

Genetic Variability, Heritability, Correlation and Path Coefficient Studies for Yield and Yield related Components of Some Promising Barley Cultivars and ~~crosses~~ (*Hordeumvulgare* L.)

Comment [WU1]: Crosses (Capitalize word)

Abstract

The goal of this research was to determine the genetic variability of yield and yield-related variables, as well as to quantify ~~direct~~ and indirect effects of trait connections. The experiment was conducted at research farm in Chaudhary Charan Singh University, Meerut, Uttarpradesh, India. The fourteen parents and their BC₁F₁ cross were examined and submitted to analysis of variance utilizing the RBD design. The varieties differed significantly for the majority of the traits and had a broad range of mean values, indicating that there were differences across the varieties examined. The phenotypic and genotypic coefficients of variance (PCV and GCV) estimates were both quite low. The biological yield had the greatest GCV and PCV values (26.57 and 40.48). The PCV values were higher than the GCV values by a small margin. The heritability of seed per spike, biological yield, flag leaf breadth, days of heading, and days of maturity was relatively high. Grain yield has a high heritability value and a high genetic progress, which is an excellent selection signal. The phenotypic and genotypic coefficients of variance (PCV and GCV) estimates were both quite low. The biological yield had the greatest GCV and PCV values (26.57 and 40.48). The PCV values were higher than the GCV values by a small margin. The heritability of seed per spike, biological yield, flag leaf breadth, days of heading, and days of maturity was relatively high. Grain yield has a high heritability value and ~~a~~ high genetic progress, which is an excellent selection signal. Days of anthesis, days of maturity, spike length were highly significant and positive correlated with yield, as were significant and ~~negative~~ correlated with grain filling period, biological yield, and highly ~~non significant~~ and ~~positive~~ correlated with harvest index, plant height, thousands seeds weight, chlorophyll content, and highly ~~non significant~~ and negative correlated with tiller number and seeds per spike, respectively.

Comment [WU2]: thedirect

Comment [WU3]: high

Comment [WU4]: negatively

Comment [WU5]: non-significant

Comment [WU6]: positively

Comment [WU7]: non- significant

~~Key words~~: Genotypic and Phenotypic variance, Heritability, Coefficient, Variability.

Comment [WU8]: Keywords

1. Introduction

Barley belongs to the genus *Hordeum* and ~~family~~ *Poaceae* (~~Von Bothmer et al., 1995~~).

Comment [WU9]: the family

Comment [WU10]: Not exist in List of References. Please check it again

Kling and Hayes, 2004). During the second half of the second millennium, barley arrived in China. One of the world's oldest food crops is barley (*Hordeum vulgare L.*). Since the early stages of agricultural developments 8,000-10,000 years ago, it has been a major cereal crop (*Giles and Bothmer, 1985*). It is a commercially significant cereal crop, ranking fourth in the world after wheat, rice, and maize in terms of both quantity produced and cultivated area (*FAO, 2014*). Barley is native to the Eastern Mediterranean, where plants are subjected to a variety of abiotic stresses in the field. It is grown in many places where the climate is unfavorable. Though it has a lower commercial value than wheat, it is used to replace wheat in dry areas where water is scarce. It is known as the poor man's crop because of its minimal input requirements and superior tolerance to rainfed conditions (*Verma et al., 2010*). Barley production in the world totals 292.9 million tonnes, with Europe producing the most (59.6%), followed by Asia (14.9%). The Russian Federation is the leading producer, with a total output of around 20.02 million tonnes, whereas India is ranked fourteenth (*USDA, 2015*). In 2017, India's barley production was 1.75 million tonnes, but according to 2008-09 statistics, barley is planted on 0.71 million hectares with a production of 1.69 million tonnes and a yield of 2394 kg ha⁻¹. Rajasthan has the most area (0.29 million ha) and production (0.89 million t) of barley, whereas Haryana has the highest yield (3491 kg ha⁻¹). Cultivated barley is a species of *Hordeum* that evolved from wild barley (*Hordeum spontaneum*), which can still be found in the Middle East. Both cultivated and wild barley have fourteen chromosomes (2n=14) and are diploid species. *Hordeum vulgare L.* is the only cultivated species with two phenotypic variants, six rowed (*Hordeum vulgare, H. hexastichum*) and two rowed (*Hordeum vulgare, H. hexastichum*) (*H. distichum*). They have the same chromosomal number (2n=14) and may intercross freely to create fertile hybrids, despite their spike morphological variances (*Poehlman, 1987*). Barley contains a lot of genetic variety, which is used to classify the species. There are many different methods to categorize barley. Identifying whether the spike has two, four, or six rows of spikelets is one technique to classify barley. The majority of cultivated barley has six rows, while wild barley has two rows. Another technique to categorize barley is to look at how the beards (awns) connect to the kernels.

