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# Research Article
# Estimate Genetic variability of Malt Barley (*Hordeum vulgare* L.)

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**Keywords**

Genetic advance, phenotypic variance, correlation coefficient, genotype

**Abstract**

Genotypic Coefficient of Variability (GCV) and Phenotypic Coefficient of Variability (PCV) were relatively higher for grain yield per plot, number of kernels per spike, spike length, plant height, grain filling period, hectoliter weight and thousand seed weight in grand mother trial. Relatively high heritability and genetic advance were recorded for spike length, thousand kernel weight, number of kernels per spike, hectoliter weight, days to maturity, grain filling period, plant height and days to heading showing better condition for effective selection in these characters. In heritability implies the presence of more additive gene effects for potential crop improvement on farmers' field. In most cases these point out that there is good scope for crop improvement through selection. From the studied genotypes most of the agronomic and quality characters were positively correlated with grain yield. This study revealed that greater yield response with better malt quality traits could be obtained through direct and indirect selection scheme in malt barley genotypes tested.

## Introduction

Individual plants in a breeding population are ideally varied for the traits identified in the breeding goals. These will include height, heading and maturity dates, disease resistance, quality parameters, and yield. Two randomly selected plants will show these variations but it will not be known whether the differences are due to genotype or the environment. The plant breeder is interested in identifying how much of the observed phenotypic variability is due to genetics and to do this must estimate heritability.

In crop improvement, only the genetic component of variation is important since only this component is transmitted to the next generation. The ratio of genetic variance to the total variance i.e. phenotypic variance is known as heritability. There are two types of heritability ($h^2$), Heritability is often used by plant breeders to quantify the precision of single field trials or of series of field trials. It is defined as the proportion of phenotypic variance among individuals in a population that is due to heritable genetic effects, also known as heritability in the narrow sense. Similarly, heritability in the broad sense is defined as the proportion of phenotypic variance that is attributable to an effect for the whole genotype, comprising the sum of additive, dominance, and epistatic effects (Nyquist 1991; Falconer and Mackay 1996). Heritability is a key parameter in quantitative genetics because it determines the response to selection. As pointed out by Holland et al. (2003), this complicates both the definition and the estimation of heritability.

When segregating generations are studied genotypic variance consists of (a) additive variance (b) dominance variance (c) and variance due to epistasis. Dominance variance is important when we are dealing with hybrids (i.e. $F_1$ generations). In self pollinated crops we release varieties only after making them homozygous lines. Hence additive variance is more important in such cases. If heritability is very high for

any character it can be improved. Improvement of characters with low heritability is very difficult. Genetic advance is the difference between the mean of the selected Plants in the original population and the mean of the progeny rose from the selected plants in the next generation.

## Materials and Methods

The study was conducted at Guagusa shekudad Woreda, Awi Administrative Zone in the 2010 main cropping season. The site is located at $11^0$91'N and $37^0$02'E latitude and longitude, 12 km away from Tilili (capital of the Woreda) along the main road from Bahir Dar to Addis Ababa. The site is characterized by an elevation of 2496 m above sea level having plain and plateau topography. Mean temperature of the area ranges from 11.2 to 25.5 $^0$C and mean annual rainfall is 1834.6 mm. The soil has a pH of 5.46, 0.098% total N, 19.73 ppm available P, 1.32% C and 2.28% OM.

### Experimental Materials and Procedures

The experiment was carried out with ten advanced malting barley genotypes where four (EH1847/F4.2p.5.2, EH1877/F4.1p.35.1, IBON-173/03 and IBON-174/03) are promising and six (HB1533, MISCAL-21, HB-52, HB-120, HOLKER and BEKA) are released genotypes. The Grandmother type experiment was conducted under rain fed conditions at one distinct sites representing barley growing agro-ecologies. One farmer conducted the grandmother trial which comprise ten test varieties with three replication in randomized complete block design. Planting date was done on June, 18, 2010. In the grandmother experiment genotypes were planted in a randomized complete block design with three replications was planted at one location. Varieties were planted at the seed rate of 75 kg $ha^{-1}$ hand drilling in plots of 3 $m^2$ with six rows measuring 0.2 m within row spacing. Fertilizer rates of 41 kg N $ha^{-1}$ and 46 kg $P_2O_5$ $ha^{-1}$ were applied. The whole rate of $P_2O_5$ was applied once during planting time whereas, N was applied in split three times (at planting, tillering and flag leaf) in equal splits. Weeding was done three times, at 35 and 55 days after planting and at heading.

