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Genotypic and Phenotypic Correlation and Path Coefficient Analysis for Yield and Yield Related Traits in Barley (*Hordeum vulgare* L.) Landraces in North Gondar, Ethiopia

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ABSTRACT

Landraces are the major genetic sources of cultivated barley in Ethiopia hence, genetic variability study in barley accession is a major source of information for barley genetic improvement program of the country. Thus, this study was initiated with the objective to assess the extent and pattern of genetic variability in Ethiopian barley accessions. Eighty-one barley accessions were evaluated for 11 morpho-agronomic traits using 9x9 simple lattice design at Debark Agricultural Research Station in 2018 main season. Analysis of variance revealed highly significant ($P \leq 0.05$) difference among accessions for all traits studied which indicated the existence of genetic variability which can be exploited in breeding. The phenotypic and genotypic correlation was positive and highly significant for grain yield with plant height, number of seeds per spike, biological yield and harvest index. Path coefficient analysis revealed maximum positive direct effect of biological yield on grain yield followed by harvest index, showing that these traits can be used for selection to improve the grain yield. In contrast, days to maturity and plant height had negative direct effects on grain yield. The study generally indicated the existence of substantial genetic variability among accessions. Thus, there is appreciable opportunity to use the existing accessions for direct selection to improve specific traits.

Keywords: *Genetic variability, Hordeum vulgare, Path coefficient analysis, Phenotypic correlation, Genotypic correlation, Path coefficient, Traits*

INTRODUCTION

Barley (*Hordeum vulgare* L.) is an annual cereal crop, which belongs to the tribe *Triticeae* of family *Poaceae* (Martin et al., 2006). It is a diploid ($2n=14$) plant with high degree of self fertilization (Martin et al., 2006). It was one of the earliest crops domesticated and is grown over a broader environmental range than any other cereal (Forster et al., 2004).

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In world production, barley ranks fourth among cereal crops, after maize, rice and wheat, with almost 147,404,262 tons obtained in 2017 (FAOSTAT, 2017). World average barley yield is 2.9 t ha^{-1} and ranges from around 8 t ha^{-1} under optimal conditions, to average yields of 1-2 t ha^{-1} in African countries bordering the Sahara desert (FAOSTAT, 2016). The total land under barley cultivation in the year of 2017/18 was 951, 993.15 ha with annual production of 2,052,996.37 tons and average yield of 2.16 tons per hectare in Ethiopia (CSA, 2018). In Ethiopia, barley is a major traditional cereal crop representing about 6.71% of the total national cereal production, and it ranks 5th in the area, after maize, sorghum, tef and wheat (CSA, 2018). It is a very important crop particularly for the highland areas where options are limited to grow other crops because of frost damage and other abiotic factors. Barley is an important crop which covers 54,841.68 ha of land with total production of 107239.38 tons in North Gondar (CSA, 2016). The productivity of barley in North Gondar Zone is 1.9 t ha^{-1} which is below the national average productivity of 2.07 t ha^{-1} (CSA, 2016).

Barley is mainly used for food and malt (CSA, 2018). It is consumed as traditional foods and in making local beverages. The straw is good for animal feed during the dry season and it is also a useful material for thatching roofs of houses and for use as bedding (Berhane Bekele et al., 2005). Barley breakfast foods and snacks are increasingly made available, driven by recent findings, which show that barley fiber contains beta- glucans and tocotrinols, chemical agents known to lower serum cholesterol levels (Asfaw Zeleke, 2000). Barley is an important crop in Ethiopian cereal production and in food security (Berhanu Bekele et al., 2005). Ethiopia was first considered to be a centre of origin for cultivated barley (Vavilov, 1926), although later it became regarded as a secondary centre of diversity because of the absence of the wild relative (Vavilov, 1951). It is cultivated in a wide range of environments, from high altitude areas (2000-3000 m.a.s.l.) to low-rainfall environments, including the Rift Valley (Wondimu Fekadu et al., 2014).

