

Genetic variability and trait association for grain yield in barley (*Hordeum vulgare* L.)

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Abstract

For yield enhancement, it is primarily important to know and predict the nature of variability available for the inter-related traits. Therefore, study was conducted to know the variability available and to comprehend the correlation among different traits for grain yield in barley accessions. Thirty-two barley accessions including two checks were sown in randomized block design with three replications at ICAR-IARI, Regional Station, Shimla, and data on seven traits *viz.*, days to maturity, plant height, spike length, grains/spike, tillers/meter, 1000-grain weight and grain yield were recorded. Sufficient genetic variability was observed among the barley lines used for the studied traits except for tillers/m. High heritability was observed for 1000 grain weight, days to maturity and plant height suggesting possible improvement of these three agronomic traits. The value of genetic advance as percent of mean was high coupled with high broad sense heritability for 1000 grain weight highlighting that the character is governed by additive genes and selection may be beneficial for such trait. Based on the correlation results at genotypic level, tillers/m (0.93) and 1000 grain weight (0.23) had higher correlation with seed yield which could be considered important traits for yield enhancement in barley. At genotypic level, 1000 grains weight showed direct positive effect on grain yield (0.22) with significant positive genotypic correlation coefficient of 0.24. The traits, spike length (4.05) followed by plant height (2.87) and days to maturity (2.14) also showed high positive direct effects but values of genotypic correlations were negative.

Keywords: Barley, heritability, correlation, path analysis, variability

1. Introduction

Barley (*Hordeum vulgare* L.) is one of the oldest crops grown by the human civilization from last 10000 years. As per archeological evidences, present day barley was domesticated from a wild relative (*Hordeum spontaneum* C. Koch) (FAO, 2008). Many barley cultivars are being cultivated all over the world having different attributes like: number of rows of grains (6-row and 2-row), spike compactness, growth habit (winter or spring), presence or absence of awns (hooded, awned or awnless), hull

adherence (hulled or naked) and colour (white, blue or black kernels). Generally, two rowed barley has less protein content than six rowed barley and contains more sugar content due to which it is used in malt industry. When fermented, two rowed barley is used as an ingredient in beer and other alcoholic beverages. Barley has high nutritive value; the grains are rich source of nutrients like thiamine, riboflavin and fiber with higher biological and medicinal values *via* reducing diabetes



and heart diseases and lowering cholesterol in human. It is also being used for various other health issues like malnutrition, hormonal imbalance, high blood pressure, kidney stones and gastric ulcers because of the presence of soluble fibers known as beta-glucans (Kumari and Vishwakarma, 2022). Barley is considered as the only possible rainfed cereal crop cultivated under low input and stressful environments, like heat, drought, and cold (Kumari *et al.*, 2020). Therefore, this old crop is likely to have new future in current situations of climate change and ever-increasing population pressure on food supply (Bishnoi *et al.*, 2022).

During 2020-21 barely was cultivated in 50.90 million hectares area with 153.47 million tonnes of production over the globe. In India, barley was grown in 0.61 million hectares area with production of 1.82 million tonnes and productivity of 29.8 q/ha (III Advance Estimates of 2020-21, Directorate of Economics and Statistics, Ministry of Agriculture and Farmers' Welfare). In India, this coarse grain crop is cultivated in different states like Rajasthan, Haryana, Uttar Pradesh, Madhya Pradesh, Bihar and Himachal Pradesh for forage or grain purpose. In the present scenario, barley is being grown under very limited area with low productivity because it is only grown by marginal farmers with low inputs (Patia *et al.*, 2018).

Breeding for enhanced grain yield relies upon the presence of genetic diversity which is an imperative for successful hybridization program (Dyulgerova, 2012). Genetic variability depicts the presence of differences among the different genotypes or individuals due to presence of different genetic composition among them and their growing environment (Falconer and Mackay, 1996). Genetic parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are crucial detecting the amount of variability present in the germplasm. Genetic advance and heritability both play an important role in effective selection of a particular trait (Kumari *et al.*, 2019). The higher heritability of the trait is an advantage for the phenotypic selection and there will be less influence of the environment (Khan *et al.*, 2013).

Since grain yield is a complex trait ensuing from interactions of several independent quantitative traits and environmental factors, hence, direct selection would not be much effective for developing improved barley lines.

