aklilu Endalkachew, Dejene Tiegist, Worede Fisseha. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield related traits in barley (Hordeum vulgare L.) landraces in north Gondar, Ethiopia. Indian Journal of Pure Applied Bioscience, 8(3), 24-36. http://dx.doi.org/10.18782/2582-2845.8082.

Allard, R.W. (1960). Principles of plant breeding. John Wiley and Sons, New York.

Dyulgerova, B., Valcheva, D., Valchev, D., Babulicova, M., Havrlentova. M. (2021). Heritability and correlation coefficient analysis for grain yield and yield-related traits in spring barley (*Hordeum vulgare* L.). Agricultural Science and Technology, 13 (2), 129-133. doi: 10.15547/ast.2021.02.021.

Bailey-Serres, J., Parker, J. E., Ainsworth, E. A., Oldroyd, G. E., and Schroeder, J. I. (2019). Genetic strategies for improving crop yields. Nature, 575(7781), 109-118.

Bishnoi, S. K., Patial, M., Lal, C., and Verma, R. P. S. (2022). Barley breeding. In Fundamentals of Field Crop Breeding. (pp. 259-308).

Burton, G.M., and Vane, E. H. De. (1953). Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated colonal material. Agronomy Journal, (45), 310-314.

Dyulgerova, B., Valcheva, D., Valchev, D., Babulicova, M., Havrlentova, M. (2021). Heritability and correlation coefficient analysis for grain yield and yield-related traits in spring barley (*Hordeum vulgare* L.). Agricultural science and technology,13(2),129-133. doi: 10.15547/ast.2021.02.021.

Geleta, N., Dagnachew, L., and Zerihun, J. (2018). Correlations and path analysis of some quantitative characters in barley (*Hordeum vulgare* L.) landraces in western Oromia, Ethiopia. African Journal of Plant Science, 13(2), 34-46. doi: 10.5897/AJPS2018.1744.

Gepts, P. (1993). The use of molecular and biochemical markers in crop evolution studies. In Evolutionary biology (pp. 51-94). Boston, MA: Springer US.

Gutierrez-Reinoso, M. A., Aponte, P. M., and Garcia-Herreros, M. (2021). Genomic analysis, progress and future perspectives in dairy cattle selection: a review. Animals, 11(3), 599.

Johnson, H.W., Robinson, H.F., and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. Agronomy Journal, 47, 314-318.

Khan, M. M. H., Rafii, M. Y., Ramlee, S. I., Jusoh, M., and Al Mamun, M. (2022). Path-coefficient and correlation analysis in Bambara groundnut (*Vigna subterranea* [L.] Verdc.) accessions over environments. Scientific reports, 12(1), 245.

Kumar, J., Kumar, M., SK Singh, and L Singh. (2017). Estimation of genetic variability and heritability in bread wheat under abiotic stress. International Journal of Pure and Applied Biosciences, 5 (1): 156-163.

Madhu, P., Manoj, K., Santosh, K. B., Dharam P., Kallol, K., P., Arun, K., S., and Silky, G. (2023). Genetic variability and trait association for grain yield in barley (*Hordeum vulgare* L.). Journal of Cereal Research, Volume, 15 (2), 284-293.

Necdet, A. (2016). Genetic variability and correlation studies in yield and yield related characters of barley (*Hordeum vulgare* L.) genotypes. Selcuk journal of agriculture and food sciences, 30(2), 88-95.

Parida, G., Saghfi, S., Eivazi, A., and Akbarzadeh, A. (2018). Study of genetic advance and broad sense heritability for grain yield and yield components of chickpea (*Cicer arietinum* L.) genotypes. Advances in Biology & Earth Sciences, 3(1), 5-12.

Patial, M., Kumar, M., Bishnoi, S. K., Pal, D., Pramanick, KK., Shukla, A.K., and Gandhi, S. (2023). Genetic variability and trait association for grain yield in barley (*Hordeum vulgare* L.). Journal of Cereal Research, 15 (2), 284-293. http://doi.org/10.25174/2582-2675/2023/133530.

Payal, A., Abhay, D., Avadhoot, B., Dharmadhikari, Parul, G., Himansuman, and Urmila. (2023). Association and path coefficient analysis among grain yield and its component traits in barley (*Hordeum vulgare* L.). Biological Forum an International Journal, 15(8a), 140-143.

Eshghi, R., and Akhundova, E. (2010). Genetic diversity in hulless barley based on agro- morphological traits and RAPD markers and comparison with storage protein analysis. African Journal of Agricultural Research, 5 (1), 097-107. doi: 10.5897/AJAR09.363.

Shiferaw, K. Abate, B. and Lakew, B. (2020). Genetic variability and association of traits in Ethiopian barley (*Hordeum vulgare* L.) genotypes. Journal of Agricultural and Crop Research, 8(1), 11-19.

Shubham, K. S., Geetam, S., Mishra, M.N., Rohit, V. S. (2023). Studies on genetic variability, heritability, genetic advance, and correlation in barley. International Research Journal of Modernization in Engineering Technology and Science. 05(06).

Swarup, S., Cargill, E. J., Crosby, K., Flagel, L., Kniskern, J., & Glenn, K. C. (2021). Genetic diversity is indispensable for plant breeding to improve crops. Crop Science, 61(2), 839-852.

Tiegist, D. (2010). Genetic diversity and population differentiation analysis of Ethiopian barley (*Hordeum vulgare* L.) landraces using morphological traits and SSR markers. Hereditas*,* 147, 154–164.

Van Rheenen, W., Peyrot, W. J., Schork, A. J., Lee, S. H., and Wray, N. R. (2019). Genetic correlations of polygenic disease traits: from theory to practice. Nature Reviews Genetics, *20*(10), 567-581.

Whan, B.R., Carlton, G.P, and Anderson, WK. (1991). Potential for increasing early vigor and total biomass in spring wheat identification of genetic improvements. Australian Journal of Agriculture Research, 42: 347-361.