Comment [WU11]: About the in-text citation and the reference list:
(1) The in-text citation format should be corrected according to the publication standards. Namely, the quoted part should be marked with numbers in square brackets "[1]" (such as [1], [2], [3] ...) instead of other forms (such as "(Von Bothmer et al., 1995; Kling and Hayes, 2004)"). Besides, the in-text citation numbers cannot be used as the sentence components. For example:
True: "... family *Poaceae* [-]." But you didn't list in list of references. Please check again and put it in order according to shown.
False: "...family *Poaceae*(*Von Bothmer et al., 1995; Kling and Hayes, 2004*)." Please revise the forms of all the in-text citations in this paper.
(2) Please ensure that for every in-text citation in the main body, there should be a corresponding reference in the reference list (and vice versa). Many of them do not exist in the list of reference.
(3) If there are two or more references cited in the same sentence or paragraph, please enclose all the reference numbers in one bracket, such as [2, 3], [6-8] and [4, 9-12].

Comment [WU12]: Not exist in the List of References. Please check it again

Comment [WU13]: Not exist in the List of References. Please check it again

Comment [WU14]: Not exist in the List of References. Please check it again

Comment [WU15]: Not exist in List of References. Please check it again

Comment [WU16]: categorize

Comment [WU17]: categorize

Comment [WU18]: Statement of the problem and objective are not articulated.

2. Materials and methods

2.1. Experimental site, Data collection, material and procedures

The experimental material for present study was obtained from Eternal University, BaruSahib,

Dist. Sirmour, H.P. The present investigation was conducted at the Research farm and Molecular laboratory of Dept. of Genetics and Plant Breeding C.C.S. University Campus, Meerut (UP) during the year 2019-2020. With three replications, the trial was set up in a Randomized Block Design (RBD). The Standard Evaluation System for barley developed by the Indian Institute of wheat and barley research was used to make observations and data records for all attributes investigated. Five sample plants were selected randomly in the middle three rows from each plot and observations were recorded on seventeen quantitative traits: Days to heading (DTH), Date of anthesis (DTA), Date of maturity (DTM), Grain filling period (GFD), Average plant height (APH), Flag leaf length (FL), Flag leaf width (FW), spike length (SL), Average tiller number (ATN), No. of grains per spike (NG), biological yield (BY), Germination percentage (GER), Chlorophyll content (CC), grain yield (GY), thousand grain yield (TGW), Harvest index (HI), were used for assessing the genetic diversity and characters association among these genotypes of barley.

Comment [WU19]: Laboratory (Capitalize word)

Comment [WU20]: Wheat

Comment [WU21]: Barley Research

Comment [WU22]: thousand-grain yield

Table no. 1: A list of barley cultivar used for evaluation and crossing in the present study

S.No.	Name of cultivar/ varieties	2 rows/ 6 rows	Remarks
1.	IITR-39	6 rows	Hulled barley
2.	PL-830	6 rows	Hulled barley
3.	PL-172	6 rows	Hulled barley
4.	PL-707	6 rows	Hulled barley
5.	PL-419	6 rows	Hulled barley
6.	PL-751	6 rows	Hulled barley
7.	PL-426	6 rows	Hulled barley
8.	PL-758	6 rows	Hulled barley
9.	IITR-104	6 rows	Hulled barley
10.	IITR-38	2 rows	Hulled barley and anthocyanin rich
11.	IITR-35	2 rows	Hulled barley
12.	VIJY-102	2 rows	Hulled barley
13.	DWRUB-52	2 rows	Hulled barley
14.	PL-838	2 rows	Hulled barley

2.2. Statistical analysis

Analysis of variance was performed using the plant breeding statistical programme SPSS software. The genotypic and phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2_b), genetic advance in percentage of mean (GA), genotypic correlation coefficients (r_g) and phenotypic correlation coefficients (r_p), genotyping and phenotyping path analysis were estimated following (Singh and

Comment [WU23]: program

Chaudhary, 1985). The estimates of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon, 1973). Heritability ~~in broad sense~~ and genetic advance were calculated according to methods given by (Allard, 1960; Singh and Chaudhary 1985). Path coefficient analysis was done using ~~R software~~.

Comment [WU24]: Plagiarism Report is found here. Please re-write it.

Comment [WU25]: ina broad sense

Comment [WU26]: R software

3. Results and discussion

Creation of genetic variability and selection for important traits is ~~erucial~~ activities that any plant breeder should apply to achieve better yield and other desirable agronomic traits, ~~However the~~ carryout effective selection the information on available genetic variation among barley genotypes. Thus effective selection not only depends on ~~estimation~~ of genetic variation among genotypes but also on the proportion of heritable variation and the expected genetic gain that would be obtained (Falconer and Mackay, 1996 and Singh, 2000). Heritable variation is useful for permanent genetic improvement (Singh, 2000). Heritability in broad sense estimates the ratio of total genetic variance, including additive, dominance and epistatic variances to the phenotypic variance (Falconer and Mackay 1996; Riaz and chaudhary 2004).

