



## Variability, Heritability and Genetic Advance of Advanced Breeding Lines of Barley (*Hordeum vulgare* L.) Under Mountain Environment of Nepal

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### Abstract

A study was conducted at Agricultural Research Station (ARS), Vijayanagar, Jumla Nepal comprising ten advanced breeding lines of barley during regular season of high hill in 2016/17 in Randomized complete block design with three replications to observe genetic variability, correlation, heritability, genetic advance and clustering of genotypes in relation to yield and yield associated traits and selection and advancement of early maturing, high yielding, disease resistant, and cold tolerance genotypes for high mountain area of Nepal. Analysis of variance revealed that characters days to heading, days to maturity, plant height and grain yield kg/ha were significant at (<0.01) and traits panicle length and thousands grain weight were significant at (<0.05) indicating presence of variation in genetic constituents. Higher broad sense heritability coupled with higher genetic advance as percent of mean was obtained in grain yield (61 and 29.78), high heritability and low genetic advance was obtained in days to maturity (63 and 3.56), low heritability and low genetic advance was obtained in plant height (16 and 4.9), medium heritability and high genetic advance was obtained in panicle length (35 and 24.81). Panicle length (0.878\*\*), thousands grain weight (0.651\*\*) and plant height (0.433\*) positively and significantly correlated with grain yield. Days to maturity and days to heading were strongly correlated (0.705\*\*). Thousands grain weight correlated with days to maturity (0.679\*\*), panicle length (0.561\*\*) and days to heading (0.403\*). Total four clusters were obtained in eighty percent euclidean similarity clustering indicating genetic closeness/distances among the genotypes. Clusture 2 carries superior two genotypes ICB-90-0203-OAP-02-ok and Chauli Jau high yielder, this coincides with the mean separation.

**Keywords:** Barley, Clustering, Correlation, Genetic advance, Heritability

### Introduction

Barley (*Hordeum vulgare* L.) belongs to the family Poaceae, tribe Triticeae and genus *Hordeum*. Cultivated barley is a self-pollinating diploid species ( $2n=2x=14$ ) with a genome size of approximately 25.3 x 10<sup>9</sup> bp equivalent to 5.5pg DNA of a haploid nucleus (Bennett and Smith, 1976). It is one of the earliest domesticated crop (Zohary and Hopf, 1993). Globally, barley ranks fourth among cereal crops after

wheat, maize and rice and is among the top ten crop plants in the world (Akar, et al., 2004).

Barley ranks in the fifth important food crop of Nepal. It is staple food for remote and food deficit mountainous area of Nepal, specially Karnali region and other high mountains. National statistics of Nepal indicates its wider range of cultivation from terai to

mountain and total area 27310 ha with production 30510 mt and 1115 kg/ha productivity. Terai, hill and mountain shares 2.77, 41.78 and 55.45 percentage of area and 4.02, 44.19 and 51.78 percentage of production of nation respectively. Which shows it's main area is mountain, mid western mountain alone contributes 25.15% area and 29.81% production to the whole nation (MOAD, 2018). Jumla district, our research venue shares 13 and 18 percentage of area and production of the country.

Barley has significance in mountainous agro ecosystem because of it's short growing period, drought tolerant, low input requirement, and good stability of yield than wheat so better fit in the cropping system of mountainous agriculture. There are two cropping system in Jumla and similar climatic zone of mountain; Rice-Barley in low land and Bean-Wheat in upland but barley fits in both cropping pattern of Jumla. It has short cropping period than wheat so farmer can plant rice after it's harvest. In upland condition bean can be planted after harvesting of barley. It is used for animal feed, brewing malts, and human consumption (Brown, 1992 and Von Bothmer et al., 2003). Barley is used to prepare roti, satu, and baby foods at mountain area of Nepal. It is considered one of the nutritious food having rich in protein, crude fibre, minerals and vitamins. Despite of its importance, barley has been considered neglected and given less priority on its research and development activities in Nepal (Adhikari, et al., 2018).