A long history of cultivation together with wide agro-ecological and cultural diversity in Ethiopia has resulted in a large number of landraces of the crop which can adapt to different environmental conditions. Among the important traits that could exist in the landraces are earliness, high nutritional quality, disease and pest tolerance, tolerance to drought and other forms of abiotic stress and characters useful for low input agriculture (Yaynu, 2011).

The low productivity is due to lack of improved varieties, poor agronomic practices, insect and disease. The long history of barley cultivation, the diverse agro ecological zones and the diverse cultural practices have resulted in a country renowned for its large number of farmers' varieties (landraces) and traditional agricultural practices (Berhanu Bekele et al., 2005). The existence of genetic diversity has special significance for the maintenance and enhancement of productivity in agricultural crops in a country like Ethiopia, which is characterized by highly varied agro-climates and diverse growing conditions (Brush, 2000).

Genetic variability in a base population plays an important role in any crop breeding program. The extent of genetic variability in the population determines the magnitude of selection. Barley landraces represent over 90% of the barley cultivated in Ethiopia due to multiple uses and adaptations to marginal environments (Hadado et al., 2009). Ethiopian barley landraces have immense variability; huge numbers of introductions have been made for yield trials for many years. However, most introduced lines were highly susceptible to scald, leaf blotch and perform poorly in a variable environments. Therefore, characterization of landraces and knowledge on the pattern of variation for important morpho-agronomic traits is needed for a proper management and a better exploitation of this gene pool (Alemayehu Assefa, 2003). Landraces need to be evaluated, characterized and properly documented so that well defined sets of samples with specific combinations of desirable traits can easily be retrieved and used in breeding programs (Berhane Gebrekidan, 1982). Ethiopian barley accessions have not been extensively studied and characterized and the genetic variability of material is not known in North Gondar.

Increasing grain production is the highest priority in Ethiopia to feed the increasing population of the country. Barley is one of the most important staple food crops in the highlands of Ethiopia. North Gondar is one of the areas where improved varieties are not widely distributed so far, particularly the potential of the area to food barley crop is not exploited due to lack of improved varieties. According to Welsh (1981), information on the extent of variability, heritability, genetic advance, correlation of yield and yield components is important to design optimum breeding strategies. Therefore, it is important to evaluate those accessions at North Gondar Zone to study the genetic variability, heritability and genetic advance since it provides information that can be utilized to improve barley yield through breeding and to identify high yielding and more adaptable varieties to improve productivity and production of Ethiopian barley.

Knowledge on the extent and pattern of genetic variability present in a population is essential for further improvement of the crop. Similarly, information on the extent and nature of interrelationships among traits helps in planning, evaluating and formulating efficient scheme of multiple trait selection. To have this type of knowledge, research on variability is paramount in plant breeding strategies. Little information is available on estimate of genetic variability and genetic relationships using morphological and agronomic traits in part of highlands of North Gondar for barley accessions. The present investigation was, therefore, concerned with the estimation of the genetic variability, heritability and correlations among yield and yield components at phenotypic and genotypic levels for designing suitable breeding programs involving barley accessions.

Objectives of the Study

To assess the extent and pattern of genetic variability in Ethiopian barley accessions. To estimate the association among grain yield and yield related traits and partition the correlation coefficients into direct and indirect effects

MATERIALS AND METHODS

Description of the Study Area

The experiment was conducted in Debark Agriculture Research Station, Debark district. The district is located at 14° 49' N and 37° 75' E about 830 km from Addis Ababa and about 125 km from Gondar town. Debark is one of the districts of the Amhara Regional State.

The altitude of Debark is 2900 meters above sea level while the minimum and maximum annual temperature ranged between 8.6 °C and 19.8 °C, respectively. Mean annual rainfall for the area was about 1044 mm. The rainy months extend from June until the end of September. However, most of the rainfall is received during the months of July and August (NMSA, 2018).

