

## Genetics Differences among Improved Malt Barley (*Hordeumvulgare*) Varieties for Yield, Yield Related Trait, North Eastern Ethiopia

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### Abstract

*The objectives of this study wereto assess the genetic variability of yield, yield related traits and to estimate direct, indirect effects of trait associations. Seventeen varieties were evaluated and subjected to the analysis of variance using RCB design, in Eastern Amhara Ethiopia. The varieties differed significantly for most of the characters and had wide range of mean values, which indicated the existence of variations among the tested varieties. Estimates of phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were generally low. The highest GCV and PCV values were recorded on grain yield (51) and plant height (60). The PCV values were slightly greater than the GCV values. Grain yield, plant height, protein content and grain size had relatively high heritability. Grain yield gives high heritability value accompanied by high genetic advance which is good indicator for selection. Grain yield had positively and significantly correlated with date of maturity. Grain yield negatively correlated with protein and positively associates with starch.*

**Key words:** *Genotypic coefficient of variance: Phenotypic coefficient of variance: Genetics advance: Heritability.*

### 1. Introduction

Barley (*Hordeumvulgare*L.) is an ancient domesticated crop belongs to the family Poaceae, it consists of 32 species with the diploid ( $2n = 2x = 14$ ), tetraploid ( $2n = 4x = 28$ ) and hexaploid ( $2n = 6x = 42$ ) cytotypes in a basic chromosome number  $x = 7$ , and self-fertility, large chromosome (6-8  $\mu\text{m}$ ) high degree of natural and easily inducible variation, ease of hybridization, ease for doubled haploid production and wide adaptation (Bothmer et al., 1992; Desimiret et al., 2004). Globally, barley ranks fourth among the cereal crops after wheat, maize and rice (FAO, 2014). It has superior nutritional quality due to the presence of beta-glucan (anti-cholesterol substance) and easily digestible due to low gluten content with high vitamin B. group. Barley is a cool-season

crop that adapted to high altitudes and grows in a wide range of agro climatic regions under several production systems.

Biological world were full of variability in which the real variability of each trait in plant breeding gave good opportunity to widen the scope of the breeding. Variability is the making of differences among individuals due to having differences in their genetic composition, the environment in which they are raised and gene and environment interaction (Allard, 1960; Falconer and Mackay, 1996). When two individual express their characters separately when the influence of an environment were identical for both, differences in expression would result from genetic variation. Information on the nature and magnitude of genetic variability present in a crop species is important for developing effective crop improvement program (Falconer and Mackay, 1996, Singh et al., 1980; Welsh, 1990; Dabholkar 1999).

When genetic variability is due to the genetic differences among individuals within a population, is the core of plant breeding which helps to magnified and widen the genetics base of a given population in trait level and support the proper management of diversity which produce permanent gain in the performance of plant and can buffer against seasonal fluctuations (Welsh, 1990; Sharma, 1998). In addition, estimation the magnitude of variation within germplasm collection and traits found in cross ability parents for important plant attributes will enable breeders to exploit genetic diversity more efficiently (Jahufer and Gawler, 2000).

The existing variability present in breeding populations can be assessed in the following way by using simple measures of variability, such as variance, standard deviation, coefficient of variability by estimating both phenotypic and genotypic various components of variance, heritability and genetic advance. Utilization of genetic resources requires proper and systematic evaluation of such resources. Therefore, the main objective of this experiment

- Assess genetic variability of malt barley for yield, yield related trait.
- Estimate direct and indirect effect of association between yield and yield related traits

## **Materials and Methods**

### **Description of the Study Area**

The experiment was conducted in Amhara region at, Mekedella (south Wollo) in 2016 main growing season. Mekdella is located 500km North of Addis Ababa, at 11<sup>0</sup>.57' N

longitude and 39.02' E latitudes, with the altitude of 2600 masl. The site received an average annual rainfall of 923mm. The soil types for both locations are litosols (GPS reading, and Kombolcha Metrological Station, 2016).