The important factors for lower productivity of barley in Nepal are fewer option of improved varieties to the farmer, low soil fertility, drought condition, inadequate agronomic management and infestation of leaf rust disease.

Increased production per unit area is the primary objective in almost crop breeding programmes. Grain yield is the most important and complex characters with which barley breeders work. Grain yield in barley is the product of several interrelated traits; hence, a successful breeding programme depends largely upon the information on the genetic variability and association of desired quantitative traits with yield. Hence, consideration of quantitative approaches for exploitation of the genetic variability available in barley cultivars is of main importance (Necdet Akgun 2016). Estimates of genetic parameters serve as a base for selection and hybridization since degree of variability for a given character is a basic prerequisite

for its improvement. The study of genotypic correlations of yield and yield related components is important to enhance selections of genotypes for improvement (Necdet Akgun 2016). Cluster analysis can be a good source to identify the variation in the germplasm and to classify based on similarity and dissimilarity index. This analysis is also useful for the selection of parents for the breeding program and crop modeling (El-Deeb and Mohamed, 1999; Jaynes et al., 2003).

Therefore, present study was conducted to identify a proper plant type for selection to improve the grain yield considering the inter relation between traits, variability, genetic advance, clustering and heritability. Advancement of cold tolerance, early maturing, high yielding, disease resistant and drought tolerance barley genotypes for mountain environment of Nepal.

## Materials and Methods

Ten advanced breeding lines of barley including one local check (chauli jau) and one released variety (Solu uwa) received from Hill Crops Research Program (HCRP), Kavre, Dolakha, Nepal were evaluated at Agricultural Research Station (ARS), Vijayanagar, Jumla during regular barley growing season of high hill (November, 2016 to June, 2017). Geographically ARS is situated at altitude of 2290 amsl and 29° 17' north latitude and 28° 10' east longitudes of mid west Nepal (ARS, 2014). This station is located at high hill region and thus is characterized by cool temperate to alpine eco belts with low rainfall. Soil of this station as developed on recent to old river, moderately deep to very deep and moderately to poor drained. The topography is gently sloppy to rolling lying in the high mountain region. Surface soil and sub-surface soils are dominantly coarse textured (Sandy loam) and are acidic to moderately alkaline in reaction. The nitrogen content of the soil is generally very low to medium while available phosphorous is high to very high and available potassium is medium to high. The organic carbon content of farm soil is low to high. The average maximum and minimum temperature is about 25°C in June and 2°C in February. There was no rainfall during October 15 to December 15, 2016. But total rainfall during barley growing period of 2016/2017 was satisfactory 244 mm with an average of 54 mm. (Meteorology office, Jumla, 2017, Annex 1). List of genotypes and recorded parameters and their abbreviation are given in Table 1. The experiment was

sown on flat bed with recommended seed rate of 40 kg/ha, on November 11<sup>th</sup> 2016 with three replications and RCBD design. Plot size was maintained 6 m<sup>2</sup> (3m x 2m) and spacing was given 25 cm between the rows and seeding done continuous on the line. Each plot

carries 8 lines of 3m length. Recommended dose of FYM and fertilizers (5 t FYM, 40:40:40 N P<sub>2</sub>O<sub>5</sub> K<sub>2</sub>O kg/ha) were applied as basal dose during land preparation. List of genotypes and recorded parameters and their abbreviation are given in Table 1.

Annex 1: Weather data of research place Jumla 2016/17.

