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Research Article

Correlation and Genetic variability Estimate of Malt Barley (*Hordeum vulgare* L.)

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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 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 general these indicate 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.

Keywords: Heritability, Genetic advance, genotypic variability, Phenotype, Correlation.

Introduction

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

Description of the Study Area

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

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.

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. Germination capacity of grain in 4ml germination test was expressed in percent within 3 days. Germination capacity of grain was done on litmus paper under laboratory.

Data Analysis

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).

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Environmental variance (σ^2_e) = error mean square

- Phenotypic variance (σ^2p) $= \pm^2_g + \pm^2_e$
- Genotypic variance (σ^2g) = 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).

$$\text{Heritability } (H^2) = \frac{\pm_g^2}{\pm_p^2} \text{x100}$$

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

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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.

$$SEg_{xy} = \sqrt{\frac{(1 - r^2 g_{xy})}{2\text{H}_x.\text{H}_y}}$$

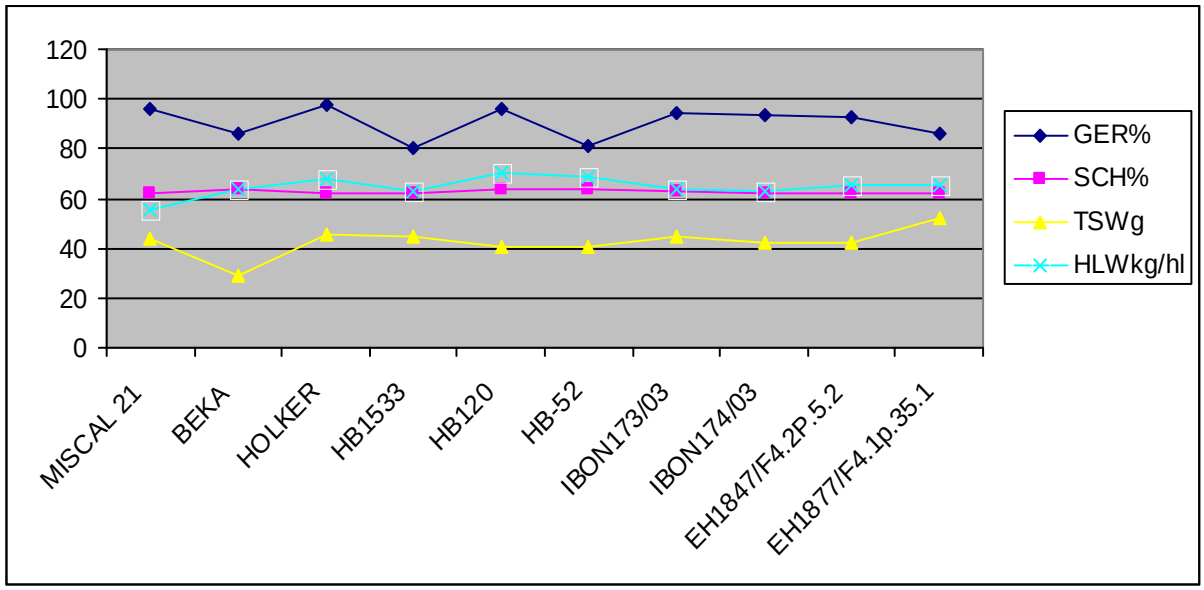
Where, H_x = Heritability value of character x

H_y = Heritability value of character y

Results and Discussion

Positive and highly significant association was observed between the following traits (Table 1 and fig); grain yield with grain filling period (r = 0.56**), plant height with grain yield (r = 0.51**), number of tiller with grain yield (r = 0.51**), crop stand with grain yield (r = 0.63**), days to maturity with grain yield (r = 0.46**). Similarly, positive and highly significant relationship was found between days to maturity with moisture content (r = 0.49**), thousand seed weight with protein content (r = 0.51**),days to heading with hectoliter weight (r = 0.63**), plant height with hectoliter weight (r = 0.79**), spike length with hectoliter weight (r = 0.47**), number of tiller with hectoliter weight (r = 0.62**), crop stand with hectoliter weight (r =0.54**), grain starch content with hectoliter weight (r = 50**), grain filling period with thousand seed weight (r = 0.52**), plant height with days to heading (r = 0.57**), days to maturity with days to heading (r = 0.84**), spike length with plant