Comment [WU27]: acrucial

Comment [WU28]: However,

Comment [WU29]: Similarity report found here.

Comment [WU30]: theestimation

The ANOVA indicated significant differences among the cultivars for Days to heading (DTH), Date of anthesis (DTA), Date of maturity (DTM), Grain filling period (GFD), Average tiller number, (ATN), No. of grains per spike (NG), biological yield (BY), Germination percentage (GER), grain yield (GY), thousand grain yield (TGW). The analysis of variance also revealed highly significant differences among the test genotypes for all the traits studied. The mean sum sequences due to test genotypes were highly significant for Date of maturity (DTM), Grain filling period (GFD), Average tiller number, (ATN), No. of grains per spike (NG), biological yield (BY), Germination percentage (GER), grain yield (GY), thousand grain yield (TGW).

The estimating of range (Minimum & Maximum), Mean Standard Error, Critical difference (5%), Critical variance (1%), environmental variance, Genotypic variance, Phenotypic variance, Genotypic coefficient of variance, Phenotypic coefficient of variance, Heritability (Broad sense), Advancement in genetics as a percentage of mean of 17 traits. The range of date of heading among the genotypes differs from 89 to 101 with a value of mean is 93.38 and CV is 3.51 percent, days of anthesis among the genotypes differs from 93 to 105 as the range with a value of mean is 99.18 and CV is 4.14% , days of maturity among genotypes differ from 114 to 126 as the range with a value of mean is 118.87, CV is 3.09 followed by the other quantitative and qualitative traits (Table no.2).

A highest GCV (26.57) and PCV (40.48) estimates for grain yield should high degree of genetic variation for this trait, However a moderate level of differences among GCV (26.57) and PCV (40.48) for grain yield indicates role of environmental variation for GCV and PCV estimates, thus have sufficient genetic variability for improvement of these traits. Some traits like number of plant germinated, seeds per spike, thousand seeds weight, average flag leaf length also had moderate values for GCV and PCV estimates, thus have sufficient genetic variability for improvement of these traits. A very low value of GCV and PCV for days of anthesis, days of heading and days of maturity harvest index, average spike length, chlorophyll content, leaf angle, days of anthesis, days of heading and days of maturity (Table no.2) showed little scope of improvement in the genotypes for these traits and similar results also reported by Yadav *et al.*, (2015).

Comment [WU31]: The highest

Comment [WU32]: However,

Comment [WU33]: having

Heritable variation is useful for permanent genetic improvement (Singh, 2000). Heritability in broad sense estimates the ratio of total genetic variance, including additive, dominance and epistatic variances to the phenotypic variance (Falconer and Mackay, 1996; Riaz and Chaudhary, 2004). Highest heritability along with highest genetic advance was recorded for biological yield, seeds per spike, thousand seeds weight and average plant height, similar results reported by (Addisu, F., & Shumet, T., 2015) (Table no.2). Hence these traits are under control for additive genes and these can be improved by selection based on phenotypic performance.

Comment [WU34]: The highest

Table no.2: Estimation of Mean, Range (Minimum & Maximum), Standard Error of mean, Critical variance (5%), Critical difference (1%), Environmental variance, Genotypic variance, Phenotypic variance, Environmental coefficient of variance, Genotypic coefficient of variance, Phenotypic coefficient of variance, Heritability (Broad sense), Genetic advance, Genetic advance as percentage of mean of seventeen different traits.