Experimental Materials and Design

For this study, 81 accessions comprising of 78 barley accessions and 3 improved barley varieties were included. Barley accessions were obtained from Ethiopian Biodiversity Institute. Among the tested accessions, there were three standard checks of released varieties (HB 1307, Agegnehu and Debark-1) adapted to North Gondar. The accessions were originally collected from diverse agro ecological locations of Ethiopia. The standard checks were obtained from Gondar Agricultural Research Center. The experiment was conducted in 2018 main cropping season. The experiment consisted of 81 accessions together with three standard checks. The trial was laid out in simple lattice experimental design. In accordance with specifications of the design, each accession was assigned randomly to the plots within a block. Each experimental plot had four rows of 2.5 meter length and 0.8 meter width. The harvestable plot size was 2.5 m* 0.4 m (1 m^2). Total plot area was used $704.55m^2$. The spacing between rows, plots, blocks and replications was 0.2 m, 0.4 m, 1 m and 1.5 m, respectively.

Data Analysis

Analysis of variance (ANOVA)

Analysis of variance was done using the procedures outlined by Gomez and Gomez (1984) with the help of SAS Computer Statistical Package version 9.2 (SAS Institute Inc., 2008). Duncan's Multiple Range Test (DMRT) was used for means separation. Estimation of the phenotypic and genotypic correlation coefficients was computed following the procedures suggested by Miller et al. (1958). The direct and indirect effects of the independent traits on grain yield were estimated by simultaneous equation using the formula as applied by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Variability among Traits

The analysis of variance for the 11 traits studied. The analysis of variance showed highly significant ($P \leq 0.01$) differences among the tested barley accessions in grain filling period, days to maturity, plant height, number of tiller per plant, spike length, number of seeds per spike, grain yield, harvest index and thousand seed weight. There was also significant difference ($P \leq 0.05$) among accessions for days to heading and biological yield (Table 1). Thus, it indicated that there was sufficient variability in the material used for this study, which provides ample scope for selecting superior and desired accessions for further improvement.

In line with this result, Nigussie Alemayehu (2001) reported the existence of significant amount of genetic variability in 36 accessions of Ethiopian barley. Berhane Lakew and Alemayehu Assefa (2011) also reported large amount of variation between populations for days to heading, days to maturity and plant height. Similarly, Tiegist Dejene (2010) reported the existence of significant variations for days to heading, days to maturity, thousand kernel weight, flag leaf length, awn length, spike length, number of seeds per spike, plant height and number of fertile tillers per plant in Ethiopian barley landraces collections.

Table 1: Mean square for quantitative traits of barley accessions studied

Traits	Replication (1)	Genotypes (80)	Error (64)	CV (%)
DH	33.8	45.47*	29.32	7.86
GFP	0.75	87.1**	39.46	12.25
DM	24.5	145.37**	19	3.63
PH (cm)	195.71	168.31**	9	3.35
SL (cm)	0.02	1.23**	0.5	9.82
NTPP	10.68	1.83**	1.11	19.9
NSPS	24.82	271.18**	36.05	17.2
BY (t ha^{-1})	0.5	4.49*	2.99	15.76
GY (t $\text{ha}^{-1)}$	0.56	1.22**	0.49	19.49
HI (%)	11.51	34.19**	18.9	13.38
TSW (gm)	120.13	94.38**	17.9	9.69

**, * significance at $P \leq 0.01$ and $P \leq 0.05$ level, respectively; numbers in parenthesis indicate degrees of freedom of each level; CV=coefficient of variation, DH=days to heading, GFP=grain filling period, DM=days to maturity, PH=plant height, SL=spike length, NTPP=number of tiller per plant, NSPS= number of seeds per spike, BY=biological yield, GY=grain yield, HI=harvest index, TSW=thousand seed weight

Associations of Traits

Phenotypic and genotypic correlation coefficients were estimated for all possible pair of traits and results are presented in Table 2.