### **Experimental Design and Field lay out**

The trial was laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 1.60m wide and 2.5 m long with a total area of 4 m<sup>2</sup> consisting of 8 rows. The spacing between rows, plot and replication was 20cm, 0.5m and 1m, respectively. Data were collected from the central six rows. The seed rate was 100 kg/ha, and seeds were drilled in each row. Fertilizer was applied in the form of Urea and Diamonium Phosphates (DAP) at the rates of 41/46 of (N/P<sub>2</sub>O<sub>5</sub>) per hectare. Half of the recommended rate was applied at planting and the remaining after 35 days of emergency for each location. All other agronomic management was applied as per recommendation.

### **Collected data**

Data were collected and recorded both in the field and in the laboratory. Data which were collected like Days to heading, Days to maturity, Plant height, Harvest index, 1000 kernel weight, Gain yield (kg/ha), Spike length, Seeds per spike, **Grain protein (GP)**: The grain protein content was analyzed by Infratic 1241 grain analyzer; Near Infrared Reflect Spectroscopy (NIRS). Around five hundred gram of malt barley grain sample was used to measure the protein content. The grains were inserted in the upper hole of NIRS then press the down arrow the NIRS start measuring the protein content minutes.

### **Result and Discussion**

Phenotypic and Genotypic Coefficient of variation the values of all the genotypic coefficient of variation (GCV) were low except for grain yield and plant height which were (16%), and (11%) respectively. The phenotypic coefficient variation (PVC), values were low to high (Table 1). The values of grain yield (23%), and spike length (25%). High heritability values obtained from plant height (60%) and protein (67%) and medium days to maturity (47%), grain yield (51%), and harvest index (56%). The other characters showed low heritability value. Grain yields (24%) had higher genetic advances. Harvest index (19%) and plant height (18%) under medium genetic advance. The other characters showed that low genetic advance..

According to Dishmukhet al., (1986) phenotypic and genotypic values greater than 20% is considered as high, between; 10-20% is medium and below 10% as low and according

to Pramoda and Gangaprasad (2007) heritability is categorized <40% low, between 40% - 59% medium, and 60% -79% high and above 80 very high. High heritability showed variation among the tested varieties as a result of the presence of difference due to the existing genetic, environmental influence and the interaction of genetic makeup and environment. High heritability values of yield, plant height, protein and grain size were supported by Chand et al., (2008), and Sunil et al., (2015). Our finding on grain size showed relatively high heritability which supported by (Briggs, 1974; Eagles et al., 1995). The value of most characters for heritability values ranged from low to medium. These were supported by previous workers, (Whanet et al., (1991). According to Singh (1990), if heritability of a character is very high, selection for such a character should be fairly easy, because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to phenotype. Al-Tabbaan and Fraihat, (2012), and Wang et al., (2006) reported that high heritability in days to heading in barley which in line with our finding. Character with low heritability should considerably difficult to practice phenotypic selection due to the masking effects of the environment.

The genetic advance as percent of mean was categorized into low ( $\leq 10\%$ ), moderate (10-20%) and high ( $\geq 20\%$ ) by Johnson et al. (1955). Higher heritability coupled with higher genetic advance was recorded for grain yield, and plant height at both locations which could help for improving the grain yield in the tested environment. The higher heritability of the trait is an advantage in phenotypic selection and easy in crop improvement for the environment. This idea was supported by Khan et al., (2008). Grain protein content showed higher heritability with low genetic advance. Different authors reported that characters possessing low genetic advance with high heritability indicate that the presence of none additive gene action, thus tell us simple selection procedure in early segregation generation may not be effective for generating desirable trait for future plant breeding. Likewise, high heritability with high genetic advance that the presence of additive gene action (Johnson et al., 1995; Singh et al., 2001). Singh, (2001) reported that genetic advance under selection refers to the improvement of characters which the value of the variety for the new population compared with the base population under one cycle of selection at a given selection intensity. Therefore, the current finding suggested that selecting the top 5% of the genotypes could result in an advance of 0.28% to 24.45 population mean for the listed characters. Genetic advance under selection value were low 0.28%, which indicates that improvements of characters of the variety genetic condition for new generation compare with base population under the first cycle selection is 0.28% at 5% selection intensity as the same time at high genetic advance the

new population compare with the base population under first cycle selection 24.45% at 5% selection intensity.