Trait s	Range		Mean	SEm	CD(5%)	CD(1%)	EV	GV	PV	ECV	GCV	PCV	Heri. (BS)	G. advance	GA as % of mean
	Maxi.	Mini.													
DTH	101.00	89.00	93.38	1.25	3.52	4.67	4.67	2.46	7.13	2.31	1.63	2.86	0.34	1.90	2.03
DTA	105.00	93.00	99.18	1.47	4.15	5.50NS	6.50	1.70	8.20	2.57	1.32	2.89	0.21	1.22	1.23
DTM	126.00	114.0	118.8	1.10	3.10	4.11	3.62	1.67	5.29	1.60	1.09	1.93	0.32	1.50	1.26
GFD	26.00	9.00	19.69	1.51	4.26	5.65	6.84	2.79	9.63	13.28	8.48	15.76	0.29	1.85	9.41
ATN	9.00	2.00	3.94	0.58	1.64	2.17NS	1.02	0.23	1.24	25.62	12.09	28.33	0.18	0.42	10.62
AFL	23.63	8.00	13.57	1.39	3.91NS	5.20NS	5.79	0.56	6.35	17.74	5.52	18.58	0.09	0.05	3.37
AFW	1.73	0.40	1.04	0.12	0.34	0.45	0.04	0.04	0.08	19.82	18.24	26.93	0.46	0.27	25.45
APH	75.70	35.33	51.58	3.42	9.64	12.80	35.11	19.10	54.21	11.49	8.47	14.27	0.35	5.34	10.36
LA	2.00	1.00	1.34	0.27	0.75NS	0.99NS	0.21	0.01	0.22	34.40	5.77	34.40	0.03	0.03	1.97
BYL	240.00	45.00	109.2	19.27	54.31	72.09	1113.5	843.26	1956.7	30.54	26.57	40.48	0.43	39.27	35.93
HI	41.18	16.12	27.10	2.48	6.98NS	9.26NS	18.40	2.91	21.31	15.83	6.29	17.03	0.14	1.30	4.79
ASL	11.00	4.67	7.24	0.56	1.57	2.09	0.93	0.21	1.14	13.33	6.30	14.75	0.18	0.40	5.54
SPS	74.66	14.00	46.22	5.92	16.69	22.15	105.17	84.42	189.58	22.19	19.88	29.79	0.45	12.63	27.33
NPG	40.00	3.00	25.01	5.69	16.4NS	21.2NS	97.13	-10.44	86.69	39.41	12.92	37.23	-0.12	-2.31	-9.24
CC	65.10	32.90	48.01	3.23	9.10NS	12.1NS	31.28	3.62	34.90	11.65	3.96	12.31	0.10	1.26	2.63
TW	72.00	22.10	48.65	2.83	7.97	10.58	23.98	81.74	105.72	10.07	18.58	21.14	0.77	16.38	33.66

YL	75.00	25.00	39.00	5.63	15.89	21.08	95.25	99.61	194.85	25.03	25.59	35.79	0.51	14.70	37.69
----	-------	-------	-------	------	-------	-------	-------	-------	--------	-------	-------	-------	------	-------	-------