Phenotypic correlations

Assessment of the pair-wise associations among different traits revealed that some of the traits are positively correlated while others are negatively correlated indicating that improving or increasing specific traits had positive or negative influence on the other traits in such degree apparent from the correlation coefficients (Table 2).

Grain yield had highly significant and positive phenotypic correlation with plant height (r_p= 0.46), number of seeds per spike (r_p= 0.30), biological yield (r_p= 0.82) and harvest index (r_p= 0.77) (Table 2). This result indicated that agronomic traits like plant height, number of seeds per spike, biological yield and harvest index could be exploited to increase grain yield in Ethiopian barley.

Alemayehu Assefa (2003) reported strong and positive association of grain yield with plant height and harvest index. The present study in agreement with grain yield had highly significant and positive associations with harvest index and biological yield in durum wheat (Arega Gashaw et al., 2007). On the other hand, grain yield had non-significant but positive phenotype correlation with grain filling period (r_p= 0.1), spike length (r_p= 0.13) and thousand seed weight (r_p= 0.12). This suggested that selection for these traits would not improve grain yield. However, grain yield had negative phenotypic correlation with days to emergence (r_p= -0.07) and number of tillers per plant (r_p= -0.00). Days to heading had highly significant and positive correlations with days to maturity (r_p= 0.61), number of seeds per spike (r_p= 0.31) and biological yield (r_p= 0.25) but negative and highly significant correlation with number of tillers per plant (r_p= -0.3) (Table 2). Madakemohekar et al. (2015) also reported that days to heading had a strong correlation (r_p=0.44) with days to maturity.

Days to maturity had strong positive phenotypic correlation with grain filling period, number of seeds per spike and biological yield. It had a strong negative phenotypic correlation with number of tiller per plant and significant and negative phenotypic correlation with spike length, indicating that delays in maturity is associated with decrease in the number of tiller per plant and spike length. Plant height had highly significant positive correlations with spike length (r_p= 0.32), biological yield (r_p= 0.48), harvest index (r_p= 0.29) and thousand seed weight (r_p= 0.32) (Table 2).

Spike length showed non-significant and positive phenotypic correlation with biological yield, grain yield and harvest index. This is in line with the report of Yetsedaw Ayenwa et al. (2015) who has reported weak positive correlation (r_p=0.25) of spike length with grain yield of malt barley. Spike length had a strong positive phenotypic correlation with number of tillers per plant (r_p=0.25), plant height (r_p=0.32) and thousand seed weight (r_p=0.34) indicating, as number of tillers per plant increases there would be a simultaneous increase of spike length. But Spike length had highly significantly positive phenotypic correlation with number of seeds per spike (r_p= 0.29). The association of these traits was direct. Number of tiller per plant had non-significantly negative phenotypic correlation with grain yield. Similarly, Karim et al. (2012) reported number of productive tillers had a negative phenotypic correlation (r_p=-0.128) with grain yield.

Number of seeds per spike had highly significant positive phenotypic correlation with grain filling period (r_p=0.37) and biological yield (r_p=0.29) indicating a simultaneous increase in number of seeds per spike, grain filling period and biological yield. Grain yield could be improved directly by improving this trait. Thus this trait could be used as a selection criterion for barley grain yield improvement. Similarly, Karim et al. (2012) indicated highly significant and positive phenotypic correlation (r_p=0.811) of number of seeds per spike with grain yield.

In addition, biological yield had highly significant positive phenotypic correlations with harvest index (r_p=0.3) and thousand seed weight (r_p=0.22). Similarly, Zerihun Jalata et al. (2011), Kefalew Taye (2016) and Budakli and Celik (2012) reported positive and highly significant correlation of harvest index with grain yield. This trait showed positive and highly significant correlation with plant height (r_p=0.29) and biological yield (r_p= 0.3). This suggested that selection of accessions for high harvest index might indicate higher biological yield and plant height. However, harvest index had positive and non significant phenotypic correlation with days to heading (r_p=0.008), grain filling period (r_p=0.07), days to maturity (r_p=0.06) and spike length (r_p=0.07). Generally, positive and significant associations of pairs of traits at phenotypic level mostly justify the possibility of correlated response to selection. The negative correlations may prohibit the simultaneous improvement of those traits.