Table1. Range, mean, phenotypic, genotypic and environmental variance and genotypic and phenotypic coefficients of variance, broad sense heritability, genetic advance and Genetics advance of mean for different characters at Mekedella 2016

Characters	Mean	SE(±)	Range	$\sigma^2_p$	$\sigma^2_g$	GCV (%)	PCV (%)	H <sup>2</sup> (%)	GA	GAM (%)
DM(days)	111.0	1.183	105-120	8.03	3.83	1.77	2.56	47.72	2.79	2.52
GF(days)	39.0	4.037	28-60	59.18	10.29	8.2	19.67	17.38	2.76	7.06
HI(%)	0.39	0.025	0.29-0.44	0.005	0.003	12.73	16.95	56.42	0.08	19.73
GY(kg/ha)	1635	152.058	1178-2156	143037	73672	16.51	23.01	51.51	401.86	24.45
TKW(g)	40.4	1.549	33.3-47	8.13	0.93	2.39	7.06	11.43	0.67	1.66
PH(cm)	63.0	3.324	42.8-80.4	84.81	51.67	11.42	14.63	60.92	11.57	18.39
GC(%)	97.9	0.592	95-99	0.99	0.27	0.53	1.18	27.53	0.57	0.58
GE(%)	98.1	0.582	96-100	0.8	0.12	0.35	1.09	14.93	0.28	0.28
Pr.(%)	9.8	0.27	8.4-12	0.67	0.45	6.8	8.3	67.15	1.13	11.5
St(%)	65.4	0.531	61.9-68.5	1.97	1.13	1.62	2.15	57.1	1.65	2.53
Ex(%)	78.5	0.868	75-82	3.09	0.83	1.16	2.24	26.92	0.98	1.24
2.8mm.s	15.8	4.127	0.7-62	209.52	158.43	79.66	91.61	75.62	22.58	142.91
2.5mm.s	54.9	2.66	29.4-78.2	144.98	123.75	20.26	21.92	85.36	21.2	38.61
2.8+2.5mm	70.8	4.539	48.4-92.1	205.88	144.06	16.95	20.27	69.97	20.71	29.26
2.2mm.s	21.1	2.928	5.3-42.2	90.88	65.16	38.33	45.27	71.7	14.1	66.95

\*SE= standard error,  $\sigma^2_p$  = phenotypic variance,  $\sigma^2_g$  = Genotypic variance, , GCV= Genotypic coefficient of variance, PCV= Phenotypic coefficient of variance, H<sup>2</sup>= broad sense heritability. GA= Genetic Advance, GAM= Genetic advance of mean express as percentage, GF= Grain filling, DM= Days to maturity, GY= Grain yield, PH=Plant height, HI=Harvest Index, TKW= Thousands seed weight, GC= Germination Capacity, GE= Germination Energy, pr=protein, st=starch, Ex= Extract

**Phenotypic and genotypic correlation of grain yield with other related characters**

Estimation of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlations between the yield and other character are presented in Table 2. The result of phenotypic correlation coefficient indicated that grain yield were positively and highly correlated with days to maturity

(0.78), grain filling period (0.75) and significantly with harvest index (0.42), thousands seeds weight (0.31), plant height (0.49). The phenotypic association of other characters showed that days to maturity positively and significantly correlate with harvest index (0.36), thousand seed weight (0.38), and plant height (0.64). Thousands seed weight to plant height (0.40). Harvest index with thousands seed weight (0.30), and grain filling to harvest index (0.27).

Estimation of genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlations between the yield and quality character is presented in Table 2. The result of phenotypic correlation coefficient indicated that grain yield were positively and highly correlated with certain characters. Wasifet al., (2015) reported that the significant correlation of plant height with grain yield which supported our findings. However, the author's finding also contradicted with the results of thousand seed weight and harvest index which had insignificantly correlation with grain yield. Days to heading (-0.43) negatively and highly correlated with grain yield. Balcha (2002 and Ahemedet al., (2012) observed that grain yield were negatively correlated with days to heading. These correlations indicated that varieties had an ability to escape moisture deficit. According to Quan (2015), biomass was positively correlated with grain yield, which is contradicted to our findings. The phenotypic correlation coefficients (PCC) were less in magnitudes than genotypic correlation coefficient (GCC) which revealed the presence of high genetic relationship among the difference. . Improve the maturity dates showed substantial yield increments since yield and days to maturity positively and significantly correlated. Days to heading with days to maturity (-0.35), and grain filling (-0.30) correlated significantly. These indicated that early heading date along with long time of maturity give reasonable yield at moisture deficits area. Here the crop tried to escape the stress (Alemuet al., 2016).