Year	Month	Average temperature (°C)		Relative Humidity (%)	Total Rainfall (mm)
		Maximum	Minimum		
2073 (Mid July 2016)	July-Aug	23.88	16.17	81.74	252.60
	Aug-Sep	25.05	14.72	77.10	102.70
	Sep-Oct	25.06	11.65	69.60	24.20
	Oct-Nov	21.41	0.74	57.08	0
	Nov-Dec	20.72	-2.23	47.9	0
	Dec-Jan	15.30	-3.96	55.46	9.70
	Jan-Feb	15.64	-2.56	58.05	24.00
	Feb-March	17.12	-0.97	54.73	53.60
	March-April	21.51	4.21	59.73	53.30
2074 (Mid June 2017)	April-May	24.34	7.90	62.05	42.80
	May-June	25.42	10.93	65.71	60.60
	June-July	25.66	15.48	73.76	180.10
	Total				803.60
	Average	21.76	6.01	63.58	66.97

Source: Meteorological Field Office, Jumla

Table 1. List of breeding lines and quantitative traits of barley used in the study

Source	En	Genotypes	Traits	Abbreviation
Hill crops Research Program (HCRP) Kavre, Diakha, NARC, Nepal	1	B86-099-2-1-0k	Days to 50% heading	DH
	2	ICB-90-0203-OAP-02-ok	Days to 90% maturity	DM
	3	ICB-90-0196-OAP-02-ok	Plant height (cm)	Pht
	4	NB-1003-37/1034	Thousands grain weight (g)	TGW
	5	B90-K-007-2-2-0-ok	Panicle length (cm)	PL
	6	LG-51	Grain yield kg per hac	Yld
	7	NB-1003-37/903		
	8	Coll # 112-14		
	9	Solu uwa (Std.-Che.)		
	10	Chauli Jau (Loc. Che.)		

Two boarder rows were excluded while recoding parameters days to heading, days to maturity, grain yield and thousands grain weight was taken on plot basis, plant height and panicle length recorded from randomly selected ten plants from inner lines of the plot. Thousands grain weight and grain yield was adjusted in 14% moisture content.

Analysis of variance done by using Genstat 18th edition, correlation was computed by using statistical software SPSS at significance level of (0.05), mean separation among the lines was done with statistical software ADEL-R and clusuring of the genotypes was done with statistical software MINITAB. The phenotypic and genotypic variances were derived according to Falconer (1964) and broad sense heritability was calculated according to Allard (1960).

Estimation and categorization of genetic advance was done according to Johnson et al. (1955). The Genetic advance as percent of mean (%mean GA) were classified as low, moderate, and high according to Robinson et al.(1949) as follows: low <10%, moderate 10–20%, and high >20%. The broad sense heritability values were ranked according to Robinson et al. (1949) as follows: low <30%, moderate 30–60%, and high >60%.

## Results and Discussion

### Analysis of variance

Analysis of variance revealed that characters days to heading, days to maturity, plant height and grain yield

kg/ha were significant at (<0.01) and traits panicle length and thousands grain weight were significant at (<0.05) (Table 2). The result showed presence of variation in genetic constituent among the genotypes for the concerned traits. Breeder can utilize the variability for selection and may use in hybridization for trait improvement, gene transfer to the other genotypes. Significant difference on barley yield and yield attributing traits were also reported by (Yadav, et al 2018 and Necdet Akgun 2016). Addisu and Shumet, 2015 also reported similar result all traits resembled significant variation in barley.

Table 2. Analysis of variance for the quantitative character of barley genotypes

SN	Traits	Rep	Treat	Error	Fcal	CV	P value
1	DH	2.53	16.50	3.90	4.20	1.37	**
2	DM	1.03	36.00	5.92	6.08	1.33	**
3	Pht	61.09	36.84	23.32	1.58	5.41	**
4	PL	1.00	3.16	1.21	2.61	16.45	*
5	TGW	3.33	35.89	11.19	3.21	10.78	*
6	Yld	92079.43	642900.89	114702.91	5.60	11.67	**

Note; DH: Days to heading, DM: Days to 90% maturity, Pht: Plant height (cm), PL: Panicle length (cm), TGW: Thousands grain weight (gm) and Yld: Grain yield (kg/ha)