Genotypic correlations

The inherent or heritable association between two variables is known as genotypic correlation. This type of correlation may be either due to pleiotropic action of genes (manifold effects of a gene) or due to linkage or both (Falconer, 1989). Generally, in a breeding program several traits are targeted simultaneously, hence the understanding of the genetic associations among those traits helps to refine the choice of the most appropriate procedures. The estimates of genotypic coefficients of correlation between all possible pairs of grain yield and yield related traits of barley accessions grown at Debark are presented in Table 2. Grain yield had highly significant and positive genotypic correlations with days to maturity (r_g= 0.28), plant height (r_g= 0.47), number of seeds per spike (r_g= 0.38), biological yield (r_g= 0.86) and harvest index (r_g= 0.84). This indicates that these traits can be improved simultaneously. However, grain yield had non-significant but positive genotypic correlation with days to heading (r_g=0.19), grain filling period (r_g=0.12), spike length (r_g= 0.14) and thousand seed weight (r_g=0.08). This suggested that selection for these traits would not improve grain yield. In line with the present study, Jimera Haile et al. (2015) stated that, grain yield was positively and significantly correlated with biological yield and harvest index at genotypic level. Days to maturity had highly significant positive genotypic correlations with days to heading (r_g=0.66), grain filling period (r_g=0.83), number of seeds per spike (r_g=0.53) and biological yield (r_g= 0.28) (Table 2). Plant height had highly significant positive correlations with spike length (r_g=0.39), biological yield (r_g= 0.52), harvest index (r_g=0.31) and thousand seed weight (r_g=0.32) (Table 6). This suggested that selection of accessions for high plant height might increase spike length, biological yield, grain yield, harvest index and thousand seed weight. However, it was positively and not significantly associated with days to heading (r_g=0.19), grain filling period (r_g=0.02), days to maturity (r_g=0.08) and number of seeds per spike (r_g=0.1).

Biological yield depicted positive and highly significant genotypic correlation with days to heading (r_g=0.29), number of seeds per spike (r_g=0.39) and harvest index (r_g=0.47), whereas it was positive and non significantly associated with grain filing period (r_g=0.15), spike length (r_g=0.19) and thousand seed weight (r_g=0.2). Number of seeds per spike showed highly significant and positive genotypic correlations with days to heading (r_g= 0.41), grain filling period (r_g= 0.4), spike length (r_g=0.26) and harvest index (r_g=0.25). Thousand seed weight showed positive and highly significant correlation with plant height (r_g=0.32) and spike length (r_g=0.44) while it had non-significant correlation with the rest of the traits.

Genotypic correlation coefficients were found to be relatively higher in magnitude than that of phenotypic correlation coefficients, which clearly indicated the presence of inherent association among various traits. Correlation among the different traits could be mainly due to the presence of linkage and of the pleiotropic effects of different genes. This is in line with the reports of Johnson et al. (1955), Kefyalew Taye

(2016) and Wasihun Legesse (2007) who explained their results of low phenotypic correlation due to the masking and modifying effects of environment on the phenotypic association among traits. Positive and significant association of pairs of traits justified the possibility of correlated response to selection and the negative and significant correlations prohibit the simultaneous improvement of those traits (Singh et al., 1990).