At genotypic correlation coefficient days to maturity (0.78) and grain filling (0.88) positively and highly correlated with grain yield. The results of these findings were supported by Dessalegn, (2000) grain yield were positively correlated with days to maturity, grain filling and plant height. Grain yield negatively and significantly correlates with days to heading (-0.55) and biomass (-0.47). These finding is similar with Kifle et al., (2016), these indicates that delayed days to heading and high biomass decrease grain yield, which means characters were highly compete the starch synthesis and biomass building. These might imply the varieties were stressed at the time of heading then plants forced to escape for grain filling for early reproduction

**Table 2. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficient of 14 quantitative characters of malt barley varieties at Mekedella 2016/2017.**

Characters	DH	DM	GF	BM	HI	GY	SKW	PH	SPS	HLW	GE	Protein	Starch	Extract
<b>DH</b>	1	-0.35*	-0.30*	0.32*	-0.93**	-0.43**	-0.28**	-0.16	0.02 <sup>ns</sup>	-0.17 <sup>ns</sup>	-0.01 <sup>ns</sup>	0.12 <sup>ns</sup>	0.11 <sup>ns</sup>	-0.04 <sup>ns</sup>
<b>DM</b>	-0.42*	1	0.18 <sup>ns</sup>	-0.02 <sup>ns</sup>	0.36**	0.78**	0.38**	0.64**	0.37 <sup>ns</sup>	-0.19 <sup>ns</sup>	-0.12 <sup>ns</sup>	-0.17 <sup>ns</sup>	0.19 <sup>ns</sup>	0.12 <sup>ns</sup>
<b>GF</b>	-0.48*	0.39 <sup>ns</sup>	1	-0.13 <sup>ns</sup>	0.27*	0.75**	0.09 <sup>ns</sup>	0.12 <sup>ns</sup>	0.1 <sup>ns</sup>	0.11 <sup>ns</sup>	-0.02 <sup>ns</sup>	-0.2 <sup>ns</sup>	0.03 <sup>ns</sup>	-0.1 <sup>ns</sup>
<b>BM</b>	0.47*	-0.22 <sup>ns</sup>	-0.52*	1	0.04 <sup>ns</sup>	-0.09 <sup>ns</sup>	0.02 <sup>ns</sup>	0.02 <sup>ns</sup>	0.05 <sup>ns</sup>	-0.11 <sup>ns</sup>	-0.28 <sup>ns</sup>	0.15 <sup>ns</sup>	-0.07 <sup>ns</sup>	0.06 <sup>ns</sup>
<b>HI</b>	-0.97*	0.4 <sup>ns</sup>	0.38 <sup>ns</sup>	-0.23 <sup>ns</sup>	1	0.42*	0.30*	0.17 <sup>ns</sup>	0.23 <sup>ns</sup>	0.13 <sup>ns</sup>	-0.1 <sup>ns</sup>	-0.06 <sup>ns</sup>	-0.14 <sup>ns</sup>	0.07 <sup>ns</sup>