### Mean separation and Variability

Mean separation of 10 wheat genotypes for six yield and yield attributing character is presented in Table 3 and Table 4. Barley genotypes exhibited considerable variation for all the traits. Panicle length resembled highest variability followed by grain yield and followed by thousand grain weight. Lowest variability was observed by days to maturity, then days to heading and plant height. The mean value of days to heading is 144.07 and it ranges from 141 to 148. Variety Solu uwa found earlier for days to heading and days to maturity (141 and 178). While genotype Coll

# 112-14 was late for days to heading and days to maturity (148 and 188.3). Genotype NB-1003-37/1034 was dwarfest (85 cm) and B86-099-2-1-0k was tallest (94 cm). Longest panicle and highest grain yield was obtained by genotype ICB-90-0203-OAP-02-ok (8.9 cm and 3462.7 kg/ha) and shortest panicle and lowest grain yield was found in genotype LG-51(5.4 cm and 2226.3 kg/ha). Highest thousands grain weight was obtained in genotype ICB-90-0196-OAP-02-ok (35 gm) and lowest in Solu uwa (22.67 gm). Local check Chauli jau (3436 kg/ha) was statistically at par with highest yielder ICB-90-0203-OAP-02-ok and mean of yield was 2902.43 kg/ha.

Table 3. Mean performance and LSD vale of the quantitative traits of barley at high hill of Nepal in 2016-2017

EN	Genotypes	DH	DM	Pht	PL	TGW	Yld
1	B86-099-2-1-0k	143.7 <sup>bc</sup>	185.7 <sup>abc</sup>	94.3 <sup>a</sup>	6.80 <sup>bc</sup>	32.67 <sup>ab</sup>	3250.3 <sup>a</sup>
2	ICB-90-0203-OAP-02-ok	144.3 <sup>bc</sup>	184.7 <sup>abc</sup>	85.6 <sup>bc</sup>	8.90 <sup>a</sup>	32.00 <sup>ab</sup>	3462.7 <sup>a</sup>
3	ICB-90-0196-OAP-02-ok	143.0 <sup>bc</sup>	186.7 <sup>ab</sup>	92.2 <sup>abc</sup>	7.07 <sup>abc</sup>	35.00 <sup>a</sup>	3167.0 <sup>ab</sup>
4	NB-1003-37/1034	148.0 <sup>a</sup>	185.0 <sup>abc</sup>	84.9 <sup>c</sup>	5.63 <sup>c</sup>	28.67 <sup>b</sup>	2178.0 <sup>c</sup>
5	B90-K-007-2-2-0-ok	142.7 <sup>bc</sup>	179.3 <sup>de</sup>	87.7 <sup>abc</sup>	5.97 <sup>bc</sup>	31.33 <sup>ab</sup>	2653.3 <sup>bc</sup>
6	LG-51	143.0 <sup>bc</sup>	184.0 <sup>bc</sup>	87.1 <sup>abc</sup>	5.47 <sup>c</sup>	31.33 <sup>ab</sup>	2226.3 <sup>c</sup>
7	NB-1003-37/903	145.0 <sup>ab</sup>	182.3 <sup>cd</sup>	93.0 <sup>abc</sup>	6.43 <sup>bc</sup>	30.00 <sup>ab</sup>	2927.7 <sup>ab</sup>
8	Coll # 112-14	148.0 <sup>a</sup>	188.3 <sup>a</sup>	87.1 <sup>abc</sup>	6.63 <sup>bc</sup>	34.00 <sup>ab</sup>	3075.0 <sup>ab</sup>
9	Solu uwa(Std.-Che.)	141.3 <sup>c</sup>	178.0 <sup>e</sup>	93.2 <sup>ab</sup>	6.30 <sup>bc</sup>	22.67 <sup>c</sup>	2648.0 <sup>bc</sup>
10	Chauli Jau (Loc. Che.)	141.7 <sup>bc</sup>	179.3 <sup>de</sup>	87.4 <sup>abc</sup>	7.73 <sup>ab</sup>	32.67 <sup>ab</sup>	3436.0 <sup>a</sup>
<b>Mean</b>		<b>144.07</b>	<b>183.3</b>	<b>89.25</b>	<b>6.69</b>	<b>31.03</b>	<b>2902.43</b>
<b>StdMSE</b>		<b>1.98</b>	<b>2.43</b>	<b>4.83</b>	<b>1.10</b>	<b>3.34</b>	<b>338.68</b>
<b>LSD</b>		<b>3.39</b>	<b>4.17</b>	<b>8.28</b>	<b>1.89</b>	<b>5.74</b>	<b>580.97</b>