### Collected Data

Plant height was measured on five randomly selected plants from ground level to the top of the spike excluding the awn. Spike length was determined from five sampled plants. Tiller number per plant was determined on five randomly sampled plants in each plot. Days to heading and days to maturity were calculated as the number of days from the day of effective rainfall to the day where 50% of the plants have fully exerted spikes and 90% of the spikes have fully matured, respectively. Grain filling period was calculated as the number of days from heading to maturity. Grain and aboveground biomass yields were measured from the central four rows at maturity. Hectoliter weight per plot was determined by weighing one liter of grain from the central four rows. Thousand seed weight from each plot was measured by weighing 1000 grains. Number of kernels per spike was determined on five randomly sampled plants from the central four rows. Protein and starch content of the grain was determined using Near Infrard spectroscopy (Infratec 1241 Grain Analyzer) and it was expressed in percent grain in 4ml germination test was expressed in percent within 3 days. Germination capacity of grain was done on litmus paper under laboratory.

### Estimation of variance components

The genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability were estimated based on the method of Burton and De vane (1953).

- Environmental variance ($\sigma^2_e$) = error mean square
- Phenotypic variance ($\sigma^2$p) = $\pm^2_g + \pm^2_e$
- Genotypic variance ( $\sigma^2$g) = MS g- MSe/r
- Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\pm^2 p}}{\bar{x}} \times 100$
- Genotypic Coefficient of variation (GCV) = $\frac{\sqrt{\pm^2 g}}{\bar{x}}$ x100

Where: $\bar{x}$ = grand mean of character

### Estimation of Heritability in Broad Sense

The inherent portion of the variability is termed as heritability (Allard, 1960). Heritability in broad sense for each character was computed according to Falconer (1989).

$$\text{Heritability } (H^2) = \frac{\pm^2_g}{\pm^2_p} \text{ x100}$$

Where: $H^2$= heritability in broad sense

$\pm^2_p$ = Phenotypic variance

$\pm^2_g$ = Genotypic variance

**Estimation of Genetic advance**

Genetic advance (GA) was calculated in accordance with the methods illustrated by Johnson *et al*. (1955) as: GA= $K*\sigma^2_p*H^2$

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

**Estimation of Phenotypic and Genotypic Correlations**

The phenotypic correlations between yield and yield related traits were estimated using the method described by Miller *et al*. (1958).

$$rp_{xy} = \frac{Covp_{xy}}{\sqrt{Vp_x Vp_y}}$$

Where, $r_{pxy}$ = phenotypic correlation coefficient between character x and y

$Cov_{pxy}$ = Phenotypic covariance between character x and y

$Vp_x$ = Phenotypic variance for character x

$Vp_y$ = Phenotypic variance for character y

$$rg_{xy} = \frac{Covg_{xy}}{\sqrt{Vg_x Vg_y}}$$

Where, $r_{gxy}$ = Genotypic correlation coefficient between character x and y

$Cov_{gxy}$ = Genotypic covariance between character x and y

$Vg_x$= Genotypic variance for character x

$Vg_y$ = Genotypic variance for character y

The coefficients of correlations at phenotypic level were tested for their significance by comparing the value of correlation coefficient with tabulated r-value at g-2 degree of freedom.

$$t = \frac{(rg_{xy})}{SEg_{xy}}$$

The calculated 't' value was compared with the tabulated 't' value at g-2 degree of freedom at 5% level of significance, where, g = number of genotypes.

$$SEg_{xy} = \sqrt{\frac{(1-r^2 g_{xy})}{2H_x.H_y}}$$

Where, $H_x$ = Heritability value of character x

$H_y$ = Heritability value of character y

## Results and Discussion

**Genetic parameter of characters**

The genotypic coefficient of variability ranged from 0 to 88.3% and phenotypic coefficient of variability from 1.26 to 41.34% suggesting that environmental conditions and genetic material had influence on the characters under the study. Major limiting factor that affect the rate of progress in plant breeding has been low heritability of quantitative traits. (Dabholkar 1992) classified heritability estimates as low (5-10%), medium (10-30%) and high (>30%).