<b>GY</b>	-0.55*	0.78**	0.88**	-0.47*	0.48 <sup>ns</sup>	1	0.31*	0.49*	0.31 <sup>ns</sup>	-0.08 <sup>ns</sup>	-0.11 <sup>ns</sup>	-0.24 <sup>ns</sup>	0.12 <sup>ns</sup>	0.02 <sup>ns</sup>
<b>SKW</b>	-0.3 <sup>ns</sup>	0.25 <sup>ns</sup>	0.18 <sup>ns</sup>	-0.32 <sup>ns</sup>	0.18 <sup>ns</sup>	0.20 <sup>ns</sup>	1	0.40*	-0.08 <sup>ns</sup>	-0.16	-0.09 <sup>ns</sup>	0.08 <sup>ns</sup>	-0.18 <sup>ns</sup>	0.1 <sup>ns</sup>
<b>PH</b>	-0.2 <sup>ns</sup>	0.65*	0.18 <sup>ns</sup>	-0.12 <sup>ns</sup>	0.2 <sup>ns</sup>	0.43 <sup>ns</sup>	0.46 <sup>ns</sup>	1	0.21 <sup>ns</sup>	-0.3	0.04 <sup>ns</sup>	0.22 <sup>ns</sup>	-0.12 <sup>ns</sup>	0.01 <sup>ns</sup>
<b>SPS</b>	0.25 <sup>ns</sup>	0.34 <sup>ns</sup>	0.34 <sup>ns</sup>	-0.21 <sup>ns</sup>	-0.06 <sup>ns</sup>	0.39 <sup>ns</sup>	-0.2 <sup>ns</sup>	0.05 <sup>ns</sup>	1	-0.1	-0.08 <sup>ns</sup>	-0.25 <sup>ns</sup>	0.12 <sup>ns</sup>	0.03 <sup>ns</sup>
<b>HLW</b>	0.02 <sup>ns</sup>	-0.22 <sup>ns</sup>	0.02 <sup>ns</sup>	-0.17 <sup>ns</sup>	-0.02 <sup>ns</sup>	-0.17 <sup>ns</sup>	-0.28 <sup>ns</sup>	-0.41 <sup>ns</sup>	-0.05 <sup>ns</sup>	1	-0.28 <sup>ns</sup>	-0.14 <sup>ns</sup>	0.03	0.12 <sup>ns</sup>
<b>GE</b>	-0.3 <sup>ns</sup>	0.12 <sup>ns</sup>	0.27 <sup>ns</sup>	-0.36 <sup>ns</sup>	0.25 <sup>ns</sup>	0.24 <sup>ns</sup>	0.28 <sup>ns</sup>	0.36 <sup>ns</sup>	0.28	-0.46	1	-0.02 <sup>ns</sup>	0.02 <sup>ns</sup>	0.04 <sup>ns</sup>
<b>Pro</b>	0.21 <sup>ns</sup>	-0.1 <sup>ns</sup>	-0.24 <sup>ns</sup>	0.26 <sup>ns</sup>	-0.16 <sup>ns</sup>	-0.21 <sup>ns</sup>	-0.01 <sup>ns</sup>	0.35 <sup>ns</sup>	-0.4	-0.23	-0.3	1	-0.67 <sup>ns</sup>	0.02 <sup>ns</sup>
<b>Sta</b>	0.24 <sup>ns</sup>	0.02 <sup>ns</sup>	-0.13 <sup>ns</sup>	-0.16 <sup>ns</sup>	-0.31 <sup>ns</sup>	-0.08 <sup>ns</sup>	-0.22 <sup>ns</sup>	-0.25 <sup>ns</sup>	0.15 <sup>ns</sup>	0.12 <sup>ns</sup>	0.2 <sup>ns</sup>	-0.67 <sup>ns</sup>	1	-0.08 <sup>ns</sup>
<b>Extra</b>	0.08 <sup>ns</sup>	-0.15 <sup>ns</sup>	-0.2 <sup>ns</sup>	0.3 <sup>ns</sup>	0.2 <sup>ns</sup>	-0.21 <sup>ns</sup>	0.03 <sup>ns</sup>	-0.1 <sup>ns</sup>	-0.11 <sup>ns</sup>	0.28 <sup>ns</sup>	-0.17 <sup>ns</sup>	0.14 <sup>ns</sup>	-0.26 <sup>ns</sup>	1