Note; DH: Days to heading, DM: Days to 90% maturity, Pht: Plant height (cm), PL: Panicle length (cm), TGW: Thousands grain weight (gm) and Yld: Grain yield (kg/ha)

### Genetic variability, heritability and genetic advance

Heritability, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and genetic advance at 5% selection intensity as percent of mean for quantitative traits of barley genotypes is given in Table 4. Our result showed PCV is higher than GCV for all traits. Higher the difference between PCV and GCV indicates higher influence of environment for the expression of traits. Higher broad sense heritability coupled with higher genetic advance as percent of mean was obtained in grain yield (61 and 29.78), high heritability and low % mean genetic advance was obtained in days to maturity (63 and 3.56), low heritability and low % mean genetic advance was obtained in plant height (16 and 4.9), medium heritability and high % mean genetic advance was obtained in panicle length (35 and 24.81). Thousands grain weight showed medium heritability and medium genetic advance as percent of mean (0.42 and 19.05) Table 4. Low heritability <20% and low % mean GA <10% was reported for plant height by (Hailu, et al., 2016) which supports our result. Hailu, et al., 2016 also support our other findings high broad sense heritability >60% for days to maturity, high genetic advance >20% for grain yield and panicle length in barley. Similarly, Yadav et al., 2018 reported medium heritability for thousands grain weight similar to our findings. Higher GCV, PCV and heritability was also reported by Jalata et al., 2011 in support to us. Addisu and Shumet, 2015 also reported similar

result high heritability for grain yield and days to maturity.

Coefficients of variation are very helpful in the estimation of the magnitude of variability which is present within a population. Low estimates for the coefficient of variation suggest lack of genetic variation among the traits in question while high values of coincident of variation indicates that selection is effective for that particular trait because of the wider genetic variability. The success of selecting genotypes with high potential in plant breeding program depends on the extent and nature of phenotypic and genotypic variability in several agronomic traits of the population. The prerequisite for coming up with a reliable breeding programme for improvement of a specific attribute in any crop could be a study on the genetic parameters, viz., variation, inheritance, and genetic advance (Atta et al., 2008).

If the value of genetic advance as percent of mean is high coupled with broad sense heritability such character may be governed by additive genes and selection may be beneficial for such traits. If Genetic advance is low the character may be governed by non additive genes and heterosis breeding may be useful. Genetic advance as percent mean ranged from 2.93% for days to heading to 29.78% for grain yield indicating that selecting the top 5% of the genotypes could result in an improvement range of 2.93% for days to maturity to 29.78% for grain yield. Similar finding, high heritability with high genetic advance for grain yield was also reported by Yadav, et al., 2019.

Adhikari et al. (2018), Singh and Upadhyay (2013), in wheat. Low genetic advance for days to maturity were reported by Adhikari et al. (2018) and Kumar et al. (2017).