In this study broad-sense heritability estimate ranged from -0.98 to 94.58 (Table 1). The lowest heritability was found for number of tillers, while the highest heritability was observed from number of kernel. According to Singh (2001), if heritability of a character is very high; say 80% or more, selection of these characters could be easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. On the other hand, for characters with low heritability, say 40 % or less, selection may be considerably difficult due to the masking effect of the environment. Heritability is moderate when it is between 40 and 80%. Highly heritable traits were observed from number of kernel (94.58%), days to maturity (80.14%) and protein content (81.94%). As reported by Eshghi and Akhundova (2010) generation mean and variance analysis indicated that additive effects were important for protein content. Therefore, it can be assumed that the phenotypes of these traits are mainly determined by its genetic constitution than environmental factor. Similarly high heritability was indicated from grain yield (52.17%), spike length (71.73%), days to heading (77.29%), plant height (75.29%), grain filling period (69.21%), crop stand (50%), hectoliter weight (70.05%), thousand seed weight (72.61%), starch content (69.84%) and germination capacity (32.01%). Similar to this finding high average heritability on test weight was reported by Therrien (2006). High heritability in grain filling period as reported by Magdalena *et a*l. (2004) in six row barley agrees with this study. Most of the variation in these traits is more genetic than environment and selection could be relatively easy.

The heritability of malt barley traits are more influenced by genetic factor, indicating a positive response for genetic gain are amenable to genetic improvement under the study area. Low heritability was showed from number of tiller (-0.98%) suggested that variability of a character is influenced more or masked by environmental factor than genetic material, showing that a negative response for genetic gain and selection of genotypes for this character is difficult. High genetic advance was observed for number of kernel, days to heading, plant height, hectoliter weight, thousand seed weight, grain filling period, crop stand and germination capacity (Table 1).

Characters with high heritability accompanied with high genetic advance will a result in better genetic gain through selection. The prediction of genetic advance is a prerequisite for crop improvement in breeding programs especially when large populations are subjected to selection (Burton,*et a*l 1953). This is facilitated by obtaining phenotypic and genotypic coefficients of variation in the absence of which field evaluation of every character would be physically less feasible. High heritability with high genetic advance indicates that selection process in these traits would certainly bring improvement in the genotypes. As reported by Burton (1952) that genotypic coefficient of variability together with heritability estimates would give a clear picture about the extent of advance to be expected from selection, therefore; the expected gain from selection would be a better indicator for selection response.

**Table 1**. Variances, Coefficient of variations and Heritability of traits on malting barley genotypes at Gusha Shenkurta in the 2010 cropping season.