- Note: DH: days to heading, DM: days to maturity, GF: Grain filling. BM: Biomass, HI: Harvest index. GY: Grain yield, SKW: Thousand kernel weight. PH: Plant height. SPS: Seed per spike, HLW: Hictoliter weight, GE: Germination energy, Pro: Protein, Sta: Starch and Extra: Extract



### **Phenotypic and Genotypic path coefficient analysis on grain yield**

The phenotypic and genotypic direct and indirect effects of different characters and component in all possible combinations are presented in Table 3. Based on phenotypic path coefficient analysis, the highest positive and favorable direct effect exerted on grain yield was days to maturity (0.6826), grain filling (0.6289), followed by biomass (0.0182). The negative direct effect exerted on grain yield also by days to heading (-0.0372), plant height (-0.0250) and harvest index (-0.0281). The negative association and negative direct effect of days to heading on grain yields were expressed by the masking effects of positive indirect effect of days to heading through biomass and harvest index.

Phenotypic and Genotypic path coefficient analysis is presented in Table 3. The direct effect of characters on grain yield showed that the relationships between the characters were good contributors to the ultimate grain yield and these characters were the main component in the improvement of the grain. The positive association direct effect of biomass with grain yield supported by (Alemuet al., 2016) but contradict idea with (Mitsiwa, 2013). In the phenotypic path coefficient analysis of these finding revealed that improving date of maturity and grain filling were the main contributor to improve grain yield of malt barley variety. Days to heading, thousands seed weight, protein, starch, and extract were negative direct effect that influence on grain yield. The negative direct effects of the above characters on grain yield indicate that improving these characters should not help. The association of plant height was positive but the direct effect were negative these indicate that the negative direct effect influenced by the counterbalance indirect effect of plant height through days to maturity (0.4369). The phenotypic path coefficient residual value is low (0.0840), which indicates the characters in phenotypic path analysis explain 91.6% the variation on grain yield. It is suggest that maximum emphasis should be given the above character in selection of malt barley variety.



**Table 3.** Estimation of phenotypic path coefficient direct (diagonal) and indirect effects of 10 characters of malt barley on grain yield conducted at Mekedela 2016.

Variable	DH	DM	GF	BM	HI	TKW	PH	Protein	Starch	Extract	GY <sup>(TP)</sup>
<b>DH</b>	<b>-0.0372</b>	-0.2389	-0.1887	0.0058	0.0262	0.0001	0.0040	0.0000	-0.0013	0.0000	-0.43**
<b>DM</b>	0.0130	<b>0.6826</b>	0.1132	-0.0004	-0.0101	-0.0001	-0.0160	0.0001	-0.0022	0.0000	0.78**
<b>GF</b>	0.0112	0.1229	<b>0.6289</b>	-0.0024	-0.0076	0.0000	-0.0030	0.0001	0.0000	0.0000	0.75
<b>BM</b>	-0.0119	-0.0137	-0.0818	<b>0.0182</b>	-0.0011	0.0000	-0.0005	-0.0001	0.0008	0.0000	-0.09
<b>HI</b>	0.0346	0.2457	0.1698	0.0007	<b>-0.0281</b>	-0.0001	-0.0043	0.0000	0.0016	0.0000	0.42
<b>TKW</b>	0.0104	0.2594	0.0566	0.0004	-0.0084	<b>-0.0003</b>	-0.0100	0.0000	0.0021	0.0000	0.31*
<b>PH</b>	0.0060	0.4369	0.0755	0.0004	-0.0048	-0.0001	<b>-0.0250</b>	-0.0001	0.0014	0.0000	0.49*
<b>Pro</b>	-0.0045	-0.1160	-0.1258	0.0027	0.0017	0.0000	-0.0055	<b>-0.0004</b>	0.0078	0.0000	-0.24
<b>Sta</b>	-0.0041	0.1297	0.0000	-0.0013	0.0039	0.0001	0.0030	0.0002	<b>-0.0116</b>	0.0000	0.12
<b>Extra</b>	0.0015	0.0819	-0.0629	0.0011	-0.0020	0.0000	-0.0003	0.0000	0.0009	<b>-0.0003</b>	0.02

(0.0840)

Note:\*\*, and \* highly significant at 0.01% and 0.05%, level respectively, rp: phenotypic correlation. DH: days to heading, DM: days to maturity, GF: Grain filling. BM: Biomass, HI: Harvest index. SKW: Thousand kernel weight. PH: Plant height. Pro: Protein, Sta: Starch, Extra: Extrac

### Conclusion

The results of this analysis of variance for different agronomic characters revealed significantly ( $p \leq 0.05$ ) difference for most of the 21 characters, except spike length, seed per spike and biomass in testing environment. Most characters showed the highest variation such as days to heading, days to maturity, grain filling and grain yield which showed that the varieties showed the wide variation which responds to drought and moisture stress, the variety differently reacts to the different environmental conditions. In general, knowing the association among characters are useful in planning, evaluating and setting selection criteria for the desired characters for selection in breeding program. Generally, days to maturity, harvest index, and grain filling showed positive phenotypic and genotypic correlation with grain yield indicating that more attention should be given to those characters to improve the grain yield of malt barley in the study area.

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