Table 4. Genetic parameters for six quantitative traits of barley tested at high hill of Nepal in 2016/17

Traits	Range	Mean	Std	Vg	Vp	H	GCV	PCV	GA	%mean GA
DFF	141-148	144.07	2.3	4.2	8.10	0.52	1.42	1.98	4.22	2.93
DM	178-188	183.33	3.5	10.026	15.95	0.63	1.73	2.18	6.52	3.56
Pht	85-94	89.25	3.5	4.5041	27.83	0.16	2.38	5.91	4.37	4.90
PL	5.4-8.9	6.69	1.0	0.6498	1.86	0.35	12.04	20.39	1.66	24.81
TGW	22.6-35	31.03	3.5	8.2333	19.42	0.42	9.25	14.20	5.91	19.05
Yld	2178-3463	2902.43	462.9	176066	290768.91	0.61	14.46	18.58	864.38	29.78

Note; DH: Days to heading, DM: Days to 90% maturity, Pht: Plant height (cm), PL: Panicle length (cm), TGW: Thousands grain weight (gm) and Yld: Grain yield (kg/ha)

### Clustering

Dendrogram generated based on UPGMA clustering method and Euclidean similarity coefficient among ten barley genotypes is given in table 5 and figure 1. Clustering was done with UPGMA clustering method with 80% euclidian similarity coefficient and four clusters were generated. Cluster 1 contains 4 genotypes (40%) out of total 10 genotypes. This cluster carries slightly higher value for all the traits than grand centroid. Similarly, two genotypes ICB-

90-0203-OAP-02-ok and Chauli jou were grouped in cluster 2. This cluster is superior among all clusters carries higher values for grain yield, panicle length and thousands grain weight but smaller values for days to heading, days to maturity and plant height than total centroid. Cluster 3 contains two genotypes LG-51 and NB-1003-37/1034 lowest yielder and lower panicle length and lower other values. Cluster 4 carries two genotypes B90-K-007-2-2-0-ok and Soluuwa inferior than grand centroid.

Table 5: Clustering of 10 genotypes of barley

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Grand centroid
DH	144.93	143	145.5	142	144.07
DM	185.75	182	184.5	178.65	183.33
Pht	91.65	86.5	86	90.45	89.25
PL	6.73	8.32	5.55	6.14	6.69
TGW	32.92	32.34	30	27	31.03
Yld	3105	3449.35	2202.15	2650.65	2902.43

Note; DH: Days to heading, DM: Days to 90% maturity, Pht: Plant height (cm), PL: Panicle length (cm), TGW: Thousands grain weight (gm) and Yld: Grain yield (kg/ha)