| Traits | $\sigma^2 g$ | $\sigma^2 e$ | $\sigma^2 p$ | Trait mean | GCV (%) | PCV (%) | $H^2$ (%) | GA | GA (%) |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | |
| GY | 0.12 | 0.11 | 0.23 | 1.61 | 21.51 | 41.34 | 52.17 | 0.25 | 15.3 |
| SPL | 0.66 | 0.26 | 0.92 | 7.72 | 10.52 | 12.42 | 71.73 | 1.37 | 17.75 |
| NK | 75.4 | 4.32 | 79.72 | 29.16 | 29.75 | 30.61 | 94.58 | 154.59 | 530.15 |
| NT | -0.0074 | 0.76 | 0.75 | 5.43 | - | 16.34 | -0.98 | -0.015 | -0.279 |
| DH | 28.63 | 8.41 | 37.04 | 83.5 | 6.4 | 7.28 | 77.29 | 59.6 | 71.38 |
| PH | 84.05 | 27.55 | 111.63 | 74.28 | 12.34 | 14.22 | 75.29 | 172.72 | 232.5 |
| GFP | 17.31 | 7.7 | 25.01 | 41.16 | 10.1 | 12.15 | 69.21 | 35.6 | 51.44 |
| STD | 22.31 | 22.31 | 44.62 | 89.33 | 5.28 | 7.47 | 50 | 46.02 | 51.52 |
| DM | 11.42 | 2.82 | 14.25 | 124.66 | 2.71 | 3.02 | 80.14 | 23.52 | 18.87 |
| HLW | 14.6 | 6.1 | 20.3 | 62.79 | 6.08 | 7.17 | 70.05 | 30.11 | 47.95 |
| TSW | 29.3 | 11.05 | 40.35 | 37.79 | 14.32 | 16.8 | 72.61 | 60.77 | 160.8 |
| GPC | 0.59 | 0.13 | 0.72 | 9.43 | 8.14 | 8.99 | 81.94 | 1.22 | 12.92 |
| SCH | 0.44 | 0.19 | 0.63 | 62.88 | 1.05 | 1.26 | 69.84 | 0.91 | 1.45 |
| GER | 44.7 | 94.91 | 139.62 | 93 | 7.18 | 12.7 | 32.01 | 92.17 | 99.1 |

$\sigma^2 g$ = Genetic variance, $\sigma^2 e$ = Environmental variance, $\sigma^2 p$ = Phenotypic variance, GCV = Genetic coefficient of variation, PCV = Phenotypic coefficient of variation, $H^2$ = Broad sense heritability, GA = Genetic advance.

**Correlation between Characters**

Spearman correlation coefficient analysis revealed that hectoliter weight, thousand seed weight, and grain filling period, plant height, kernel number, tiller number, crop stand, days to maturity, grain protein content, germination capacity and biomass yield were positively correlated with grain yield (Table 2, Fig 1 and 2). Hectoliter weight, grain filling period and biomass yield had highly significant (P<0.01) association with grain yield. While plant height and crop stand had significant (P<0.05) association with grain yield. Characters are highly related among themselves and with yield. Positive and significant association of pairs of characters justified the possibility of correlated response to select and the negative and significant correlations prohibit the simultaneous improvement of those traits (Singh *et al*., 1990).

Highly significant and positive association were observed between hectoliter weight with plant height (r= 0. 48**), biomass yield with hectoliter weight (r= 0.59**), thousand seed weight with grain filling period (r= 0.64**), protein content with thousand seed weight (r= 0.46**), days to heading with days to maturity (r= 0.47**), days to heading with grain starch content (r= 0.66**), grain filling period with protein content (r= 0.58**), plant height with spike length (r= 0.48**), kernel number with plant height (r=0.64**), days to maturity with plant height (r= 0.73**), grain starch content with plant height (r= 0.47**), biomass yield with plant height (r= 0.78**), kernel number with days to maturity (r=0.54**), biomass yield with kernel number (r= 0.69**), tiller number with crop stand (r= 0.47**) and days to maturity with biomass yield (r= 0.58**). Positive and significant correlation was observed for hectoliter weight with days to maturity (r= 0.46*), days to heading with plant height (r= 0.41*), grain filling period with biomass yield (r= 0.39*), spike length with number of kernel (r= 0.38*), spike length with grain starch content (r= 0.43*), number of tiller with biomass yield (r= 0.40*) and crop stand with biomass yield (r= 0.40*). Negative and non significant association was indicated for number of kernel with thousand seed weight (r= -0.27) and this result agree with a report of Mohammad and Komatsuda (2007).

Generally, positive and significant association of pairs of characters justified the possibility of correlated response to select. The negative and significant correlation prohibits the simultaneous improvement of those traits. The non significant coefficient of correlation indicates that selection for these different traits could be done separately and independently.