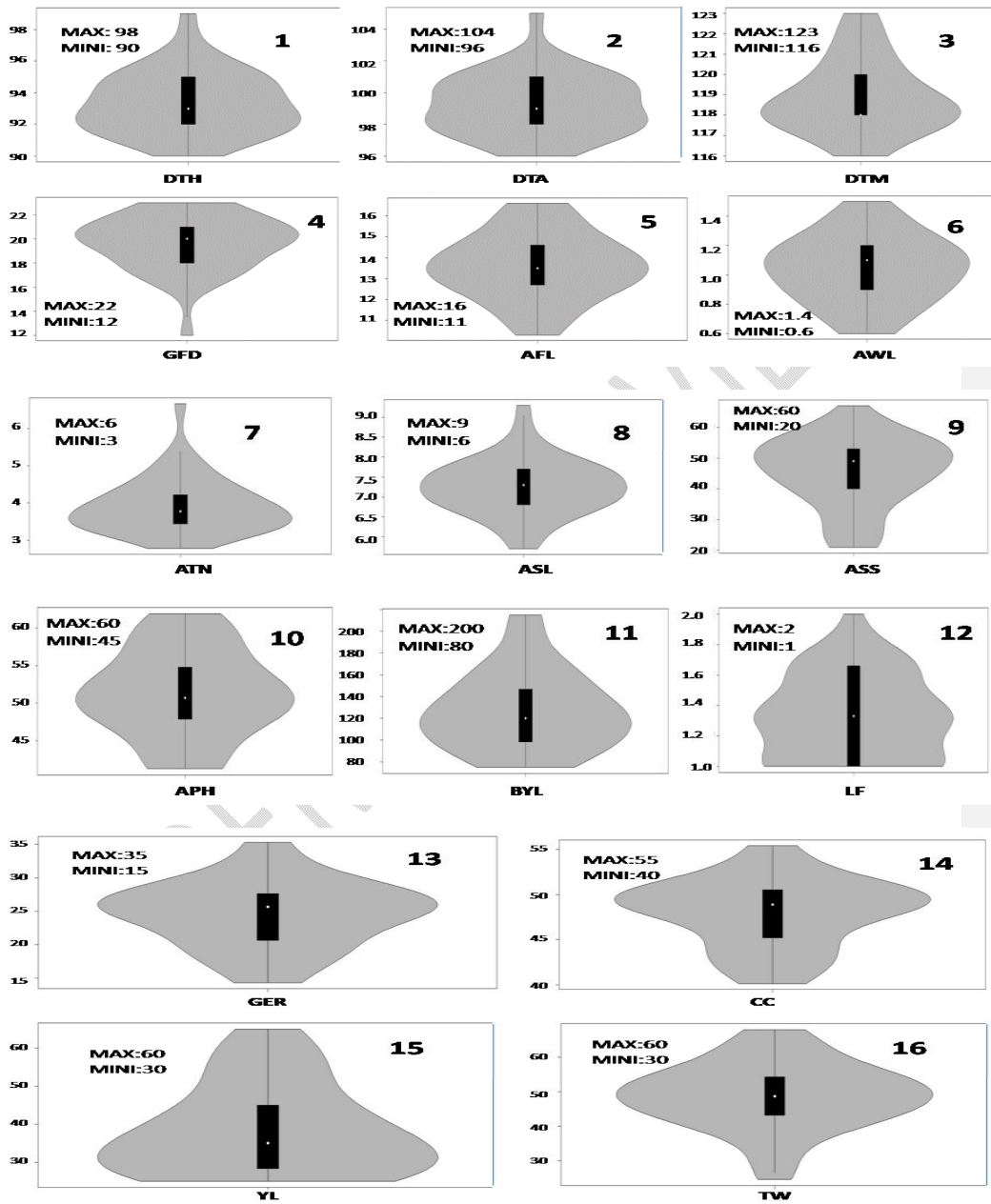


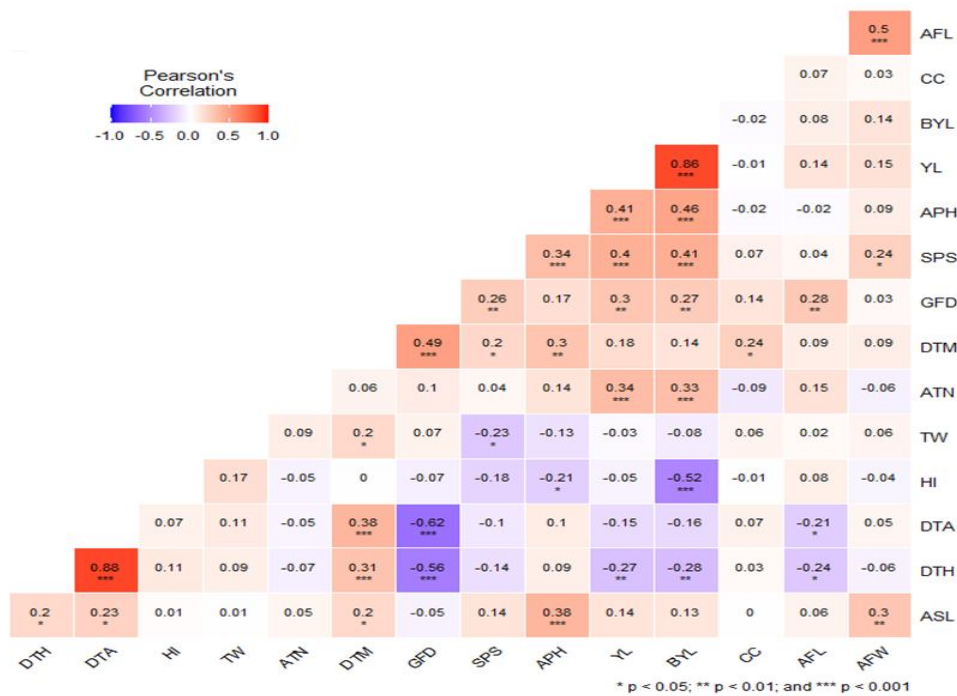
Figure 1: Violin plot (A box or marker indicating the inter quartile range; and possibly all sample points for 16 different traits).