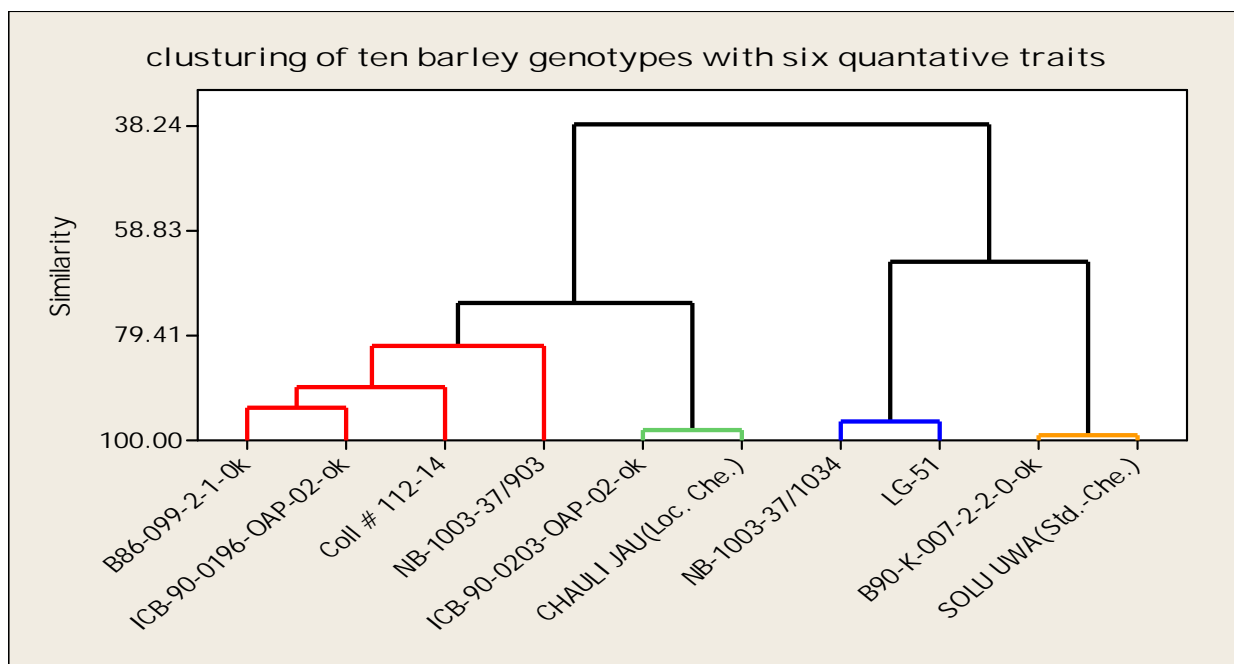


Figure 1: Dendrogram of barley genotypes based on six quantitative characters

**Correlation**

Correlation is very important tool in plant breeding because we can use indirect selection to improve another targeted parameter. There are positive and negative effect in correlation which results in simultaneous changes in related character. Phenotypic correlation between six parameters of 10 genotypes of barley is given in table 6. Panicle length (0.878\*\*), thousands grain weight (0.651\*\*) and plant height (0.433\*) positively and significantly correlated with grain yield. Days to maturity and days to heading were strongly correlated (0.705\*\*). These parameter contribute higher yield. Thousands grain weight correlated with days to maturity (0.679\*\*), panicle length (0.561\*\*) and days to heading (0.403\*). Panicle length showed positive association with plant height

(0.397\*) and thousands grain weight and days to heading also has positive correlation (0.403\*). Adhikari et al., 2018 reported similar finding positive correlation of grain yield with spike length (0.46\*\*), plant height (0.26\*) and thousand grain weight (0.25\*). Singh et al. 2014, reported significantly positive association of spike length, plant height and thousand grain weights on barley grain yield. Al-Tabbal and Al-Fraihat, 2012 also reported result to our findings plant height, thousand grain weight significantly correlated with grain yield. Significant positive correlation between days to flowering and maturity were reported by Lodhi et al., 2015 and Mohtashami 2015. Breeder can select barley genotypes indirectly having longer panicle, more thousands grain weight and taller plant for grain yield increment.

Table 6: Phenotypic correlation coefficient between six parameters of barley

	DH	DM	Pht	PL	TGW
DM	0.705**				
Pht	0.131	0.226			
PL	0.228	0.341	0.397*		
TGW	0.403*	0.679**	0.274	0.561**	
Yld	0.093	0.299	0.433*	0.878**	0.615**

Note; DH: Days to heading, DM: Days to 90% maturity, Pht: Plant height (cm), PL: Panicle length (cm), TGW: Thousands grain weight (gm) and Yld: Grain yield (kg/ha)

## Conclusion

Obtained results indicates presence of sufficient genetic variability for the studied traits showing genotypes are suitable for breeding purpose. Result resembled high heritability coupled with high genetic advance as percent of mean for grain yield, medium heritability and high genetic advance as percent of mean was found in panicle length and Thousand grain weight also have more GA so these traits ; grain yield, panicle length and TGW may be governed by additive gene, selection of these traits would be more effective for genetic improvement for grain yield of barley. Mean separation and clustering showed barley genotypes ICB-90-0203-OAP-02-ok and Chauli Jau are superior among the tested genotypes can be selected for registration and/or recommendation for general cultivation at high hill region of Nepal. Parameters plant height, panicle length and thousands grain weight contribute for higher grain yield. We can select plants having longer panicle and higher grain weight for higher grain yield of barley.

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## Conflict of Interest

The authors declare that there is no conflicts of interest regarding publication of this manuscript.

## Author's contribution

N.H. Ghimire: Designed and performed experiment, analyzed data and wrote the paper  
P.M. Mahat: Performed experiment, data recorded

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