Table 2: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among 11 traits in 81 barley accessions studied

Trait	DE	DH	GFP	DM	PH	SL	NTPP	NSPS	BY	GY	HI	TSW
DH	0.31**	1	0.14ns	0.66**	0.19ns	-0.11ns	-0.46**	0.41**	0.29**	0.19ns	0.09ns	-0.03ns
GFP	0.47**	0.006ns	1	0.83**	0.02ns	-0.07ns	-0.08ns	0.4**	0.15ns	0.12ns	0.08ns	0.2ns
DM	0.57**	0.61**	0.78**	1	0.08ns	-0.11ns	-0.32**	0.53**	0.28**	0.23*	0.12ns	0.14ns
PH	-0.26**	0.14ns	-0.05ns	0.04ns	1	0.39**	-0.2ns	0.1ns	0.52**	0.47**	0.31**	0.32**
SL	-0.26**	-0.08ns	-0.14ns	-0.16*	0.32**	1	0.24*	0.26*	0.19ns	0.14ns	0.05ns	0.44**
NTPP	-0.13ns	-0.30**	-0.09ns	-0.26**	-0.07ns	0.25**	1	-0.27**	-0.15ns	-0.14ns	-0.08ns	0.08ns
NSPS	0.38**	0.31**	0.37**	0.48**	0.09ns	0.29**	-0.23**	1	0.39**	0.38**	0.25*	-0.39**
BY	-0.11ns	0.25**	0.11ns	0.25**	0.48**	0.15*	-0.00ns	0.29**	1	0.86**	0.47**	0.2ns
GY	-0.07ns	0.15*	0.1ns	0.18*	0.46**	0.13ns	-0.00ns	0.30**	0.82**	1	0.84**	0.08ns
HI	0.004ns	0.008ns	0.07ns	0.06ns	0.29**	0.07ns	-0.02ns	0.19*	0.30**	0.77**	1	-0.06ns
TSW	-0.14ns	0.008ns	0.16*	0.13ns	0.32**	0.34*	0.05ns	-0.36**	0.22**	0.12ns	-0.01ns	1

*, ** and ns, significant at 5%, 1% probability level and non significant, respectively; DH=days to heading, GFP=grain filling period, DM=days to maturity, PH=plant height, SL= spike length, NTPP=number of tiller per plant, NSPS= number of seeds per spike, BY=biological yield, GY=grain yield, HI=harvest index, TSW=thousand seed weight

Path Coefficient Analysis

Path coefficient analysis was computed to estimate the contribution of individual traits to grain yield. It is performed to understand the causes and effects of chain relationships of different yield contributing traits with yield. The path coefficient analysis was conducted using grain yield as dependent variable and all other traits studied as independent variables. Path coefficient analysis was done for those which showed significant correlations with grain yield. In this study, the phenotypic and genotypic direct and indirect effects of different traits on grain yield are presented in Tables 3 and 4.

Phenotypic direct and indirect effects of various traits on grain yield

The phenotypic path coefficient analysis revealed that biological yield and harvest index exerted high and favorable direct effects on grain yield. They had also positive and highly significant correlation with grain yield (Table 3). High values of direct effects suggest that the true relationship and direct selection for these traits may also increase and give better response for improvement of grain yield and can be major selection criteria in barley breeding programs. Similarly, Kefyalew Taye (2016) also reported a strong positive direct effect of biological yield on grain yield of barley (0.6). On the other hand, harvest index had positive indirect effect on seed yield through days to heading, number of seeds per spike and biological yield but it had negative indirect effect through days to maturity and plant height. Totally the direct and indirect effects of days to maturity on grain yield were positive and small in magnitude (0.07). Thus, direct selection based on plant height could not be effective to improve barley grain yield. Rather, indirect selection via biological yield would be effective for barley grain yield improvement.

Direct effect of harvest index on grain yield was high in magnitude and positive (0.573). Thus, direct selection based on this trait would be promising for barley grain yield improvement. Kefyalew Taye (2016) also indicated a high positive direct effect (0.759) of harvest index on grain yield of Ethiopian barley. Majumder et al. (2008) found positive direct effects of harvest index on grain yield of spring wheat varieties. Furthermore, Gadisa *et al*. (2014) reported that days to maturity, biological yield per plot, and harvest index had direct effect on grain yield.