height (r = 0.46**), number of kernel with plant height (r = 0.58**), number of tiller with plant height (r = 0.62**),crop stand with plant height (r = 0.62**), days to maturity with plant height (r = 0.67**), grain starch content with plant height (r =0.55**),number of kernel with spike length (r = 0.46**), number of tiller with spike length (r = 0.59**), crop stand with spike length (r = 0.59**), grain starch content with spike length (r = 0.48**), number of tiller with crop stand (r = 0.68**). Positive and significant ($p<0.05$) correlation was also observed between grain yield and thousand seed weight (r = 0.45*), days to heading with moisture content (r = 0.42*), number of tiller with moisture content (r =0.43*) and crop stand with grain starch content (r = 0.44*). The association between grain yield and thousand seed weight is positive and highly significant as reported by Kiflu (2009) and does not agree with this finding. As reported by Fox *et al.* (2000) test weight has a positive relationship to important malt quality traits and also agrees with this finding. Most of the studied genotypes quality traits showed positive correlation between them and yield also positively correlated with grain protein content. The positive correlations of grain yield with agronomic and quality traits are desirable for the achievement of varietal selection on malt barley genotypes. On the contrary negative and highly significant relation ship was observed between malt barley genotypes traits of grain starch content with grain protein content (r = -0.77**), germination capacity with plant height (r = -0.60**), germination capacity with number of tillers (r = -0.53**), crop stand with germination capacity (r = -0.50**), germination capacity with days to maturity (r = -0.64**) and germination capacity with grain starch content (r = -0.49**). Negative and non significant correlation was observed from grain protein content with grain moisture content (r = -0.15), number of kernel with grain moisture content (r = -0.03), hectoliter weight with grain filling period (r = -0.13), thousand seed weight with spike length (r = -0.05), number of kernel with thousand seed weight (r= -0.06); this agree with the results reported by Sameri & Komatsuda (2007).



Genetic parameter of characters

In mother trial broad sense heritability estimate was ranged from -0.77% to 96.3% (Table 2). The highest heritability was recorded for number of kernel while the lowest heritability was observed from crop stand. Similarly highly heritable on stem length, grain weight and grain number per spike were reported by Lalic *et al.*(2010). The studied malt barely genotypes revealed that highly heritable traits were recorded for spike length (78.5%), days to heading (77.3%), plant height (72.9), grain filling period (41.9%), days to maturity (64.1%), hectoliter weight (66.9%), thousand seed weight (76.3%), grain protein content (47.2%), grain starch content (52.4%) and number of tiller (34.4%) while medium heritability was observed for grain yield (15.7%) and germination capacity (20.2%). This study agrees with Chand *et al.* (2008) that thousand grain weight and number of grains per spike were highly heritable but not agree with days to maturity as he reported lowest value of heritability. Low heritability was recorded for crop stand (-0.8%).

Table 1 Spears man correlation coefficient of the main traits of malting barley genotypes studied at GushaShinkurta 2010 cropping season (Mother trial).

	GY	MC	PC	HLW	TSW	DTH	GFP	PH	SPL	NK	NT	STD	DM	SCH	GER
GY															
MC	0.183														
PC	0.112	-0.152													
HLW	0.254	0.381*	-0.258												
TSW	0.455*	0.19	0.513**	0.172											
DTH	0.141	0.425*	-0.411*	0.630**	0.08										
GFP	0.563**	0.033	0.348	-0.138	0.520**	-0.333									
PH	0.516**	0.32	-0.201	0.796**	0.269	0.579**	0.131								
SPL	0.257	0.175	-0.034	0.470**	-0.058	0.062	0.049	0.468**							
NK	0.386*	-0.037	-0.173	0.367*	-0.061	0.283	0.117	0.580**	0.467**						
NT	0.511**	0.433*	0.023	0.624**	0.259	0.175	0.259	0.624**	0.590**	0.17					
STD	0.633**	0.259	-0.049	0.514**	0.351	0.098	0.355	0.626**	0.596**	0.394*	0.682**				
DM	0.467**	0.493**	-0.265	0.542**	0.314	0.840**	0.165	0.672**	0.049	0.344	0.383*	0.28			
SCH	0.168	0.266	-.774**	0.502**	-0.319	0.387*	-0.155	0.555**	0.480**	0.344	0.390*	0.441*	0.342		
GER	-0.412*	-0.449*	0.24	-0.434*	-0.138	-0.355	-0.365*	-0.609**	-0.307	-0.414*	-0.531**	-0.502**	-.646**	-.495**	-