Table no. 2: Genotypic correlation and phenotypic correlation

Traits	DT H	DTA	DTM	GFD	ATN	AFL	AFW	APH	BYL	HI	ASL	SPS	CC	TW	YL
DT H	1**	0.96*	0.10 N	-0.67*	0.18NS	-0.69*	0.19NS	0.23NS	-0.02NS	0.08NS	0.46*	-0.36*	-0.43**	0.13NS	-0.06NS
DT A	0.89**	1**	0.17 NS	-0.64**	0.23 NS	-0.26 NS	0.02 NS	0.11 NS	0.04 NS	0.14NS	0.65**	-0.56**	-0.37*	0.20NS	0.04 NS
DT M	0.27**	0.29**	1**	0.63**	-0.07 NS	0.14 NS	0.04 NS	0.80**	0.60**	-0.4*	0.33*	0.21 NS	0.12NS	0.34*	0.49**
GFD	-0.62**	-0.70**	0.47**	1**	-0.23 NS	0.32 NS	0.01 NS	0.53**	0.43**	-0.42**	-0.25**	0.61**	0.39*	0.10NS	0.34*
AT N	-0.03NS	-0.03 NS	0.13 NS	0.12 NS	1**	-0.13 NS	-0.47**	0.50**	0.54**	-0.42**	-0.38*	-0.08 NS	-0.62**	0.09NS	0.38*
AFL	-0.30**	-0.24**	0.04 NS	0.25**	0.20*	1**	0.79**	-0.44**	0.14 NS	1.06**	0.33*	0.30 NS	-0.02NS	0.32NS	0.53**
AF W	-0.07NS	0.01 NS	0.04 NS	0.01 NS	-0.04 NS	0.50**	1**	-0.23 NS	0.27 NS	-0.01NS	0.47**	0.43**	0.13NS	0.11NS	0.32 NS
AP H	0.10NS	0.03 NS	0.26**	0.16 NS	0.13 NS	0.04 NS	0.08 NS	1**	0.80**	-0.64**	0.47**	0.73**	-0.05NS	0.37*	0.65**
BY L	-0.24*	-0.16 NS	0.26**	0.34**	0.30**	0.21*	0.17 NS	0.44**	1**	-0.26 NS	0.18 NS	0.85**	0.36*	0.21NS	0.95**
HI	0.06NS	0.06 NS	-0.0 NS	-0.11 NS	-0.05 NS	0.04 NS	-0.06 NS	-0.17 NS	-0.47**	1**	0.46**	-0.63**	-0.06NS	0.53**	0.03 NS
ASL	0.20*	0.23*	0.21*	-0.05 NS	0.05 NS	0.07 NS	0.29**	0.38**	0.12 NS	0.02NS	1**	0.04 NS	-0.31NS	0.06NS	0.31 NS
SPS	-0.11NS	-0.10 NS	0.25**	0.28**	0.02 NS	0.08 NS	0.25**	0.32**	0.31**	-0.15 NS	0.13 NS	1**	-0.08NS	0.43**	0.72**
CC	0.01NS	9e-04 NS	0.15 NS	0.11 NS	-0.09 NS	0.08 NS	0.08 NS	-0.10 NS	-0.04 NS	0.03 NS	-0.08 NS	0.05 NS	1* 0.01NS	0.01NS	0.35*
TW	0.08NS	-0.08 NS	0.18*	0.05 NS	0.08 NS	0.03 NS	0.04 NS	-0.16 NS	-0.09 NS	0.18 NS	0.13 NS	-0.24*	0.03NS	1* 0.01NS	0.35*
YL	-0.24**	-0.16 NS	0.25**	0.33**	0.32**	0.22*	0.16 NS	0.38**	0.86**	0.09 NS	0.13 NS	0.38**	-0.03NS	0.03NS	1**

Comment [WU35]: Make good format for your table.

Fig 2: pearsons Correlation



3.1.Path coefficient analysis

Phenotypic and Genotypic path coefficient analysis is presented in Table no.4&5. The direct effect of characters on grain yield showed that the relationships between the characters were good contributors to the ultimate grain yield and these characters were the main component in the improvement of the grain. Genotypic correlation coefficients were partitioned by using path analysis method to find out the direct and indirect effects of yield contributing traits towards the grain yield. Path analysis (Table no.4&5) revealed that the highest positive direct effect and genotypic correlation with grain yield was obtained by biological yield, harvest index, days of anthesis, date of maturity, grain filling period, seeds per spike, days of heading, flag leaf length, similar results reported by (Jouyban, et al., 2015). Plant height, thousands seeds weight, spike length, flag leaf width, effective tiller number and chlorophyll content had negative direct effect with significant genetic correlation with grain yield. On the other hand, days to heading had positive indirect effect with anthesis, maturity, flag leaf width, harvest index, chlorophyll content and negative indirect effects with grain filling period, tiller number, flag leaf length, plant

Comment [WU36]: Similarity Report is found

Comment [WU37]: thepath

Comment [WU38]: were

height, biological yield, spike length, thousands seeds weight. The residual effect of the present study was -0.0055, indicating that about 98 percent of variability in grain yield might be contributed by these 16 yield contributing traits studied in the path analysis. This gives an impression that some other minor characters than those involved in the present study also contributed to the variability of grain yield.