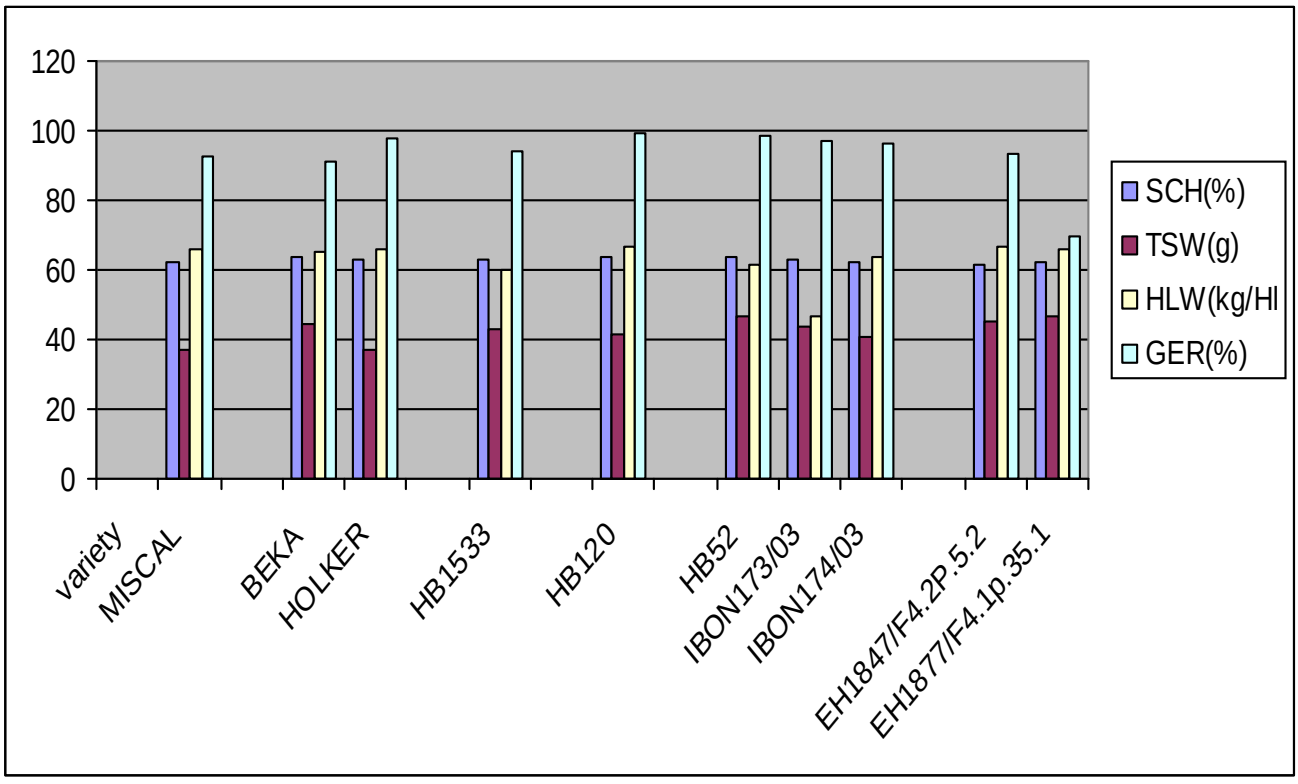


Figure 1 The relation ship between germination capacity, grain starch content, thousand seed weight and hectoliter weight.