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

This finding agrees with Daniel (2010) except in spike length he reported highly heritable. According to Jalata *et al.* (2011) heritability in broad sense was high for all important quantitative characters measured. High genetic advance was revealed from number of kernels, days to heading, plant height, thousand seed weight, germination capacity and hectoliter weight. These indicate that there is good capacity for crop improvement through selection.

High amount of genetic variability among the population indicated an increased opportunity for the selection of desirable genotypes as the variation is heritable one. The traits possessing low genetic advance with high heritability indicates that the presence of non additive gene action, thus simple selection procedure in early segregating generations will not be effective for screening of the desirable traits.

The quality traits of grain starch content, grain protein content, hectoliter weight and thousand seed weight are useful for malting and brewing industry. These traits vary depending on genotype and field environments. In the population under the study**,** genetic effects formed the major part of variability for plant height, number of kernel, days to maturity, spike length, days to heading, hectoliter weight, thousand seed weight, grain starch content and grain protein content. As a result, genetic improvement in the grain yield per plant would be easier through indirect selection for component traits such as agronomic and quality traits than through direct selection for grain yield. The estimated values of mean effects were highly significant which indicated that studied characters were quantitatively inherited. High heritability estimates indicate the presence of large number of fixable additive factor and hence these traits may be improved by selection. The effectiveness of selection depends up on genetic advance of the characters selected along with heritability. High genetic coefficient of variation along with high heritability and genetic advance provide better information than other parameters alone. High heritability with high genetic advance indicates the control of additive gene and selection may be effective for those characters

Table 2 Variances, Coefficient of variations and Heritability of traits of malting barley genotypes at Gusha Shinkurta in the 2010 cropping season. (Mother trial)

Traits	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 p$	Traits mean	GCV (%)	PCV (%)	H^2 (%)	GA	GA (%)
GY	0.16	0.86	1.02	3.06	12.86	33	15.68	0.34	11.11
SPL	1.02	0.28	1.3	8.21	12.3	13.89	78.46	2.1	25.57
NK	105.88	4.09	109.97	31.03	33.16	33.79	96.28	217.8	701.9
NT	0.63	1.19	1.83	6.6	12.87	20.49	34.43	1.28	19.39
DTH	31.06	9.14	40.2	84.96	6.56	7.46	77.26	63.86	75.16
PH	165.29	61.51	226.8	88.3	14.56	17.1	72.88	341.56	386.8
GFP	5.79	8	13.79	43.4	5.55	8.56	41.99	11.95	27.5
STD	-0.93	121.39	120.46	89.5	-	12.26	-0.77	-1.74	-1.94
DM	14.59	8.18	22.77	128.37	2.98	3.32	64.07	30.06	23.42
HLW	13.91	6.85	20.77	64.59	5.77	7.06	66.97	28.7	44.45
TSW	31.27	9.7	40.97	42.57	13.14	15.04	76.32	64.24	150.9
PC	0.42	0.47	0.89	10.2	6.36	9.24	47.19	0.86	8.46
SCH	0.33	0.3	0.63	62.69	0.91	1.26	52.38	0.68	1.08
GER	18.96	71.61	90.57	90.4	4.82	10.52	20.23	37.37	41.34
MC	-0.011	0.64	0.62	9.79	-	10.16	-1.77	-0.026	-0.26

$\sigma^2 g$= 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.

Conclusion

As a final point, 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 representing 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 marginal environments

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