Therefore, for a successful barley yield improvement, selection based on yield components can be effective tool. Therefore, understanding of inter-relationship among component characters helps in identifying the character selection during improvement of the related complex trait. In plant breeding programmes, the understanding of degree of association between yield and attributing traits helps in improvement of yield involving correlation studies of various traits linked directly or indirectly. Yield components can be estimated from variances and covariances of correlation coefficients. Degree of association and genetic or non-genetic relationships between two or more characters are helpful for selection (Shrimali *et al.*, 2017).

Path analysis partition the correlation coefficient in direct and indirect effects of independent characters on yield (dependent character). Therefore, path coefficients are analysed from simple correlation coefficients. Knowledge about the extent and nature of interrelationship among characters promotes formulating efficient selection scheme of multiple trait, as it enables direct and indirect selection of component characters.

Estimation of variability for yield and potential yield traits becomes essential before planning a suitable breeding strategy for genetic improvement (Kumari *et al.*, 2019). Therefore, the present study was formulated with the objective to identify genetic variability and heritability of the different traits among barley accessions for future breeding program. Along with this, the study also focuses to estimate the extent of association between pairs of characters at genotypic and phenotypic levels and thereby compare the direct and indirect effects of the characters for the improvement of yield *via* yield contributing traits which can result in potential selection criterion for development of improved barley cultivars with enhanced yield.

2. Material and Methods

2.1 Experimental Procedure

The study was conducted at ICAR- Indian Agricultural Research Institute Regional Station, situated at Tutikandi Center, Shimla, Himachal Pradesh which is located at 32° N latitude and 77°E longitudes at an altitude of 1900 m above mean sea level. This location falls under Northern Hill Zone of India. Thirty-two barley accessions



including two checks BHS400 and BHS 380 were grown in randomized block design with three replications during Rabi 2019-20. Row to row and plant to plant distance was maintained at 23cm and 10cm, respectively. All recommended package of practices were done to raise a good crop.

2.2 Data collection

Plant height was measured as the average distance from the soil surface to the tips of spikes, excluding awns. The data pertaining to days to maturity (days), 1000 grain weight (g) and yield(Q/ha) were recorded on plot basis; for tillers/m (number) on number of tillers in 1 meter, whereas, for remaining traits viz, plant height (cm), spike length (cm), grains/spike (number) was recorded from five random plants.

2.3 Statistical analysis

Analysis of variance (ANOVA) was done according to OP-STAT software. Phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), genetic advance (GA), heritability broad sense (h^2_{bs}), genetic advance in percentage (GA%), phenotypic correlation coefficients (PCV), genotypic correlation coefficients (GCV), were estimated according to Singh and Chaudhary (1985). Path coefficients of yield with other traits were worked out following Dewey and Lu (1959).

Path analysis was conducted using correlation considering grain yield as the response variable and days to maturity, 1000 grain weight, tillers/m, plant height, spike length and grains/spike as predictor variables. To satisfy the assumption of additivity for the path-coefficient analysis, yield and yield trait data were logarithmically transformed prior to analysis. Tests of significance of phenotypic correlation coefficients of yield and its components and plant traits by t-test were obtained through the Statistical Analysis System (SAS, 1987).

Following formulas were used for calculation as given by different researchers.

Genotypic coefficient of variation (GCV)

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

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where

$\sqrt{\sigma_g^2}$ = genotypic standard deviation

\bar{X} = population mean

Phenotypic coefficient of variation (GCV)

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$\sqrt{\sigma_p^2}$ = phenotypic variance

\bar{X} = population mean

Heritability (%) (Broad Sense)

$$\text{Heritability (h}^2_{bs}\text{)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2 = genotypic variance and

σ_p^2 = phenotypic variance

Genetic advance (%)

The genetic advance (GA) ensuing from the selection of 5 per cent superior individuals was computed as per Burton and De Vane (1953) and Johnson *et al.* (1955):

$$GA = K \times \sigma_p \times h^2_{bs}$$

Where,

$K = 2.06$ (selection differential at 5% selection intensity)

h^2_{bs} = heritability (broad sense)

σ_p = phenotypic standard deviation

Genetic advance expressed as percent of mean (GA %) =

$$\frac{\text{Expected GA}}{\text{Grand mean}} \times 100$$

For categorizing the magnitude of different parameters, the following limits were used:

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

Heritability in broad sense (Johnson *et al.*, 1955): >60% - high; 30 - 60% - moderate; <30% - low

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

Phenotypic coefficient of correlation

$$r_{p_{xy}} = \frac{\sigma_{p_{xy}}}{(\sigma^2_{p_x} \times \sigma^2_{p_y})^{1/2}} \times 100$$