Comment [WU39]: The impression

Table no. 4: Genotypic Path analysis

Traits	DTH	DTA	DTM	GFD	ATN	AFL	AFW	APH	BYL	HI	ASL	SPS	CC	TW
DTH	0.074	0.258	0.018	-0.111	-0.028	-0.088	0.029	-0.079	-0.034	0.003	-0.100	-0.042	0.069	-0.038
DTA	0.071	0.266	0.030	-0.106	-0.036	-0.034	-0.004	-0.040	0.058	0.049	-0.141	-0.065	0.052	-0.057
DTM	0.007	0.046	0.173	0.104	0.011	0.019	-0.007	-0.272	0.705	-0.133	-0.072	0.025	-0.018	-0.097
GFD	-0.050	-0.172	0.111	0.163	0.037	0.041	-0.003	-0.179	0.501	-0.141	0.054	0.070	-0.055	-0.030
ATN	0.013	0.062	-0.012	-0.039	-0.155	-0.017	0.069	-0.169	0.638	-0.143	0.083	-0.010	0.087	-0.027
AFL	-0.051	-0.071	0.026	0.053	0.021	0.126	0.115	0.148	0.172	0.354	-0.073	0.034	0.003	-0.091
AFW	-0.015	0.007	0.008	0.003	0.074	0.100	-0.145	0.080	0.318	-0.006	-0.101	0.049	-0.019	-0.031
APH	0.017	0.032	0.140	0.087	-0.078	-0.055	0.034	-0.337	0.938	-0.215	-0.103	0.084	0.007	0.104
BYL	-0.002	0.013	0.105	0.070	-0.085	0.019	-0.040	-0.272	1.163	-0.087	-0.039	0.098	-0.050	0.060
HI	0.001	0.039	-0.069	-0.069	0.067	0.134	0.002	0.218	-0.307	0.332	-0.100	-0.073	0.010	-0.150
ASL	0.034	0.174	0.058	-0.041	0.060	0.043	-0.068	-0.161	0.213	0.154	-0.215	0.005	0.044	0.018
SPS	-0.027	-0.152	0.038	0.100	0.014	0.038	-0.063	-0.249	1.000	-0.211	-0.009	0.114	0.012	0.122
CC	-0.036	-0.100	0.022	0.064	0.097	-0.003	-0.020	0.017	0.421	-0.023	0.068	-0.010	-0.139	-0.004
TW	0.010	0.054	0.060	0.018	-0.015	0.041	-0.016	0.125	-0.247	0.177	0.014	-0.050	-0.002	-0.281

Table no. 5: Phenotypic path analysis

Traits	DTH	DTA	DTM	GFD	ATN	AFL	AFW	APH	BYL	HI	ASL	SPS	CC	TW
DTH	-0.012	-0.167	0.043	0.123	0.000	0.010	-0.002	-0.002	-0.267	0.035	-0.003	-0.003	0.000	-0.003
DTA	-0.010	-0.186	0.046	0.139	0.000	0.008	0.001	-0.001	-0.185	0.033	-0.003	-0.003	0.000	-0.003
DTM	-0.003	-0.055	0.155	-0.093	0.001	-0.001	0.001	-0.006	0.294	-0.043	-0.003	0.006	0.002	-0.006
GFD	0.007	0.131	0.073	-0.197	0.001	-0.009	0.000	-0.004	0.388	-0.062	0.001	0.007	0.001	-0.002
ATN	0.000	0.006	0.021	-0.025	0.005	-0.007	-0.001	-0.003	0.334	-0.003	-0.001	0.001	-0.001	-0.003
AFL	0.004	0.046	0.006	-0.050	0.001	-0.034	0.014	-0.001	0.234	0.000	-0.001	0.002	0.001	-0.001
AFW	0.001	-0.004	0.007	-0.003	0.000	-0.017	0.027	-0.002	0.196	-0.036	-0.004	0.006	0.000	-0.002
APH	-0.001	-0.006	0.042	-0.033	0.001	-0.001	0.002	-0.021	0.497	-0.097	-0.005	0.008	-0.001	0.005
BYL	0.003	0.031	0.041	-0.069	0.002	-0.007	0.005	-0.009	1.111	-0.255	-0.002	0.010	-0.001	0.003
HI	-0.001	-0.011	-0.012	0.023	0.000	0.000	-0.002	0.004	-0.522	0.541	0.000	-0.004	0.000	-0.006
ASL	-0.002	-0.044	0.034	0.011	0.000	-0.002	0.008	-0.008	0.136	0.013	-0.013	0.003	0.000	0.000
SPS	0.001	0.020	0.040	-0.057	0.000	-0.003	0.007	-0.007	0.437	-0.083	-0.002	0.025	0.001	0.008
CC	0.000	0.000	0.024	-0.023	0.000	-0.003	0.000	0.002	-0.046	0.002	0.000	0.001	0.012	-0.001
TW	-0.001	-0.016	0.029	-0.012	0.000	-0.001	0.001	0.003	-0.101	0.099	0.000	-0.006	0.000	-0.032

Conclusion

The present study entitled “Genetic variability, heritability, correlation and path coefficient studies for yield and yield related components of some promising barley cultivars and crosses (*Hordeum vulgare L*), was undertaken in barley for phenotypic characterization and to evaluate divergence among barley genotypes. In each variety five plants were selected for various morphological observations. Phenotypic data for various morphological traits were analyzed, with the help of some statistical tools like of Mean,

Comment [WU40]: Report for similarity

Comment [WU41]: In each variety,

Comment [WU42]: analyzed

Range (Minimum & Maximum), Standard Error of mean, Critical variance (5%), Critical difference(1%), Environmental variance, Genotypic variance, Phenotypic variance, Environmental coefficient of variance, Genotypic coefficient of variance, Phenotypic coefficient of variance, Heritability (Broad sense), Genetic advance. Higher genotypic coefficient of variation was found in no. biological yield, grains yield and followed by seed per spike, average flag leaf width, thousand grains yield and higher phenotypic coefficient variation was found in biological yield and followed by grains yield, average flag leaf width, leaf area, and germination percentage respectively. Genetic advance highest in biological yield followed by seeds per spike, thousand grain yield and grains yield (Table no.2). Therefore in correlation study revealed that days to anthesis, average spike length showed strongly positive association with biological yield, grain yield per genotype and grain filling period, average flag leaf length, seeds per spike and chlorophyll content showed negative association with many traits. Therefore obtained results indicates presence of sufficient genetic variability for the studied traits showing genotypes are suitable for breeding purpose.