Days to heading and number of seeds per spike exerted favorable but weak influences on grain yield, whereas days to heading had some negative influences at phenotypic level. The negative direct effects of days to maturity and plant height on grain yield would indicate that the selection for these traits would not be rewarding for yield improvement. The results of path coefficient analysis showed that biological yield and harvest index had high and favorable direct effects on grain yield. Genetic improvement in grain yield can be accelerated if yield contributing traits are used as selection criteria. For this purpose, it is necessary not only identify indirect linkage to gain yield, but also understanding of the genetic bases controlling this trait for easy handling (Garcia et al., 2011).

On the other hand, days to maturity and plant height had negative direct effects on grain yield. Day to maturity exerted positive indirect effect on grain yield through days to heading, number of seeds per spike, biological yield and harvest index. Likewise, plant height exerted favorable indirect effect on grain yield through biological yield and harvest index. Indirect and positive effects of biological yield were exhibited through days to heading, number of seeds per spike and harvest index on grain yield. The results of residual effect (R=0.16) revealed that 84% of the yield of barley was contributed by the traits studied in this experiment. The role of other independent variables which had not been included in this experiment was expected to influence grain yield only by 16% (Table 3). This result indicates the adequacy of the traits that were included in this study.

Table 3: Phenotypic path coefficient of direct (bold diagonal) and indirect effects (off diagonal) of quantitative traits on grain yield in 81 barley accessions

Traits	DH	DM	PH	NSPS	BY	HI
DH	**0.017**	-0.197	-0.004	0.002	0.169	0.005
DM	0.103	**-0.322**	-0.001	0.002	0.169	0.039
PH	0.025	-0.013	**-0.025**	0.000	0.324	0.166
NSPS	0.053	-0.155	-0.002	**0.005**	0.196	0.109
BY	0.042	-0.081	-0.012	0.001	**0.674**	0.172
HI	0.002	-0.019	-0.007	0.001	0.202	**0.573**

Residual effect =0.16

DH=days to heading, DM=days to maturity, PH=plant height, NSPS=number of seeds per spike, BY=biological yield, HI=harvest index

Genotypic path coefficient analysis of grain yield

The genotypic direct and indirect effects of different traits on grain yield are presented in Table 4. Path coefficient analysis at genotypic level showed that number of seeds per spike (0.06), biological yield (0.59) and harvest index (0.56) had positive direct effect on grain yield, which showed that these yield components positively affected grain yield in barley. The strong direct positive effects of biological yield and harvest index on grain yield indicate selection based on these traits can be effective for yield improvement in barley. The genotypic direct effects of these traits ranged between 0.06 for number of seeds per spike and 0.59 for biological yield. Whereas days to maturity (-0.09) and plant height (-0.039) showed negative direct effects. The direct negative effects of these traits seemed to be emphasized because the effects of these traits were towards declining grain yield (Table 4). Similar to these results, Alemayehu Assefa (2003) reported that days to heading and plant height had negative direct effects on grain yield. Biological yield exerted the highest direct effect on grain yield. Kefyalew Taye (2016) reported higher and positive direct effect of biological yield (0.6) and harvest index (0.75) on grain yield. Similarly, Solomon Gelalcha and Hanchinal (2013) also reported a strong positive direct effect of biological yield (0.805) and harvest index (0.97) on grain yield of wheat.

The genotypic indirect effects had considerable contribution to their total correlation. Days to maturity had positive indirect effects through number of seeds per spike, biological yield and harvest index. The indirect effects of days to maturity were negative through plant height and very small in magnitude. The indirect effect of plant height on grain yield via biological yield and harvest index was relatively large. Positive indirect effects of harvest index on grain yield were exhibited via seeds per spike, harvest index and biological yield. The genotypic positive indirect effects of the phenological traits on grain yield would provide a better means of increasing grain yield and clarify their true relationship (Khan et al., 2013).

Unfavorable and negative indirect effects of number of seeds per spike on grain yield were through days to maturity and plant height. Biological yield exhibited positive and indirect effect on grain yield via number of seeds per spike and harvest index. Biological yield exhibited negative and indirect effect on grain yield via days to maturity and plant height. Biological yield exhibited positive and significant indirect effect on grain yield via number of seeds per spike and harvest index. Biological yield exhibited negative and non significant indirect effect on grain yield via days to maturity and plant height.