Where,

$\sigma_{p_{xy}}$ = phenotypic covariance between two characters x and y

$\sigma^2_{p_x}$ = phenotypic variance of character x

$\sigma^2_{p_y}$ = phenotypic variance of character y

Genotypic coefficient of correlation

$$r_{g_{xy}} = \frac{\sigma_{g_{xy}}}{(\sigma^2_{g_x} \times \sigma^2_{g_y})^{1/2}} \times 100$$

Where,

$\sigma_{g_{xy}}$ = genotypic covariance between two characters, x and y

$\sigma^2_{g_x}$ = genotypic variance of character x

$\sigma^2_{g_y}$ = genotypic variance of character y

3. Results and Discussion

3.1 Mean performance of barley lines for seven different traits

Based on the mean values of thirty-two barley lines the range of various traits were; days to maturity varied

Table.1 Mean values for different traits in thirty-two barley accessions.

Genotypes	Days to maturity (Days)	Plant height (cm)	Spike length (cm)	Grains/spike (Number)	Tillers/m (Number)	1000 grains weight (g)	Grain yield (Q/ha)
BBM 828	169.00	84.67	8.50	46.67	50.00	36.00	23.57
BBM 829	171.00	85.33	10.83	45.00	77.33	48.00	25.80
BBM 830	167.00	85.67	9.50	45.00	59.67	43.00	29.37
BBM 831	167.00	85.17	9.00	44.33	60.00	52.00	21.93
BBM 832	173.00	70.67	9.67	48.67	102.00	33.00	33.92
BBM 833	170.67	90.33	9.83	43.67	49.33	34.67	32.00
BBM 834	174.67	85.67	8.17	35.67	65.33	35.00	23.00
BMM 835	169.00	79.67	9.33	42.67	67.67	36.00	32.36
BBM 836	175.00	79.50	10.33	45.33	66.67	41.67	31.79
BBM 837	168.00	88.00	8.67	38.33	90.67	52.33	29.37
BBM 838	172.00	85.33	10.33	35.33	59.00	36.00	33.00
BBM 839	174.00	82.00	9.17	46.67	80.00	36.67	25.31
BBM 840	169.00	86.00	8.83	50.33	81.67	39.00	33.30
BBM 841	181.33	85.33	8.17	45.00	56.00	43.00	28.99
BBM 842	181.00	80.67	8.17	40.00	61.33	41.33	28.60
BBM 843	181.00	101.50	9.33	52.67	69.33	39.67	35.26

from (167-186.7 days), plant height (67.5-101.5 cm), spike length (6.67-10.83 cm), grains/spike (34.33-52.67), tillers/m (49-102), 1000 grain weight (33-52.33 g) and grain yield (19.61-35.26 Q/ha). Comparative study of barley accessions for seven traits showed clear distinction of genotypes. BBM830 (167 days) and BBM831 (167 days) were most early to mature. In case of plant height BBM850 (67.50 cm) was shortest as compare to other genotypes. For spike the accession BBM829 (10.83) had longest spike length. BBM840 (50.33) and BHS400 (50.33) had highest number of grains/spike. For tillers/m accession BBM832 (102.00) was having highest number of tillers/m. BBM837 (52.33g) had highest 1000 grain weight among thirty-two genotypes. Highest grain yield was shown by BBM843 (35.26 Q/ha) among all the genotypes (Table1). Patial *et al.* (2018) and Katiyaret *al.* (2020) in barley also reported different better performing lines than check in their study involving different barley accessions and cultivars.



BBM 844	182.67	87.00	8.33	45.33	49.00	47.00	29.18
BBM 845	180.33	79.33	7.83	46.00	60.67	35.00	34.60
BBM 846	183.00	83.17	8.17	39.67	58.33	51.00	31.01
BBM 847	181.00	93.00	8.17	40.67	57.67	40.67	25.12
BBM 848	168.00	79.67	8.50	42.67	59.33	37.67	21.55
BBM 849	186.00	73.83	8.33	42.00	66.00	40.67	29.27
BBM 850	183.33	67.50	7.00	34.67	52.67	41.67	30.05
BBM 851	186.00	72.67	8.50	37.33	57.67	34.33	19.61
BBM 852	186.67	76.50	7.50	35.33	83.33	35.00	21.26
BBM 853	183.67	67.83	6.83	37.00	69.33	36.00	20.87
BBM 854	183.67	85.00	8.83	34.33	86.00	40.33	26.67
BBM 855	184.00	68.83	6.67	39.67	61.33	44.33	29.66
BBM 856	184.00	80.83	7.33	38.00	67.00	49.00	30.92
BBM 857	184.00	84.50	7.00	38.00	49.33	40.00	20.39
BHS 400©	170.00	82.67	9.67	50.33	68.00	41.00	33.00
BHS 380©	173.00	70.17	8.83	35.00	65.50	36.00	21.31
Mean	176.94	81.50	8.60	41.92	65.85	40.53	27.88
Range	167-186.7	67.5-101.5	6.67-10.83	34.33-52.67	49-102	33-52.33	19.61-35.26
C.D. (5%)	2.61	8.26	1.63	7.95	25.83	4.49	7.14
SE(m)	0.92	2.92	0.58	2.81	9.11	1.58	2.77
SE(d)	1.30	4.12	0.81	3.97	12.89	2.24	3.92
C.V.	0.90	6.20	11.59	11.59	23.97	6.77	17.23