Comment [WU43]: A Higher

Comment [WU44]: Is highest

Comment [WU45]: strong

Comment [WU46]: a negative

Comment [WU47]: indicate presence

Comment [WU48]: purposes

Comment [WU49]: Write acknowledgment for the Institution and another individual who assist you during the time of the research.

Acknowledgements

XXX: xxxxxx

Abbreviations

XXX: xxxxxx

Comment [WU50]: The list of Abbreviations in the body should be listed here.

References

- [1] Addisu, F., & Shumet, T. (2015). Variability, heritability and genetic advance for some yield and yield related traits in barley (*Hordeum vulgare* L.) landraces in Ethiopia. *International Journal of Plant Breeding and Genetics*, 9(2), 68-76.
- [2] Allard, R. W., Jain, S. K., & Workman, P. L. (1968). The genetics of inbreeding populations. *Advances in genetics*, 14, 55-131.
- [3] Bourne, T. F., & Poehlman, J. M. (1987). Evaluation of barley yellow dwarf tolerance from plant traits in two winter x spring barley crosses. *Euphytica*, 36(2), 585-589.

- [4] Bothmer, R. von, and N Jacobson. 1985. Origin, taxonomy, and related species. In Barley, ed. D. C. Rasmuson, 19-56. Madison, Wis.
- [5] Breeding, P., & Singh, B. D. (1985). Kalyani publishers. *New delhi*.
- [6] Falconer, D. S. (1996). *Introduction to quantitative genetics*. Pearson Education India.
- [7] Hill, W. G., & Mackay, T. F. (2004). DS Falconer and Introduction to quantitative genetics. *Genetics*, 167(4), 1529-1536.
- [8] Jain, S.K. and Allard, R.W., 1960. Population studies in predominantly self-pollinated species. I. Evidence for heterozygote advantage in a closed population of barley. *Proceedings of the National Academy of Sciences of the United States of America*, 46(10), p.1371.
- [9] Jouyban, A., Give, H. S., & Noryan, M. (2015). Relationship between agronomic and morphological traits in barley varieties under drought stress condition. *Intl. Res. J. Appl. Basic. Sci*, 9(9), 1507-1511.
- [10] Karsai, I., Hayes, P. M., Kling, J., Matus, I. A., Mészáros, K., Láng, L., ...& Sato, K. (2004). Genetic variation in component traits of heading date in *Hordeum vulgare* subsp. *spontaneum* accessions characterized in controlled environments. *Crop science*, 44(5), 1622-1632.
- [11] Karthikeyan, P., Anbuselvam, Y., Elangaimannan, R., & Venkatesan, M. (2010). Variability and heritability studies in rice (*Oryza sativa* L.) under coastal salinity. *Electronic Journal of Plant Breeding*, 1(2), 196-198.
- [12] Narwal, S., Kumar, D., Sheoran, S., Verma, R. P. S., & Gupta, R. K. (2017). Hullless barley as a promising source to improve the nutritional quality of wheat products. *Journal of food science and technology*, 54(9), 2638-2644.
- [13] Riaz, R., & Chowdhry, M. A. (2003). Genetic analysis of some economic traits of wheat under drought condition. *Asian Journal of Plant Sciences*.
- [14] Singh, V. P., Man, S., & Lal, J. P. (2000). Gamma ray and EMS induced genetic variability for quantitative traits in urdbean (*Vignamungo* L. Hepper). *Indian Journal of Genetics & Plant Breeding*, 60(1), 89-96.

- [15]Solomon, G. (2013). Correlation and path analysis in yield and yield components in spring bread wheat (*Triticum aestivum* L.) genotypes under irrigated condition in Southern India. *African Journal of Agricultural Research*, 8(24), 3186-3192.
- [16]Von Bothmer, R., Giles, B. E., & Jacobsen, N. (1986). Crosses and genome relationship in the *Hordeum patagonicum* group. *Genetica*, 71(1), 75-80.
- [17]Yadav, S. K., Singh, A. K., Pandey, P., & Singh, S. (2015). Genetic variability and direct selection criterion for seed yield in segregating generations of barley (*Hordeum vulgare* L.). *American Journal of Plant Sciences*, 6(09), 1543.

UNDER PEER REVIEW