Generally, trait association between yield and yield related traits in this particular study indicated various magnitude of association which can be carefully looked into, while exploiting in selection to improve traits of interest in Ethiopian barley breeding. According to Singh and Chaudhary (1977), whenever a trait has positive correlation and high positive indirect effects but negative direct effect on the economic trait like grain yield, emphasis should be given to the indirect effects.

Table 3: Genotypic path coefficient of direct (bold diagonal) and indirect effects (off diagonal) of quantitative traits on grain yield in 81 barley accessions

Traits	DM	PH	NSPS	BY	HI
DM	**-0.0923**	-0.0031	0.0332	0.1679	0.068
PH	-0.0074	**-0.0385**	0.0063	0.3118	0.175
NSPS	-0.0489	-0.0039	**0.0627**	0.2339	0.141
BY	-0.0259	-0.02	0.0244	**0.5997**	0.265
HI	-0.011081	-0.01194	0.01567	0.2818	**0.564**

Residual effect = 0.11; DH=days to heading, DM=days to maturity, PH=plant height, NSPS= number of seeds per spike, BY=biological yield, HI=harvest index

CONCLUSION

Knowledge of the nature and magnitude of variation existing in breeding materials, interrelationships between quantitatively inherited traits and partitioning their direct and indirect effects on grain yield are of great importance to design breeding strategies. The analysis of variance in this study revealed significant variation among the test genotypes for all the traits studied. Spike length, number of seeds per spike and grain yield had high phenotypic and genotypic coefficients of variation. The existence of high degree of genotypic variability among the tested barley accessions in morpho-agronomic traits indicated the availability of great potential for future improvement of the crop. Genotypic correlations were found to be higher in magnitude than that of phenotypic correlations for the majority of the traits studied. This indicated that genetic factors played a major role in the associations among the majority of the traits. Grain yield was highly significantly and positively correlated with plant height, number of seeds per spike, biological yield and harvest index at both genotypic and phenotypic levels. This indicates that these characters could be improved simultaneously.

Path coefficient analysis revealed that biological yield and harvest index were major contributors of grain yield. This implies that selection criteria that focused on these traits would have a tremendous value for yield improvement. Residual effect was 0.11 and 0.16 at phenotypic and at genotypic levels, respectively. This showed that the twelve traits explained 89% at genotypic and 84% at phenotypic levels of the variability in grain yield. This further elucidated that the yield attributing traits chosen in the study explained much of the variability in the accessions.

The observed variability within the barely accessions in grain yield and other agronomic traits, indicates the potential for further improvement through directional selection and hybridization.

By combining the above results together, breeders can design effective and efficient genetic improvement methods such as selection and hybridization for wise utilization of the available resources. However, it is important to be emphasized that the results and conclusions made is based on data obtained from one year field evaluation at a single location. Therefore, evaluation of more number of accessions in multiple environments would be necessary in order to get comprehensive results and draw valid recommendations and conclusions. Further research on selected accessions will save a lot of time for the breeder in future.

Abbreviations

CSA	Central Statistical Agency
EBI	Ethiopian Biodiversity Institute
FAO	Food and Agricultural Organization
LSD	Least Significance Difference Test
SAS	Statistical Analysis System

Authors' contributions

EA initiated the research, wrote the research proposal, conducted the research, did data entry and analysis and wrote the manuscript. TD and FK were involved in analysis, methodology, writing, reviewing and editing of research proposal and manuscript. All authors read and approved the final manuscript.

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Competing interests

The authors declare that they have no competing interests.

Availability of data and materials

The authors want to declare that they can submit the data at whatever time based on your request. The datasets used and/or analyzed during the current study will be available from the corresponding author on reasonable request.

Consent for publication

Not applicable.

Ethics approval and consent to participate

Not applicable since the study involved barley plants.

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