3.2 Analysis of variance

Analysis of variance of different genotypes for seven different traits showed significant differences among them. All the traits except tillers/m showed significant differences among the genotypes indicating sufficient variability for

the traits in the material opted for the study (Table 2). Hailu *et al.* (2016) and Raikwar *et al.* (2014) also reported significant variation among barley genotypes for different traits in their study that can be used for improvement of the trait of interest.

Table.2: Mean squares analysis for morphological traits in different barley accessions

Source of variation	Degree of freedom	Days to maturity (days)	Plant height (cm)	Spike length (cm)	Grains/spike (number)	Tillers/ meter (number)	1000 grain weight (g)	Yield (Q/ha)
Replication	2	1.34	32.09	5.40	14.26	1,731.5	24.219	86.76
Treatments	31	138.56**	174.03**	3.27*	78.79*	486.07	90.04**	68.28*
Error	62	2.53	25.50	0.99	23.61	249.14	7.52	27.20

** and * significance at the 0.01 and 0.05 levels

3.3 Variability parameters

Genetic variability is an important tool which helps in formulation of breeding strategies for the crop improvement, based upon the information on genetic

properties of the population (Pandey *et al.*, 2011). Total variation based on the genotypic effects is measure of genotypic and phenotypic variance which is known as broad sense heritability (Allard, 1960).



Moderate genotypic coefficient of variations (GCV) was observed for grain yield (13.96), tillers/m (13.49), 1000 grain weight (12.94), grains/spike (10.23) and spike length (10.12) (Table 3). These characters with moderate GCV value indicate greater potential for selection. High phenotypic coefficient of variation (PCV) was recorded for tillers/m (27.50) and grain yield (22.15). Moderate (PCV) values were observed for traits like, grains/spike (15.46), spike length (15.39), 1000 grain weight (14.60) and plant height (10.62). Days to maturity showed lowest PCV and GCV values. In present study, in general high PCV values were observed than GCV indicating environment influence for traits expression. The similar trend has also been reported by Singh and Upadhyay (2013) in wheat. High heritability was observed for days to maturity (94.70), 1000 grain weight (78.53) and plant height (66.00). Moderate heritability values were recorded for grains/spike (43.78), spike length (43.28) and grain yield (39.50). All the traits showed moderate genetic advance except

1000 grain weight (high genetic advance of 23.62) and days to maturity (low genetic advance of 7.62). Higher heritability coupled with higher genetic advance was observed for 1000 grain weight. High heritability along with moderate genetic advance was observed for plant height. High heritability and low genetic advance were observed for days to maturity. The high heritability for 1000 grain weight, days to maturity and plant height suggests that the three characters are inherited from the parents to their offspring and thereby indicates a possible improvement of these three agronomic traits. These findings reinforce the results of previous studies that find high heritability value in these agronomic traits (Kumar *et al.*, 2002; Yadav *et al.*, 2004; Therrien, 2006; Mishra *et al.*, 2007; Iannucciet *al.*, 2021). This genetic variability may be exploited in the breeding program for improvement of barley yield and its related traits. Patial *et al.* (2016) also reported the importance of these traits and variability present for enhancing variability in barley breeding gene pool.