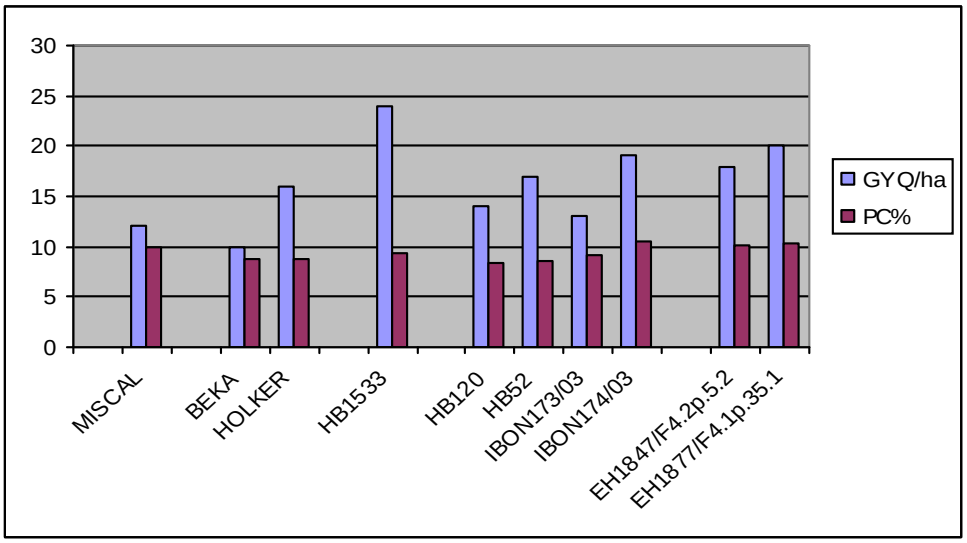


Figure 2 The relation ship between mean grain yield and protein content of ten malt barley cultivars.

**Table 2** Spears man correlation coefficient of the main traits of malting barley genotypes studied at Gusha shinkurta 2010 cropping season. (Grand mother)

| | GY | HLW | TSW | DTH | GFP | PH | SPL | NK | NT | STD | DM | PC | SCH | GER | BMY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GY | | | | | | | | | | | | | | | |
| HLW | 0.670** | | | | | | | | | | | | | | |
| TSW | 0.344 | 0.13 | | | | | | | | | | | | | |
| DTH | -0.347 | -0.144 | -0.556** | | | | | | | | | | | | |
| GFP | 0.582** | 0.337 | 0.648** | -0.728** | | | | | | | | | | | |
| PH | 0.391* | 0.481** | -0.071 | 0.419* | -0.012 | | | | | | | | | | |
| SPL | -0.039 | 0.29 | -0.347 | 0.287 | -0.322 | 0.487** | | | | | | | | | |
| NK | 0.479** | 0.355 | -0.272 | 0.254 | 0.122 | 0.641** | 0.381* | | | | | | | | |
| NT | 0.254 | 0.186 | 0.151 | -0.093 | 0.211 | 0.213 | 0.276 | 0.283 | | | | | | | |
| STD | 0.386* | 0.213 | 0.076 | -0.277 | 0.329 | 0.151 | 0.211 | 0.261 | 0.479** | | | | | | |
| DM | 0.309 | 0.460* | -0.017 | 0.471** | 0.147 | 0.739** | 0.186 | 0.542** | 0.13 | -0.116 | | | | | |
| PC | 0.27 | 0.002 | 0.466** | -0.775** | 0.581** | -0.493** | -0.388* | -0.172 | -0.162 | 0.188 | -0.372* | | | | |
| SCH | -0.207 | 0.002 | -0.316 | 0.665** | -0.524** | 0.478** | 0.430* | 0.105 | 0.208 | 0.045 | 0.274 | -0.859** | | | |
| GER | 0.087 | 0.187 | -0.138 | 0.026 | -0.115 | 0.238 | 0.196 | 0.162 | 0.181 | 0.032 | 0.115 | -0.312 | 0.224 | | |
| BMY | 0.760** | 0.595** | 0.194 | -0.023 | 0.396* | 0.784** | 0.294 | 0.692** | 0.402* | 0.405* | 0.585** | -0.128 | 0.16 | 0.297 | |

**. Correlation is significant at the 0.01 level (2-tailed)
*. Correlation is significant at the 0.05 level (2-tailed)

## Conclusion

Finally, it can be stated that estimates of genetic parameters help in understanding the role of various plant traits in establishing the growth behavior of cultivars under a given set of environmental conditions. Genetic analysis leads us to a clear understanding of different morphological, physiological and genetic characters and also the type and extent of their contribution to grain yield. Mostly the studied characters showed high heritability ($H^2$) coupled with high genetic influence indicating that, these plant traits can be further improved through individual plant selection. Variability between traits and genetic character and integration of information are the area of research priority and can lead us to understand the plant responses under different growing conditions and trivial environments.

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