Table 3: Genetic parameters for grain yield and its contributing traits in barley

Traits	Days to Maturity (days)	Plant height (cm)	Spike length (cm)	Grains/spike (number)	Tillers/m (number)	1000 grain weight (g)	Grain yield (Q/ha)
GCV	3.80	8.63	10.12	10.23	13.49	12.94	13.96
PCV	3.91	10.62	15.39	15.46	27.50	14.60	22.15
Heritability (h^2_{ns}) (%)	94.70	66.00	43.28	43.78	24.07	78.53	39.50
Genetic Advance (GA)(%)	7.62	14.44	13.72	13.94	13.64	23.62	18.02

The value of genetic advance as percent of mean was high coupled with broad sense heritability for 1000 grain weight highlighting that the character is governed by additive genes and selection may be beneficial for such trait. For trait like days to maturity, low genetic advance suggests non-additive genes and heterosis breeding may be useful.

Genetic advance as percent mean ranged from (7.62 %) for days to maturity to (23.62 %) for 1000 grain weight indicating that selecting the top 5% of the genotypes could result in an improvement range of 7.62% for days to maturity to 23.62% for 1000 grain weight (g). Similar finding of moderate heritability with moderate genetic advance for grain yield was also been reported (Yadav *et al.*, 2019; Singh and Upadhyay, 2013; Afzal *et al.*, 2021). Low genetic advance for days to maturity was also reported by Adhikari *et al.* (2018) and Kumar *et al.* (2017).

3.4 Correlation coefficient

Genetic association between different traits can be worked out which can be a helpful tool in selection procedure. At genotypic level tillers/m (0.91) and 1000 grains weight (0.24) exhibited significant positive correlation with grain yield whereas, remaining traits had negative correlation with grain yield (Table 4). Among yield contributing traits, at genotypic level, days to maturity had significant positive correlation with plant height (0.27); plant height showed significant positive correlation with spike length (0.86) and grains/spike (0.32); spike length had significant positive correlation with grains/spike (0.30) (Table 4). Kumari



and Vishwakarma(2022) reported significant association between different yield and its contributing traits which are coherent to present study.

At phenotypic level the traits viz., grains/spike (0.44), spike length (0.33), plant height (0.24), tillers/m (0.22) and 1000 grain weight (0.26) showed significant positive correlation with grain yield. Plant height showed significant positive correlation with spike length (0.23), grains/spike (0.31), 1000 grain weight (0.22). Spike length had significant positive phenotypic correlation with grains/spike (0.33) and tillers/m (0.23).

The genotypic correlation coefficient values were higher as compared to phenotypic correlation coefficient that indicated that there was negligible influence of the environment.Zeng and Chen (2001), Dyulgerova and Valcheva (2014) and Singh *et al.*, 2017 also reported the higher values of genotypic correlation coefficient.

Correlation is an important tool in plant breeding for indirect selection to improve a targeted trait like grain yield.

Based on the correlation results at genotypic level, tillers/m and 1000 grain weight had higher correlation with grain yield which could be considered important traits for yield enhancement in barley. A positive correlation between tiller/m and seed yield means the increase in the number of tillers will increase the resulting barley grain yield. This is understandable because barley grains appear along the stem of plant, so the higher the appearance of tillers of a plant, more likely it is to produce spikes and therefore more yield. Besides tillers/m, the 1000 grain weight also leads to increase in grain yield which is evident in the present study. Several previous study reports have also found similar results (Singh *et al.*, 2008; Patial *et al.*, 2018; Adhikari *et al.*, 2018)

Table 4: Phenotypic and Genotypic correlation of grain yield with different traits in barley

Traits		Plant height (cm)	Spike length (cm)	Grains/spike (number)	Tillers/m (number)	1000 grain weight (g)	Grain yield (Q/ha)
Days to maturity (days)	P	-0.24*	-0.52**	-0.31**	-0.08NS	-0.01NS	-0.10NS
	G	0.27**	-0.66**	-0.26*	-0.67**	-0.05NS	-0.14NS
Plant height (cm)	P		0.23*	0.31**	-0.09NS	0.22*	0.24*
	G		0.86**	0.32**	-0.42**	0.19NS	-0.03NS
Spike length (cm)	P			0.33**	0.23*	0.03NS	0.33**
	G			0.30**	-0.10NS	0.18NS	-0.19NS
Grains/spike (number)	P				0.13NS	0.10NS	0.44**
	G				-1.33**	-0.18NS	0.01NS
Tillers/m (number)	P					0.03NS	0.22*
	G					-0.10NS	0.91**
1000 grain weight (g)	P						0.26*
	G						0.24*

** and * significance at the 0.01 and 0.05 levels

3.5 Path Coefficient Analysis

Yield is generally considered as polygenic character which is controlled by various other traits or components, therefore, selection based only on correlation analysis could neglect other indirect causes which may create misleading results (Uddin *et al.*, 2015). Path analysis splits correlation coefficients into direct and indirect

effects which may not be provided by simple correlation estimates of yield and other traits. Therefore, in this study, it is assumed that grain yield was the end product of days to maturity, plant height, spike length, grains/spike, tillers/m and 1000 grain weight. The residual that represents other factors affecting grain yield but not included in this study was also considered.



Table 5: Direct and indirect effects of different traits at phenotypic and genotypic level on grain yield in barley.

Traits		Days to maturity (days)	Plant height (cm)	Spike length (cm)	Grains/spike (number)	Tillers/m (number)	1000 grain weight (g)	Yield (Q/ha)
Days to maturity (days)	P	0.17	-0.02	-0.13	-0.11	-0.01	-0.00	0.10NS
	G	2.14	-0.78	2.68	0.07	0.04	-0.01	-0.14NS
Plant height (cm)	P	-0.04	0.09	0.05	0.11	-0.01	0.03	0.24*
	G	0.58	2.87	-3.48	-0.08	0.03	0.04	-0.03NS
Spike length (cm)	P	-0.09	0.02	0.25	0.11	0.03	0.00	0.33**
	G	1.42	2.47	4.05	-0.08	0.00	0.04	-0.19NS
Grains/spike (number)	P	-0.05	0.03	0.08	0.35	0.01	0.01	0.44**
	G	0.56	0.92	-1.25	-0.27	0.09	-0.04	0.01NS
Tillers/m (number)	P	0.01	-0.00	0.06	0.04	0.13	0.00	0.22*
	G	1.44	-1.22	0.44	0.36	-0.07	-0.02	0.91**
1000 grain weight (g)	P	-0.00	0.02	0.00	0.03	0.00	0.15	0.26*
	G	0.11	0.57	-0.73	0.05	0.00	0.22	0.24*

Residual effect at phenotypic and genotypic levels (0.069) and (0.043) respectively

** and * significant at the 0.01 and 0.05 levels

Path coefficient analysis revealed that at phenotypic level, grains/spike (0.35) had highest positive direct effect on yield followed by spike length (0.25). Phenotypic correlations were also positive and significant ($r=0.44$ and 0.33), respectively. At genotypic level, 1000 grains weight showed direct positive effect on grain yield (0.22) with significant positive genotypic correlation coefficient of 0.24. The traits, spike length (4.05) followed by plant height (2.87) and days to maturity (2.14) also showed high positive direct effects. However, these traits showed negative genotypic correlation coefficient of -0.19, -0.03 and -0.14, respectively. From this result, it was indicated that there is a true relationship between grain yield and 1000 grain weight and grain yield. Similarly, Adhikari *et al.* (2018) Madic *et al.* (2005) reported that a positive direct effect of 1000 grain weight on grain yield.

The trait tillers/m showed negative genotypic direct effect, however the genotypic correlation coefficient was significantly high (0.91). The high significant correlation coefficient of tillers/m with grain yield was due to the indirect effects of days to maturity and spike length. This highlights that there was no true association between number of tillers/m and grain yield. This is in agreement with the findings of Hailu *et al.* (2016) where path coefficient analysis revealed that number of tillers

exhibited negative direct effect (-0.042) on seed yield in barley research. Maximum of the indirect effect of different traits on grain yield was contributed by plant height and spike length.

The variability for grain yield and other traits not studied in the present experiment can be determined by studying the residual effect at phenotypic and genotypic levels. The residual effect at phenotypic level was observed as (0.069) and (0.043) at genotypic level. Which means the characters in the path analysis expressed the variability in grain yield by 93.1% and 95.7% at phenotypic and genotypic level, respectively and the remaining 6.9% and 4.3% needs additional characterization for the future breeding program. Similar result reported by Aliet *al.*, (2008) and Mollasadeghiand Shahryari (2011).

Conclusion

It is evident from the results that 1000-grain weight had high heritability with high genetic advance which could be considered as an important trait in barley breeding program. Additional traits like plant height also showed high heritability and moderate genetic advance, and spike length also showed moderate values of heritability and genetic advance highlighting importance of these traits. The trait, 1000 grain weight also showed positive



significant genotypic and phenotypic correlation with grain yield and showed direct effect for grain yield. The correlation coefficient at phenotypic level of plant height and spike length was also significantly positive and these two traits highlighted the potential traits for indirect selection for grain yield improvement in barley. In relation to the barley breeding program to obtain high yielding barley varieties, the trait 1000 grain weight, plant height and spike length can be used as the selection criteria.

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